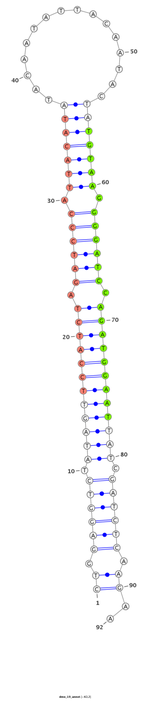
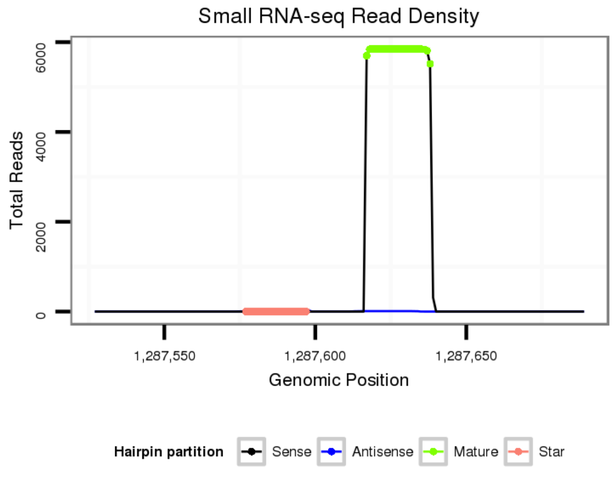
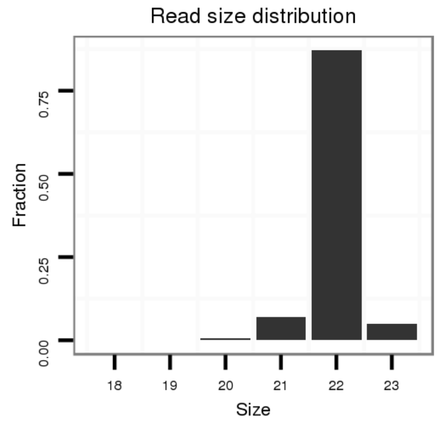
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_19	**scaffold_6308:1287577-1287639 +**	**confident**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

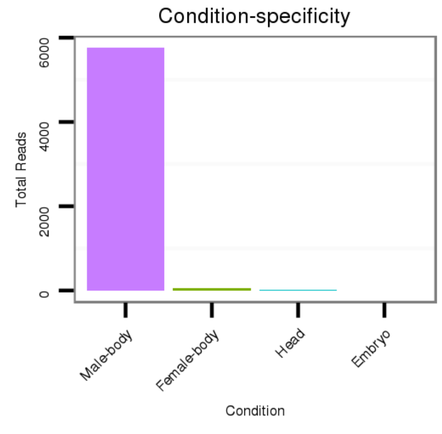
Legend: mature star mismatch in alignment mismatch in read

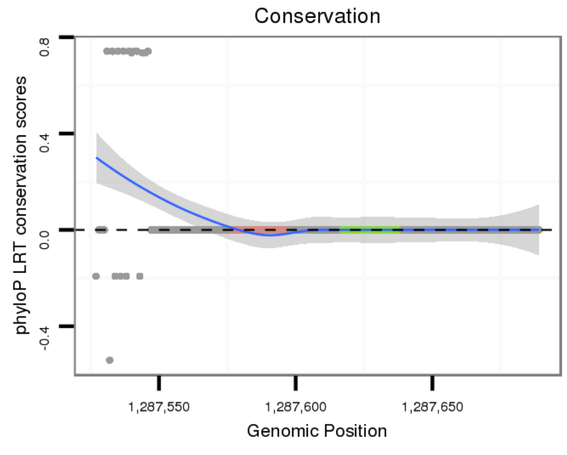
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dmoj\GI10984-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACGATCTATATATGTTCCCATAACAGGGTCTGCTGCTGGAGGTCTATAGTTCCATCTAGATCCCATTACATATACAATATTACAATACTATGTAAGGGGATCCAGATGGAATTATCGATCTCAAGAAGCTGAGTTTGCTATGGATCACAGTGAAATAGTTGAA **********(((.(((((((.(((((((((((((.(((((((.(((((((.....)))))))))))))))))))))))))))))))))))))**********..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head	V049 head	M060 embryo	V041 embryo
.....TGTAAGGGGATCCAGATGGAAT.....	22	0	1	5080.00	5080	5006	48	16	5	2	3
.....TGTAAGGGGATCCAGATGGAATC.....	23	1	1	407.00	407	401	6	0	0	0	0
.....TGTAAGGGGATCCAGATGGAATT.....	23	0	1	291.00	291	288	3	0	0	0	0
.....TGTAAGGGGATCCAGATGGAA.....	21	0	1	284.00	284	277	4	2	1	0	0
.....TGTAAGGGGATCCAGATGGAAC.....	22	1	1	163.00	163	162	0	0	1	0	0
.....GTAAGGGGATCCAGATGGAAT.....	21	0	1	122.00	122	118	4	0	0	0	0
.....TGTAAGGGGATCCAGATGGA.....	20	0	1	32.00	32	31	0	1	0	0	0
.....GTAAGGGGATCCAGATGGAATC.....	22	1	1	30.00	30	29	1	0	0	0	0
.....TGTAAGGGGATCCAGATGGAATTC.....	24	1	1	19.00	19	19	0	0	0	0	0
.....GTAAGGGGATCCAGATGGAATT.....	22	0	1	18.00	18	18	0	0	0	0	0
.....TGTAAGGGGATCCAGATGGAATG.....	23	1	1	15.00	15	14	1	0	0	0	0
.....TGTAAGGGGATCCAGATGGAATA.....	23	1	1	13.00	13	13	0	0	0	0	0
.....TGTAAGGGGATCCAGATGGAAA.....	22	1	1	11.00	11	11	0	0	0	0	0
.....GTAAGGGGATCCAGATGGAAC.....	21	1	1	9.00	9	9	0	0	0	0	0
.....TAAGGGGATCCAGATGGAATTC.....	22	1	1	8.00	8	8	0	0	0	0	0
.....TGTAAGGGGATCCAGATGG.....	19	0	1	8.00	8	8	0	0	0	0	0
.....TGTAAGGGGATCCAGATGGAATTT.....	24	1	1	7.00	7	7	0	0	0	0	0
.....TAAGGGGATCCAGATGGAATTT.....	22	1	1	7.00	7	7	0	0	0	0	0
.....TGTAAGGGGATCCAGATGGAG.....	21	1	1	6.00	6	6	0	0	0	0	0
.....GTAAGGGGATCCAGATGGAA.....	20	0	1	5.00	5	5	0	0	0	0	0
.....TGTAAGGGGATCCAGATGGAATTG.....	24	1	1	4.00	4	4	0	0	0	0	0
.....TGTAAGGGGATCCAGATGGAAG.....	22	1	1	3.00	3	3	0	0	0	0	0
.....GTAAGGGGATCCAGATGGAATA.....	22	1	1	3.00	3	3	0	0	0	0	0
.....TGTAAGGGGATCCAGATGGAATAT.....	24	2	1	3.00	3	3	0	0	0	0	0
.....TAAGGGGATCCAGATGGAAT.....	20	0	1	2.00	2	1	0	0	0	0	1
.....TAAGGGGATCCAGATGGAA.....	19	0	1	2.00	2	2	0	0	0	0	0
.....TGTAAGGGGATCCAGATGGAATTA.....	24	0	1	2.00	2	2	0	0	0	0	0
.....TCCATCTAGATCCCATTACATC.....	22	1	1	2.00	2	1	1	0	0	0	0
.....GTAAGGGGATCCAGATGGAATG.....	22	1	1	2.00	2	2	0	0	0	0	0
.....AGGGGATCCAGATGGAAT.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TAAGGGGATCCAGATGGAATT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TGTAAGGGGATCCAGATGGTC.....	21	2	1	1.00	1	1	0	0	0	0	0
.....GTAAGGGGATCCAGATGGAATTT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TGTAAGGGGATCCAGATGGAATTTC.....	25	2	1	1.00	1	1	0	0	0	0	0
.....TGTAAGGGGATCCAGATGC.....	19	1	1	1.00	1	1	0	0	0	0	0
.....TAAGGGGATCCAGATGGAATGT.....	22	2	1	1.00	1	1	0	0	0	0	0
.....AAGGGGATCCAGATGGAAC.....	19	1	1	1.00	1	1	0	0	0	0	0
.....TCCATCTAGATCCCATTACAT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TGTAAGGGGATCCAGATGGAATCT.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TGTAAGGGGATCCAGATGGAACC.....	23	2	1	1.00	1	1	0	0	0	0	0
.....TGTAAGGGGATCCAGATGGAAAA.....	23	2	1	1.00	1	1	0	0	0	0	0
.....TGTAAGGGGATCCAGATGGC.....	20	1	1	1.00	1	1	0	0	0	0	0
.....GTAAGGGGATCCAGATGGA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TAAGGGGATCCAGATGGAACAT.....	22	3	1	1.00	1	1	0	0	0	0	0
.....TCCATCTAGATCCCATTACATA.....	22	0	1	1.00	1	0	1	0	0	0	0
.....TGTAAGGGGATCCAGATG.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TGTAAGGGGATCCAGAAT.....	18	2	5	0.20	1	1	0	0	0	0	0

Anti-sense strand reads

TGCTAGATATATACAAGGGTATTGTCCCAGACGACGACCTCCAGATATCAAGGTAGATCTAGGGTAATGTATATGTTATAATGTTATGATACATTCCCCTAGGTCTACCTTAATAGCTAGAGTTCTTCGACTCAAACGATACCTAGTGTCACTTTATCAACTT **********(((.(((((((.(((((((((((((.(((((((.(((((((.....)))))))))))))))))))))))))))))))))))))**********..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V056 head	V049 head	V041 embryo
.....AGGTAGATCTAGGGTAATGTAT.....	22	0	1	10.00	10	5	1	1	0	2	1
.....GGTAGATCTAGGGTAATGTAT.....	21	0	1	9.00	9	3	2	3	1	0	0
.....TGGTAGATCTAGGGTAATGTAT.....	22	1	1	9.00	9	8	1	0	0	0	0
.....TGATACATTCCCCTAGGTCTAC.....	22	0	1	4.00	4	1	1	2	0	0	0
.....CAAGGTAGATCTAGGGTAATGT.....	22	0	1	3.00	3	3	0	0	0	0	0
.....ATGATACATTCCCCTAGGTCTAC.....	23	0	1	2.00	2	0	2	0	0	0	0
.....GATACATTCCCCTAGGTCTAC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TCAAGGTAGATCTAGGGTAATGT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....ACGACCTCCAGATATCAAGG.....	20	0	1	1.00	1	0	1	0	0	0	0
.....ATGATACATTCCCCTAGGTCT.....	21	0	1	1.00	1	0	1	0	0	0	0
.....GGGTAGATCTAGGGTAATGTAT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....ATGATACATTCCCCTAGGTCTA.....	22	0	1	1.00	1	0	1	0	0	0	0
.....TCAAGGTAGATCTAGGGTAA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GGTAGATCTAGGGTAATGTATA.....	22	0	1	1.00	1	0	0	0	1	0	0
.....AGGTAGATCTAGGGTAATGTA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....AAGGTAGATCTAGGGTAATGTAT.....	23	0	1	1.00	1	0	0	1	0	0	0
.....ATACATTCCCCTAGGTCTACCT.....	22	0	1	1.00	1	0	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1287527-1287689 +	dmo_19	ACGATCTATATATGTTCCCATAACAGGGTCTGCTGCTGGAGGTCTATAGTTCCATCTAGATCCCATTACATATACAATATTACAATACTATGTAAGGGGATCCAGATGGAATTATCGATCTCAAGAAGCTGAGTTTGCTATGGATCACAGTGAAATAGTTGAA
droKik1	scf7180000302798:195250-195266 -		G---TGTGTGTCTGTTTCCA----------

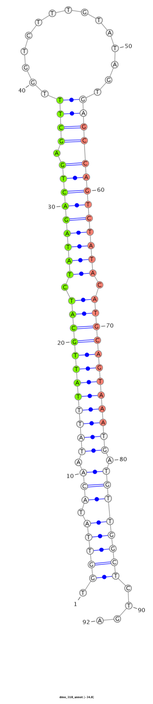
Generated: 09/08/2015 at 06:14 PM

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

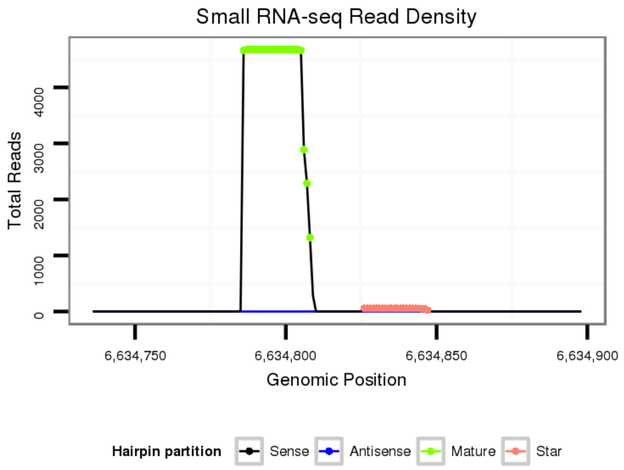
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_318	**scaffold_6540:6634786-6634848 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

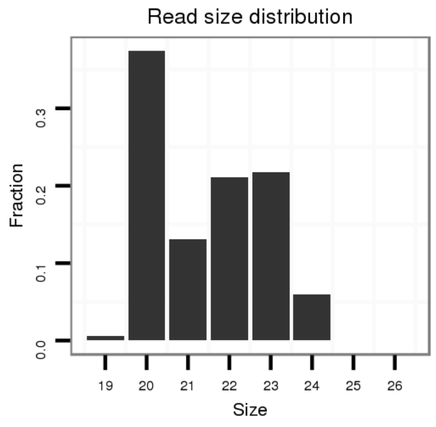
Legend: mature star mismatch in alignment mismatch in read

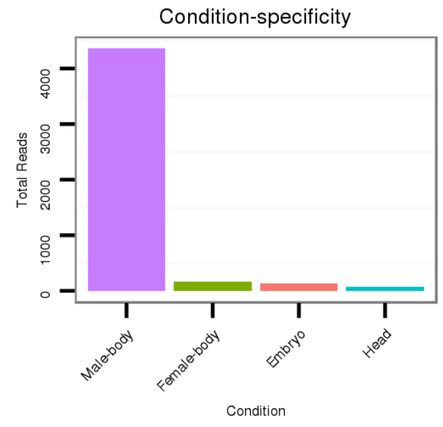
Predicted structure

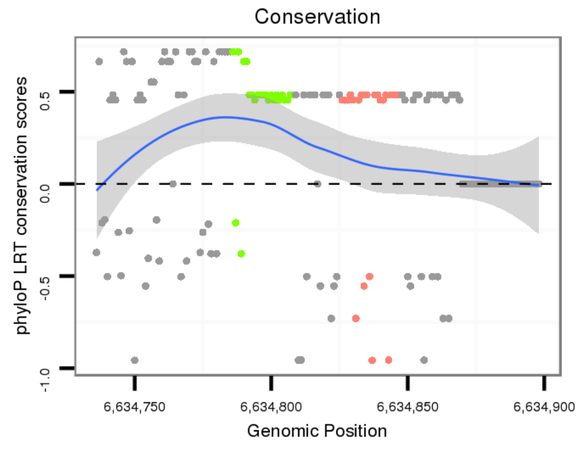


Show Alternate Folds









Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGTGTGTGAGTGCCCGTGAATAGAGTCCCTTTAAATGGTTATACAATATTTATTGCATCTATAGACTGAGCTTTGGTCTTTGTATAGTGAGCCAGTCTATACATGCAGTAAATGATGTTGGCTCTGATCTAATGTCAACTGCAAAGGAACCAAGCAATGGCCA **********.(((((.(((.(((((((((((.(((((((((.((((.............)))))))))))).)))))))))))).)))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V056 head	V049 head	V041 embryo
..........TATTGCATCTATAGACTGAG..........	20	0	1	1764.00	1764	1722	21	1	9	11	0
..........TATTGCATCTATAGACTGAGCTT..........	23	0	1	1027.00	1027	859	54	86	9	12	7
..........TATTGCATCTATAGACTGAGCT..........	22	0	1	964.00	964	917	35	2	5	5	0
..........TATTGCATCTATAGACTGAGC..........	21	0	1	595.00	595	556	19	7	7	5	1
..........TATTGCATCTATAGACTGAGCTTT..........	24	0	1	282.00	282	259	10	5	5	1	2
..........TATTGCATCTATAGACTGAGCTTC..........	24	1	1	135.00	135	126	6	3	0	0	0
..........TATTGCATCTATAGACTGAGT..........	21	1	1	94.00	94	93	0	0	1	0	0
..........TATTGCATCTATAGACTGAGCTTCT..........	25	2	1	30.00	30	28	2	0	0	0	0
..........TATTGCATCTATAGACTGAGCTC..........	23	1	1	29.00	29	24	0	5	0	0	0
..........GCCAGTCTATACATGCAGTAAA..........	22	0	1	25.00	25	9	4	7	0	0	5
..........GCCAGTCTATACATGCAGTAA..........	21	0	1	23.00	23	14	3	4	0	1	1
..........TATTGCATCTATAGACTGAGCTTTC..........	25	1	1	23.00	23	22	1	0	0	0	0
..........TATTGCATCTATAGACTGAGCTA..........	23	1	1	20.00	20	13	4	2	1	0	0
..........TATTGCATCTATAGACTGA..........	19	0	1	18.00	18	14	2	0	1	1	0
..........TATTGCATCTATAGACTGAGCTTTT..........	25	1	1	14.00	14	13	0	0	1	0	0
..........TATTGCATCTATAGACTGAGA..........	21	1	1	12.00	12	10	2	0	0	0	0
..........ATTGCATCTATAGACTGAGCTT..........	22	0	1	9.00	9	0	9	0	0	0	0
..........TTATTGCATCTATAGACTGAGCT..........	23	0	1	6.00	6	4	0	2	0	0	0
..........GCCAGTCTATACATGCAGT..........	19	0	1	6.00	6	5	0	1	0	0	0
..........TATTGCATCTATAGACTGAGCTTA..........	24	1	1	5.00	5	5	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTTTT..........	26	2	1	5.00	5	5	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTCA..........	25	2	1	4.00	4	4	0	0	0	0	0
..........TATTGCATCTATAGACTGAT..........	20	1	1	4.00	4	4	0	0	0	0	0
..........ATTGCATCTATAGACTGAG..........	19	0	1	3.00	3	1	2	0	0	0	0
..........TATTGCATCTATAGACTGAGCTCA..........	24	2	1	3.00	3	3	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTG..........	24	1	1	3.00	3	2	1	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTTCC..........	26	2	1	3.00	3	2	1	0	0	0	0
..........TTATTGCATCTATAGACTGAG..........	21	0	1	3.00	3	3	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTG..........	23	1	1	3.00	3	3	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCC..........	22	1	1	3.00	3	1	0	2	0	0	0
..........TATTGCATCTATAGACTGAGCTTCC..........	25	2	1	3.00	3	3	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTCTG..........	26	3	1	2.00	2	2	0	0	0	0	0
..........GCCAGTCTATACATGCAGTA..........	20	0	1	2.00	2	1	1	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTAAA..........	26	3	1	2.00	2	1	1	0	0	0	0
..........TTATTGCATCTATAGACTGAGC..........	22	0	1	2.00	2	1	0	1	0	0	0
..........ATTGCATCTATAGACTGAGC..........	20	0	1	2.00	2	0	2	0	0	0	0
..........TATTGCATCTATAGACTGAGG..........	21	1	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTTCCC..........	27	3	1	1.00	1	1	0	0	0	0	0
..........GCCAGTCTATACATGCAGTAATCC..........	24	3	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCAA..........	23	2	1	1.00	1	0	1	0	0	0	0
..........GTGAGCCAGTCTATACATGCAGTAAA..........	26	0	1	1.00	1	1	0	0	0	0	0
..........ATTGCATCTATAGACTGAGCT..........	21	0	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCCCT..........	25	3	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTCC..........	24	2	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTTTC..........	26	2	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCA..........	22	1	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTGT..........	25	2	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTTGC..........	26	1	1	1.00	1	1	0	0	0	0	0
..........GCCAGTCTATACATGCAGTAAT..........	22	1	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGTA..........	22	2	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTTGG..........	26	0	1	1.00	1	0	1	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTAT..........	25	2	1	1.00	1	1	0	0	0	0	0
..........TGAGCCAGTCTATACATGCAG..........	21	0	1	1.00	1	1	0	0	0	0	0
..........ATTGCATCTATAGACTGAGCTTC..........	23	1	1	1.00	1	0	1	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTCAA..........	26	3	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAA..........	20	1	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTAA..........	25	2	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTAA..........	24	2	1	1.00	1	1	0	0	0	0	0
..........GCCAGTCTATACATGCAGTAAC..........	22	1	1	1.00	1	0	1	0	0	0	0
..........TTATTGCATCTATAGACTGAGCTT..........	24	0	1	1.00	1	1	0	0	0	0	0
..........GCCAGTCTATACATGCAGTAT..........	21	1	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTAG..........	19	2	6	0.17	1	1	0	0	0	0	0

Anti-sense strand reads

ACACACACTCACGGGCACTTATCTCAGGGAAATTTACCAATATGTTATAAATAACGTAGATATCTGACTCGAACCAGAAACATATCACTCGGTCAGATATGTACGTCATTTACTACAACCGAGACTAGATTACAGTTGACGTTTCCTTGGTTCGTTACCGGT **********.(((((.(((.(((((((((((.(((((((((.((((.............)))))))))))).)))))))))))).)))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body
..........ATTGCATCTATAGACTGAGCT..........	21	0	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCCT..........	25	3	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTCC..........	24	2	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTTTC..........	26	2	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCA..........	22	1	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTGT..........	25	2	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTTGC..........	26	1	1	1.00	1	1	0	0	0	0	0
..........GCCAGTCTATACATGCAGTAAT..........	22	1	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGTA..........	22	2	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTTGG..........	26	0	1	1.00	1	0	1	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTAT..........	25	2	1	1.00	1	1	0	0	0	0	0
..........TGAGCCAGTCTATACATGCAG..........	21	0	1	1.00	1	1	0	0	0	0	0
..........ATTGCATCTATAGACTGAGCTTC..........	23	1	1	1.00	1	0	1	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTCAA..........	26	3	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAA..........	20	1	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTTAA..........	25	2	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTGAGCTAA..........	24	2	1	1.00	1	1	0	0	0	0	0
..........GCCAGTCTATACATGCAGTAAC..........	22	1	1	1.00	1	0	1	0	0	0	0
..........TTATTGCATCTATAGACTGAGCTT..........	24	0	1	1.00	1	1	0	0	0	0	0
..........GCCAGTCTATACATGCAGTAT..........	21	1	1	1.00	1	1	0	0	0	0	0
..........TATTGCATCTATAGACTAG..........	19	2	6	0.17	1	1	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:6634736-6634898 +	dmo_318	TGTGTGTGAGTGCCCGTGAATAGAGTCCCTTTAAATGGTTATACAATATTTATTGCATCTATAGACTGAGCTTTGGTCTTTGTATAGTGAGCCAGTCTATACATGCAGTAAATGATGTTGGCTCTGATCTAATGTCAACTGCAAAGGAACCAAGCAATGGCCA
droVir3	scaffold_12855:6286781-6286909 +	dvi_197	CGTGCGGTGTTTGTGTGT---GTGTCC-TTCATATGGCAATACAATATTTATTGCATCTATAGACTGAGCTTTCCTTTTT-AATATAAAGCCAGCGCTTTGGATGACTAAATGTGAGTTACCTTTAAGCGAATG----------
droGri2	scaffold_14906:7794704-7794747 -		TGCA----TTTGTGA----GTAAAGTCC-T---AATGGTAAACCCATATTTGTGC----------

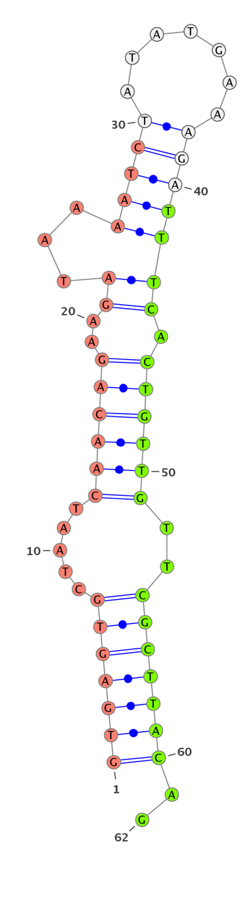
Generated: 09/08/2015 at 08:07 PM

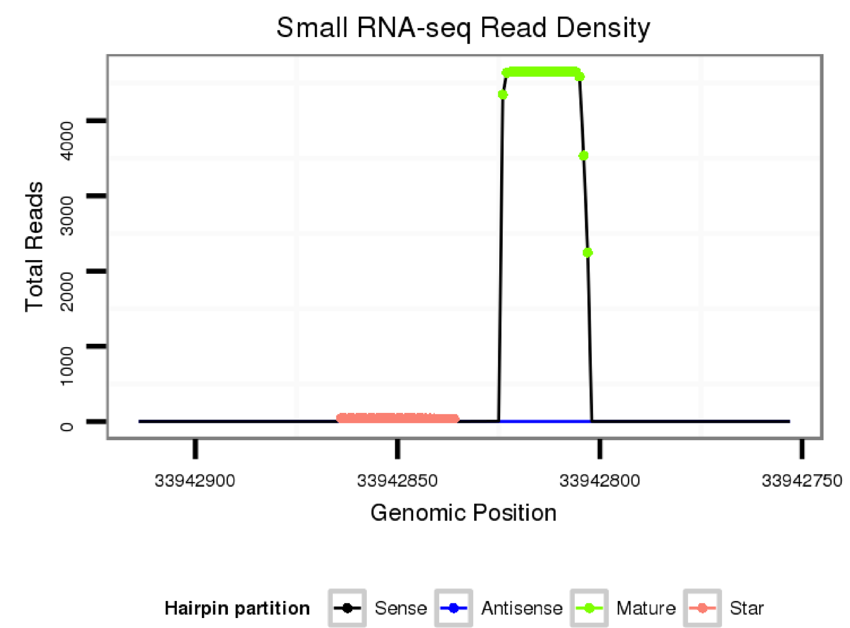
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

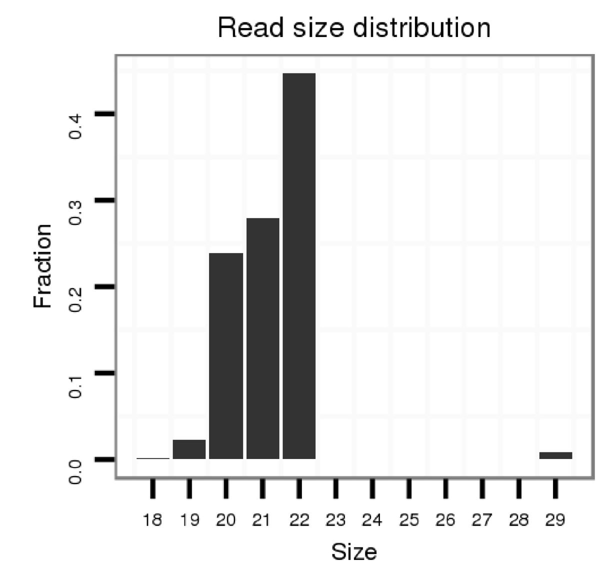
ID: dmo_2176	Coordinate: scaffold_6540:33942803-33942864 -	Confidence: confident	Class: Mirtron	Genomic Locale: intron	[View on UCSC Genome Browser {Cornell Mirror}]

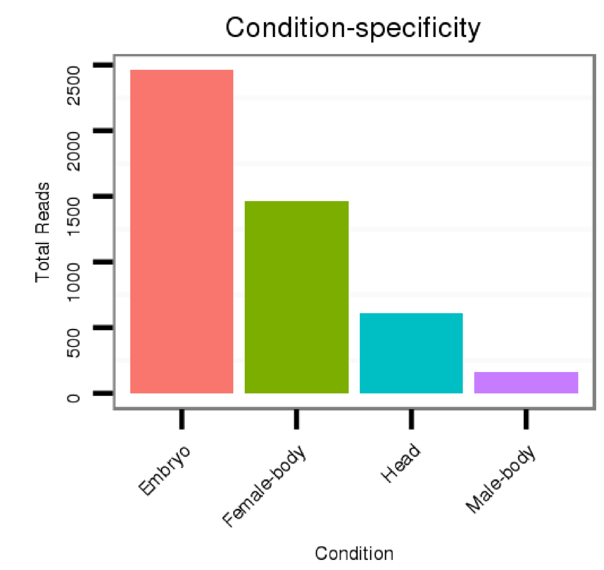
Legend: mature star mismatch in alignment mismatch in read

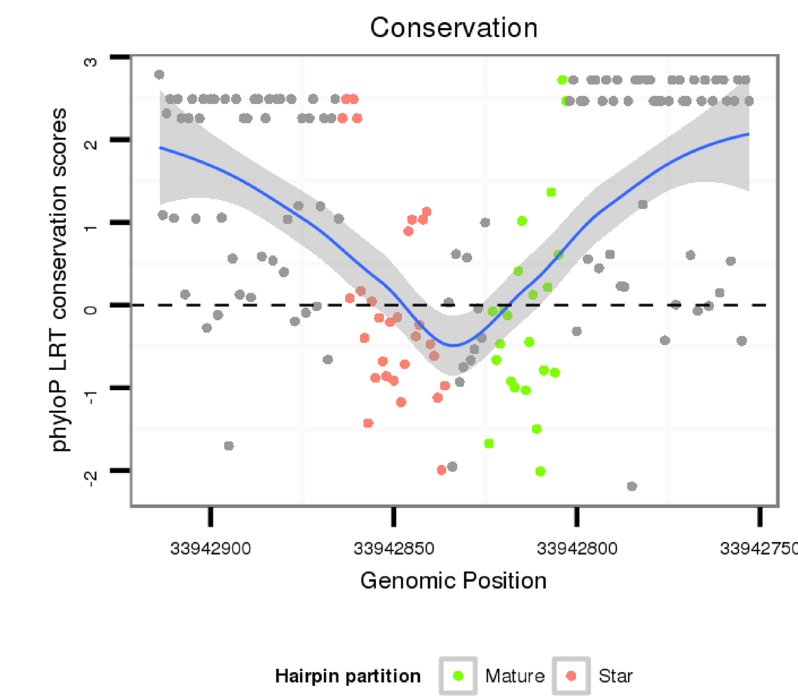
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI21936-in]; CDS [Dmoj\GI21936-cds]; CDS [Dmoj\GI21936-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGGACTGTGAACTGAAGCTGTTGCCCATACACTTTCTTACACAATCGGAAGTGAGTGCTAATCAACAGAAGATAAAATCTATATGAAAGATTTCACTGTTGTTCGCTTACAGGTGGGCAATGAGGAAGCGATGATGCGCCAATGGTTGGATGTGTGTGTCAC **(((((((.....((((((..((...(((((.......))))))).))))))..)))))))..**	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V056 head	V049 head	V041 embryo	V110 male body
....TTTCACTGTTGTTCGCTTACAG..	22	0	1	2098.00	2098	1771	222	24	19	59	3
....TTTCACTGTTGTTCGCTTACA...	21	0	1	1173.00	1173	259	574	140	106	57	37
....TTTCACTGTTGTTCGCTTAC..	20	0	1	1003.00	1003	140	469	152	122	13	107
....TTCACTGTTGTTCGCTTACAG..	21	0	1	137.00	137	93	39	0	0	5	0
....TTTCACTGTTGTTCGCTTACAGT...	23	1	1	137.00	137	99	16	3	1	18	0
....TTCACTGTTGTTCGCTTACA...	20	0	1	111.00	111	10	73	8	6	3	11
....TTTCACTGTTGTTCGCTTACAGA...	23	1	1	78.00	78	57	14	3	0	4	0
....TTCACTGTTGTTCGCTTACAGT...	22	1	1	69.00	69	52	4	1	2	10	0
....TTTCACTGTTGTTCGCTTA...	19	0	1	65.00	65	1	36	12	12	1	3
....TTCACTGTTGTTCGCTTAC..	19	0	1	42.00	42	1	33	3	2	0	3
....GTGAGTGCTAATCAACAGAAGATAAAATC...	29	0	1	38.00	38	37	0	0	0	0	1
....TTTCACTGTTGTTCGCTTACAGC...	23	1	1	37.00	37	35	2	0	0	0	0
....TTTCACTGTTGTTCGCTTACAC..	22	1	1	35.00	35	35	0	0	0	0	0
....TTCACTGTTGTTCGCTTACAGA...	22	1	1	24.00	24	15	8	0	0	1	0
....TTCACTGTTGTTCGCTTACAGC...	22	1	1	23.00	23	23	0	0	0	0	0
....TTTCACTGTTGTTCGCTTACT...	21	1	1	12.00	12	4	3	2	2	1	0
....TTTCACTGTTGTTCGCTTACAA..	22	1	1	11.00	11	2	6	0	0	3	0
....TCACTGTTGTTCGCTTACAG..	20	0	1	9.00	9	4	4	0	0	1	0
....TTTCACTGTTGTTCGCTTACC...	21	1	1	7.00	7	0	1	2	4	0	0
....TTTCACTGTTGTTCGCTTAA..	20	1	1	6.00	6	2	4	0	0	0	0
....TTTCACTGTTGTTCGCTTACAT..	22	1	1	3.00	3	1	0	1	1	0	0
....TTTCACTGTTGTTCGCTTACAAA...	23	2	1	2.00	2	1	1	0	0	0	0
....TTTCACTGTTGTTCGCTTACG...	21	1	1	2.00	2	0	2	0	0	0	0
....TCACTGTTGTTCGCTTACAGA...	21	1	1	2.00	2	0	2	0	0	0	0
....TTTCACTGTTGTTCGCTTACAGG...	23	0	1	2.00	2	2	0	0	0	0	0
....TTTCACTGTTGTTCGCTTAT..	20	1	1	2.00	2	0	0	0	0	0	2
....TTTCACTGTTGTTCGCTT..	18	0	1	2.00	2	0	0	0	1	1	0
....TTCACTGTTGTTCGCTTACT...	20	1	1	2.00	2	0	2	0	0	0	0
....TCACTGTTGTTCGCTTAC..	18	0	1	2.00	2	0	2	0	0	0	0
....TCACTGTTGTTCGCTTACA...	19	0	1	2.00	2	0	2	0	0	0	0
....ATTTCACTGTTGTTCGCTTACAGT...	24	1	1	1.00	1	1	0	0	0	0	0
....CACTGTTGTTCGCTTACAGC...	20	1	1	1.00	1	1	0	0	0	0	0
....TTTCACTGTTGTTCGCTTACTT..	22	2	1	1.00	1	1	0	0	0	0	0
....TTTCACTGTTGTTCGCTTACATC...	23	2	1	1.00	1	0	1	0	0	0	0
....AAGATTTCACTGTTGTTCGCTTA..	23	0	1	1.00	1	0	1	0	0	0	0
....CACTGTTGTTCGCTTACAG..	19	0	1	1.00	1	0	1	0	0	0	0
....GTGAGTGCTAATCAACAGAA..	20	0	1	1.00	1	0	1	0	0	0	0
....ATTTCACTGTTGTTCGCTTACA...	22	0	1	1.00	1	0	1	0	0	0	0
....TTCACTGTTGTTCGCTTACAA..	21	1	1	1.00	1	0	0	0	0	1	0
....ATGAAAGATTTCACTGTTGTTCGCTTA..	27	0	1	1.00	1	0	1	0	0	0	0
....CACTGTTGTTCGCTTACA...	18	0	1	1.00	1	0	1	0	0	0	0
....TTTCACTGTTGTTCGCTTAG..	20	1	1	1.00	1	0	0	1	0	0	0
....TTCACTGTTGTTCGCTTA...	18	0	1	1.00	1	0	1	0	0	0	0
....ATTTCACTGTTGTTCGCTTAC..	21	0	1	1.00	1	1	0	0	0	0	0
....GTGAGTGCTAATCAACAGAAGATAA...	25	0	1	1.00	1	1	0	0	0	0	0
....GTGAGTGCTAATCAACAGAAG...	21	0	1	1.00	1	0	0	0	0	1	0
....TTTCACTGTTGTTCGCTTATG...	21	2	1	1.00	1	0	0	0	0	1	0
....TTTCACTGTTGTTCGCTTACAGAA..	24	2	1	1.00	1	0	1	0	0	0	0
....TTCACTGTTGTTCGCTTACAC..	21	1	1	1.00	1	1	0	0	0	0	0
....GTGAGTGCTAATCAACAGAAGATAAA..	26	0	1	1.00	1	0	1	0	0	0	0
....ATTTCACTGTTGTTCGCTTACAG..	23	0	1	1.00	1	1	0	0	0	0	0
....GTGAGTGCTAATCAACAGAAGATA..	24	0	1	1.00	1	0	0	0	0	1	0
....TTTCACTGTTGTTCGCTTACAGAAA...	25	3	1	1.00	1	1	0	0	0	0	0
....TTCACTGTTGTTCGCTTACCT..	21	2	1	1.00	1	1	0	0	0	0	0
....TCACTGTTGTTCGCTTACAA..	20	1	1	1.00	1	0	1	0	0	0	0
....GTGAGTGCTAATCAACAGAAGATAAAA...	27	0	1	1.00	1	0	1	0	0	0	0
....TTTCACTGTTGTTCGCTTT...	19	1	2	0.50	1	0	0	0	0	0	1
....TTTCACTGTTGTTCGCTTTA..	20	2	3	0.33	1	0	0	0	1	0	0

Anti-sense strand reads

ACCTGACACTTGACTTCGACAACGGGTATGTGAAAGAATGTGTTAGCCTTCACTCACGATTAGTTGTCTTCTATTTTAGATATACTTTCTAAAGTGACAACAAGCGAATGTCCACCCGTTACTCCTTCGCTACTACGCGGTTACCAACCTACACACACAGTG **(((((((.....((((((..((...(((((.......))))))).))))))..)))))))..**	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_6540:33942753-33942914 -	dmo_2176	TGGACTGTGAACTGAAGCTGTTGCCCATACACTTTCTTACACAATCGGAAGTGAGTGC--TAATCA--ACAGAAGATAAAATCTATA---T-------------------------------G------------------------------------AA---AGATTTCACTGTTGT--TCG------CTTACAGGTGGGCAATGAGGAAGCGATGATGCGCCAATGGTTGGATGTGTGTGTCAC
droVir3	scaffold_12822:1328550-1328707 -	dvi_2469	TGGACTGCGAGCTGAAGCTGCTGCCCATACACTTTCTAACACAAACAGAGGTGAGTTT--GCG---GCCAA----ATTCGAA-------TTTCACT--TGTA--CTTGACCATC------TTTT--CTG------ATTGCAGGTGGGGAATGAGGAGACCATGATGCGTCAATGGCTGGACGTTTGTGTCAC
droGri2	scaffold_15074:2546878-2547041 +		TGGACTGCGAGCTTAAACTCCTACCCATACACTTTTTATCGCAGTCGGAGGTCAGTTC--GAA---CAACA----ATTCCCAATT---CAAA-------AT-------------------C-----------------------------------GAA-CTAACTAAGTATTTTACCTCA------CTTCCAGGTTGGCAATGAGGAGACCATGATGCGTCAATGGTTGGACGTGTGTGTCAC
droWil2	scf2_1100000004902:10787357-10787412 -		T---TTTAGGTGGGCAACGAGGAGTCGATAATGCGTCAATGGCTAGACGTTTGTGTAAC
dp5	2:5533852-5534010 +		TGGACTGCGAGCTCAAGCTCTTGCCCATACATTTTCTCACACAGTCGGAGGTGAGAAT--GCA---ACTGA----AAGATCTGTA---A-------------------------------A------------------------------------GAA-GAAACTGATTCGTTAATTTCT------TTGACAGGTTGGCAATGAGGAGTCAATGATGCGCCAATGGCTGGATGTTTGCGTAAC
droPer2	scaffold_19:1250580-1250738 +		TGGACTGCGAGCTCAAGCTCTTGCCCATACATTTTCTCACACAGTCGGAGGTGAGAAT--GCA---ACTGA----AAGATCTGTA---A-------------------------------A------------------------------------GAA-GAAACTGATTCGTTAATTTCT------TTGACAGGTTGGCAATGAGGAGTCAATGATGCGCCAATGGCTGGATGTTTGCGTAAC
droAna3	scaffold_13250:62462-62632 -		TGGACTGCGAGCTTAAACTCTTGCCAATACATTTCTTACACAATCTGAGGTGAGATT--TCT---ATCCA----TATA--TG------------------TGTACTTAAATAGAGGTGAA------------------------------------CTA-GAAAATAATATGATTA--TGT------TATGCAGGTGGGCAATGAAGAATCTATGATGCGTCAATGGCTGGACGTGTGTGTAAC
droBip1	scf7180000396413:618022-618182 -		TGGACTGCGAGCTGAAACTCTTGCCAATACATTTCTCACACAATCTGAGGTGAGATA--TTAATCATGTGCAGT--AGTTT------------------------G---------------------CAAATT-AA---------------------------CTAGAAAATA------TTTA--TAA------TGTACAGGTTGGCAATGAAGAATCTATGATGCGCCAGTGGCTGGACGTGTGTGTAAC
droKik1	scf7180000302461:159822-159983 +		TGGATTGTGACTGAAACTGTTGCCTATCCATTTCCTCACCCAGTCCGAGGTAAGGGA--ATAATAATTTGAAAA--ATATA-----------------------A---------------------CGTTTT-TT-----------------------CTAC--GAGAATT------CTAT--CTT------TTTGCAGGTGGGTAACGAAGAGACCATGATGCGCCAGTGGCTTGACGTGTGCGTTAC
droFic1	scf7180000454104:1315736-1315959 +		TGGACTGCGAGCTGAAACTATTACCCATACACTTTCTCACCCAGTCCGAGGTGAGAGA--TAATGA-----AAATATATTGCATTTTCTTTGTGGGAAATTATAAAGTTCTAATTTGATATTCGTATTTAA----AATACATTTG---GAGT-------ACGGTT---------------A------------------------------------GCT-AATTAAATTTAATGTC--TAC------TTTGCAGGTGGGCAACGAGGAGTCGATGATGCGCCAATGGCTCGACGTGTGCGTGAC
droEle1	scf7180000491047:110351-110415 +		TGGACTGTGAGCTGAAGCTTTTGCCCATACATTCCTCACACAGTCCGAGGTGAGAGA--TTATTA---A---
droRho1	scf7180000777865:308496-308559 -		TTG--C--TTC------CTTGCAGGTGGGCAACGAGGAGTCGATGATGCGCCAGTGGCTGGATGTGTGCGTAAC
droBia1	scf7180000302402:3011974-3012159 -		TGGACTGCGAGCTTAAGCTGTTGCCAATACATTTCCTCACTCAGTCCGAGGTGAGATT--TGTAGA--TACAT----ATATCTTGCA---GAT-----------------------------------TTTACTAAGGTATAATGCTATGTTTACTAAT-----------TA----TTGT--TGCTATATATTGCAGGTGGGCAACGAGGAGTCGATGATGCGCCAATGGCTGGACGTGTGCGTGAC
droTak1	scf7180000415653:574311-574475 -		TGGACTGCGAGCTGAAACTATTGCCCATACATTTCCTCACACAGTCCGAGGTGAGAGA--TTAGAG---AT----ATTATTGCTGTATCATA-------AC--------------------T--CTT-TT-----------------------AAAC--------TATTATTTGC--TAC------CTTTTAGGTGGGCAACGAGGAGTCAATGATGCGCCAATGGCTGGACGTGTGCGTAAC
droEug1	scf7180000407136:160743-160898 +		TGGACTGCGAGCTGAAATTATTACCCATACATTTCCTCACACAGTCTGAGGTAAGTGA--TC--TTAA----AGATGAT----------TTACTAT--TATT---------------A------------------------------------ATA-AAAATAAAATC--------GC------TTTGCAGGTAGGCAACGAGGAATCAATGATGCGCCAGTGGCTTGATGTGTGCGTAAC
dm3	chr3R:5532713-5532878 -		TGGACTGCGAGCTGAAACTTTTGCCCATACATTTCTTACACAGTCGGAGGTGAGAGC--TTA---TTCAA----ATATCCTGTA---GAAC-------ATTGTG---------------A------------------------------------GCT-TAGACATTTCCGTTCC--TTG------CCTGCAGGTTGGCAACGAGGAGTCAATGATGCGTCAATGGCTGGACGTGTGCGTAAC
droSim2	3r:15501523-15501688 +	dsi_9275	TGGACTGCGAGCTGAAACTTTTGCCCATTCATTTCTTACACAGTCGGAGGTGAGAGC--TTA---TTCAA----ATAGCCTGTG---GAAC-------ATTGTG---------------A------------------------------------GCT-TAGACATTTCCGTTCC--TTG------CTTGCAGGTTGGCAACGAGGAGTCGATGATGCGTCAATGGCTGGACGTGTGCGTAAC
droSec2	scaffold_0:16372165-16372330 +		TGGACTGCGAGCTGAAACTTTTGCCCATACATTTCTTACACAGTCGGAGGTGAGAGC--TTA---TTCAA----ATATCCTGTG---GAAC-------ATTGGG---------------A------------------------------------GCT-TAGACATTTCCGTTCC--TTG------CTTGCAGGTTGGCAACGAGGAGTCGATGATGCGGCAATGGCTGGACGTGTGCGTAAC
droYak3	3R:9579202-9579367 -		TGGACTGCGAGCTGAAACTTTTGCCCATACATTTCTTACACAATCGGAGGTGAGAGT--TTA---TTTTA----ATATCATATG---GAAC-------ATTGTG---------------A------------------------------------GCA-GAGACATTTCCGTTCC--CTA------CTTGCAGGTTGGCAACGAGGAGTCGATGATGCGTCAATGGCTGGACGTGTGCGTGAC
droEre2	scaffold_4770:16072318-16072485 +		TGGACTGCGAGCTGAAACTTTTGCCCATACATTTCTTACACAATCGGAGGTGAGAGCCCTTC---CTTAA----ATATAATTTG---GATT-------ACTGTA---------------A------------------------------------GCA-GAGATATATCCATTCC--TTA------CTTGCAGGTTGGCAACGAGGAGTCGATGATGCGTCAATGGCTGGACGTGTGCGTGAC

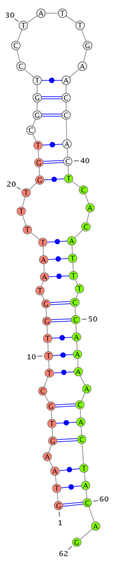
Generated: 09/08/2015 at 10:34 PM

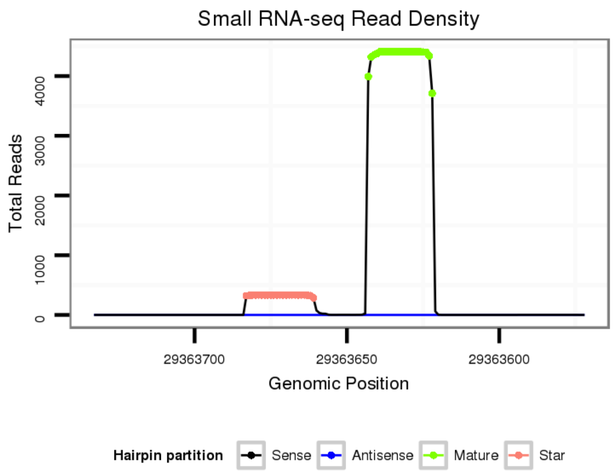
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

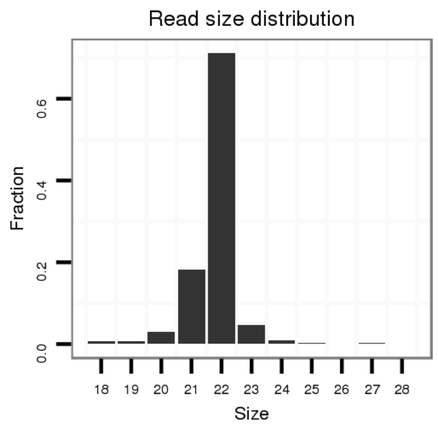
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_212	**scaffold_6540:29363622-29363683 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

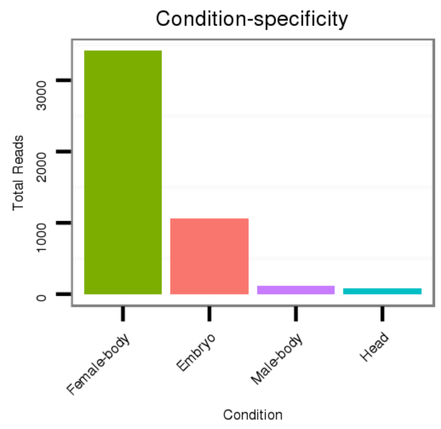
Legend: mature star mismatch in alignment mismatch in read

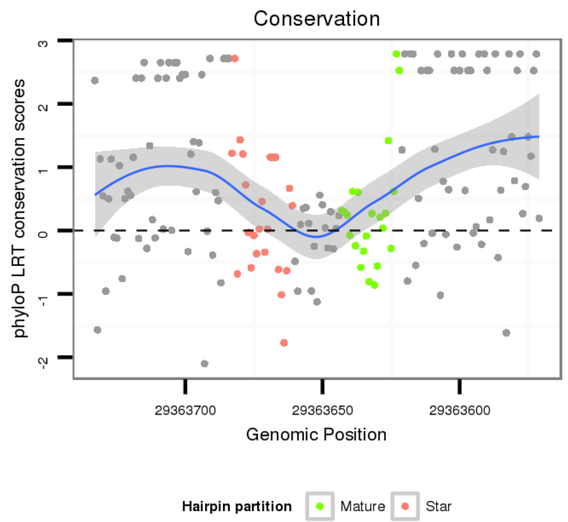
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI22194-in]; CDS [DmojGI22194-cds]; CDS [DmojGI22194-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GTCCTGGAGCCCAACCGCAATTTGATGACATGGGTCAGACACTACTCAATGTAAGTGCTTTGGTAATTTTGGTCGGTCCTATTGAACCACTCACATTTCCAAAACACTACAGCTCTTTCGACGACTCATCTCGGAGGGATTGACGGACACCATTGAGTTGCA **********(((.(((.(((((.(((...(((.(((.....)))))).)))..)))).)))))).)))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V110 male body	V056 head	V049 head	V041 embryo
.....TCACATTTCCAAAACACTACAG.....	22	0	1	3288.00	3288	2453	800	1	18	11	5
.....TCACATTTCCAAAACACTACA.....	21	0	1	572.00	572	464	100	0	3	5	0
.....CACATTTCCAAAACACTACAG.....	21	0	1	265.00	265	253	12	0	0	0	0
.....GTAAGTGCTTTGGTAATTTTGGT.....	23	0	1	207.00	207	35	49	80	18	10	15
.....CACATTTCCAAAACACTACAGT.....	22	1	1	73.00	73	21	44	2	2	4	0
.....TCACATTTCCAAAACACTAC.....	20	0	1	57.00	57	45	12	0	0	0	0
.....CACATTTCCAAAACACTACA.....	20	0	1	45.00	45	45	0	0	0	0	0
.....GTAAGTGCTTTGGTAATTTTGGTC.....	24	0	1	40.00	40	3	13	19	1	0	4
.....TCACATTTCCAAAACACTACAGC.....	23	0	1	40.00	40	24	15	0	1	0	0
.....TCACATTTCCAAAACACTACAGT.....	23	1	1	37.00	37	9	24	0	2	1	1
.....ACATTTCCAAAACACTACAG.....	20	0	1	34.00	34	22	12	0	0	0	0
.....GTAAGTGCTTTGGTAATTTTGG.....	22	0	1	33.00	33	9	2	8	6	6	2
.....ATTTCCAAAACACTACAG.....	18	0	1	27.00	27	17	10	0	0	0	0
.....CATTTCCAAAACACTACAG.....	19	0	1	20.00	20	15	5	0	0	0	0
.....TCACATTTCCAAAACACTACAA.....	22	1	1	19.00	19	17	2	0	0	0	0
.....GTAAGTGCTTTGGTAATTTTGGC.....	23	1	1	17.00	17	1	15	0	1	0	0
.....CACATTTCCAAAACACTACAGC.....	22	0	1	16.00	16	8	8	0	0	0	0
.....GTAAGTGCTTTGGTAATTTTGGTCGGT.....	27	0	1	15.00	15	4	2	7	1	1	0
.....CTCACATTTCCAAAACACTACAG.....	23	0	1	13.00	13	7	6	0	0	0	0
.....TCACATTTCCAAAACACTACAC.....	22	1	1	11.00	11	1	10	0	0	0	0
.....GTAAGTGCTTTGGTAATTTTGGTCG.....	25	0	1	10.00	10	7	0	3	0	0	0
.....GTAAGTGCTTTGGTAATTTTG.....	21	0	1	7.00	7	2	0	1	3	0	1
.....TCACATTTCCAAAACACTACAGA.....	23	1	1	7.00	7	2	5	0	0	0	0
.....CACATTTCCAAAACACTACAA.....	21	1	1	6.00	6	6	0	0	0	0	0
.....TCACATTTCCAAAACACTACAT.....	22	1	1	5.00	5	3	0	0	2	0	0
.....CTCACATTTCCAAAACACTACA.....	22	0	1	5.00	5	4	1	0	0	0	0
.....TAAGTGCTTTGGTAATTTTGGT.....	22	0	1	4.00	4	3	0	1	0	0	0
.....GTAAGTGCTTTGGTAATTTTGGTCGGTC.....	28	0	1	4.00	4	4	0	0	0	0	0
.....CACATTTCCAAAACACTAC.....	19	0	1	4.00	4	4	0	0	0	0	0
.....TCACATTTCCAAAACACTACAGCT.....	24	0	1	4.00	4	2	0	1	0	1	0
.....ACATTTCCAAAACACTACA.....	19	0	1	3.00	3	2	0	0	1	0	0
.....TCACATTTCCAAAACACT.....	18	0	1	3.00	3	3	0	0	0	0	0
.....TAAGTGCTTTGGTAATTTTGG.....	21	0	1	3.00	3	2	0	1	0	0	0
.....ACTCACATTTCCAAAACACTACAG.....	24	0	1	3.00	3	3	0	0	0	0	0
.....TCACATTTCCAAAACACTACAGG.....	23	1	1	3.00	3	2	1	0	0	0	0
.....TCACATTTCCAAAACACTA.....	19	0	1	3.00	3	0	3	0	0	0	0
.....CATTTCCAAAACACTACA.....	18	0	1	3.00	3	3	0	0	0	0	0
.....ACATTTCCAAAACACTACAGT.....	21	1	1	3.00	3	2	1	0	0	0	0
.....GTAAGTGCTTTGGTAATTTT.....	20	0	1	2.00	2	1	0	0	1	0	0
.....TAAGTGCTTTGGTAATTTTGGTC.....	23	0	1	2.00	2	1	0	1	0	0	0
.....GTAAGTGCTTTGGTAATTTTGGTCGG.....	26	0	1	2.00	2	0	2	0	0	0	0
.....TCACATTTCCAAAACACTACAGCC.....	24	1	1	2.00	2	2	0	0	0	0	0
.....CACATTTCCAAAACACTACAGA.....	22	1	1	2.00	2	1	1	0	0	0	0
.....AGTGCTTTGGTAATTTTGGC.....	20	1	1	1.00	1	0	1	0	0	0	0
.....CTCACATTTCCAAAACACTACAT.....	23	1	1	1.00	1	0	1	0	0	0	0
.....AAGTGCTTTGGTAATTTTG.....	19	0	1	1.00	1	1	0	0	0	0	0
.....ATTGAACCACTCACATTTCCAAAACAC.....	27	0	1	1.00	1	0	1	0	0	0	0
.....GTAAGTGCTTTGGTAATTTTGGTA.....	24	1	1	1.00	1	0	0	0	0	0	1
.....CTCACATTTCCAAAACACTAC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....CACATTTCCAAAACACTACATA.....	22	2	1	1.00	1	1	0	0	0	0	0
.....TCACATTTCCAAAACACTACAGCTC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TCACATTTCCAAAACACTACT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....AAGTGCTTTGGTAATTTTGGTC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....CACATTTCCAAAACACTACAGTC.....	23	2	1	1.00	1	1	0	0	0	0	0
.....AATTTTGGTCGGTCCTATTGA.....	21	0	1	1.00	1	0	0	1	0	0	0
.....TCACATTTCCAAAACACTACAGAGG.....	25	3	1	1.00	1	1	0	0	0	0	0
.....AAGTGCTTTGGTAATTTTGGTCG.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TGTAAGTGCTTTGGTAATTTTGG.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GTAAGTGCTTTGGTAATTTTGAC.....	23	2	1	1.00	1	0	1	0	0	0	0
.....TTGACGGACACCATTGAGTTG..	21	0	1	1.00	1	1	0	0	0	0	0
.....GTAAGTGCTTTGGTAATTTTGGTCGGC.....	27	1	1	1.00	1	0	1	0	0	0	0
.....TCACATTTCCAAAACACTACG.....	21	1	1	1.00	1	0	1	0	0	0	0
.....TCACATTTCCAAAACACTACAGCA.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TAAGTGCTTTGGTAATTTTGGC.....	22	1	1	1.00	1	0	1	0	0	0	0
.....ATTTCCAAAACACTACAC.....	18	1	1	1.00	1	0	1	0	0	0	0
.....CCACTCACATTTCCAAAACA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....CACATTTCCAAAACACTACAC.....	21	1	1	1.00	1	1	0	0	0	0	0
.....CACATTTCCAAAACACTACAGTA.....	23	2	1	1.00	1	0	1	0	0	0	0
.....TTTCCAAAACACTACAGTCA.....	20	3	11	0.09	1	1	0	0	0	0	0

Anti-sense strand reads

CAGGACCTCGGGTTGGCGTTAAACTACTGTACCCAGTCTGTGATGAGTTACATTCACGAAACCATTAAAACCAGCCAGGATAACTTGGTGAGTGTAAAGGTTTTGTGATGTCGAGAAAGCTGCTGAGTAGAGCCTCCCTAACTGCCTGTGGTAACTCAACGT **********(((.(((.(((((.(((...(((.(((.....)))))).)))..)))).)))))).)))))..**********	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_6540:29363571-29363733 -	dmo_212	GTCCTGGAGCCCAACCGC------AATTTGATGACATGGGTCAGACACTACT------CAATGTAAGTGCTTT--GG----------------TAATTTTGGT-CGG---TC-CTA----------TTGAA---CCA-CTCACA--------------------TTTCCAAA------ACACTACAGCTCTTTCGACGACTCATCTCGGAGGGATTGACGGACACCATTGAGTTGCAA
droVir3	scaffold_13047:12453791-12453943 +	dvi_16654	---------CCAGTCAC------AGTCTGATGACATGGGTCAGGCGCTGCT------CAATGTAAGTGCTTT--GG----------------TAATTTTGGT-TGT---TC-CAA----------GTGAA---CCA-CTCACA--------------------TTTCCAAA------ACACTACAGCTCTTTCGACGACTTATCTCGGAGGGATTGACGGAGACAATTGAGATGCAA
droGri2	scaffold_14830:672690-672859 -	dgr_111	GCCACAGCGCCAGCCGGAGGCACAGCTGGAGGACATGGGACAGACACTGCG------CAATGTAAGTGCTTT--GG----------------CAATTTCGGGT-CGT---TGTCCA----------GCGAA---CCA-CTCACA--------------------TTTCCAAA------ACACTGCAGCTTTCAGCGCGCTCAACTCGGAAGGACTAACGGAGACGATCGAGCTGCAA
droWil2	scf2_1100000004921:3101048-3101204 +		GTTCCGGAGCCCTACCGC------AATACGAGGATATGGGTCAGAGGTTGCG------TAATGTCAGTGAGA---------------------CAAA-TTAAT---------GGGT---TTTTGAG---TA---------ATTTTAAT--------G---A--T---TTTCAGACCTAACTTCCGAGGGACTAACGGATTCAATTGAGAATGCAG
dp5	2:42007-42169 -		GAGAGGAGGCTGCCCC------AATACGACGACATGGGACAGAGCTGCG------GAATGTGAGTGATATTTGAAGAT----------------TAG---------T---------GTCCAATCTCTATT---TA---------ATTCCAAC--------T---T---TTT---TT------GAATTTAAGCTCTTTCGACGCCTCACTTCTGAAGGATTAACGACTAATTGAGATCCAG
droPer2	scaffold_7:2832405-2832567 -		GAGAGGAGGCTGCCCC------AATACGACGACATGGGACAGAGCTGCG------GAATGTGAGTTATATTTGAAGAT----------------TAG---------T---------GTCCAATCTCTATT---TA---------ATTCCAAC--------T---T---TTT---TT------GAATTTAAGCTCTTTCGACGCCTCACTTCTGAAGGATTAACGACTAATTGAGATCCAG
droAna3	scaffold_13340:14472496-14472650 +		GAGAGGAGGACTGCCGC------AGTATGAGGAAATGGGTCAGACTTTAAG------AAATGTAAGAAATA---------------------CTA--TTAT----TTATTA----------CTTAA---AAA-CATATA--------------------ATGACTTG------TTATGGCAGCTTTTCAGCGCCTCTCTCCTCGAGGGATTGACGGATCTCATTGAGATGCAA
droBip1	scf7180000395971:697067-697218 -		GAGAGGGGGTCCTGCCTC------AGTACGAGGAAATGGGACAGACCTTAAG------AAATGTAAGTAATA---------------------TTAA-CTAAA-TT---------TTGTA---AT------------------CATATTATGACGTT------TTGTGGCAGCTTTTCAGCGCCTCTCCTCTGAGGGATTGACGGATCTCATTGAGATGCAG
droKik1	scf7180000301923:202838-203005 +		GGCAGGAGGAGCCCTGCCGC------AATACGAGGAAATGGGACAAACCTCAG------GAATGTGAGTGGAGTTGGGAAGA----------CAC---------T---------TATAAATCACTTTTATAA---A---------TTTTATG--------T---T---TTCTTTA------CATTTGCAGTTGTTTAGACCGCTCTCCTCTCGAGGGCTTGACGGACCTCATTGAGATGCAA
droFic1	scf7180000454106:2111191-2111350 +		GAGAAGGCTGTCTGCCGC------AGTACGAGGAAATGGGACAGACCTCAG------GAATGTGAGTAATT---------------------GTGC-TTAAAGTT---------TTGT---ATAG---------ATTCAA---------CATTTAATAACATT------CATTTGCAGCTTTTCAGCGCCTCTAGCTCTGAGGGACTGACCGATCTCATTGAAACGCAG
droEle1	scf7180000491194:220510-220666 -		GTCACTTTTC--------------GGAACGACTTTAAATTTTAAAAATATTATTAAGT-GGTGGTAACCCCTTAAAGTT----TA----------ACTT---------TT---ATA---TTTTTTTTA------T---------A--AATTTAAATCC------CTTTTGCAGCTTTTCAGACGCCTTAGCTCTGAGGGATTGACGGACGCTTATAGAGATGCAG
droRho1	scf7180000779488:280687-280850 -		GAGATGGAGCCCTGCCGC------AATACGAGGAGATGGGCAGACGCTGAG------GAATGTGAGTATAAG---TT------TCTTTAAAGTT----TA----------AGCT---------AT------------ATTTTTTTA------T---------T--TTTACAATATC------CATTTACAGCTTTTTAGACGCCTAACTCTGAGGGATTGACGGATCTCATTGAGATGCAG
droBia1	scf7180000302402:7801029-7801184 -		GGCAAGGAAGAGTGCCGC------ACTTTGAGGAGATGGGCAGACCTGAG------GAATGTAAGTAGAT---------------------ATTC-TTTT----CTT---------TTGAA---AT------TCTGTATA---------CT----TATGCATT------TATTTGCAGCTCTTTAGCGACTGAGCTCTGAGGGATTAACGGATCTAATTGAAATGCAG
droTak1	scf7180000415364:57343-57398 +		--TGACGGACACCATTGAGTTG..
droEug1	scf7180000407340:34244-34404 +		GGCAAGGAGGTACGCCAC------AGTACGAAGAGATGGGACAAACTCTGAG------GAATGTGAGTAGAT---------------------TTGG-TTGT----TT---------T----TA---------ATATGAATTTTGTTTAAT-T--TTGCCATT------CACTTACAGCTTTTCAGCGCCTAAGCTCTGAGGGATTAACGGATCTTATTGAAATGCAG
dm3	chr3R:5068718-5068873 -		GGCAGGAGGAGTCTGCCGC------AGTACGAGGAGATGGGACAGACCTTGGG------TAATGTATGTGGAT---------------------TAGA-TCAAAATT---------GTAT---AA---------ATTGTAAA--------T---T---GTTCCTTT------AACGTGCAGCTCTTTAGACCCTTAAGCTCTGAGGGATTAACGGATCTATTGAGATGCAG
droSim2	3r:15944725-15944883 +	dsi_1222	GAGAGGAGGTCTGCCGC------AGTACGAGGAGATGGGACAGACTCTGGG------TAATGTAAGTGGAT---------------------TAGA-TCAAAATT---------GTAT---AA---------ATGGTAAA--------T---T---GTT---GGTAATTTAACTTGCAGCTCTTTAGACCCTTAAGCTCTGAGGGTTTAACGGATCTCATTGAGATGCAG
droSec2	scaffold_0:16813354-16813509 +		GAGAGGAGGTCTGCCGC------AGTACGAGGAGATGGGACAGACCTGGG------TAATGTAAGTGGAT---------------------TGGA-TCAAAATT---------GTAT---AA---------ATGGTAAA--------T---T---GTTCCTT------AACTTGCAGCTCTTTAGACCCTTAAGCTCTGAGGGTTTAACGGATCTCATTGAGATGCAG
droYak3	3R:9121138-9121300 -		GAGAGGAAGTCTGCCGC------AGTACGAGGAGATGGGACAGACCTGGG------GAATGTAAGTGTAAC--TT---------------TAATGTAA-TTAAAGTC---------ATAT---GA---------ATTGTAAT--------T---T---ATTCCTCC------AACTTGAAGCTTTTAGACCCTTAAGCTCTGAGGGCCTAACGGATCTCATTGAGATGCAG
droEre2	scaffold_4770:16531450-16531605 +		GAGAGGAAGTCTGCCGC------AGTACGAGGAGATGGGACAGACCTGGG------CAATGTAAGCGGAT---------------------TAAA-CTAGAGCT---------ATAT---GC---------CCTCTAAT--------T---T---GTAGCTT------AACTTGCAGCTTTTTAGACGCCTTAGCTCTGAGGGCTTAACGGATCTCATTGAGATGCAG

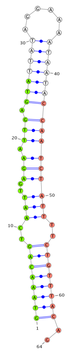
Generated: 09/08/2015 at 10:34 PM

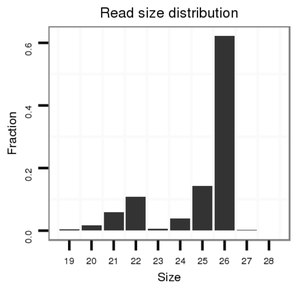
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	3
rescue.candidate	0

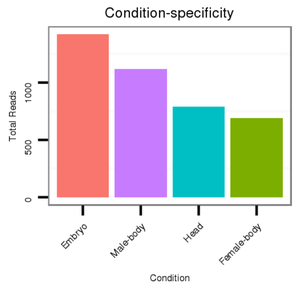
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2402	**scaffold_6680:8002455-8002518 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Comell Mirror]]

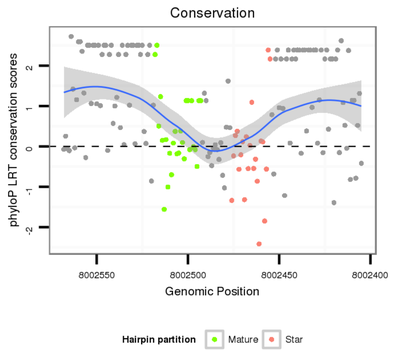
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annnotation

intron [DmojGI12223-in]; CDS [DmojGI12223-cds]; CDS [DmojGI12223-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTCCATGGATCTCATCAAGAGCAATGAGTTGCTCCAAAACATGAGCGAAGGTAAACAGTCAATTGAGAATTGAGTATTATAGGAAAATAATACCAATCTATTTTCTGTTTACAGGAGAGCGTGAAGAGATTATTTTATATATTCAGCGCGTTAGTGCACGCCTA	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V110 male body	M046 female body	V056 head	V041 embryo	V049 head
(((((((..(((..(((.(((.(((.(((((((.....)))))))))))))))..)))))))..)))))..*												
.....CCAATCTATTTTCTGTTTACAGT.....	23	1	1	5431.00	5431	4532	89	355	166	177	112
.....GTAAACAGTCAATTGAGAATTGAGTA.....	26	0	1	2501.00	2501	420	875	228	537	297	144
.....CCAATCTATTTTCTGTTTACAGT.....	23	1	1	1016.00	1016	1010	1	5	0	0	0
.....GTAAACAGTCAATTGAGAATTGAGT.....	25	0	1	567.00	567	237	196	28	39	49	18
.....CCAATCTATTTTCTGTTTACAG.....	22	0	1	416.00	416	200	1	193	9	8	5
.....CAATCTATTTTCTGTTTACAGT.....	22	1	1	267.00	267	197	5	47	4	8	6
.....CCAATCTATTTTCTGTTTACA.....	21	0	1	215.00	215	55	4	133	4	13	6
.....GTAAACAGTCAATTGAGAATTGAGTAA.....	27	1	1	144.00	144	2	97	1	16	19	9
.....GTAAACAGTCAATTGAGAATTGAG.....	24	0	1	144.00	144	21	28	17	10	62	6
.....GTAAACAGTCAATTGAGAATTGAGTT.....	26	1	1	143.00	143	70	42	27	2	1	1
.....CCAATCTATTTTCTGTTTACAA.....	23	1	1	81.00	81	60	0	17	1	3	0
.....GTAAACAGTCAATTGAGAATTGAGC.....	25	1	1	71.00	71	67	2	0	0	2	0
.....GTAAACAGTCAATTGAGAATTGAGTAAA.....	28	2	1	41.00	41	1	34	2	3	1	0
.....CCAATCTATTTTCTGTTTAC.....	20	0	1	41.00	41	9	0	27	4	0	1
.....CAATCTATTTTCTGTTTACAGC.....	22	1	1	39.00	39	39	0	0	0	0	0
.....CCAATCTATTTTCTGTTTACAC.....	22	1	1	35.00	35	32	0	3	0	0	0
.....CCAATCTATTTTCTGTTTACAGTT.....	24	2	1	32.00	32	24	1	1	1	5	0
.....AATCTATTTTCTGTTTACAGT.....	21	1	1	31.00	31	25	0	6	0	0	0
.....CCAATCTATTTTCTGTTTACAGTC.....	24	2	1	29.00	29	9	7	10	0	3	0
.....CCAATCTATTTTCTGTTTACAGG.....	23	0	1	17.00	17	16	0	1	0	0	0
.....CAATCTATTTTCTGTTTACAG.....	21	0	1	17.00	17	1	0	15	0	1	0
.....GTAAACAGTCAATTGAGAATTGAGTCC.....	27	2	1	17.00	17	9	7	0	1	0	0
.....CAATCTATTTTCTGTTTACA.....	20	0	1	14.00	14	0	0	14	0	0	0
.....GTAAACAGTCAATTGAGAATTG.....	22	0	1	14.00	14	1	3	3	1	4	2
.....CTATTTTCTGTTTACAGT.....	18	1	4	10.25	41	33	0	7	0	1	0
.....CCAATCTATTTTCTGTTTACACC.....	23	2	1	10.00	10	10	0	0	0	0	0
.....GTAAACAGTCAATTGAGAATTGAGCCC.....	26	2	1	10.00	10	8	2	0	0	0	0
.....CCAATCTATTTTCTGTTTACACT.....	23	2	1	10.00	10	7	0	1	1	0	1
.....CAATCTATTTTCTGTTTACAGA.....	22	1	1	9.00	9	4	0	5	0	0	0
.....CCAATCTATTTTCTGTTTACATT.....	23	2	1	9.00	9	4	0	0	2	0	3
.....GTAAACAGTCAATTGAGAATTGA.....	23	0	1	9.00	9	6	0	3	0	0	0
.....GTAAACAGTCAATTGAGAATTGAGTT.....	26	1	1	9.00	9	3	0	1	1	4	0
.....ATCTATTTTCTGTTTACAGT.....	20	1	1	8.00	8	7	0	1	0	0	0
.....GTAAACAGTCAATTGAGAAT.....	20	0	1	8.00	8	1	3	2	0	2	0
.....GTAAACAGTCAATTGAGAATTGAGTAT.....	27	0	1	8.00	8	1	4	1	1	1	0
.....AATCTATTTTCTGTTTACACT.....	21	1	1	8.00	8	8	0	0	0	0	0
.....AACAGTCAATTGAGAATTGAGTA.....	24	0	1	8.00	8	5	1	2	0	0	0
.....GTAAACAGTCAATTGAGAATTGAGTAG.....	27	1	1	7.00	7	2	3	2	0	0	0
.....CCAATCTATTTTCTGTTTACAT.....	22	1	1	6.00	6	4	0	2	0	0	0
.....AACAGTCAATTGAGAATTGAGTA.....	23	0	1	6.00	6	6	0	0	0	0	0
.....TAAACAGTCAATTGAGAATTGAGTA.....	25	0	1	6.00	6	0	0	6	0	0	0
.....AAACAGTCAATTGAGAATTGAGT.....	23	0	1	5.00	5	3	2	0	0	0	0
.....GTAAACAGTCAATTGAGAATTGAGC.....	25	1	1	5.00	5	5	0	0	0	0	0
.....GTAAACAGTCAATTGAGAA.....	19	0	1	5.00	5	2	1	1	0	1	0
.....GTAAACAGTCAATTGAGAATTGAGTCCC.....	28	3	1	4.00	4	1	2	1	0	0	0
.....CAGTCAATTGAGAATTGAGTA.....	21	0	1	4.00	4	3	0	0	0	1	0
.....GTAAACAGTCAATTGAGAATTGAGA.....	25	1	1	4.00	4	2	0	1	0	1	0
.....GTAAACAGTCAATTGAGAATTC.....	22	1	1	4.00	4	1	3	0	0	0	0
.....CTATTTTCTGTTTACAGC.....	18	1	3	3.67	11	11	0	0	0	0	0
.....ACAGTCAATTGAGAATTGAGTA.....	22	0	1	3.00	3	3	0	0	0	0	0
.....TAAACAGTCAATTGAGAATTGAG.....	23	0	1	3.00	3	0	0	3	0	0	0
.....ACCAATCTATTTTCTGTTTACAG.....	23	0	1	3.00	3	2	0	1	0	0	0
.....GTAAACAGTCAATTGAGAATTGAC.....	24	1	1	3.00	3	3	0	0	0	0	0
.....GTAAACAGTCAATTGAGAATTGAGTATT.....	28	0	1	3.00	3	0	1	2	0	0	0
.....GTAAACAGTCAATTGAGAATTGAGTAAAG.....	29	3	1	3.00	3	1	1	1	0	0	0
.....CAATCTATTTTCTGTTTAC.....	19	0	1	3.00	3	1	0	2	0	0	0
.....AATCTATTTTCTGTTTACAG.....	20	0	1	3.00	3	2	0	1	0	0	0
.....ATCTATTTTCTGTTTACAG.....	19	0	1	3.00	3	0	0	3	0	0	0
.....TCTATTTTCTGTTTACAGT.....	19	1	2	3.00	6	4	0	0	1	1	0
GTCCATGGATCTCATCAAGAGC.....	22	0	1	2.00	2	0	2	0	0	0	0
.....GTAAACAGTCAATTGAGAATTGAGTCA.....	27	2	1	2.00	2	0	2	0	0	0	0
.....CAATCTATTTTCTGTTTACAC.....	21	1	1	2.00	2	0	0	2	0	0	0
.....ACCAATCTATTTTCTGTTTACAGT.....	24	1	1	2.00	2	2	0	0	0	0	0
.....ATCTATTTTCTGTTTACAGC.....	20	1	1	2.00	2	2	0	0	0	0	0
.....TAAACAGTCAATTGAGAATTGAGTG.....	25	1	1	2.00	2	0	0	2	0	0	0
.....CCAATCTATTTTCTGTTTACAA.....	22	1	1	2.00	2	1	0	1	0	0	0
.....AAACAGTCAATTGAGAATTGAGC.....	23	1	1	2.00	2	2	0	0	0	0	0
.....CCAATCTATTTTCTGTTTA.....	19	0	1	2.00	2	0	0	0	0	0	2
.....CCAATCTATTTTCTGTTTACAAT.....	23	2	1	2.00	2	2	0	0	0	0	0
.....CCAATCTATTTTCTGTTTACAAC.....	23	2	1	2.00	2	2	0	0	0	0	0
.....GTAAACAGTCAATTGAGAATTGAGTACC.....	28	2	1	2.00	2	0	2	0	0	0	0
.....CAATCTATTTTCTGTTTACAGTT.....	23	2	1	2.00	2	0	0	1	1	0	0
.....TAAACAGTCAATTGAGAATTGAGT.....	24	0	1	2.00	2	0	0	2	0	0	0
.....AGTCAATTGAGAATTGAGTA.....	20	0	1	2.00	2	2	0	0	0	0	0
.....AATCTATTTTCTGTTTACA.....	19	0	1	2.00	2	0	0	2	0	0	0
.....GTAAACAGTCAATTGAGAATTGAGCCCC.....	27	3	1	2.00	2	2	0	0	0	0	0
.....GTAAACAGTCAATTGAGAATT.....	21	0	1	2.00	2	0	0	2	0	0	0
.....AATCTATTTTCTGTTTACAGA.....	21	1	1	2.00	2	1	0	1	0	0	0
.....CAGTCAATTGAGAATTGAGTG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....ACCAATCTATTTTCTGTTTACA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....CCAATCTATTTTCTGTTTACATA.....	23	2	1	1.00	1	1	0	0	0	0	0
.....GTAAACAGTCAATTGAGAATTGCC.....	24	2	1	1.00	1	1	0	0	0	0	0
.....GTAAACAGTCAATTGAGAATCC.....	22	2	1	1.00	1	1	0	0	0	0	0
.....CCAATCTATTTTCTGTTTACAC.....	21	1	1	1.00	1	0	0	1	0	0	0
.....CAATCTATTTTCTGTTTACAGTC.....	23	2	1	1.00	1	0	0	1	0	0	0
.....GTAAACAGTCAATTGAGAATTGAGTG.....	26	1	1	1.00	1	0	1	0	0	0	0
.....TCTATTTTCTGTTTACAC.....	18	1	1	1.00	1	1	0	0	0	0	0
.....GTAAACAGTCAATTGAGAATTGAG.....	24	1	1	1.00	1	0	0	0	0	0	1

Anti-sense strand reads

CAGGTACCTAGAGTAGTTCTCGTTACTCAACGAGGTTTTGTACTCGCTTCCATTTGTCAGTTAACTCTTAACTCATAATATCCTTTTATTATGGTTAGATAAAAGACAAATGTCCTCTCGCACTTCTCTAATAAAATATATAAGTCGCGCAATCACGTGCGGAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V049 head	V056 head
(((((((..(((..(((.(((.(((.(((((((.....)))))))))))))))..)))))))..)))))..*							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6680:8002405-8002568 -	dmo_2402	GTCCATGGATCTCATCAAGAGCAATGAGTTGCTCCAAAACATGAGCGAAGGTAAACAGT----------CA----------A---TTGA-----GAATTGAGTATTA----------TAG----------GA--------AAATAATA-CA--------A---TC--TATTTT-CTGTTTACAGGAGAGCGTGAAGAGATTATTTTATATTCAGCGCGTTAGTGCACGCCTA
droVir3	scaffold_13049:20291595-20291759 +	dvi_20739	GTCCATGGATCTCATCAAGAGCAACGAAATGCTCAAAACATGAGCGAGGGTAAACAGA----------TTTTGAGTACAATGTAAAT----------A---TTG-----------------------------AAAAC-TAA--ATTGGATACGA--TTTAAT---------ACTAGCGAGCGGAGCGAGATCATGTTGTACATTCAGCGCGTTAGTTACGCGCGTT
droGri2	scaffold_15110:16611261-16611432 +		GTCCATGGATCTCATCAAGAGCAACGAAATGCTCAAAATATGAGCGAGGTAGTAATAA----------AGACCCTA----------A---TTG-----------------------------ACA--GAA--CAT-TTA--AACGTTTAA-AATCATCATT---AC-TTTAATTGTGACGAGCGCGAGCGGAAGAGATTATGTTGTACATTCAGCGCGTTAGTGCGCGCGTT
droWil2	scaf2_1100000004949:1844158-1844267 -		GTCCATGGATCTCATCAAGAAGCAATGAAATGCTCAAAACATGAGCGAAGGTAGTAATAA----------A---TTGCTGA-----AAAGAATCTATTA----------GAC----------A---CA--TA-----------------------------TAACGTATAC
dp5	XR_group6:236972-237146 +		GTCGATGGATCTGATCAAGAGCAATGATAAACGTCACAACATGAGCGAGGTCTAGTAGTAGA----------A---TTG-----------------------------TGTTCACATAATACCTCACG--GAA-ACGCGGA--AACGGATAA-CAA-TGTAAT---CCC-TCTCTT-TCCCCGTAGCCGAGCCGAGCGAGATCATGTTGTACATTCAGCGCGTTAGCTCACGCGTG
droPer2	scaffold_12:922864-923038 +		GTCGATGGATCTGATCAAGAGCAATGATAAACGTCACAACATGAGCGAGGTCTAGTAGTAGA----------A---TTG-----------------------------TGTTCACATAATACCTCACG--GAA-AGCGGA--AACGGATAA-CAA-TGTAAT---CCC-TCTCTT-TCCCCGTAGCCGAGCCGAGCGAGATCATGTTGTACATTCAGCGCGTTAGCTCACGCGTG
droAna3	scaffold_13337:17347358-17347530 +		GTCCATGGATCTATCAAGACAACGAAATGATCACAACATGAGCGAGGTCGTATCGCTT----------AA----------A---TTG-----------------------------ATTTCATACG--AGGTTGCATTTTAA--AACAATACGTTACTTGCATT---AA-TATATTCTGACGAGCGAGAAGAGATCATGTTGTATTCAGCGAGTCGCGCGTG
droBip1	scf7180000396741:648783-648938 +		GTCCATGGATCTAATCAAGAGCAACGAAATGATCACAACATGAGCGAGGTATACGATT----------GC----------TTT-----------------------------TCTATCAAAAGGGT----------T---------------A---TATATT---CAA-TCTCTT-CTATACAGCAGTCGATGAGAAGAGATTATGTTGTATATTCAGCGAGTCGCGATCG
droKik1	scf7180000302686:1242198-1242424 +		GTCCATGGATCTGATTAAGAGCAATGAAATGCTCACAACATGACGAAGGTCGAGAAAGGGACTAAAGATCTCGAAATAATAAGATGAGTAACGAATACGCATTATCGAA-------GTTACATCTATAACTTCTTTAC----------TTT-----------------------------TC----------TTTCG--ATATT---AATT-------A---TTT---TATTGATAGA-C-CGCATTTGAGCTGATCGCGAGAGATCATGTTGTACATTCAGCGCGTTAGCTCACGCGTG
droFic1	scf7180000454065:1794625-1794784 +		GTCCATGGATCTGATCAAGAGCAACGAAATGATCACAACATGAGCGAAGGTATGCGAT----------GGT---TA----------A---CCA-----G----------AAA----------TTATGTACATAATTCATTATC---A---------A---TTTTTGAGCTGATCGTAACGTGAGAGATCATGTTGTACATCAGCGAGTTAGCTCACGCGTG
droEle1	scf7180000491000:903568-903631 -		CTA----------A---TTG-----------------------------TTT-----------------------------TCTATCAAAAGGGT----------T---------------A---TATATT---CAA-TCTCTT-CTATACAGCAGTCGATGAGAAGAGATTATGTTGTATATTCAGCGAGTCGCGATCG
droRho1	scf7180000770847:5989-6060 +		ACTAATT----------A---TTG-----------------------------TTT-----------------------------TCTATCAAAAGGGT----------T---------------A---TATATT---TTATTTTAGCCGAACGGAGAGATCATGTTGTACATTCAGCGAGTTAGCTCACGCGTG
droBia1	scf7180000302334:881527-881584 +		GTCCATGGATCTGATCAAGAGCAACGAAATGATCACAACATGAGCGAGGTCGAAGT----------A---TTG-----------------------------TCTATCAAAAGGGT----------T---------------A---TATATT---CAA-TCTCTT-CTATACAGCAGTCGATGAGAAGAGATTATGTTGTACATTCAGCGAGTCGCGATCG
droTak1	scf7180000415795:938032-938090 -		GTCCATGGATCTGATCAAGAGCAACGAAATGATCACAACATGAGCGAGGTCGAGAGT----------A---TTG-----------------------------TCTATCAAAAGGGT----------T---------------A---TATATT---CAA-TCTCTT-CTATACAGCAGTCGATGAGAAGAGATTATGTTGTACATTCAGCGAGTCGCGATCG
droEug1	scf7180000408844:246318-246504 -		GTCCATGGATCTGATCAAGAGCAACGAAATGATCACAACATGACGAGGTATAGAGT----------GTTTTGAACATTTAGATCACTA----------CCCCATTTGTTTAAGTTTGC----------A---TTG-----------------------------TTTTACT---AACT--------A---TTG---T---TCTTACTCTTTCTTCCTTGGAGCTGATCGTAACGTGAGATTATGTTGTACATTCAGCGAGTTAGCTCACGCGTG
dm3	chr3L:15515246-15515509 -		GTCCATGGATCTGATCAAGAGCAACGAAATGATCACAACATGAGCGAAGGTAGTGACAGT----------G---------------------ATTCTTAAAACTAATTTGAACCCTCATTTGTTCA---TA-CTTTACTAAATTGTGTATTTCGAAGTCGGAAGTAATGGTTTCTGATGACAAACTAAGTAAAGGGTTATTCATAGTTGACTG----------TG----------A---CA--TA-----------------------------GCTAATGT---TG---T---A---CACTTTCTTCTTTGGAGCTGATCGTAACGTGAGATTATGTTGTACATTCAGCGAGTCGCGTCG
dmoSim2	scaffold_6:8002455-8002518 -		TAAT-CAG----------A---TTG-----------------------------TTT-----------------------------TCTATCAAAAGGGT----------T---------------A---TATATT---CAA-TCTCTT-CTATACAGCAGTCGATGAGAAGAGATTATGTTGTATATTCAGCGAGTCGCGATCG
droYak3	3L:18030836-18030908 -		ACTAATTTATC----------A---TTG-----------------------------TTT-----------------------------TCTATCAAAAGGGT----------T---------------A---TATATT---CAA-TCTCTT-CTATACAGCAGTCGATGAGAAGAGATTATGTTGTATATTCAGCGAGTCGCGATCG
droEre2	scaffold_4784:17772850-17772921 -		ACTAATTGATCT----------A---TTG-----------------------------TTT-----------------------------TCTATCAAAAGGGT----------T---------------A---TATATT---CAA-TCTCTT-CTATACAGCAGTCGATGAGAAGAGATTATGTTGTATATTCAGCGAGTCGCGATCG

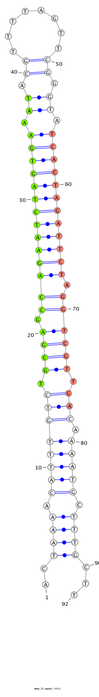
Generated: 09/08/2015 at 10:34 PM

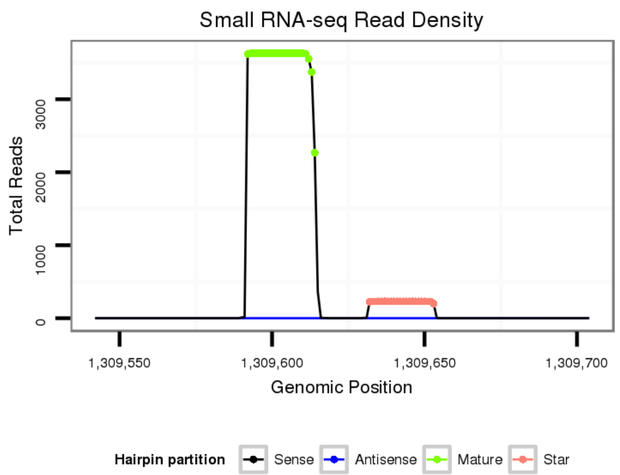
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

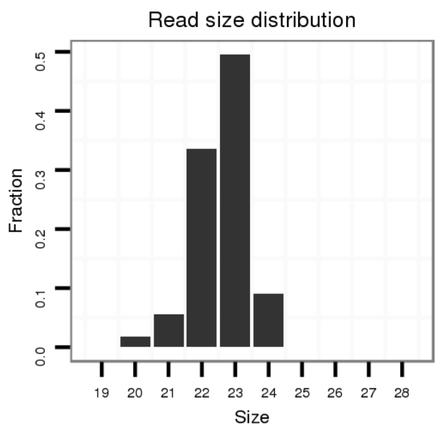
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_27	**scaffold_6308:1309592-1309654 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

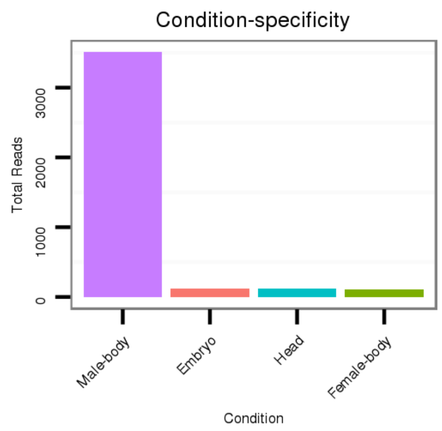
Legend: mature star mismatch in alignment mismatch in read

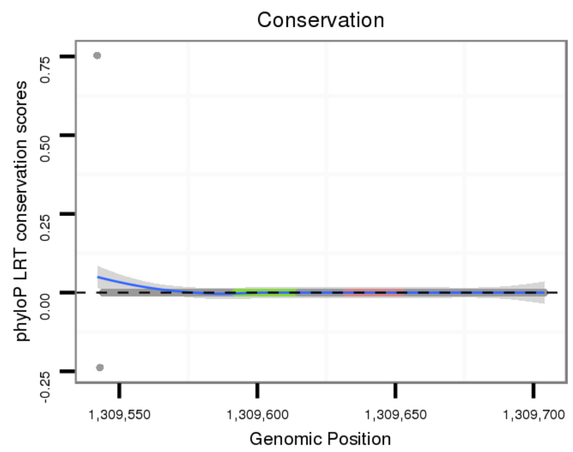
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATTCAATTTGTAATCGGTCTATAGAAAAAATCTAAACTAAAACATTTGTCTGCGAGCCAGAATCTAGTGAAATACGTTTTAGTTCGGGTATCACTAGATTCTAGGTCGTTGACAAAATGCTTTGCTTTGCAACAGAAAAATCGGAAACCCATCAAATGTGTAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V056 head	V049 head	V041 embryo
**********..((((.(((((((((.((((.(((((((((((((((.((.((........)).)).)))))))))))))).)))))))..)))).)))))...**********											
.....TGCGAGCCAGAATCTAGTGAAAT.....	23	0	1	1896.00	1896	1812	22	14	28	13	7
.....TGCGAGCCAGAATCTAGTGAAA.....	22	0	1	1101.00	1101	997	18	38	11	11	26
.....TGCGAGCCAGAATCTAGTGAAATA.....	24	0	1	351.00	351	339	3	2	5	1	1
.....TCACTAGATTCTAGGTCGTTGA.....	22	0	1	187.00	187	136	32	5	8	4	2
.....TGCGAGCCAGAATCTAGTGAA.....	21	0	1	179.00	179	142	7	9	4	12	5
.....TGCGAGCCAGAATCTAGTGAAATC.....	24	1	1	88.00	88	87	1	0	0	0	0
.....TGCGAGCCAGAATCTAGTGA.....	20	0	1	65.00	65	36	9	1	9	5	5
.....TGCGAGCCAGAATCTAGTGAAAA.....	23	1	1	65.00	65	64	0	0	1	0	0
.....TGCGAGCCAGAATCTAGTGAAATAA.....	25	1	1	51.00	51	50	0	0	1	0	0
.....TCACTAGATTCTAGGTCGTTG.....	21	0	1	26.00	26	18	1	2	2	1	2
.....TGCGAGCCAGAATCTAGTGAAATAAA.....	26	2	1	20.00	20	20	0	0	0	0	0
.....TCACTAGATTCTAGGTCGTTGAT.....	23	1	1	15.00	15	13	2	0	0	0	0
.....TCACTAGATTCTAGGTCGTTGT.....	22	1	1	9.00	9	9	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAATCA.....	25	2	1	9.00	9	9	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAATAT.....	25	1	1	7.00	7	7	0	0	0	0	0
.....TCTGCGAGCCAGAATCTAGTGA.....	22	0	1	7.00	7	1	1	5	0	0	0
.....TGCGAGCCAGAATCTAGTGAAATT.....	24	1	1	6.00	6	4	1	0	0	1	0
.....TCACTAGATTCTAGGTCGTTGAA.....	23	1	1	6.00	6	3	1	1	1	0	0
.....CACTAGATTCTAGGTCGTTGA.....	21	0	1	6.00	6	0	6	0	0	0	0
.....GCGAGCCAGAATCTAGTGAAAT.....	22	0	1	5.00	5	4	1	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAATAC.....	25	0	1	5.00	5	5	0	0	0	0	0
.....TCACTAGATTCTAGGTCGTTGAC.....	23	0	1	5.00	5	5	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTG.....	19	0	1	5.00	5	4	1	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAG.....	22	1	1	4.00	4	3	1	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAC.....	22	1	1	4.00	4	4	0	0	0	0	0
.....TCTGCGAGCCAGAATCTAGTG.....	21	0	1	3.00	3	1	0	0	2	0	0
.....TATCACTAGATTCTAGGTCGTTG.....	23	0	1	3.00	3	2	0	1	0	0	0
.....TGCGAGCCAGAATCTAGTGAATT.....	22	1	1	3.00	3	3	0	0	0	0	0
.....GCGAGCCAGAATCTAGTGAAATA.....	23	0	1	3.00	3	2	1	0	0	0	0
.....TCACTAGATTCTAGGTCGTTGG.....	22	1	1	3.00	3	3	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAATAG.....	25	1	1	2.00	2	2	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGTT.....	20	1	1	2.00	2	2	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAATCT.....	25	2	1	2.00	2	2	0	0	0	0	0
.....GAGCCAGAATCTAGTGAAAT.....	20	0	1	2.00	2	2	0	0	0	0	0
.....CTGCGAGCCAGAATCTAGTGAAA.....	23	0	1	2.00	2	0	0	2	0	0	0
.....TCACTAGATTCTAGGTCGTTGATC.....	24	2	1	2.00	2	2	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAATACGT.....	27	0	1	2.00	2	2	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAATAAAA.....	27	3	1	2.00	2	2	0	0	0	0	0
.....TCACTAGATTCTAGGTCGTT.....	20	0	1	2.00	2	0	1	0	0	1	0
.....GCGAGCCAGAATCTAGTGAAA.....	21	0	1	2.00	2	1	0	0	0	1	0
.....TGCGAGCCAGAATCTAGTGAAATTT.....	25	2	1	2.00	2	2	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAATACA.....	26	1	1	2.00	2	2	0	0	0	0	0
.....TCACTAGATTCTAGGTCGTTGAGC.....	24	2	1	2.00	2	2	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAT.....	21	1	1	2.00	2	1	0	0	0	1	0
.....GCGAGCCAGAATCTAGTGAA.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TCTGCGAGCCAGAATCTAGTGAAA.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TCACTAGATTCTAGGTCGTTTC.....	22	2	1	1.00	1	0	1	0	0	0	0
.....TCACTAGATTCTAGGTCGTTGAAG.....	24	2	1	1.00	1	0	0	1	0	0	0
.....CGAGCCAGAATCTAGTGAAATAA.....	23	1	1	1.00	1	0	0	1	0	0	0
.....CTGCGAGCCAGAATCTAGTGAAAT.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAATTAA.....	26	3	1	1.00	1	1	0	0	0	0	0
.....TCACTAGATTCTAGGTCGTTGAG.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAATATCA.....	27	3	1	1.00	1	1	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAATAAT.....	26	2	1	1.00	1	1	0	0	0	0	0
.....TATCACTAGATTCTAGGTCGT.....	21	0	1	1.00	1	0	0	1	0	0	0
.....TATCACTAGATTCTAGGTCGTT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGC.....	20	1	1	1.00	1	1	0	0	0	0	0
.....TCACTAGATTCTAGGTCGTTGACT.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAATATA.....	26	2	1	1.00	1	1	0	0	0	0	0
.....TCACTAGATTCTAGGTCGTC.....	20	1	1	1.00	1	1	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAAAT.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TCACTAGATTCTAGGTCGTTGC.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAAC.....	23	1	1	1.00	1	0	0	1	0	0	0
.....TGCGAGCCAGAATCTAGTGAATAT.....	24	3	1	1.00	1	1	0	0	0	0	0
.....TCACTAGATTCTAGGTCGTTGACG.....	24	1	1	1.00	1	0	1	0	0	0	0
.....TGCGAGCCAGAATCTAGTC.....	19	1	1	1.00	1	0	1	0	0	0	0
.....CTAGATTCTAGGTCGTTGACA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAATCAA.....	26	3	1	1.00	1	1	0	0	0	0	0
.....GCGAGCCAGAATCTAGTGAAATAG.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAATACGTT.....	28	0	1	1.00	1	1	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAATA.....	23	2	1	1.00	1	0	0	0	0	0	1
.....TGCGAGCCAGAATCTAGTGAAATTA.....	25	2	1	1.00	1	1	0	0	0	0	0
.....TGCGAGCCAGAATCTAGTGAAATACGTC.....	28	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

TAAGTTAAACATTAGCCAGATATCTTTTTTAGATTTGATTTTGTAAACAGACGCTCGGTCTTAGATCACTTTATGCAAAATCAAGCCCATAGTGATCTAAGATCCAGCAACTGTTTTACGAAACGAAACGTTGTCTTTTTAGCCTTTGGGTAGTTTACACATT	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V049 head
**********..((((.(((((((((.((((.(((((((((((((((.((.((........)).)).)))))))))))))).)))))))..)))).)))))...**********							
.....AACGAAACGTTGTCTTTTTAGCCTTT.....	26	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1309542-1309704 +	dmo_27	ATTCAATTTGTAATCGGTCTATAGAAAAAATCTAAACTAAAACATTTGTCTGCGAGCCAGAATCTAGTGAAATACGTTTTAGTTCGGGTATCACTAGATTCTAGGTCGTTGACAAAATGCTTTGCTTTGCAACAGAAAAATCGGAAACCCATCAAATGTGTAA
droEle1	scf7180000491249:2203261-2203262 +		AA----------

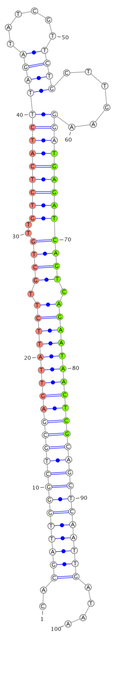
Generated: 09/08/2015 at 08:02 PM

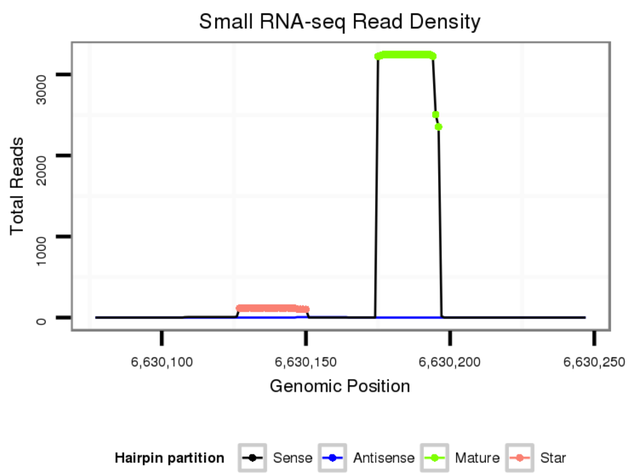
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

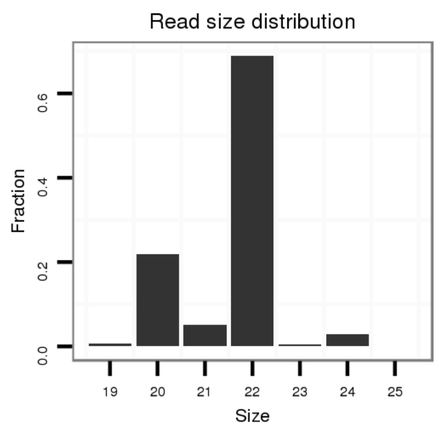
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_34	**scaffold_6540:6630127-6630197 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

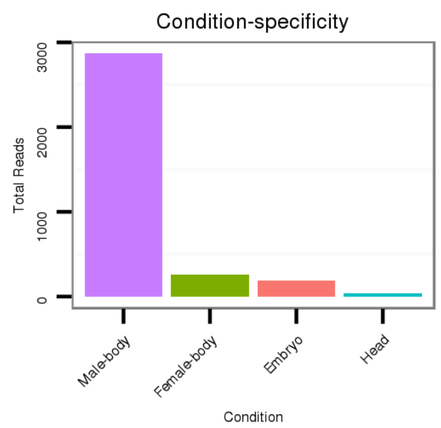
Legend: mature star mismatch in alignment mismatch in read

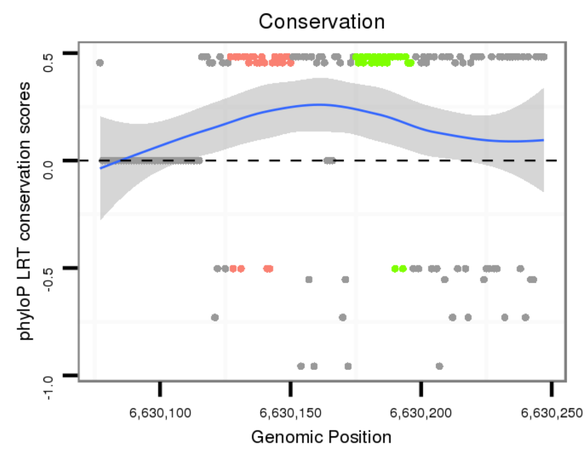
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GCCTAGTTAAGATTATGTGGAATAACTCAGCCCTTCACGATTGGGCTGCGAGTTATTCTTGCTGTTGTCTCATCTTAGATATCGTTCTGCTTGAAGGATGAGATCAGTCAGAATAACTCGCAGCTCAATTGATAAGCAACAAGATTTTTTTAAAATATATATAAAATTTAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V056 head	V049 head	V041 embryo
**********..(((((((((((((((((((((((.((((..((((((((((((((.....))))).....)))))))))))))).))))))))))))))))))))....**********											
.....TGAGATCAGTCAGAATAACTCG.....	22	0	1	2317.00	2317	2005	214	46	20	17	15
.....TGAGATCAGTCAGAATAACT.....	20	0	1	719.00	719	698	14	6	0	1	0
.....TGAGATCAGTCAGAATAACTC.....	21	0	1	152.00	152	103	26	21	1	1	0
.....TGAGATCAGTCAGAATAACTCGT.....	23	1	1	130.00	130	124	2	1	2	1	0
.....TGAGATCAGTCAGAATAACTCT.....	22	1	1	125.00	125	123	0	0	2	0	0
.....AGTTATTCTTGCTGTTGTCTCATC.....	24	0	1	101.00	101	1	2	98	0	0	0
.....TGAGATCAGTCAGAATAACTCC.....	22	1	1	51.00	51	37	1	12	1	0	0
.....TGAGATCAGTCAGAATAACTA.....	21	1	1	43.00	43	42	1	0	0	0	0
.....TGAGATCAGTCAGAATAACTCGTC.....	24	2	1	27.00	27	23	4	0	0	0	0
.....TGAGATCAGTCAGAATAAC.....	19	0	1	22.00	22	22	0	0	0	0	0
.....TGAGATCAGTCAGAATAACTCA.....	22	1	1	21.00	21	20	1	0	0	0	0
.....TGAGATCAGTCAGAATAACTCGA.....	23	1	1	14.00	14	11	2	1	0	0	0
.....TGAGATCAGTCAGAATAAA.....	19	1	1	13.00	13	12	1	0	0	0	0
.....TGAGATCAGTCAGAATAACTCGC.....	23	0	1	13.00	13	9	2	2	0	0	0
.....GAGATCAGTCAGAATAACTCG.....	21	0	1	10.00	10	6	4	0	0	0	0
.....TGAGATCAGTCAGAATAACTCGTCT.....	25	3	1	10.00	10	10	0	0	0	0	0
.....TGAGATCAGTCAGAATAACTCGTT.....	24	2	1	10.00	10	10	0	0	0	0	0
.....TGAGATCAGTCAGAATAACTT.....	21	1	1	8.00	8	8	0	0	0	0	0
.....AGATCAGTCAGAATAACTCG.....	20	0	1	8.00	8	7	1	0	0	0	0
.....TGAGATCAGTCAGAATAACA.....	20	1	1	8.00	8	8	0	0	0	0	0
.....TGAGATCAGTCAGAATAACTAA.....	22	2	1	7.00	7	7	0	0	0	0	0
.....TGAGATCAGTCAGAATAACTAAA.....	23	3	1	6.00	6	6	0	0	0	0	0
.....CCTTCACGATTGGGCTGCG.....	19	0	1	6.00	6	1	2	2	1	0	0
.....AGTTATTCTTGCTGTTGTCT.....	20	0	1	6.00	6	6	0	0	0	0	0
.....TGAGATCAGTCAGAATAAAA.....	20	2	2	5.50	11	11	0	0	0	0	0
.....AGATCAGTCAGAATAACTCGC.....	21	0	1	5.00	5	5	0	0	0	0	0
.....TGAGATCAGTCAGAATAACTCCA.....	23	2	1	4.00	4	4	0	0	0	0	0
.....AGTTATTCTTGCTGTTGTC.....	19	0	1	3.00	3	3	0	0	0	0	0
.....AGATCAGTCAGAATAACTCGT.....	21	1	1	3.00	3	3	0	0	0	0	0
.....GAGTTATTCTTGCTGTTGTCT.....	21	0	1	3.00	3	3	0	0	0	0	0
.....AGATCAGTCAGAATAACTCGTT.....	22	2	1	2.00	2	2	0	0	0	0	0
.....TGAGATCAGTCAGAATAACTCTA.....	23	2	1	2.00	2	2	0	0	0	0	0
.....AGTTATTCTTGCTGTTGTCTC.....	21	0	1	2.00	2	2	0	0	0	0	0
.....TGAGATCAGTCAGAATAACTCTT.....	23	2	1	2.00	2	2	0	0	0	0	0
.....TGAGATCAGTCAGAATAACTCGTCA.....	25	3	1	2.00	2	2	0	0	0	0	0
.....AGATCAGTCAGAATAACTCGTC.....	22	2	1	2.00	2	2	0	0	0	0	0
.....TGAGATCAGTCAGAATAACTAT.....	22	2	1	2.00	2	2	0	0	0	0	0
.....AGTTATTCTTGCTGTTGTCC.....	20	1	1	2.00	2	2	0	0	0	0	0
.....TTAGATATCGTTCTGCTTGAA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GAGATCAGTCAGAATAACTCGT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TATTCTTGCTGTTGTCTCATC.....	21	0	1	1.00	1	0	0	1	0	0	0
.....TGAGATCAGTCAGAATAACTAC.....	22	2	1	1.00	1	1	0	0	0	0	0
.....CTTCACGATTGGGCTGCG.....	18	0	1	1.00	1	0	0	1	0	0	0
.....TGAGATCAGTCAGAATAACTCGG.....	23	1	1	1.00	1	1	0	0	0	0	0
.....GATCAGTCAGAATAACTCA.....	19	1	1	1.00	1	0	0	1	0	0	0
.....TGAGATCAGTCAGAATAACC.....	20	1	1	1.00	1	1	0	0	0	0	0
.....GAGATCAGTCAGAATAACTCA.....	21	1	1	1.00	1	0	1	0	0	0	0
.....GGATGAGATCAGTCAGAATAACTCG.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TGAGATCAGTCAGAATAACTCTTT.....	24	3	1	1.00	1	1	0	0	0	0	0
.....GAGTTATTCTTGCTGTTGTCTC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TGAGATCAGTCAGAATAACTCGCT.....	24	1	1	1.00	1	0	0	1	0	0	0
.....AGTTATTCTTGCTGTTGTCTCAT.....	23	0	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

CGGATCAATTCTAATACACCTTATTGAGTCGGGAAGTGCTAACCCGACGCTCAATAAGAACGACAACAGAGTAGAATCTATAGCAAGACGAACTTCCTACTCTAGTCAGTCTTATTGAGCGTCGAGTTAACTATTCGTTGTTCTAAAAAAATTTTATATATATTTTAAATA	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head	V049 head	M060 embryo
**********..(((((((((((((((((((((((.((((..((((((((((((((.....))))).....)))))))))))))).))))))))))))))))))))....**********										
.....GGTAGAATCTATAGCAAGA.....	19	1	1	33.00	33	3	30	0	0	0
.....GGTAGAATCTATAGCAAG.....	18	1	1	18.00	18	0	16	0	2	0
.....GTAGAATCTATAGCAAGA.....	18	0	1	6.00	6	0	6	0	0	0
.....TGGTAGAATCTATAGCAAG.....	19	2	1	1.00	1	1	0	0	0	0
.....TGAGTAGAATCTATAGCAAG.....	20	1	1	1.00	1	1	0	0	0	0
.....ATGAGTAGAATCTATAGCAAG.....	21	2	1	1.00	1	1	0	0	0	0
.....TTGGTAGAATCTATAGCAAG.....	20	3	4	0.25	1	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:6630077-6630247 +	dmo_34	GCCTAGTTAAGATTATGTGGAATAACTCAGCCCTTCACGATTGGGCTGCGAGTTATTCTTGCTGTTGTCTCATCTTAGATATCGTTCTGCTTGAAGGATGAGATCAGTCAGAATAACTCGCAGCTCAATTGATAAGCAAC----------AAGATTTTTTTAAAATATATATAAAATTTAT
droVir3	scaffold_12855:6282867-6283021 +	dvi_14	G----------ATTGGTTTGTGAATTGTTCTTGCTGCGTCTCATGTTACATTTGGTTC---TTGCTCGATGAGATCAGTCAGAACAATTCGTAACTCAGTCCAAAATCGAGCTTGTTTCTATTTAACTGGTTTACTGCGATTTACCTGGAAGATATACACATATTTAT

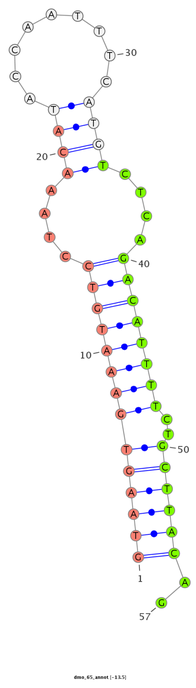
Generated: 09/08/2015 at 08:02 PM

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

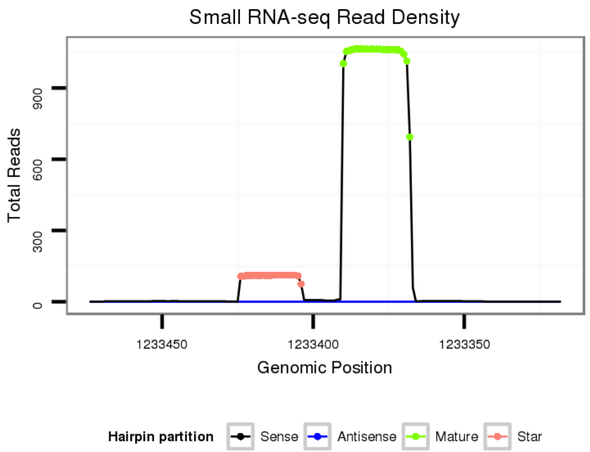
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_65	**scaffold_6328:1233368-1233424 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

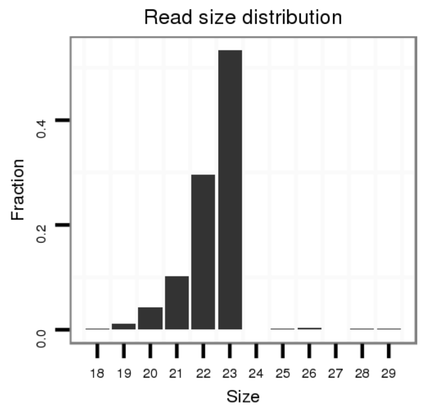
Legend: mature star mismatch in alignment mismatch in read

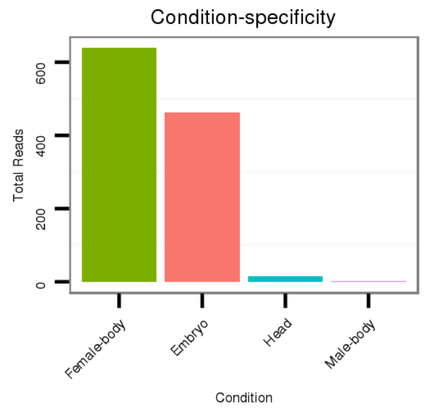
Predicted structure

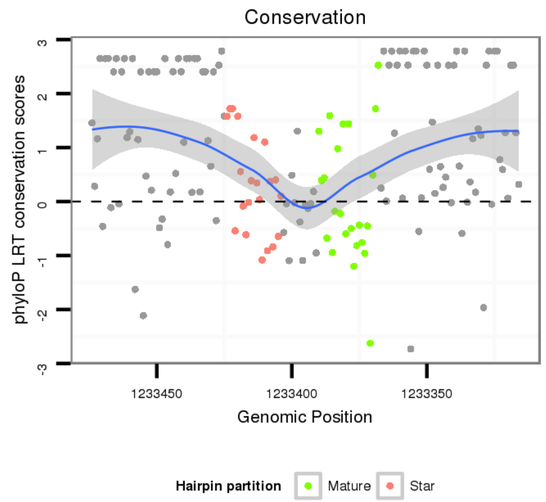


Show Alternate Folds









Flybase annnotation

intron [DmojGI16206-in]; CDS [DmojGI16206-cds]; CDS [DmojGI16206-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATGTCATACATCAGTTCTCATCGCGTTTGCGCTGCAAGTTCGCCTCGCAGGTAAGTGAAATGTCCTAAACATACCAATTTCATGTCTCAGACATTTTCTGCTTACAGATCCAAGAGTCGAAGATGATGGCCACACAGCTGAGCACAGATTATAGGGG **********(((((((((((((....((((.....))))....))))))))).))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V041 embryo	V056 head	V049 head	V110 male body
.....TCTCAGACATTTTCTGCTTACAGT.....	24	1	1	1789.00	1789	942	374	400	33	22	18
.....TCTCAGACATTTTCTGCTTACAG.....	23	0	1	597.00	597	230	346	19	2	0	0
.....TCTCAGACATTTTCTGCTTACA.....	22	0	1	300.00	300	90	201	3	3	3	0
.....TCTCAGACATTTTCTGCTTACAGC.....	24	1	1	274.00	274	256	16	1	1	0	0
.....CTCAGACATTTTCTGCTTACAGT.....	23	1	1	71.00	71	19	46	4	0	0	2
.....GTAAGTGAAATGTCCTAAACA.....	21	0	1	68.00	68	48	4	16	0	0	0
.....TCTCAGACATTTTCTGCTTACAGA.....	24	0	1	52.00	52	18	19	15	0	0	0
.....GTAAGTGAAATGTCCTAAAC.....	20	0	1	33.00	33	29	0	1	1	0	2
.....TCTCAGACATTTTCTGCTTACAGTC.....	25	2	1	31.00	31	15	10	1	2	1	2
.....CTCAGACATTTTCTGCTTACAG.....	22	0	1	30.00	30	1	29	0	0	0	0
.....TCTCAGACATTTTCTGCTTAC.....	21	0	1	27.00	27	12	15	0	0	0	0
.....TCTCAGACATTTTCTGCTTACACT.....	24	2	1	20.00	20	16	3	0	0	1	0
.....CTCAGACATTTTCTGCTTACA.....	21	0	1	17.00	17	1	16	0	0	0	0
.....TCTCAGACATTTTCTGCTTACAC.....	23	1	1	16.00	16	14	2	0	0	0	0
.....TCTCAGACATTTTCTGCTTACAGTAA.....	26	3	1	16.00	16	12	4	0	0	0	0
.....TCTCAGACATTTTCTGCTTACAGTA.....	25	2	1	14.00	14	11	2	1	0	0	0
.....TCTCAGACATTTTCTGCTTACACC.....	24	2	1	12.00	12	12	0	0	0	0	0
.....TCTCAGACATTTTCTGCTTA.....	20	0	1	11.00	11	3	4	0	0	4	0
.....CAGACATTTTCTGCTTACAGT.....	21	1	1	9.00	9	8	1	0	0	0	0
.....TCAGACATTTTCTGCTTACAGT.....	22	1	1	9.00	9	3	3	3	0	0	0
.....AGACATTTTCTGCTTACAGT.....	20	1	1	8.00	8	2	2	4	0	0	0
.....TCTCAGACATTTTCTGCTTACAA.....	23	1	1	7.00	7	0	7	0	0	0	0
.....TCTCAGACATTTTCTGCTTACATT.....	24	2	1	6.00	6	4	0	1	0	1	0
.....TCTCAGACATTTTCTGCTT.....	19	0	1	5.00	5	0	2	1	1	1	0
.....CTCAGACATTTTCTGCTTACAGC.....	23	1	1	4.00	4	3	1	0	0	0	0
.....GACATTTTCTGCTTACAGT.....	19	1	1	4.00	4	3	0	0	0	1	0
.....CTCAGACATTTTCTGCTTACAGA.....	23	0	1	3.00	3	0	3	0	0	0	0
.....GTAAGTGAAATGTCCTAAA.....	19	0	1	3.00	3	0	2	0	1	0	0
.....TCTCAGACATTTTCTGCTTACAGAA.....	25	1	1	3.00	3	2	1	0	0	0	0
.....AGACATTTTCTGCTTACAGC.....	20	1	1	3.00	3	2	1	0	0	0	0
.....TCTCAGACATTTTCTGCTTACAGG.....	24	1	1	3.00	3	2	1	0	0	0	0
.....AGACATTTTCTGCTTACAG.....	19	0	1	3.00	3	0	3	0	0	0	0
.....TGTCTCAGACATTTTCTGCTTACAG.....	25	0	1	2.00	2	2	0	0	0	0	0
.....TACCAATTTCATGTCTCAGACATTTT.....	26	0	1	2.00	2	2	0	0	0	0	0
.....CTCAGACATTTTCTGCTTACAGTA.....	24	2	1	2.00	2	0	2	0	0	0	0
.....TCTCAGACATTTTCTGCTTC.....	20	1	1	2.00	2	0	2	0	0	0	0
.....TCTCAGACATTTTCTGCTTACAT.....	23	1	1	2.00	2	2	0	0	0	0	0
.....TCAGACATTTTCTGCTTACA.....	20	0	1	2.00	2	0	2	0	0	0	0
.....TCTCAGACATTTTCTGCTTACAGAAA.....	26	2	1	2.00	2	0	2	0	0	0	0
.....TCAGACATTTTCTGCTTACAG.....	21	0	1	1.00	2	1	0	0	0	0	1
.....ATACATCAGTTCTCATCGCGT.....	21	0	1	1.00	1	0	0	0	0	0	1
.....TCTCAGACATTTTCTGCTTACAGCC.....	25	2	1	1.00	1	1	0	0	0	0	0
.....ATACATCAGTTCTCATCGCGTTTGC.....	25	0	1	1.00	1	0	1	0	0	0	0
.....CAGACATTTTCTGCTTACACT.....	21	2	1	1.00	1	1	0	0	0	0	0
.....AAGTGAAATGTCCTAAACA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....GATCCAAGAGTCGAAGAT.....	18	0	1	1.00	1	0	1	0	0	0	0
.....TCTCAGACATTTTCTGCT.....	18	0	1	1.00	1	0	1	0	0	0	0
.....GTAAGTGAAATGTCCTAAACG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....CTCAGACATTTTCTGCTTACAGAA.....	24	1	1	1.00	1	1	0	0	0	0	0
.....AGATCCAAGAGTCGAAGATGATGGCC.....	26	0	1	1.00	1	0	0	0	0	0	1
.....GTCCTAAACATACCAATTTCATGTCTCAG.....	29	0	1	1.00	1	0	1	0	0	0	0
.....TCTCAGACATTTTCTGCTTT.....	20	1	1	1.00	1	0	1	0	0	0	0
.....GTCTCAGACATTTTCTGCTTA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....AAGTGAAATGTCCTAAAC.....	18	0	1	1.00	1	1	0	0	0	0	0
.....CAAGAGTCGAAGATGATGGCCA.....	22	0	1	1.00	1	0	0	0	0	0	1
.....GTAAGTGAAATGTCCTAAACAT.....	22	0	1	1.00	1	0	1	0	0	0	0
.....TGCGCTGCAAGTTCGCCTC.....	19	0	1	1.00	1	0	1	0	0	0	0
.....AAGTGAAATGTCCTAAACATACCAAT.....	26	0	1	1.00	1	0	1	0	0	0	0
.....ATTTCATGTCTCAGACATTTTCTGCTTAC.....	29	0	1	1.00	1	0	1	0	0	0	0
.....CAGACATTTTCTGCTTACA.....	19	0	1	1.00	1	0	1	0	0	0	0
.....CTCAGACATTTTCTGCTTAC.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TCTCAGACATTTTCTGCTTACTT.....	23	2	1	1.00	1	1	0	0	0	0	0
.....ATTTCATGTCTCAGACATTTTCTGCTTA.....	28	0	1	1.00	1	0	1	0	0	0	0
.....CAGACATTTTCTGCTTACAG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TGTCTCAGACATTTTCTGCTTACA.....	24	0	1	1.00	1	0	1	0	0	0	0
.....CAGACATTTTCTGCTTACAGA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TGTCTCAGACATTTTCTGCTTACAGA.....	26	0	1	1.00	1	1	0	0	0	0	0
.....TCTCAGACATTTTCTGCTTACATTC.....	25	3	1	1.00	1	0	0	0	0	0	1
.....GTAAGTGAAATGTCCTAAACATACCA.....	26	0	1	1.00	1	0	1	0	0	0	0
.....GTAAGTGAAATGTCCTAAACATACCAAT.....	28	0	1	1.00	1	0	1	0	0	0	0
.....CAGACATTTTCTGCTTAC.....	18	0	1	1.00	1	0	1	0	0	0	0
.....TCTCAGACATTTTCTGCTTACATC.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TCTCAGACATTTTCTGCTTACC.....	22	1	1	1.00	1	1	0	0	0	0	0
.....CGCGTTTGCGCTGCAAGTTCGCCTCGCA.....	28	0	1	1.00	1	0	1	0	0	0	0
.....TAAGTGAAATGTCCTAAACATACCA.....	25	0	1	1.00	1	0	1	0	0	0	0
.....AGACATTTTCTGCTTACACC.....	20	2	2	0.50	1	1	0	0	0	0	0
.....ACATTTTCTGCTTACAGG.....	18	1	2	0.50	1	1	0	0	0	0	0

Anti-sense strand reads

TACAGTATGTAGTCAAGAGTAGCGCAAACGCGACGTTCAAGCGGAGCGTCCATTCACTTTACAGGATTTGTATGGTTAAAGTACAGAGTCTGTAAAAGACGAATGTCTAGGTTCTCAGCTTCTACTACCGGTGTGTCGACTCGTGTCTAATATCCCC **********(((((((((((((....((((.....))))....))))))))).))))))..**********	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_6328:1233316-1233474 -	dmo_65	ATGTCATACATCAGTTCTCATCGCGTTTGCGCTGCAAGTTCGCCTCGCAGGTAAGTGA----------A-ATGTCC----TAA-ACA--TACCA--------------------ATTTCATGT---CTCA----------------GACATTTTCT-GCTTACAGATCCAAGAGTCGAAGATGATGGCCACACAGCTGAGCACAGATTATAGGGGCA
droVir3	scaffold_13042:2338545-2338712 +		ATGTTATACATCAGTTCTCGTCGCGTTTAGGCTGCAAATTCGCCTCCAGGTATGTGG----------C-ATGTGC----AAC-ATATGCAACGACTTTTCATTTTGCAT----------------TGTTTC-TCTTACAGATTCAGGAGTCCAAAATGATGGCCACACAGCTGAGCACAGACTATCGGGGCA
droGri2	scaffold_15203:5171567-5171624 +		TT----------GCA--GCA----------GCA----------GCA----------GATCCAGACTCGAAAATGTGGCCACACAGATGAGCACAGATTATCGGGGCA
droWil2	scf2_1100000004909:9861649-9861822 -		ATGTCATACATCAGTTTTCTCCAGTTTTAGGCTGCAAATTTGCCTCGCAGGTAAGTTT----------AGATCCCC----AAGAACA--AACCA----------------AAAAAAGATTTTATTAA--CCTGTTTTT-------TCTTTTCGGATTAATTAGATCCAGGATTCCAAGATGGTCGCTTCACAGTTGACCACCGATTATCGGTGGCG
dp5	XL_group1:11651723-11651896 +		ATGTCATTCACCAGTTCTCGCCGCCGCGTTCGGCTGCAAGTTTGCCTCGCAGGTAAGTCTTTAGAGTGGGTTA-ATGCGG----TGGAATT--TGGCA----------------GAATTAGTCT---CTTA----------------TCATTTGGAATGTTGAGGTCCAGGACTCGAAGATGTGGCCTTCACAGTTGACAACTGATTATCGGTGGCG
droPer2	scaffold_14:1114287-1114460 +		ATGTCATTCACCAGTTCTCGCCGCGCGTTCGGCTGCAAGTTTGCCTCGCAGGTAAGTCTTTAGAGTAGGTTA-ATGCGG----TGGAATT--TAGCA----------------GAATCAGTCT---CTTA----------------TCATTTGGAATGTTACAGGTCCAGGACTCGAAATGTGGCCTTCACAGTTGACAAGTGATTATCGGTGGCG
droAna3	scaffold_13117:1702075-1702240 -		ATGTCATTCACCAGTTCTCGCCGCGTATCCGCTGCAAGTTTGCCTCGCAGGTAGGTGG----------AGG-C---TACCTAT-TG-GGCCCAA----------------CTGG---TTACTAA--CACTGTTCTACTTTAACG--------TGGCCAGGTCCAGGAGTCTAAGATGGTGGCCTTCACAGCTGACGACGACTACAAGGGCA
droBip1	scf7180000396425:415190-415355 +		ATGTCATTCACCAGTTATCGCCGCGTATCCGCTGCAAGTTTGCCTCGCAGGTAGGTGG----------AGG-C---CACCAAT-TG-GCGCCAA----------------ATG---TTACTAA--CACGGTTCTTCTCTAATG--------CCGGCAGGTCCAGGAGTCTAAGATGGTGGCCTGCAGCTGACGACGACTACAAGGGCA
droKik1	scf7180000302344:494063-494235 +		ATGTCATTCATCAGTTTACGCCGCCGTGTGCGCTGCAAGTTTGCCGCCAGGTATGAGT----------GTG-C---------------AGTGCTTCTCCATACAGCCTACACAGCCTCATAT---CACATCCCTGA----------ATATCGA-ATCCACAGATCCAGGACTCCAAAATGCGTGCCAGCCAAATATCCGACGATTATCGTGGCA
droFic1	scf7180000453955:964633-964734 -		ACGTGATCACCAGTTCACTCGTCGTTGAGGTGCAAGTTCGCCGCCGCA----------GCA----------GCA----------GCA----------GTTCCAGGACTCGAAGCTGGTGGCCACCCAGCTGACGGGCGACTACCGGGGCA
droEle1	scf7180000490484:74939-75040 -		ATGTGATGCATCAGTTGACATCTCGGCTGCGTTGCAAGTTCGCCTCCCA----------GCA----------GCA----------GCA----------GTTCCAGGACTCGAAATTGGTGGCCACCCAGCTGACTGGAGACTATCGGCGGCC
droRho1	scf7180000780108:298363-298464 -		ACGTGATCACCAGTTCACATCTCGACTGCGGTGCAAGTTCGCCTCGCA----------GCA----------GCA----------GCA----------GTTCCAGGACTCGAAGTTGGTGGCCACCCAGCTGACGGGGGACTATCGGGGTC
droBia1	scf7180000302291:218833-218934 +		ACGTTATCATCAGCTAACCTGTCGACTGAGGTGTAAGTTTGCGTCGCA----------GCA----------GCA----------GCA----------GTTCAGGACTCAAAGTTGGTGGTAACCCAGTTTTCGGGGGACTATCGCGGCA
droTak1	scf7180000415401:739858-739959 +		ATGTGATCATCAGCTGACCTGTCGACTGAGGTGTAAGTTTGCCTCGCA----------GCA----------GCA----------GCA----------GTTCCAGGACTCGAAGTTGGTGGCTACCCAGCTGACGGGCGACTATCGGCGGCA
droEug1	scf7180000409581:132282-132383 -		ACGTCATTCATCAGCTAACATCACGACTACGGTGCAAATTTGCCTCACA----------GCA----------GCA----------GCA----------GTTCAGGACTCAAAGCTGGTTGCCACCCAATTGTCGGGTGACTATCGGCGGCA
dm3	chr2R:2113645-2113746 +		ACGTTATCCATCAACTGACCTGTCGTTTGAGGTGCAAGTTTGCCTCGCA----------GCA----------GCA----------GCA----------GTTCCAGGACTCAAAGCTGGTGGCACCCAGCTGACGGGGGACTATCGGCGGCA
droSim2	2r:3111681-3111782 +		ACATTATCCATCAACTGACATCTCGCCTGAGGTGCAAGTTTGCCTCGCA----------GCA----------GCA----------GCA----------GTTCCAGGACTCAAAGTTGGTGGCACCCAGCTCACGGGGGACTATCGGCGGCA
droSec2	scaffold_26:756369-756470 +		ACATTATCCATCAACTGACCTGTCGCCTGAGGTGCAAGTTTGCCTCGCA----------GCA----------GCA----------GCA----------GTTCCAGGACTCAAAGTTGGTGGCACCCAGCTCACGGGGGACTATCGGCGGCA
droYak3	2L:20358616-20358717 -		ACGTTATCATCAACTGACGTGTCGTCTAAGGTGCAAGTTTGCCTCGCA----------GCA----------GCA----------GCA----------GTTCCAGGACTCAAAGTTGGTGGCCACACAGCTCACGGGAGATTATCGCGGCA
droEre2	scaffold_4929:20213668-20213769 -		ACGTTATCCATCAACTGACGTGTCGTCTGAGGTGCAAGTTTGCCTCCCA----------GCA----------GCA----------GCA----------GTTCCAGGACTCGAAATTGGTGGCCACCCAGCTCACGGGAGACTATCGCGGCA

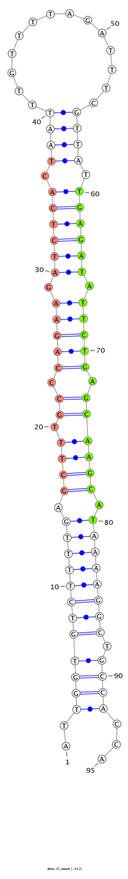
Generated: 09/08/2015 at 10:36 PM

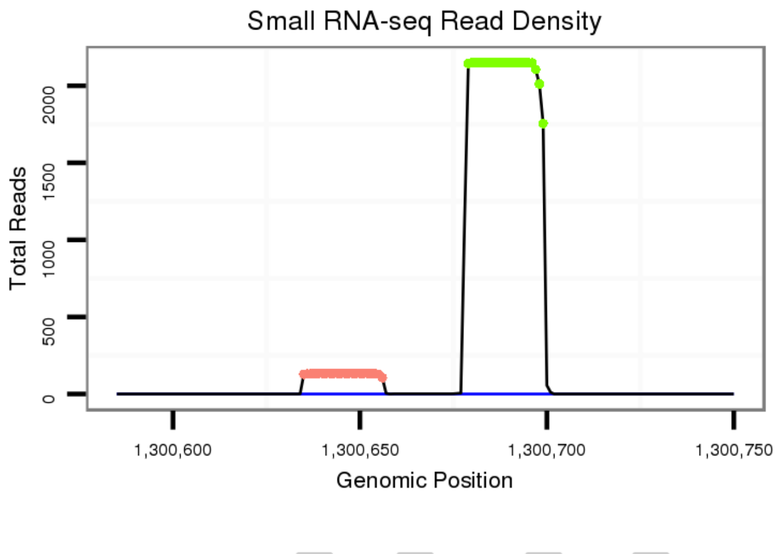
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

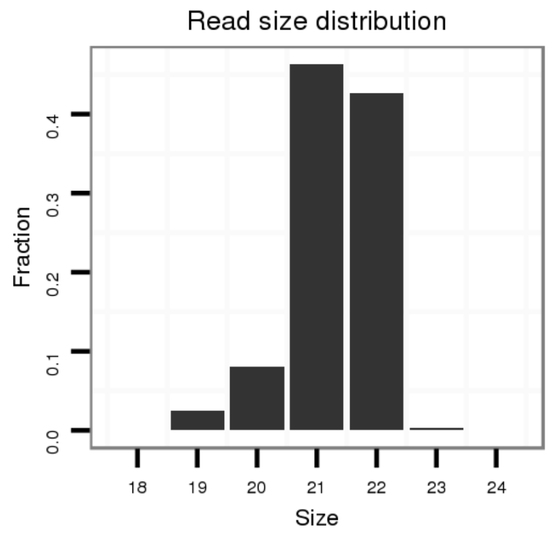
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_37	**scaffold_6308:1300635-1300700 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

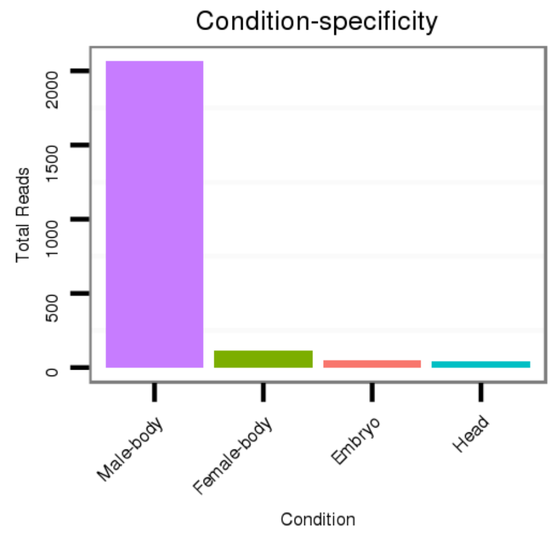
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dmoj\GI10984-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TATATTATTGTGAATCATATATATTTATATATCTAATTGGTGTCTTTTGAGCTTTGCCCAGAAGATCTCACTAATTTGTTTTAGATTTCGTTATTGAGATATTCTGAGCAAGCATAAAAGGCTGCCACCAGCAACAGCTGATACAAAGAGAGTTTTCCCGAGTGGT	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V056 head	V049 head	V041 embryo
..................................**..(((((((((((.((((.((.(((((.((((((.((((((.((((.............)))).))))))..))))))..))))))..))))))..))))))..))))...**.....TGAGATATTCTGAGCAAGCAT.....	21	0	1	864.00	864	796	38	12	15	3	0
.....TTGAGATATTCTGAGCAAGCAT.....	22	0	1	829.00	829	733	43	31	14	5	3
.....TGAGATATTCTGAGCAAGCATT.....	22	1	1	290.00	290	268	13	4	5	0	0
.....TTGAGATATTCTGAGCAAGCA.....	21	0	1	164.00	164	158	5	0	1	0	0
.....TGAGATATTCTGAGCAAGCATTC.....	23	2	1	129.00	129	122	6	0	1	0	0
.....TGAGATATTCTGAGCAAGCATC.....	22	1	1	126.00	126	121	4	0	1	0	0
.....GCTTTGCCCAGAAGATCTCACT.....	22	0	1	98.00	98	90	2	2	2	1	1
.....TGAGATATTCTGAGCAAGCA.....	20	0	1	89.00	89	79	9	0	0	1	0
.....TTGAGATATTCTGAGCAAGC.....	20	0	1	83.00	83	81	0	0	0	2	0
.....TTGAGATATTCTGAGCAAGCATC.....	23	1	1	71.00	71	68	1	1	1	0	0
.....TTGAGATATTCTGAGCAAG.....	19	0	1	42.00	42	41	1	0	0	0	0
.....TGAGATATTCTGAGCAAGCATA.....	22	0	1	40.00	40	36	3	1	0	0	0
.....TGAGATATTCTGAGCAAGCATG.....	22	1	1	30.00	30	26	2	0	1	1	0
.....GCTTTGCCCAGAAGATCTCAC.....	21	0	1	21.00	21	21	0	0	0	0	0
.....TGAGATATTCTGAGCAAGCATTT.....	23	2	1	21.00	21	21	0	0	0	0	0
.....TTGAGATATTCTGAGCAAGCATT.....	23	1	1	19.00	19	18	0	0	1	0	0
.....GCTTTGCCCAGAAGATCTCACTC.....	23	1	1	15.00	15	13	2	0	0	0	0
.....TGAGATATTCTGAGCAAGC.....	19	0	1	12.00	12	10	2	0	0	0	0
.....TTGAGATATTCTGAGCAAGT.....	20	1	1	9.00	9	8	1	0	0	0	0
.....TTGAGATATTCTGAGCAAGCAA.....	22	1	1	9.00	9	9	0	0	0	0	0
.....TGAGATATTCTGAGCAAGCATAA.....	23	0	1	7.00	7	7	0	0	0	0	0
.....TGAGATATTCTGAGCAAGCAC.....	21	1	1	6.00	6	3	0	3	0	0	0
.....TGAGATATTCTGAGCAAGCAA.....	21	1	1	6.00	6	6	0	0	0	0	0
.....TGAGATATTCTGAGCAAGCATTCT.....	24	3	1	5.00	5	5	0	0	0	0	0
.....TTGAGATATTCTGAGCAAGCATA.....	23	0	1	5.00	5	5	0	0	0	0	0
.....TTGAGATATTCTGAGCAAGCATTT.....	24	2	1	5.00	5	5	0	0	0	0	0
.....TTGAGATATTCTGAGCAAGCATCT.....	24	2	1	5.00	5	5	0	0	0	0	0
.....TGAGATATTCTGAGCAAGCATTCC.....	24	3	1	5.00	5	5	0	0	0	0	0
.....TGAGATATTCTGAGCAAGCATCC.....	23	2	1	5.00	5	5	0	0	0	0	0
.....GCTTTGCCCAGAAGATCTCA.....	20	0	1	5.00	5	5	0	0	0	0	0
.....TTGAGATATTCTGAGCAAGCATTC.....	24	2	1	4.00	4	3	1	0	0	0	0
.....GAGATATTCTGAGCAAGCAT.....	20	0	1	4.00	4	1	3	0	0	0	0
.....TTGAGATATTCTGAGCAAGCATAA.....	24	0	1	3.00	3	3	0	0	0	0	0
.....TTGAGATATTCTGAGCAAGCATCC.....	24	2	1	3.00	3	3	0	0	0	0	0
.....TGAGATATTCTGAGCAAGCAG.....	21	1	1	3.00	3	3	0	0	0	0	0
.....TGAGATATTCTGAGCAAGT.....	19	1	1	3.00	3	3	0	0	0	0	0
.....TTGAGATATTCTGAGCAAGA.....	20	1	1	2.00	2	2	0	0	0	0	0
.....GCTTTGCCCAGAAGATCTCACTA.....	23	0	1	2.00	2	2	0	0	0	0	0
.....CTTTGCCCAGAAGATCTCACT.....	21	0	1	2.00	2	0	1	0	0	1	0
.....TGAGATATTCTGAGCAAGCATGT.....	23	2	1	2.00	2	2	0	0	0	0	0
.....TTGAGATATTCTGAGCAAGCATG.....	23	1	1	2.00	2	2	0	0	0	0	0
.....TTTGCCCAGAAGATCTCACTA.....	21	0	1	2.00	2	0	2	0	0	0	0
.....TTGAGATATTCTGAGCAAGCAC.....	22	1	1	2.00	2	1	0	1	0	0	0
.....TGAGATATTCTGAGCAAGCATTTT.....	24	3	1	2.00	2	2	0	0	0	0	0
.....ATTGAGATATTCTGAGCAAGCA.....	22	0	1	2.00	2	1	1	0	0	0	0
.....TGAGATATTCTGAGCAAGCATTG.....	23	2	2	2.00	4	4	0	0	0	0	0
.....TTGAGATATTCTGAGCAAT.....	19	1	1	1.00	1	1	0	0	0	0	0
.....GAGATATTCTGAGCAAGCATC.....	21	1	1	1.00	1	0	0	1	0	0	0
.....AGCTTTGCCCAGAAGATCTCAC.....	22	0	1	1.00	1	0	1	0	0	0	0
.....CTTTGCCCAGAAGATCTCACTA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TGAGATATTCTGAGCAAGCATAT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....GCTTTGCCCAGAAGATCTC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TTGAGATATTCTGAGCAA.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TTTGTTTTAGATTTCGTTAT.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TATTGAGATATTCTGAGCAAGCAT.....	24	0	1	1.00	1	1	0	0	0	0	0
.....GAGATATTCTGAGCAAGCA.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TTGAGATATTCTGAGCAAGCAAT.....	23	2	1	1.00	1	1	0	0	0	0	0
.....TTATTGAGATATTCTGAGCAAG.....	22	0	1	1.00	1	0	1	0	0	0	0
.....TGAGATATTCTGAGCAAGCATAAAAAAA.....	28	3	1	1.00	1	0	1	0	0	0	0
.....TTGCCCAGAAGATCTCACT.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TATTGAGATATTCTGAGCAA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TGAGATATTCTGAGCAAGCAGT.....	22	2	1	1.00	1	1	0	0	0	0	0
.....GATATTCTGAGCAAGCATTC.....	20	2	1	1.00	1	0	1	0	0	0	0
.....GAGATATTCTGAGCAAGCATAA.....	22	0	1	1.00	1	0	1	0	0	0	0
.....AGATATTCTGAGCAAGCAT.....	19	0	1	1.00	1	0	1	0	0	0	0
.....CTTTGCCCAGAAGATCTCACTC.....	22	1	1	1.00	1	1	0	0	0	0	0
.....GCTTTGCCCAGAAGATCTCAA.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TTGAGATATTCTGAGCAAGCAG.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TTGAGATATTCTGAGCAAGCATAT.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TGAGATATTCTGAGCAAGCATAC.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TGAGATATTCTGAGCAAGCACT.....	22	2	2	0.50	1	1	0	0	0	0	0
.....TTGAGATATTCTGAGCAAGTT.....	21	2	2	0.50	1	1	0	0	0	0	0
.....TTGAGATATTCTGAGCAAGCT.....	21	1	2	0.50	1	1	0	0	0	0	0
.....TTGAGATATTCTGAGCAAGCATTG.....	24	2	2	0.50	1	1	0	0	0	0	0
.....TGAGATATTCTGAGCAATT.....	19	2	3	0.33	1	1	0	0	0	0	0
.....TGAGATATTCTGAGCAAAA.....	19	2	7	0.29	2	2	0	0	0	0	0
.....ATATTCTGAGCAAGCATCC.....	19	2	5	0.20	1	1	0	0	0	0	0
.....TGAGATATTCTGAGCATC.....	18	2	8	0.13	1	1	0	0	0	0	0
.....TGAGATATTCTGAGCATT.....	18	2	10	0.10	1	1	0	0	0	0	0
.....TGAGATATTCTGAGCAATGT.....	20	3	11	0.09	1	1	0	0	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1300585-1300750 +	dmo_37	TATATTATTGTGAATCATATATATTTATATATCTAATTGGTGTCTTTTGAGCTTTGCCCAGAAGATCTCACTAATTTGTTTTAGATTTCGTTATTGAGATATTCTGAGCAAGCATAAAAGGCTGCCACCAGCAACAGCTGATACAAAGAGAGTTTTCCCGAGTGGT

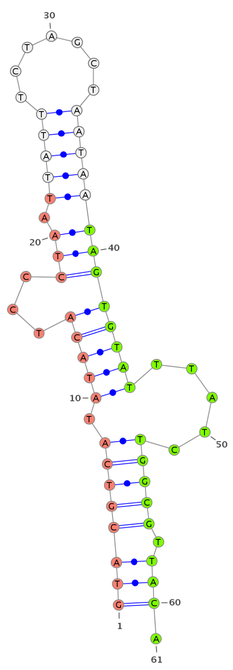
Generated: 09/08/2015 at 08:02 PM

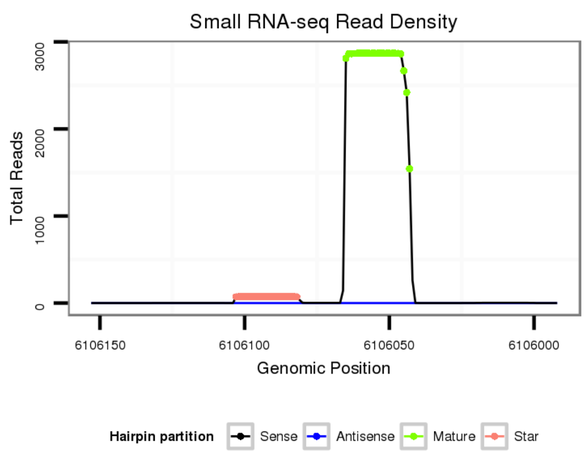
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

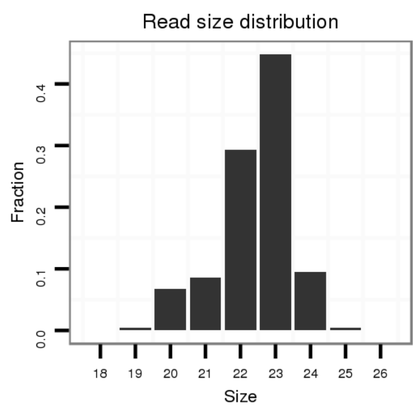
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2373	**scaffold_6680:6106042-6106103 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

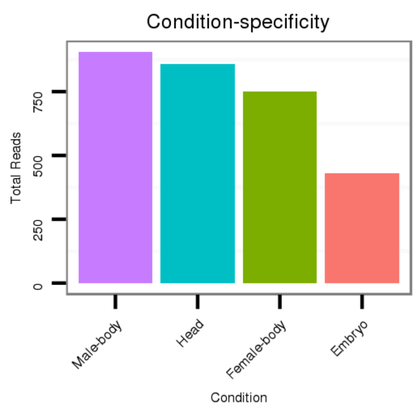
Legend: mature star mismatch in alignment mismatch in read

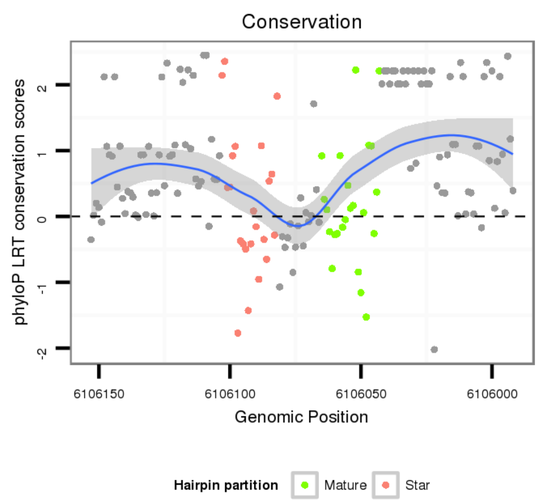
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI12323-in]; CDS [Dmoj\GI12323-cds]; CDS [Dmoj\GI12323-cds]; utr3 [utr3_plus_4620]; utr5 [utr5_plus_8240]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CTGGCGACGCAAAACGCTGCGTACGCCCAACGACAGTCCCACTAAGAATCGTACGTCATATACATCCCTAATTATTTCTAGCTAATAATAGTGTATTTATCTGGCGTTACAGAAGTTCCTGACAAAGAGCTAAGCGGCAAGAGCGCCAATGAGACCGCCAAC **********(((((((((.(((((...(((.(((((.......)))))))))))))).....)))))).)))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head	V049 head	M060 embryo	V041 embryo
.....TAGTGTATTTATCTGGCGTTACA.....	23	0	1	1214.00	1214	423	203	173	145	123	147
.....TAGTGTATTTATCTGGCGTTAC.....	22	0	1	798.00	798	230	233	152	128	47	8
.....TAGTGTATTTATCTGGCGTTACAG.....	24	0	1	232.00	232	61	79	25	14	32	21
.....TAGTGTATTTATCTGGCGTTA.....	21	0	1	232.00	232	77	76	46	33	0	0
.....TAGTGTATTTATCTGGCGTT.....	20	0	1	182.00	182	71	29	45	35	1	1
.....ATAGTGTATTTATCTGGCGTTAC.....	23	0	1	67.00	67	24	8	18	15	2	0
.....ATAGTGTATTTATCTGGCGTTACA.....	24	0	1	45.00	45	10	9	9	2	11	4
.....GTACGTCATATACATCCCTAAT.....	22	0	1	38.00	38	1	29	0	0	7	1
.....GTACGTCATATACATCCCTAATT.....	23	0	1	29.00	29	0	14	0	0	15	0
.....AGTGTATTTATCTGGCGTTACA.....	22	0	1	19.00	19	0	14	2	0	2	1
.....ATAGTGTATTTATCTGGCGTTACAG.....	25	0	1	14.00	14	1	6	2	0	5	0
.....AGTGTATTTATCTGGCGTTA.....	20	0	1	12.00	12	0	12	0	0	0	0
.....TAGTGTATTTATCTGGCGTTACAT.....	24	1	1	12.00	12	4	3	2	1	2	0
.....TAGTGTATTTATCTGGCGTTACT.....	23	1	1	11.00	11	5	1	3	1	1	0
.....TAGTGTATTTATCTGGCGTTAT.....	22	1	1	11.00	11	3	4	3	1	0	0
.....AGTGTATTTATCTGGCGTTAC.....	21	0	1	10.00	10	0	8	1	1	0	0
.....AGTGTATTTATCTGGCGTTACAG.....	23	0	1	8.00	8	0	7	1	0	0	0
.....TAGTGTATTTATCTGGCGTTACAGT.....	25	1	1	7.00	7	2	3	0	0	2	0
.....ATAGTGTATTTATCTGGCGTTA.....	22	0	1	7.00	7	2	2	3	0	0	0
.....ATAGTGTATTTATCTGGCGTT.....	21	0	1	7.00	7	1	2	3	1	0	0
.....TAGTGTATTTATCTGGCGT.....	19	0	1	6.00	6	0	4	1	1	0	0
.....TAGTGTATTTATCTGGCGTTACAGC.....	25	1	1	4.00	4	0	4	0	0	0	0
.....AGTGTATTTATCTGGCGTT.....	19	0	1	4.00	4	1	3	0	0	0	0
.....TAGTGTATTTATCTGGCGTTACAA.....	24	1	1	3.00	3	1	2	0	0	0	0
.....TAGTGTATTTATCTGGCGTTACAGTT.....	26	2	1	3.00	3	2	1	0	0	0	0
.....GTACGTCATATACATCCCTAA.....	21	0	1	3.00	3	0	3	0	0	0	0
.....GTATTTATCTGGCGTTACAG.....	20	0	1	2.00	2	0	1	0	0	1	0
.....TAGTGTATTTATCTGGCGTTT.....	21	1	1	2.00	2	2	0	0	0	0	0
.....TAGTGTATTTATCTGGCGTTACC.....	23	1	1	2.00	2	0	0	0	2	0	0
.....TAGTGTATTTATCTGGCGTTACAC.....	24	1	1	2.00	2	0	0	0	1	1	0
.....TGTATTTATCTGGCGTTACA.....	20	0	1	2.00	2	2	0	0	0	0	0
.....TAGTGTATTTATCTGGCG.....	18	0	1	2.00	2	0	0	0	2	0	0
.....ACGTCATATACATCCCTAAT.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TACGTCATATACATCCCTAATTA.....	23	0	1	1.00	1	0	1	0	0	0	0
.....TATTTCTAGCTAATAATAGTGT.....	22	0	1	1.00	1	0	0	1	0	0	0
.....CGTACGTCATATACATCCCTAATT.....	24	0	1	1.00	1	0	0	0	0	1	0
.....GCTAAGCGGCAAGAGCGCCAATGAGA.....	26	0	1	1.00	1	0	1	0	0	0	0
.....TAGTGTATTTATCTGGCGTTACAGAA.....	26	0	1	1.00	1	1	0	0	0	0	0
.....GTATTTATCTGGCGTTACAT.....	20	1	1	1.00	1	0	1	0	0	0	0
.....ATAGTGTATTTATCTGGCGTTAA.....	23	1	1	1.00	1	0	1	0	0	0	0
.....AATAGTGTATTTATCTGGCGTTACAG.....	26	0	1	1.00	1	0	1	0	0	0	0
.....ATAGTGTATTTATCTGGCGTTAT.....	23	1	1	1.00	1	0	0	1	0	0	0
.....GGCAAGAGCGCCAATGAGA.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TACGTCATATACATCCCTAATT.....	22	0	1	1.00	1	0	1	0	0	0	0
.....ATAGTGTATTTATCTGGCGTTACT.....	24	1	1	1.00	1	0	0	1	0	0	0
.....TAGTGTATTTATCTGGCGTTACAGA.....	25	0	1	1.00	1	0	0	0	0	1	0
.....GTACGTCATATACATCCCTAATTA.....	24	0	1	1.00	1	0	0	0	0	0	1
.....TAGTGTATTTATCTGGCGTTAG.....	22	1	1	1.00	1	0	0	1	0	0	0
.....TGTATTTATCTGGCGTTACAG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TATTTATCTGGCGTTACAG.....	19	0	1	1.00	1	0	1	0	0	0	0
.....GTATTTATCTGGCGTTACA.....	19	0	1	1.00	1	0	0	0	0	1	0
.....TAGTGTATTTATCTGGCGTC.....	20	1	1	1.00	1	0	0	1	0	0	0
.....TAGTGTATTTATCTGGCGTTCT.....	22	2	1	1.00	1	0	0	1	0	0	0
.....TAGTGTATTTATCTGGCGTTTG.....	22	2	1	1.00	1	0	0	1	0	0	0
.....GTGTATTTATCTGGCGTTACAG.....	22	0	1	1.00	1	0	1	0	0	0	0
.....TATTTCTAGCTAATAATAGTGTAT.....	24	0	1	1.00	1	0	1	0	0	0	0
.....ATAGTGTATTTATCTGGCGTTACAGC.....	26	1	1	1.00	1	0	0	0	0	1	0
.....GTACGTCATATACATCCCTAATG.....	23	1	1	1.00	1	0	0	0	0	1	0
.....TAGTGTATTTATCTGGCGTTAA.....	22	1	1	1.00	1	0	1	0	0	0	0
.....TAGTGTATTTATCTGGCGTTACTC.....	24	2	1	1.00	1	1	0	0	0	0	0
.....ATAGTGTATTTATCTGGCGTTACAGT.....	26	1	1	1.00	1	1	0	0	0	0	0
.....TAGTGTATTTATCTGGCGTTAGT.....	23	2	1	1.00	1	0	0	0	1	0	0
.....TAGTGTATTTATCTGGCGTTACG.....	23	1	1	1.00	1	0	0	0	1	0	0
.....TAGTGTATTTATCTGGCGTTACATT.....	25	2	1	1.00	1	0	0	0	1	0	0
.....TACGCCCAACGACAGTCCCACTAAGA.....	26	0	1	1.00	1	0	1	0	0	0	0
.....GCGGCAAGAGCGCCAATGA.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TAGTGTATTTATCTGGCGTG.....	20	1	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

GACCGCTGCGTTTTGCGACGCATGCGGGTTGCTGTCAGGGTGATTCTTAGCATGCAGTATATGTAGGGATTAATAAAGATCGATTATTATCACATAAATAGACCGCAATGTCTTCAAGGACTGTTTCTCGATTCGCCGTTCTCGCGGTTACTCTGGCGGTTG **********(((((((((.(((((...(((.(((((.......)))))))))))))).....)))))).)))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	M060 embryo	V056 head	V049 head	V041 embryo
.....TAGTGTATTTATCTGGCGTTACA.....	23	0	1	1214.00	1214	203	423	123	173	145	147
.....TAGTGTATTTATCTGGCGTTAC.....	22	0	1	798.00	798	233	230	47	152	128	8
.....TAGTGTATTTATCTGGCGTTACAG.....	24	0	1	232.00	232	79	61	32	25	14	21
.....TAGTGTATTTATCTGGCGTTA.....	21	0	1	232.00	232	76	77	0	46	33	0
.....TAGTGTATTTATCTGGCGTT.....	20	0	1	182.00	182	29	71	1	45	35	1
.....ATAGTGTATTTATCTGGCGTTAC.....	23	0	1	67.00	67	8	24	2	18	15	0
.....ATAGTGTATTTATCTGGCGTTACA.....	24	0	1	45.00	45	9	10	11	9	2	4
.....GTACGTCATATACATCCCTAAT.....	22	0	1	38.00	38	29	1	7	0	0	1
.....GTACGTCATATACATCCCTAATT.....	23	0	1	29.00	29	14	0	15	0	0	0
.....AGTGTATTTATCTGGCGTTACA.....	22	0	1	19.00	19	14	0	2	2	0	1
.....ATAGTGTATTTATCTGGCGTTACAG.....	25	0	1	14.00	14	6	1	5	2	0	0
.....AGTGTATTTATCTGGCGTTA.....	20	0	1	12.00	12	12	0	0	0	0	0
.....TAGTGTATTTATCTGGCGTTACAT.....	24	1	1	12.00	12	3	4	2	2	1	0
.....TAGTGTATTTATCTGGCGTTACT.....	23	1	1	11.00	11	1	5	1	3	1	0
.....TAGTGTATTTATCTGGCGTTAT.....	22	1	1	11.00	11	4	3	0	3	1	0
.....AGTGTATTTATCTGGCGTTAC.....	21	0	1	10.00	10	8	0	0	1	1	0
.....AGTGTATTTATCTGGCGTTACAG.....	23	0	1	8.00	8	7	0	0	1	0	0
.....TAGTGTATTTATCTGGCGTTACAGT.....	25	1	1	7.00	7	3	2	2	0	0	0
.....ATAGTGTATTTATCTGGCGTTA.....	22	0	1	7.00	7	2	2	0	3	0	0
.....ATAGTGTATTTATCTGGCGTT.....	21	0	1	7.00	7	2	1	0	3	1	0
.....TAGTGTATTTATCTGGCGT.....	19	0	1	6.00	6	4	0	0	1	1	0
.....TAGTGTATTTATCTGGCGTTACAGC.....	25	1	1	4.00	4	4	0	0	0	0	0
.....AGTGTATTTATCTGGCGTT.....	19	0	1	4.00	4	3	1	0	0	0	0
.....TAGTGTATTTATCTGGCGTTACAA.....	24	1	1	3.00	3	2	1	0	0	0	0
.....TAGTGTATTTATCTGGCGTTACAGTT.....	26	2	1	3.00	3	1	2	0	0	0	0
.....GTACGTCATATACATCCCTAA.....	21	0	1	3.00	3	3	0	0	0	0	0
.....GTATTTATCTGGCGTTACAG.....	20	0	1	2.00	2	1	0	0	0	1	0
.....TAGTGTATTTATCTGGCGTTT.....	21	1	1	2.00	2	0	2	0	0	0	0
.....TAGTGTATTTATCTGGCGTTACC.....	23	1	1	2.00	2	0	0	0	0	2	0
.....TAGTGTATTTATCTGGCGTTACAC.....	24	1	1	2.00	2	0	0	0	0	1	1
.....TGTATTTATCTGGCGTTACA.....	20	0	1	2.00	2	0	2	0	0	0	0
.....TAGTGTATTTATCTGGCG.....	18	0	1	2.00	2	0	0	0	0	2	0
.....ACGTCATATACATCCCTAAT.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TACGTCATATACATCCCTAATTA.....	23	0	1	1.00	1	0	1	0	0	0	0
.....TATTTCTAGCTAATAATAGTGT.....	22	0	1	1.00	1	0	0	0	1	0	0
.....CGTACGTCATATACATCCCTAATT.....	24	0	1	1.00	1	0	0	1	0	0	0
.....GCTAAGCGGCAAGAGCGCCAATGAGA.....	26	0	1	1.00	1	0	1	0	0	0	0
.....TAGTGTATTTATCTGGCGTTACAGAA.....	26	0	1	1.00	1	1	0	0	0	0	0
.....GTATTTATCTGGCGTTACAT.....	20	1	1	1.00	1	0	1	0	0	0	0
.....ATAGTGTATTTATCTGGCGTTAA.....	23	1	1	1.00	1	0	1	0	0	0	0
.....AATAGTGTATTTATCTGGCGTTACAG.....	26	0	1	1.00	1	0	1	0	0	0	0
.....ATAGTGTATTTATCTGGCGTTAT.....	23	1	1	1.00	1	0	0	1	0	0	0
.....GGCAAGAGCGCCAATGAGA.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TACGTCATATACATCCCTAATT.....	22	0	1	1.00	1	0	1	0	0	0	0
.....ATAGTGTATTTATCTGGCGTTACT.....	24	1	1	1.00	1	0	0	1	0	0	0
.....TAGTGTATTTATCTGGCGTTACAGA.....	25	0	1	1.00	1	0	0	0	0	1	0
.....GTACGTCATATACATCCCTAATTA.....	24	0	1	1.00	1	0	0	0	0	0	1
.....TAGTGTATTTATCTGGCGTTAG.....	22	1	1	1.00	1	0	0	1	0	0	0
.....TGTATTTATCTGGCGTTACAG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TATTTATCTGGCGTTACAG.....	19	0	1	1.00	1	0	1	0	0	0	0
.....GTATTTATCTGGCGTTACA.....	19	0	1	1.00	1	0	0	0	0	1	0
.....TAGTGTATTTATCTGGCGTC.....	20	1	1	1.00	1	0	0	1	0	0	0
.....TAGTGTATTTATCTGGCGTTCT.....	22	2	1	1.00	1	0	0	1	0	0	0
.....TAGTGTATTTATCTGGCGTTTG.....	22	2	1	1.00	1	0	0	1	0	0	0
.....GTGTATTTATCTGGCGTTACAG.....	22	0	1	1.00	1	0	1	0	0	0	0
.....TATTTCTAGCTAATAATAGTGTAT.....	24	0	1	1.00	1	0	1	0	0	0	0
.....ATAGTGTATTTATCTGGCGTTACAGC.....	26	1	1	1.00	1	0	0	0	0	1	0
.....GTACGTCATATACATCCCTAATG.....	23	1	1	1.00	1	0	0	0	0	1	0
.....TAGTGTATTTATCTGGCGTTAA.....	22	1	1	1.00	1	0	1	0	0	0	0
.....TAGTGTATTTATCTGGCGTTACTC.....	24	2	1	1.00	1	1	0	0	0	0	0
.....ATAGTGTATTTATCTGGCGTTACAGT.....	26	1	1	1.00	1	1	0	0	0	0	0
.....TAGTGTATTTATCTGGCGTTAGT.....	23	2	1	1.00	1	0	0	0	1	0	0
.....TAGTGTATTTATCTGGCGTTACG.....	23	1	1	1.00	1	0	0	0	1	0	0
.....TAGTGTATTTATCTGGCGTTACATT.....	25	2	1	1.00	1	0	0	0	1	0	0
.....TACGCCCAACGACAGTCCCACTAAGA.....	26	0	1	1.00	1	0	1	0	0	0	0
.....GCGGCAAGAGCGCCAATGA.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TAGTGTATTTATCTGGCGTG.....	20	1	1	1.00	1	0	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6680:6105992-6106153 -	dmo_2373	CTGGCGACGCAAAACGCTGCGTACGCCCAACGACAGTCCCACTAAGAATCGTACGTCATATACATCCCTAATTA----------TTTCTAGCTAATAATAGTG----------TATTTATCT--GGC-----GTTACAGAAGTTCCTGACAAAGAGCTAAGCGGCAAGA---GCGCCAATGAGACCGCCAAC
droVir3	scaffold_13049:9242168-9242328 +		CTGGCGACGCAAAAGTCTGCGCACGCCCAACGACAGTCCCACTAAGAATCGTAAGTAATATGT-CCCCTAATG-----------C--TAAACAGTTAATAATCAAA----------TCTTTATAT---TCA-----TTTGCAGAAGTTCCTGACAAAGAGCTGAGCGGCAAAA---GCGCTAATGAGAGCGCAAAC
droGri2	scaffold_15110:5012800-5012976 +		CTGGCGACGCAGAACGCAGCCACGCCCAACGACAGCCCCACTAAGAATCGTGAGTGACGA--------ATTGACAGTTCGCCAATTTTGGTG-CAGTTACTA---ATC----GAT----AATTGT--TAACTTCTAT-TTGCCTCGCAGAAGTTCCTGATAAAGAGCTGAGTGGCAAGA---GTGCCAATGAGAGCGCCAAC
droWil2	scf2_1100000004837:848631-848791 +		CTGGCGACGCAAAAAGCCACGTACACCCAACGAAAGTCCCACTAAAAATCGTATGTTATG----------C----------CAT---AAT---AGTACTAATTTGTATTAAATCATT---AAATCCTTT-----TTTATAGAAGTTCCTGATAAAGAGCTTAGCAGCAACAAGAGTGTCAATGAGAGCGCCAAC
dp5	XR_group6:1775224-1775279 -		CTGGCGACGCAAGATGGCCCGCGCACCCAACGACAGTCCCACTAAAAATCGTAAGT----------]----------
droPer2	scaffold_9:70017-70072 -		CTGGCGACGCAAGATGGCCCGCGCACCCCACGACAGTCCCACTAAAAATCGTAAGT----------]----------
droAna3	scaffold_13337:16558818-16558971 -		CTGGAGACGCAAGTTGCCACGCCACATCCAACGACAGTCCCACTAAAAATCGTGAGTTTTAG-------TTATTG----TTT-------T--TATATATTAG--ATTATCT----------ACCTGTATTATCC-----TTTTAGAAGTTCCTGATAGAGAGCTCAGCAGCAAATA---GGCTC---AGAGACCGCCAAC
droBip1	scf7180000396641:84105-84260 -		CTGGAGACGCAAGTTGCCACGCAAACTCCAACGAAAGTCCCACTAAAAATCGTAAGAAGAGTAC---TTTTTTTAT----------AAA-AAGACCC-----TTT----------AATATTATTATTTTTTTGAATTTTAGAAGTTCCTGATAGAGAGCTGGTCAGCAATA---GGCTC---TGAGACCGCCAAC
droKik1	scf7180000302486:2753570-2753667 +		TCATA----------TGAATTTAT----------ATT-CTGATAATTCTATATC----------GATTCA--TATCAT-----CCTGCAGAAGTTCCTGATAGAGAGCTTAGCAGCAATA---GGCTC---GGAGACCGCCAAC
droFic1	scf7180000453839:1439753-1439809 +		CTGGCGACGCAAGCTGCCACGCACACCCAACGACAGTCCCACTAAAAATCGTAAGTC----------]----------
droEle1	scf7180000491249:7386135-7386191 -		CTGGCGACGCAAGCTGCCACGCCACACCCAACGACAGTCCCACTAAAAATCGTAAGTC----------]----------
droRho1	scf7180000779672:7654-7714 +		CTGGCGACGCAAGCTGCCACGCCACACCCAACGACAGTCCCACTAAAAATCGTAAGTC----------]----------GCAAT
droBia1	scf7180000302334:299548-299623 -		T----------]----------AATAATCC----------AATACAATTATCAT-----CTTGCAGAAGTTCCTGATAGAGAGCTTAGCAGCAATA---GGCTC---GGAGACCGCCAAC
droTak1	scf7180000414445:350678-350818 +		ACATTGCTTGTAAAGAATGTACATTATCTAAAGG---CT-TTGAAACGA----------ACGATAATTC----------AAT-CCGATAATAATAATCC----------ATTATATTTATCAT-----CTTGCAGAAGTTCCTGATAGAGAGCTCAGCAGCAATA---GGCTC---GGAACAGCCAAC
droEug1	scf7180000409711:1284017-1284135 -		TTGGCGACGCAAGCTGCCACGCCACACCCAACGACAGTCCCACTAAAAATCGTAAGTCTCGG----------]----------TTTTTGGGAGATCACGAAG----------TTAATG---TAGGGT-----GTTTG----------]----------AGAGGGTTTA---GAAA---TGA----GTTAGG
dm3	chr3L:16057292-16057373 +		A----------]----------]------GATAGTAATATTTC----------AATATAATTACCAT-----TTTGCAGAAGTTCCTGATAGAGAGCTCCGCACCAATA---GGCTC---GGAGACCGCCAAC
droSim2	3L:15676301-15676399 +		ACGTTT----------]----------GGTAATCG----------AAT-CAGATAGTAATAATCC----------AATATAATTACAAC-----TTTGCAGAAGTTCCTGATAGAGAGCTCAGCAGCAATA---GGCTC---GGAGACCGCCAAC
droSec2	scaffold_0:8157272-8157370 +		ACGTTT----------]----------GGTAATCG----------AAT-CAGATAGTAATAATCC----------AATATAATTACCAT-----TTTGCAGAAGTTCCTGATAGAGAGCTCAGCAGCAATA---GGCTC---GGAGACCGCCAAC
droYak3	3L:18622676-18622800 +		CAA----------TCCCTTGAAGAGCAGTAATTGGCAA-CGGTCTGTAATCG----------AAT-CAGATAGTAATAATCC----------AATATAATTACCAT-----TTTGCAGAAGTTCCTGATAGAGAGCTTAGCAGCAATA---GGCTC---GGAGACCGCCAAC
droEre2	scaffold_4784:18304148-18304223 +		T----------]----------AATATAATC----------AATATAATTATCAT-----TTTGCAGAAGTTCCTGATAGAGAGCTTAGCAGCAATA---GGCTC---GGAGACCGCCAAC

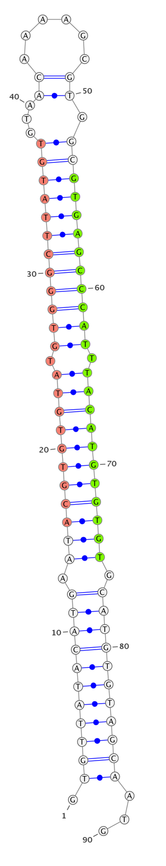
Generated: 09/08/2015 at 07:00 PM

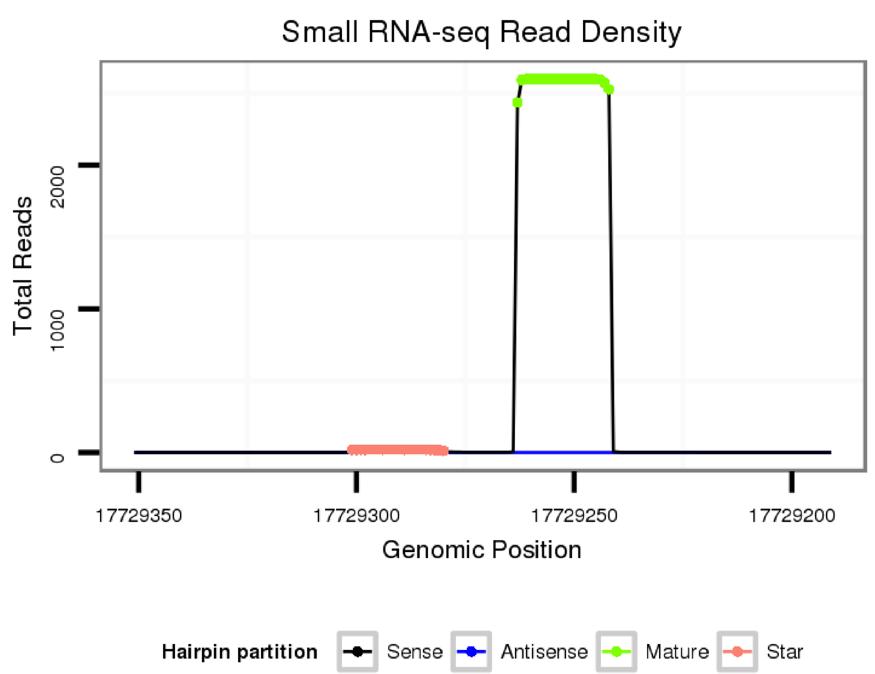
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

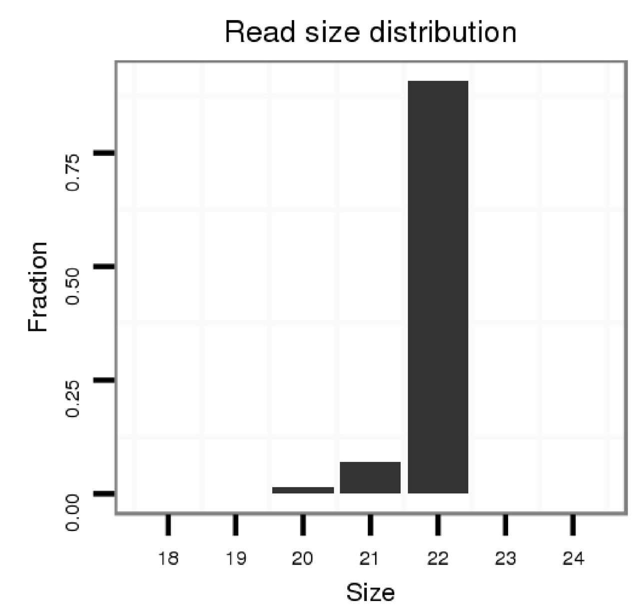
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_40	**scaffold_6680:17729241-17729301 -**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

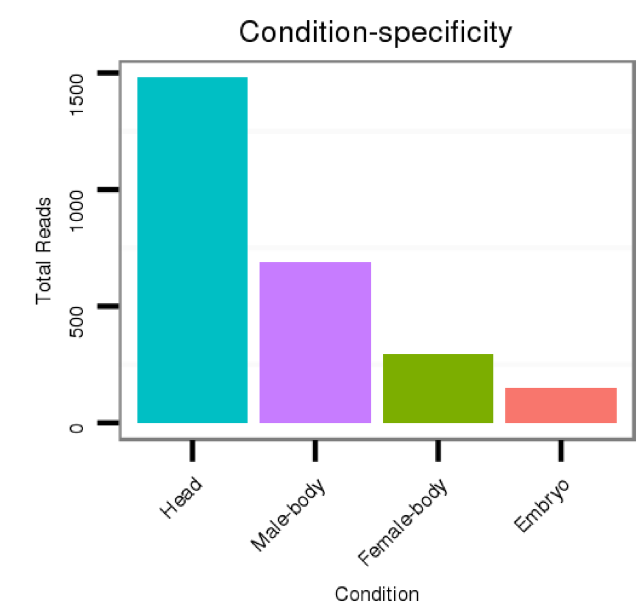
Legend: mature star mismatch in alignment mismatch in read

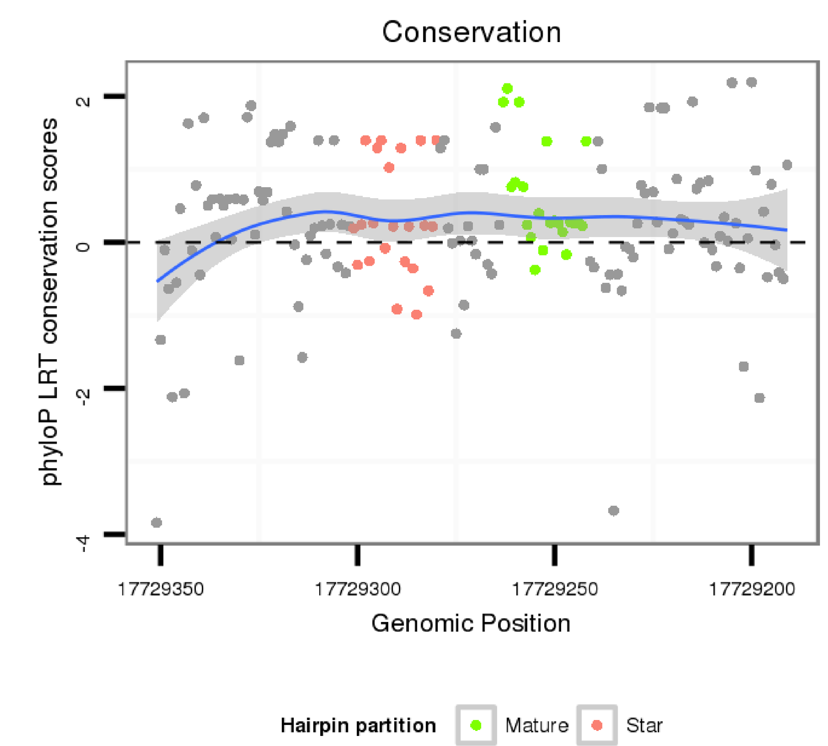
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI11630-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GTTAGTTATATGTGTGTGTGTGGGTGCGTGTGTGTGTGTTATACATGAATACGTGTGTATGTGGGCTTATGTGTAACAAAAGCGTGGCGTGAGCCCATTTACATGTGTGTGCATGTGTAGCAATGGCTGCTGGTACCGCAATAGTTTGCTAAAATTCCGTT **********************************.((((((((((.((((((((((.((((((((((((...((......)).)))))))))))).))))))))))).)))))))))))...***********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head	V110 male body	V049 head	M046 female body	M060 embryo	V041 embryo
GTGAGCCCATTTACATGTGTGT	22	0	1	2369.00	2369	800	641	584	223	70	51
TGAGCCCATTTACATGTGTGT	21	0	1	143.00	143	29	25	19	50	13	7
GTGAGCCCATTTACATGTGTGTC	23	1	1	85.00	85	11	57	5	12	0	0
GTGAGCCCATTTACATGTGTG	21	0	1	36.00	36	13	7	10	4	2	0
GTGAGCCCATTTACATGTGTGTT	23	1	1	36.00	36	7	14	3	9	2	1
GTGAGCCCATTTACATGTGTGC	22	1	1	34.00	34	6	1	4	3	19	1
TGAGCCCATTTACATGTGTGTC	22	1	1	32.00	32	6	12	5	9	0	0
GTGAGCCCATTTACATGTGT	20	0	1	24.00	24	8	7	6	2	0	1
TGAGCCCATTTACATGTGTGTT	22	1	1	21.00	21	7	8	2	4	0	0
GTGAGCCCATTTACATGTGTGA	22	1	1	15.00	15	3	4	1	5	1	1
ACGTGTGTATGTGGGCTTATGT	22	0	1	8.00	8	0	3	1	3	1	0
ACGTGTGTATGTGGGCTTATGTC	23	1	1	7.00	7	0	6	0	1	0	0
TGAGCCCATTTACATGTGTG	20	0	1	7.00	7	0	0	2	4	1	0
GAGCCCATTTACATGTGTGT	20	0	1	6.00	6	0	0	0	5	1	0
ACGTGTGTATGTGGGCTTATG	21	0	1	5.00	5	1	3	0	0	1	0
CGTGAGCCCATTTACATGTGTGT	23	0	1	5.00	5	2	1	2	0	0	0
TGAGCCCATTTACATGTGTGTA	22	1	1	5.00	5	1	2	0	1	1	0
GTGAGCCCATTTACATGTGTGG	22	1	1	4.00	4	1	0	2	0	0	1
TGAGCCCATTTACATGTGTGTGC	23	0	1	3.00	3	0	1	1	1	0	0
GTGAGCCCATTTACATGTGTGTA	23	1	1	3.00	3	2	0	0	0	0	1
GTGAGCCCATTTACATGTGTGTTT	24	2	1	3.00	3	1	1	0	1	0	0
TGAGCCCATTTACATGTGTGC	21	1	1	2.00	2	0	0	0	0	2	0
TGAGCCCATTTACATGTGTGA	21	1	1	2.00	2	0	0	1	1	0	0
TGAGCCCATTTACATGTGTGTGT	23	1	1	2.00	2	0	1	1	0	0	0
TGAGCCCATTTACATGTGTGTTT	23	2	1	2.00	2	1	1	0	0	0	0
ACGTGTGTATGTGGGCTTATGC	22	1	1	2.00	2	0	1	0	0	1	0
GTGAGCCCATTTACATGTGTGTCT	24	2	1	2.00	2	0	1	0	1	0	0
ACGTGTGTATGTGGGCTTA	19	0	1	2.00	2	0	1	0	1	0	0
TGAGCCCATTTACATGTGTGTAA	23	2	1	2.00	2	0	0	0	1	0	1
TGAGCCCATTTACATGTGT	19	0	1	2.00	2	0	1	0	1	0	0
TACGTGTGTATGTGGGCTTATG	22	0	1	2.00	2	0	1	0	1	0	0
GTGTATGTGGGCTTATGTGTAA	22	0	1	1.00	1	0	1	0	0	0	0
GTGAGCCCATTTACATGTGC	20	1	1	1.00	1	0	0	0	0	1	0
ACGTGTGTATGTGGGCTTC	19	1	1	1.00	1	0	0	1	0	0	0
ACGTGTGTATGTGGGCTTATGTGT	24	0	1	1.00	1	0	0	0	1	0	0
CGTGAGCCCATTTACATGTGTGTT	24	1	1	1.00	1	0	0	0	1	0	0
AGCCCATTTACATGTGTGT	19	0	1	1.00	1	0	0	0	0	1	0
GTGAGCCCATTTACATGTGTGTTG	24	2	1	1.00	1	0	1	0	0	0	0
TGAGCCCATTTACATGTGTGTTA	23	2	1	1.00	1	0	0	0	0	1	0
ACGTGTGTATGTGGGCTT	18	0	1	1.00	1	0	0	0	1	0	0
TGTAACAAAAGCGTGGCGTGAGCC	24	0	1	1.00	1	1	0	0	0	0	0
GTGAGCCCATTTACATGTGTGTTTC	25	3	1	1.00	1	0	1	0	0	0	0
GTGAGCCCATTTACATGT	18	0	1	1.00	1	1	0	0	0	0	0
GCATGTGTAGCAATGGCTGC	20	0	1	1.00	1	0	1	0	0	0	0
GAGCCCATTTACATGTGTGTT	21	1	1	1.00	1	0	0	0	1	0	0
GCCCATTTACATGTGTGT	18	0	1	1.00	1	0	0	0	1	0	0
TGAGCCCATTTACATGTG	18	0	1	1.00	1	0	0	0	0	1	0
TGAGCCCATTTACATGTGTGTCT	23	2	1	1.00	1	1	0	0	0	0	0
TGTGTAACAAAAGCGTGG	18	0	1	1.00	1	0	0	0	1	0	0
GTGAGCCCATTTACATGTGTGTTTT	25	3	1	1.00	1	0	1	0	0	0	0
GTGAGCCCATTTACATGTG	19	0	1	1.00	1	0	0	1	0	0	0
TGAGCCCATTTACATGTGTGCC	22	2	1	1.00	1	1	0	0	0	0	0
GAGCCCATTTACATGTGTGTAA	22	2	1	1.00	1	0	0	0	1	0	0
ATACGTGTGTATGTGGGCTTAT	22	0	1	1.00	1	1	0	0	0	0	0
TGAGCCCATTTACATGTGTGTG	22	0	1	1.00	1	0	0	1	0	0	0
GTGAGCCCATTTACATGTGTGTAA	24	2	1	1.00	1	0	0	0	1	0	0
GTGAGCCCATTTACATGTGTC	21	1	1	1.00	1	0	0	1	0	0	0
GTGAGCCCATTTACATGTGCTA	22	3	2	0.50	1	0	0	1	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6680:17729191-17729351 -	dmo_40	GTTAGTTATAT--G----------T-------------------GTGTGTGTGGGTGCGTGTGTGTGTG--TTATACATGAATACGTGTGTATGTGGGCTTATGTGTAACA-AAAGCGTGGCGTGAGCC-----------------CATTTACAT------GTGTGTGCATGTGTAGCAATGGC------------TGCTG-GTACCGCAA-TAGTTTGCTAAAATTCCG-TT
droVir3	scaffold_13049:23117616-23117755 -		TCAGCTTTTAT--A--TATGC-AT-GTA----TATGCATGTATGTGTGCGTGCCTGTGTTT-------------ATTGAAAGCGTG---GCGTGAGCT-----------G------TGTATGTGT------ATATGTGTATGTTCTGCAATGGC------------TGCCGGTAACCGCTA-TAGTTTGCTAAAGTGCCG-TT
droGri2	scaffold_15110:18383161-18383346 -		TACGCTTGTAT--G----------T-------------------GTGTGTTTTTGTGTGT-------------ACAGCAAGCATGGCGTGAGACATATACATAAGAGTGT-ATTTGTAAGCATGTATGTGTAAGCAAATATATGTA-A-GCA---------------AA----TATATGTAAGCATGCATGTGT------AAGCTTATATATATTGTAATGGC------------TGCCGTTTACCGCAA-ATTTCTGTTAAATTGCCG-TT
droWil2	scf2_1100000004963:1347390-1347454 +		GTTATCCATGT--G----------T-------------------GTGTGTGTGTGTGTGTGTGTGTG-----TATGTGTGTACGT--GTGTACGTT---TGTGTG---T
dp5	3:662562-662727 -		TT-----G--TGTG----------T-------------------GTTTGTGTGTGTTTGTGTGTGCG--------GC--ATGTACGTATATGAGTGTGT--GTGTGCTTAAGTGTGTGG-AAGTCGTTGG-------TGCTGTT----G------TTATGTGGGCATTGGTGTGTGCATCAGCAGCAGCAGGAGCAGCAGCAGCAGCAGCTTGGCA----------ACTAAAATGCAA-TT
droPer2	scaffold_47:303237-303330 +		AT-----G--TATGC---------------------------ACATACATATGTGTGT-------------ATGCGAAAAGTG---GCGTGAGCC----------------------------------AAGACAGTGATGGC------------CGCTCTTTACCGTTT-GCATTTGACAAACTCCCT-CT
droKik1	scf7180000302441:2804703-2804761 +		G---CGTGAGCT----------------------------------TGCATCGCAATGGC------------TGCCCTTTACCGTTT-GATTATGCCGAATTCAATGTT
droFic1	scf7180000453784:308173-308228 +		G---CGTGAGCT----------------------------------TGACCCGCTATGGC------------TGCCCTTTACCGTTTTGATATTGCAAAAATCCC----
droEle1	scf7180000491255:2441410-2441509 +		AT-----A--CATAC-------AT-ACA----TATATATGTAT------------GTATGC-------------ATGTCAAATGTG---GCGTGAGCT----------------------------------TAAACCGCGATGGC------------TGCCCTTTACCGTTT-GTTTTTTCTTAGCTCCCG-CT
droBia1	scf7180000302402:6167107-6167221 +		TTTAGTTGTGT--G----------T-------------------GTGTGTGTGTGTGTGTGTGTGTGTA--ATGTATGTAAATGTGTGTGT--GGGTGTGTGGGTGTGTGG-GTGTCGG-----------------------------TG---TGCACGTGT-GTTTGTGTAGAATATCTATTG
droTak1	scf7180000415667:133545-133561 -		T--TTGTCAAACCCCCG-CT
droEug1	scf7180000409456:173137-173195 +		G---CGTGAGCT----------------------------------TGAAACACGATGGC------------TGCCCTTTACCGTTT-GTTTTTGTCAAATTCCCGCTT
dm3	chr3L:13987584-13987584 +		G--
droSim2	3L:13659090-13659197 +		TGTGTATATGT--A-----------CATACATATGTACATAT---------------------ATACAACGTATATAAGCAATG---GCGTGAGCT----------------------------------TGAGCCTCGATGGC------------TGCCCTTTACCGTTT-CTTATTGTCAAATTCCCG-CT
droSec2	scaffold_9:1955946-1956072 -		GT-----G--TGTGTGTGTTTA--T-------------------GTGTGTGTGTGTGTGTGTGTGTGTG--TAGTATGTGAGTGTATACGTGTGTGTGTATGTGTGTG-T-GAA---------------TG----CGTGTGTGTGTGTGTGTGTGT------GTGTGTTTATATACAGAGGTGG--
droYak3	3L:14075339-14075451 +		GT-----G--TATAAGTATATA--TACAAATGTACGTACATAT---------------------GTACACAGTATATACGCAATG---GCGTGAGCT----------------------------------TGAACCGCGATGGC------------TGCCCTTTACCGTTT-CTTATTGTTAAATTCCCG-CT
droEre2	scaffold_4784:13979507-13979614 +		TATACGTATAT--A-----------CAATTGTATATAATTAT---------------------GTACGCAGTATATAAGCAATG---GCGTGAGCT----------------------------------TGAGCCTCGATGGC------------TGCCCTTTACCGTTT-CTTATTGCCAAATTCCCG-CT

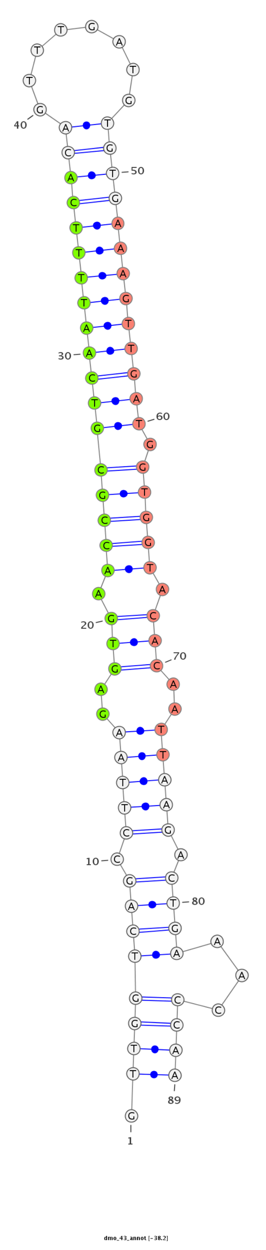
Generated: 09/08/2015 at 07:33 PM

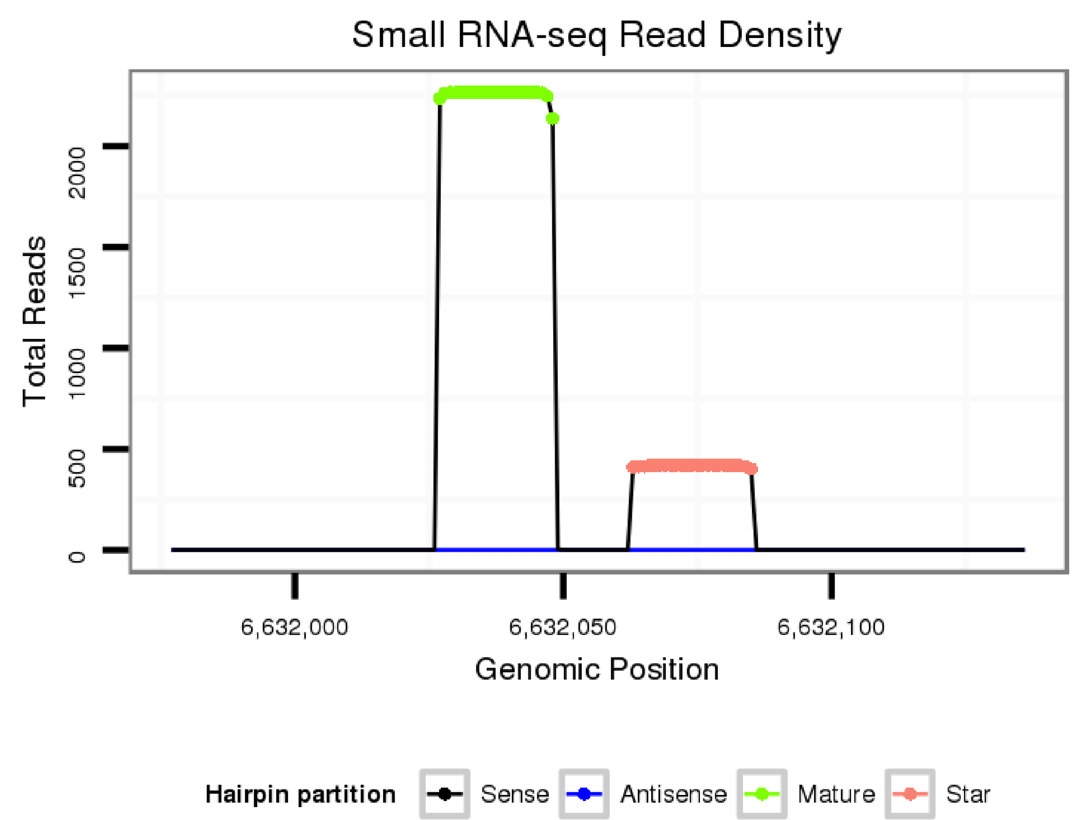
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

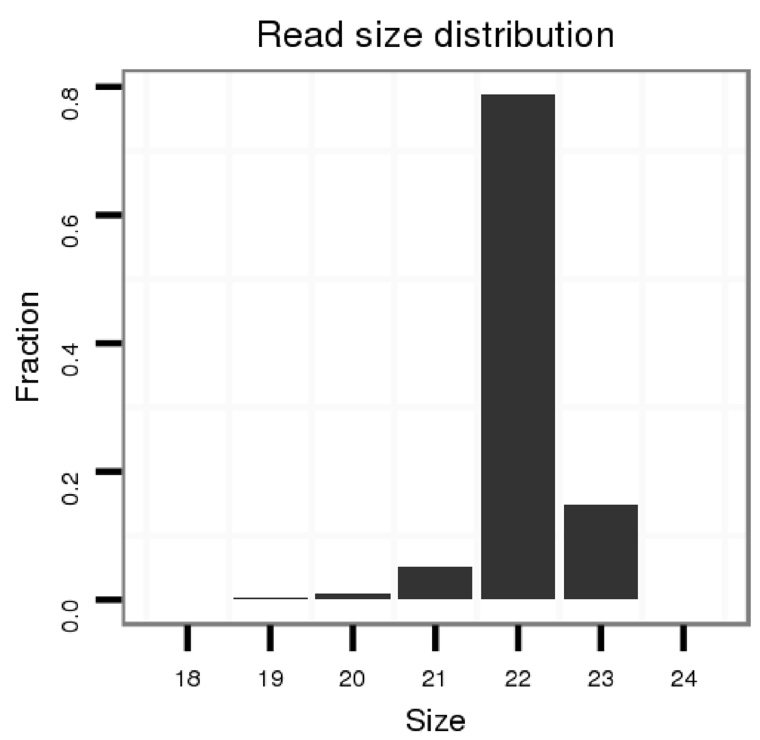
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_43	**scaffold_6540:6632027-6632086 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

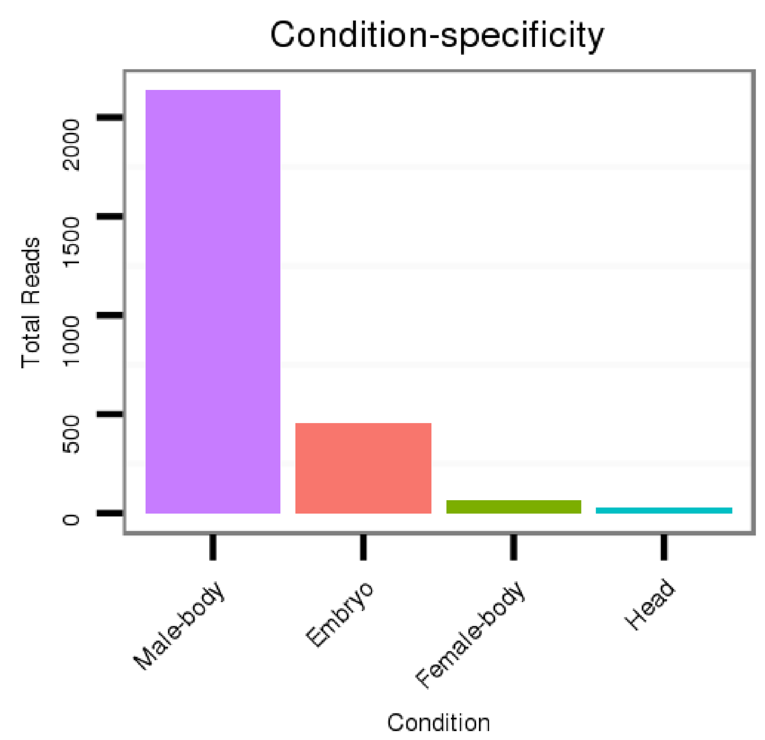
Legend: mature star mismatch in alignment mismatch in read

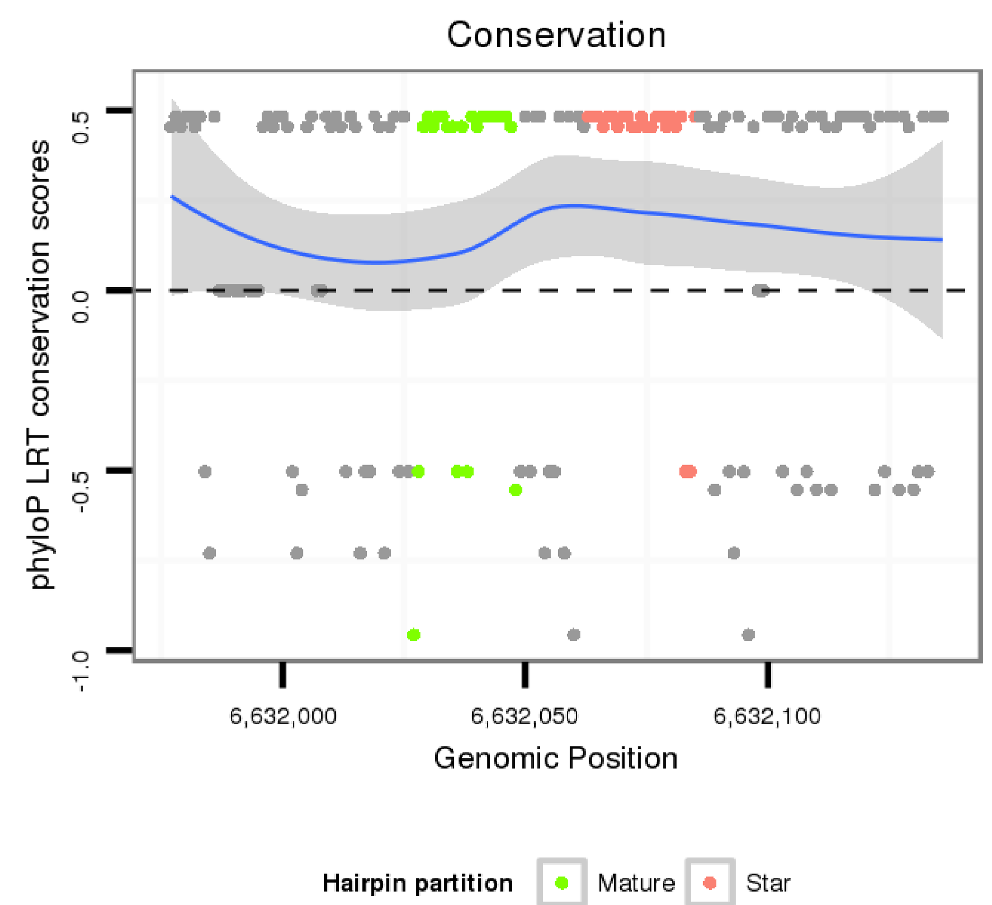
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTGTTGTGCAACGATGTCGGTGTTCAGTGTTCAGTGTTGGTCAGCCTTAAGAGTGAACCGCGTCAATTTTCACAGTTTGATGTGTGAAAGTTGATGGTGGTACACAATTAAGACTGAAACCCAAAAGCATCGTATCTGAAAATACTATAAATCAGTTAAA **********************************.(((((((.(((((..(((.((((((((((((((((((........)))))))))))))).))))).)))..))))).))))...))))***********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M060 embryo	M046 female body	V056 head	V041 embryo	V049 head
....GAGTGAACCGCGTCAATTTTCA..	22	0	1	2103.00	2103	1996	30	33	20	16	8
....AAAGTTGATGGTGGTACACAATT...	23	0	1	393.00	393	1	380	11	0	1	0
....GAGTGAACCGCGTCAATTTTC...	21	0	1	110.00	110	92	7	10	1	0	0
....GAGTGAACCGCGTCAATTTTCAA...	23	1	1	32.00	32	27	0	4	1	0	0
....AGTGAACCGCGTCAATTTTCA..	21	0	1	26.00	26	20	1	5	0	0	0
....GAGTGAACCGCGTCAATTTTCC..	22	1	1	26.00	26	26	0	0	0	0	0
....GAGTGAACCGCGTCAATTTT..	20	0	1	17.00	17	16	0	1	0	0	0
....AAAGTTGATGGTGGTACACAATC...	23	1	1	15.00	15	0	15	0	0	0	0
....GAGTGAACCGCGTCAATTTTCACC..	24	1	1	14.00	14	14	0	0	0	0	0
....AAAGTTGATGGTGGTACACAAT..	22	0	1	12.00	12	0	10	2	0	0	0
....GAGTGAACCGCGTCAATTTTCG..	22	1	1	6.00	6	4	0	0	1	1	0
....GAGTGAACCGCGTCAATTTTCAC...	23	0	1	4.00	4	4	0	0	0	0	0
....GTTGATGGTGGTACACAATT...	20	0	1	4.00	4	0	4	0	0	0	0
....GAGTGAACCGCGTCAATTT...	19	0	1	3.00	3	2	0	1	0	0	0
....AAGTTGATGGTGGTACACAATT...	22	0	1	3.00	3	0	2	1	0	0	0
....GAGTGAACCGCGTCAATTTTCT..	22	1	1	3.00	3	3	0	0	0	0	0
....AAAGTTGATGGTGGTACACAA...	21	0	1	3.00	3	1	1	1	0	0	0
....GTGAACCGCGTCAATTTTCA..	20	0	1	3.00	3	3	0	0	0	0	0
....GAGTGAACCGCGTCAATTTTCAG...	23	1	1	2.00	2	2	0	0	0	0	0
....GAGTGAACCGCGTCAATTTC..	20	1	1	2.00	2	2	0	0	0	0	0
....AAAGTTGATGGTGGTACACA..	20	0	1	2.00	2	0	0	2	0	0	0
....TTGATGGTGGTACACAATT...	19	0	1	2.00	2	0	2	0	0	0	0
....AAAGTTGATGGTGGTACACAT...	21	1	1	1.00	1	0	0	1	0	0	0
....GAGTGAACCGCGTCAATTA...	19	1	1	1.00	1	1	0	0	0	0	0
....GAGTGAACCGCGTCAATTTTCCA...	23	2	1	1.00	1	1	0	0	0	0	0
....GAGTGAACCGCGTCAATTTTCACA..	24	0	1	1.00	1	1	0	0	0	0	0
....AAAGTTGATGGTGGTACACAATG...	23	1	1	1.00	1	0	1	0	0	0	0
....AAAGTTGATGGTGGTACACAATTT..	24	1	1	1.00	1	0	1	0	0	0	0
....GAGTGAACCGCGTCAATTTTCATC..	24	2	1	1.00	1	1	0	0	0	0	0
....GAGTGAACCGCGTCAATTTTCAAC..	24	2	1	1.00	1	1	0	0	0	0	0
....GAACCGCGTCAATTTTCA..	18	0	1	1.00	1	1	0	0	0	0	0
....AAAGTTGATGGTGGTACAC...	19	0	1	1.00	1	0	0	1	0	0	0
....AAAGTTGATGGTGGTACAT...	19	1	1	1.00	1	0	0	0	0	0	1
....GAGTGAACCGCGTCAATTTCA...	21	2	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:6631977-6632136 +	dmo_43	GTGTTGTGCAACGATGTCGGTGTTCAGTGTTCAGTGTTGGTCAGCCTTAAGAGTGAACCGCGTCAATTTTCACAGTTTGATGTGT-------GAAAGTTGATGGTGGTACACAATTAAGACTGAAACCCAAAAGCATCGTATCTG-------AAAATACTATAAATCAGTTAAA
droVir3	scaffold_12855:6284314-6284474 +	dvi_220	GTGTTGTAAA---------GTGTTCGTAGT--AGTGCTGTCTAGACTCAGCGGTGAACCACATCAATTTTCTTAATTGAGTTTCTAAATGCAGAAAGTTGATGGTGGTACACAGCTAAGTCTACAGGC--AAAACAACATTTCAGATAACATAAAATACAACAATTCTATCAAA

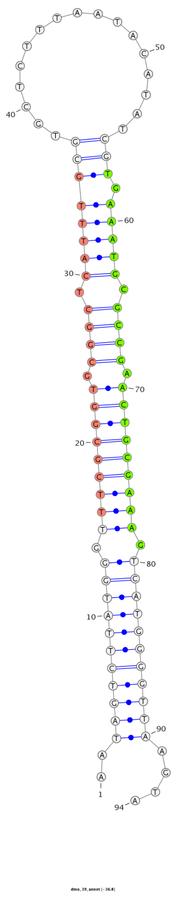
Generated: 09/08/2015 at 08:03 PM

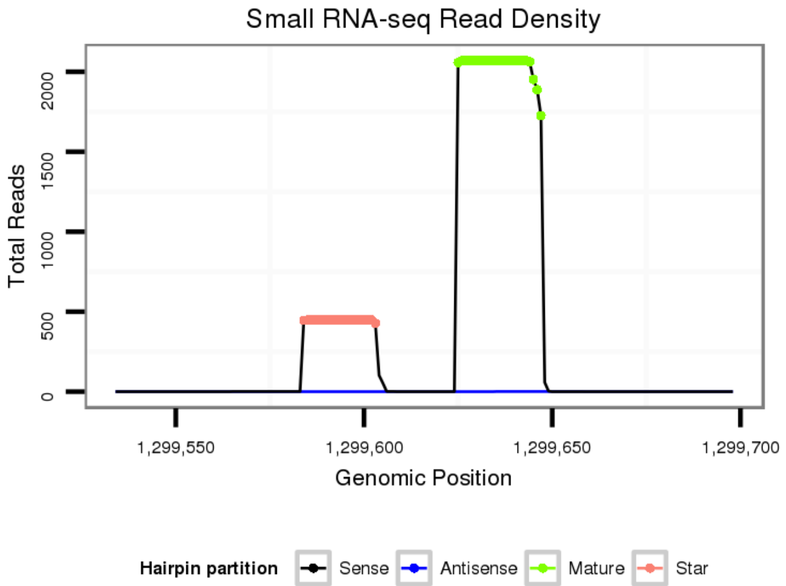
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

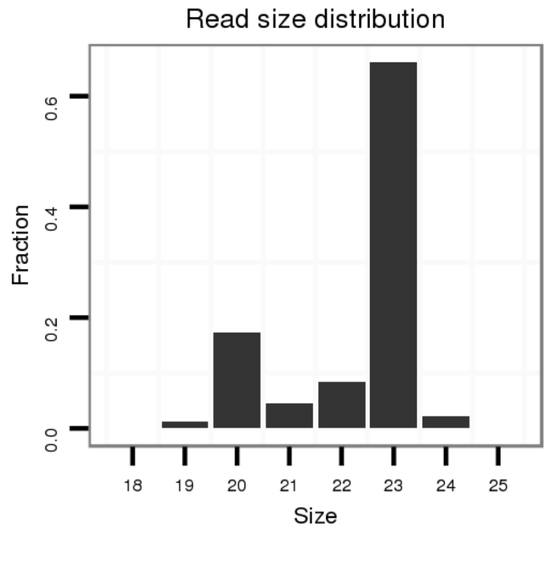
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_39	**scaffold_6308:1299584-1299648 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

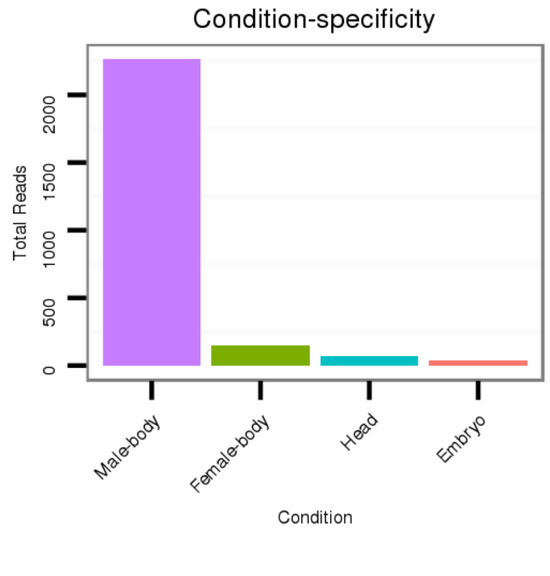
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dmoj\GI10984-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GGAAAATTTCTATAGTGAGATCAATTGACGTTTGGAATAGTCTTATGGGTTTCGCGGTGCGGCTCATTTGCGTGCTCTTTAATACATATCGTGAAATGCGCCGAACTGCGAAAGTCATGGGGTTAAGTAAACAACGTGAATTATCTACATACAAACCAATATAAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head	M060 embryo	V049 head	V041 embryo
**********..(((((((((((.(((((((((.((((.(((((((((.....)))).)))))).))))..)))))))))..)))))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head	M060 embryo	V049 head	V041 embryo
.....TGAAATGCGCCGAACTGCGAAAG.....	23	0	1	1663.00	1663	1598	26	19	13	5	2
.....TTCGCGGTGCGGCTCATTTG.....	20	0	1	325.00	325	249	57	11	0	7	1
.....TGAAATGCGCCGAACTGCGAAA.....	22	0	1	158.00	158	146	9	2	0	1	0
.....TGAAATGCGCCGAACTGCGA.....	20	0	1	109.00	109	92	10	2	0	4	1
.....TGAAATGCGCCGAACTGCGAA.....	21	0	1	62.00	62	55	6	0	0	0	1
.....TGAAATGCGCCGAACTGCGAAAGT.....	24	0	1	54.00	54	53	0	0	1	0	0
.....TTCGCGGTGCGGCTCATTTGCG.....	22	0	1	51.00	51	31	5	4	1	3	7
.....TTCGCGGTGCGGCTCATTTGC.....	21	0	1	48.00	48	17	19	2	6	2	2
.....TGAAATGCGCCGAACTGCGAAAA.....	23	1	1	37.00	37	34	2	1	0	0	0
.....TTCGCGGTGCGGCTCATTT.....	19	0	1	20.00	20	13	4	3	0	0	0
.....TGAAATGCGCCGAACTGCGAAAGA.....	24	1	1	20.00	20	19	1	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAAGC.....	24	1	1	14.00	14	14	0	0	0	0	0
.....TTCGCGGTGCGGCTCATTTGT.....	21	1	1	12.00	12	8	1	1	0	2	0
.....TGAAATGCGCCGAACTGCGAAAT.....	23	1	2	12.00	24	24	0	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAT.....	22	1	1	10.00	10	10	0	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAAGTT.....	25	1	1	8.00	8	8	0	0	0	0	0
.....TGAAATGCGCCGAACTGCG.....	19	0	1	8.00	8	3	1	2	0	1	1
.....TTCGCGGTGCGGCTCATTTT.....	20	1	1	7.00	7	4	2	0	0	1	0
.....TTCGCGGTGCGGCTCATTTGCGC.....	23	1	1	6.00	6	5	0	0	0	1	0
.....TGAAATGCGCCGAACTGCGAAAC.....	23	1	1	6.00	6	5	1	0	0	0	0
.....TTCGCGGTGCGGCTCATTTC.....	20	1	1	5.00	5	4	1	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAAGG.....	24	1	1	4.00	4	4	0	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAAGTA.....	25	1	1	4.00	4	4	0	0	0	0	0
.....GAAATGCGCCGAACTGCGAAA.....	21	0	1	4.00	4	3	1	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAAGTC.....	25	0	1	4.00	4	4	0	0	0	0	0
.....GAAATGCGCCGAACTGCGAAAG.....	22	0	1	4.00	4	0	4	0	0	0	0
.....TTCGCGGTGCGGCTCATTTA.....	20	1	1	4.00	4	3	1	0	0	0	0
.....TTCGCGGTGCGGCTCATTTGA.....	21	1	1	4.00	4	3	0	1	0	0	0
.....TGAAATGCGCCGAACTGCGAAAAA.....	24	2	1	3.00	3	3	0	0	0	0	0
.....TTCGCGGTGCGGCTCATTTGCC.....	22	1	1	3.00	3	2	1	0	0	0	0
.....TGAAATGCGCCGAACTGCGATT.....	22	2	1	3.00	3	3	0	0	0	0	0
.....TGAAATGCGCCGAACTGCGAT.....	21	1	1	3.00	3	3	0	0	0	0	0
.....TTCGCGGTGCGGCTCATTTGCGTC.....	24	1	1	2.00	2	2	0	0	0	0	0
.....GAAATGCGCCGAACTGCGAA.....	20	0	1	2.00	2	0	2	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAAAAA.....	25	3	1	2.00	2	2	0	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAAGCA.....	25	2	1	2.00	2	2	0	0	0	0	0
.....TTCGCGGTGCGGCTCATTC.....	19	1	1	2.00	2	2	0	0	0	0	0
.....GAAATGCGCCGAACTGCGA.....	19	0	1	2.00	2	0	2	0	0	0	0
.....TTCGCGGTGCGGCTCATTC.....	19	1	1	2.00	2	2	0	0	0	0	0
.....GAAATGCGCCGAACTGCGA.....	19	0	1	2.00	2	0	2	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAAAG.....	24	2	1	2.00	2	2	0	0	0	0	0
.....TGAAATGCGCCGAACTGCGAATT.....	23	2	2	2.00	4	4	0	0	0	0	0
.....TCGCGGTGCGGCTCATTT.....	18	0	1	1.00	1	0	1	0	0	0	0
.....TCGCGGTGCGGCTCATTTG.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TTCGCGGTGCGGCTCATTTTTT.....	22	3	1	1.00	1	1	0	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAAGAG.....	25	2	1	1.00	1	1	0	0	0	0	0
.....TTCGCGGTGCGGCTCATTTGCGTGC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAAGATT.....	26	3	1	1.00	1	1	0	0	0	0	0
.....TTCGCGGTGCGGCTCATTTGG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAAGTTCA.....	27	3	1	1.00	1	1	0	0	0	0	0
.....TTCGCGGTGCGGCTCATTTGTA.....	22	2	1	1.00	1	1	0	0	0	0	0
.....TTGGAATAGTCTTATGGGT.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TTCGCGGTGCGGCTCATC.....	18	1	1	1.00	1	1	0	0	0	0	0
.....AATGCGCCGAACTGCGAAAG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TTCGCGGTGCGGCTCATTTAA.....	21	2	1	1.00	1	1	0	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAAGTTC.....	26	2	1	1.00	1	1	0	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAG.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TTCGCGGTGCGGCTCATTTGTC.....	22	2	1	1.00	1	1	0	0	0	0	0
.....TTCGCGGTGCGGCTCATTTTT.....	21	2	1	1.00	1	0	0	1	0	0	0
.....TGAAATGCGCCGAACTGCGAAACG.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TGAAATGCGCCGAACTGCGT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....TTCGCGGTGCGGCTCATTTGCGCC.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TTCGCGGTGCGGCTCATTTGAC.....	22	2	1	1.00	1	1	0	0	0	0	0
.....TCGCGGTGCGGCTCATTTGCG.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TTCGCGGTGCGGCTCATTG.....	19	1	1	1.00	1	1	0	0	0	0	0
.....TTCGCGGTGCGGCTCATTTGCA.....	22	1	1	1.00	1	0	1	0	0	0	0
.....TTCGCGGTGCGGCTCATTTGCGT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TTCGCGGTGCGGCTCATTTGCGA.....	23	1	1	1.00	1	0	1	0	0	0	0
.....TGAAATGCGCCGAACTGCGTTT.....	22	3	2	1.00	2	2	0	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAATA.....	24	2	2	0.50	1	1	0	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAATC.....	24	2	2	0.50	1	1	0	0	0	0	0
.....AAATGCGCCGAACTGCGAA.....	19	0	2	0.50	1	1	0	0	0	0	0
.....TGAAATGCGCCGAACTGCGAAATG.....	24	2	2	0.50	1	1	0	0	0	0	0
.....TGAAATGCGCCGAACTGCGATTT.....	23	3	4	0.25	1	1	0	0	0	0	0

Anti-sense strand reads

CCTTTTAAAGATATCACTCTAGTTAACTGCAAACCTTATCAGAATACCCAAAGCGCCACGCCGAGTAAACGCACGAGAAATTATGTATAGCACTTTACGCGGCTTGACGCTTTCAGTACCCCAATTCATTTGTTGCACTTAATAGATGTATGTTTGGTTATATTT	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body
**********..(((((((((((.(((((((((.((((.(((((((((.....)))).)))))).))))..)))))))))..)))))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body
.....GCTTGACGCTTTCAGTACCCCAAT.....	24	0	1	1.00	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1299534-1299698 +	dmo_39	GGAAAATTTCTATAGTGAGATCAATTGACGTTTGGAATAGTCTTATGGGTTTCGCGGTGCGGCTCATTTGCGTGCTCTTTAATACATATCGTGAAATGCGCCGAACTGCGAAAGTCATGGGGTTAAGTAAACAACGTGAATTATCTACATACAAACCAATATAAA

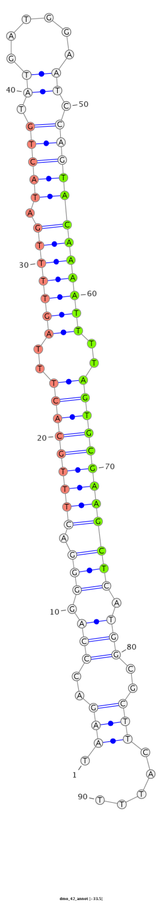
Generated: 09/08/2015 at 08:03 PM

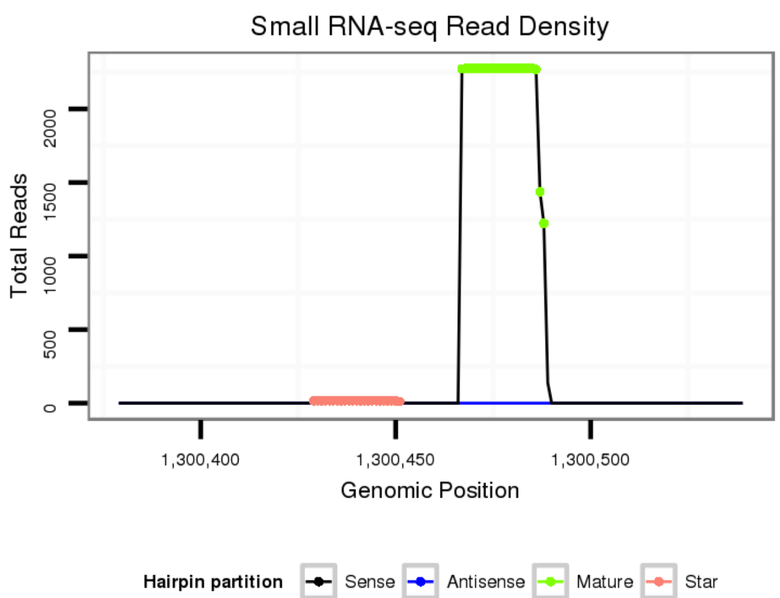
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

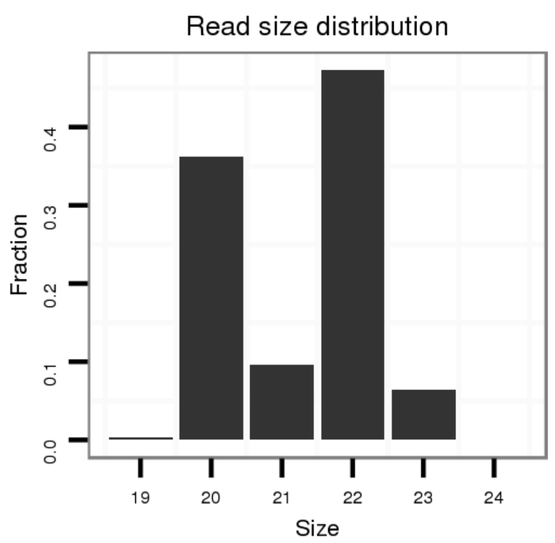
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_42	**scaffold_6308:1300429-1300489 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

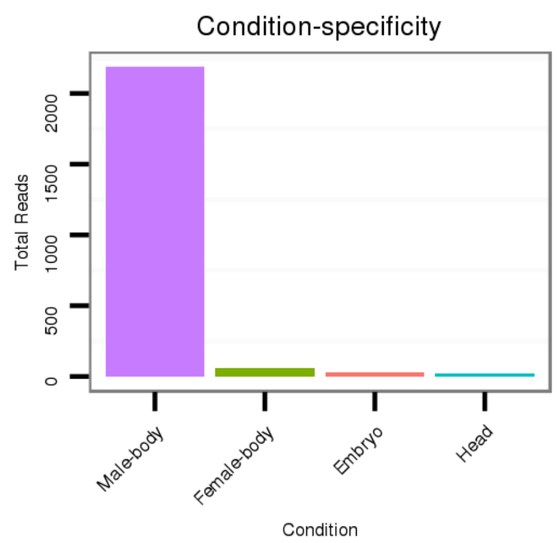
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dmoj\GI10984-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TATATATCTATATTATATTTGAATCTATACTTGATTAAGACCCAGGGGACTTTGCACTTTAGTTTTGATACTGTATGATGGAATCCAGTACAAAATTTTAGTGCGAAGCTCATGGCGCTTCATTTTGACAAATACAGAGTTTTATTTGTTCATTATTCATG **********.(((..(((.(((.(((((((((..(((((((.(((((.((.....)).)))))))))))..)))))))))))).)))..)))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V056 head	V049 head	V041 embryo
.....TACAAAATTTTAGTGCGAAGCT.....	22	0	1	1080.00	1080	1019	31	17	8	4	1
.....TACAAAATTTTAGTGCGAAG.....	20	0	1	831.00	831	815	12	0	4	0	0
.....TACAAAATTTTAGTGCGAAGC.....	21	0	1	216.00	216	205	5	5	1	0	0
.....TACAAAATTTTAGTGCGAAGCTC.....	23	0	1	137.00	137	131	2	0	4	0	0
.....TACAAAATTTTAGTGCGAAGCTT.....	23	1	1	30.00	30	28	0	1	1	0	0
.....TACAAAATTTTAGTGCGAAGCC.....	22	1	1	29.00	29	26	1	2	0	0	0
.....TACAAAATTTTAGTGCGAAGCTTC.....	24	2	1	22.00	22	21	1	0	0	0	0
.....TACAAAATTTTAGTGCGAAGCTA.....	23	1	1	12.00	12	11	1	0	0	0	0
.....TTTGCACTTTAGTTTTGATACTG.....	23	0	1	10.00	10	5	3	0	0	0	2
.....TACAAAATTTTAGTGCGAAGCA.....	22	1	1	9.00	9	8	1	0	0	0	0
.....TACAAAATTTTAGTGCGAA.....	19	0	1	8.00	8	7	1	0	0	0	0
.....TACAAAATTTTAGTGCGAAGT.....	21	1	1	7.00	7	7	0	0	0	0	0
.....TACAAAATTTTAGTGCGAAGA.....	21	1	1	5.00	5	5	0	0	0	0	0
.....TACAAAATTTTAGTGCGAAGCTCC.....	24	1	1	5.00	5	5	0	0	0	0	0
.....TACAAAATTTTAGTGCGAAGCTCT.....	24	1	1	5.00	5	4	0	0	0	1	0
.....TACAAAATTTTAGTGCGAAGCCA.....	23	2	1	5.00	5	5	0	0	0	0	0
.....TTTGCACTTTAGTTTTGATACT.....	22	0	1	4.00	4	2	2	0	0	0	0
.....ACAAAATTTTAGTGCGAAGCT.....	21	0	1	3.00	3	1	1	1	0	0	0
.....TACAAAATTTTAGTGCGAAGCCT.....	23	2	1	3.00	3	3	0	0	0	0	0
.....TACAAAATTTTAGTGCGAAGCTTG.....	24	2	1	3.00	3	3	0	0	0	0	0
.....TACAAAATTTTAGTGCGAAGCTCTC.....	25	2	1	2.00	2	2	0	0	0	0	0
.....TACAAAATTTTAGTGCGAAGTC.....	22	2	1	2.00	2	2	0	0	0	0	0
.....TACAAAATTTTAGTGCGAAGCTTCC.....	25	3	1	2.00	2	2	0	0	0	0	0
.....TTTGCACTTTAGTTTTGATACC.....	22	1	1	2.00	2	0	0	2	0	0	0
.....TACAAAATTTTAGTGCGAAGCTTCC.....	25	3	1	2.00	2	2	0	0	0	0	0
.....TTTGCACTTTAGTTTTGATACC.....	22	1	1	2.00	2	0	0	2	0	0	0
.....TTTGCACTTTAGTTTTGATACTC.....	23	1	1	2.00	2	1	1	0	0	0	0
.....TACAAAATTTTAGTGCGAAA.....	20	1	2	1.50	3	3	0	0	0	0	0
.....CAAAATTTTAGTGCGAAGCC.....	20	1	1	1.00	1	0	0	1	0	0	0
.....AAAATTTTAGTGCGAAGCT.....	19	0	1	1.00	1	0	1	0	0	0	0
.....ACTTTGCACTTTAGTTTTGATACTC.....	25	1	1	1.00	1	1	0	0	0	0	0
.....TACAAAATTTTAGTGCGAAT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....TACAAAATTTTAGTGCGAAGCTTTC.....	25	3	1	1.00	1	1	0	0	0	0	0
.....TACAAAATTTTAGTGCGAAGCTATC.....	25	3	1	1.00	1	1	0	0	0	0	0
.....ACAAAATTTTAGTGCGAAGCTC.....	22	0	1	1.00	1	0	1	0	0	0	0
.....TACAAAATTTTAGTGCGAAGCTTT.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TTTGCACTTTAGTTTTGATACTGTC.....	25	1	1	1.00	1	1	0	0	0	0	0
.....TTTGCACTTTAGTTTTGATACTGA.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TTGCACTTTAGTTTTGATACTGT.....	23	0	1	1.00	1	0	0	0	1	0	0
.....TTTGCACTTTAGTTTTGATACTGT.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TACAAAATTTTAGTGCGAAGCTCATC.....	26	1	1	1.00	1	1	0	0	0	0	0
.....TTTGCACTTTAGTTTTGATAC.....	21	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

ATATATAGATATAATATAAACTTAGATATGAACTAATTCTGGGTCCCCTGAAACGTGAAATCAAAACTATGACATACTACCTTAGGTCATGTTTTAAAATCACGCTTCGAGTACCGCGAAGTAAAACTGTTTATGTCTCAAAATAAACAAGTAATAAGTAC **********.(((..(((.(((.(((((((((..(((((((.(((((.((.....)).)))))))))))..)))))))))))).)))..)))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo
.....TACAAAATTTTAGTGCGAAGCTCCC.....	27	3	1	1.00	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1300379-1300539 +	dmo_42	TATATATCTATATTATATTTGAATCTATACTTGATTAAGACCCAGGGGACTTTGCACTTTAGTTTTGATACTGTATGATGGAATCCAGTACAAAATTTTAGTGCGAAGCTCATGGCGCTTCATTTTGACAAATACAGAGTTTTATTTGTTCATTATTCATG

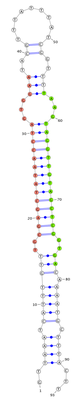
Generated: 09/08/2015 at 08:02 PM

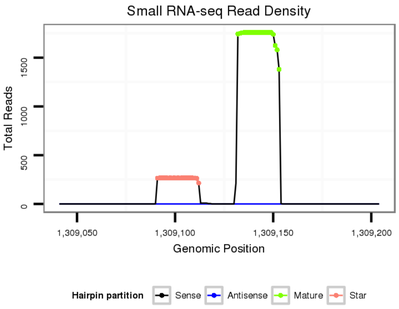
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

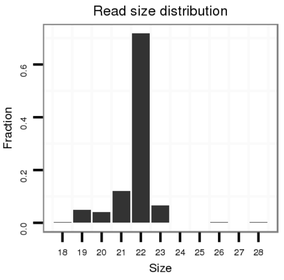
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_38	**scaffold_6308:1309091-1309154 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

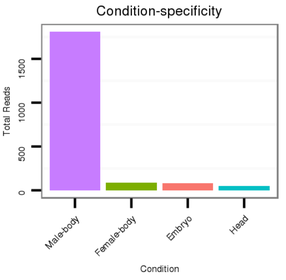
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
	1. dmo_61 scaffold_6308:1308803-1308824 + 2. dmo_38 scaffold_6308:1309091-1309112 +

Sense Strand Reads

hide 3p reads | show mid mismatch reads

```
ACTATATGTGCAATCAGTATATAGCAAAAATCTAAGTTAAATCATTTGTTTGCGAGCTATAACCTAGTGGAATACGTTTATTTATCGGTTTTAAGTAGGTTGTAGCTCGGTGACAAAATGCTTTACTTTGCAACAGGAAAATCGGGAAATCTAACATCGATATA
**********************************..((((.(((((((((..(((((((((((((((...(((..((.(.........).)..)))...)))))))))))))))..)))).)))))).))))...**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V041 embryo	M060 embryo	V056 head	V049 head
22	0	1	1236.00	1236	1099	40	39	17	23	18
22	0	2	202.50	405	362	19	8	8	5	3
21	0	1	180.00	180	166	10	2	2	0	0
23	0	1	128.00	128	116	6	1	2	1	2
22	1	1	122.00	122	113	1	1	0	5	2
19	0	1	76.00	76	73	0	0	3	0	0
21	0	4	46.25	185	155	16	0	6	5	3
20	0	1	39.00	39	38	1	0	0	0	0
20	0	1	32.00	32	30	1	0	0	0	1
23	1	1	23.00	23	22	0	0	1	0	0
23	1	1	21.00	21	20	0	1	0	0	0
22	0	1	18.00	18	14	2	1	0	1	0
19	0	1	15.00	15	13	1	0	1	0	0
23	1	2	13.50	27	22	3	0	1	1	0
21	0	1	11.00	11	11	0	0	0	0	0
22	1	4	7.25	29	27	0	0	2	0	0
21	1	1	6.00	6	6	0	0	0	0	0
22	1	1	6.00	6	6	0	0	0	0	0
26	0	2	5.50	11	10	0	0	0	0	1
21	0	1	5.00	5	1	4	0	0	0	0
22	2	1	5.00	5	5	0	0	0	0	0
23	1	2	5.00	10	9	1	0	0	0	0
20	0	4	4.50	18	15	3	0	0	0	0
23	2	4	4.25	17	15	1	0	0	1	0
23	1	1	4.00	4	4	0	0	0	0	0
23	1	1	4.00	4	4	0	0	0	0	0
22	1	1	4.00	4	4	0	0	0	0	0
18	0	1	4.00	4	3	1	0	0	0	0
28	0	2	4.00	8	8	0	0	0	0	0
21	1	1	3.00	3	3	0	0	0	0	0
23	2	1	3.00	3	3	0	0	0	0	0
23	0	1	3.00	3	1	1	1	0	0	0
23	2	1	3.00	3	3	0	0	0	0	0
20	0	1	3.00	3	2	0	0	1	0	0
19	0	1	3.00	3	3	0	0	0	0	0
19	0	1	2.00	2	2	0	0	0	0	0
24	2	1	2.00	2	2	0	0	0	0	0
22	2	1	2.00	2	2	0	0	0	0	0
19	1	1	2.00	2	2	0	0	0	0	0
24	1	1	2.00	2	1	0	0	0	1	0
20	1	1	2.00	2	2	0	0	0	0	0
23	2	1	2.00	2	2	0	0	0	0	0
22	1	1	2.00	2	1	0	0	0	1	0
23	1	1	2.00	2	2	0	0	0	0	0
20	0	1	2.00	2	0	2	0	0	0	0
24	3	1	2.00	2	2	0	0	0	0	0
21	0	2	2.00	4	1	3	0	0	0	0
19	0	5	1.80	9	7	1	0	0	0	1
23	0	2	1.50	3	3	0	0	0	0	0
24	2	2	1.50	3	3	0	0	0	0	0
22	1	4	1.50	6	6	0	0	0	0	0
22	0	4	1.25	5	4	0	0	0	1	0
21	1	1	1.00	1	1	0	0	0	0	0
24	1	1	1.00	1	1	0	0	0	0	0
24	2	1	1.00	1	1	0	0	0	0	0
24	1	1	1.00	1	1	0	0	0	0	0
22	2	1	1.00	1	1	0	0	0	0	0
25	2	1	1.00	1	1	0	0	0	0	0
22	2	1	1.00	1	1	0	0	0	0	0
24	2	1	1.00	1	0	0	0	0	0	1
18	0	1	1.00	1	1	0	0	0	0	0
24	2	1	1.00	1	1	0	0	0	0	0
23	2	1	1.00	1	1	0	0	0	0	0
24	0	1	1.00	1	0	0	0	1	0	0
22	1	1	1.00	1	0	0	0	0	0	1
23	3	1	1.00	1	1	0	0	0	0	0
23	1	2	1.00	2	2	0	0	0	0	0
28	1	2	1.00	2	2	0	0	0	0	0
23	0	2	1.00	2	1	1	0	0	0	0
25	1	2	1.00	2	2	0	0	0	0	0
21	0	5	0.80	4	4	0	0	0	0	0
23	0	5	0.60	3	2	0	1	0	0	0
23	0	2	0.50	1	0	1	0	0	0	0
20	0	2	0.50	1	1	0	0	0	0	0
25	1	2	0.50	1	1	0	0	0	0	0
24	2	2	0.50	1	0	0	0	0	0	1
23	3	2	0.50	1	1	0	0	0	0	0
22	1	2	0.50	1	0	1	0	0	0	0
20	2	2	0.50	1	1	0	0	0	0	0
24	0	2	0.50	1	0	0	1	0	0	0
26	0	2	0.50	1	1	0	0	0	0	0
26	2	2	0.50	1	1	0	0	0	0	0
23	1	5	0.40	2	2	0	0	0	0	0
20	1	3	0.33	1	1	0	0	0	0	0
23	2	4	0.25	1	1	0	0	0	0	0
21	1	4	0.25	1	1	0	0	0	0	0
21	3	4	0.25	1	1	0	0	0	0	0
22	2	4	0.25	1	1	0	0	0	0	0
21	0	4	0.25	1	1	0	0	0	0	0
21	1	4	0.25	1	1	0	0	0	0	0
22	0	5	0.20	1	0	0	0	1	0	0
21	3	5	0.20	1	1	0	0	0	0	0
20	0	5	0.20	1	0	1	0	0	0	0
19	2	5	0.20	1	0	0	1	0	0	0

Anti-sense strand reads

```
TGATATACACGTTAGTCATATATCGTTTTTAGATTCAATTTAGTAAACAAACGCTCGATATTGGATCACCTTATGCAAATAAATAGCCAAAATTCATCCAACATCGAGCCACTGTTTTACGAAATGAAACGTTGTCCTTTTAGCCCTTTAGATTGTAGCTATAT
**********************************..((((.((((((((..(((((((((((((((...(((..((.(.........).)..)))...)))))))))))))))..)))).)))))).))))...**********************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head	M046 female body	V110 male body
23	1	1	1.00	1	0	0	0
24	0	1	1.00	1	0	0	0
24	1	1	1.00	1	0	0	0
24	2	1	1.00	1	0	0	0
23	2	1	1.00	1	0	0	0
22	2	1	1.00	1	0	0	0
21	2	1	1.00	1	0	0	0
20	2	1	1.00	1	0	0	0
19	2	1	1.00	1	0	0	0
18	2	1	1.00	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1309041-1309204 +	dmo_38	ACTATATGTGCAATCAGTATATAGCAAAAATCTAAGTTAAATCATTTGTTTGCGAGCTATAACCTAGTGGAATACGTTTATTTATCGGTTTTAAGTAGGTTGTAGCTCGGTGACAAAATGCTTTACTTTGCAACAGGAAAATCGGGAAATCTAACATCGATATA

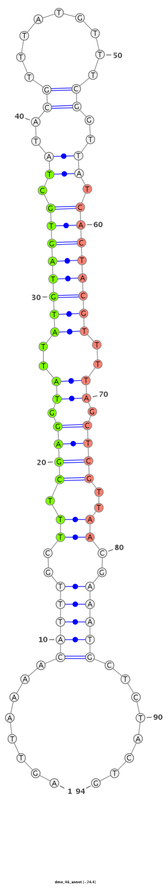
Generated: 09/08/2015 at 08:04 PM

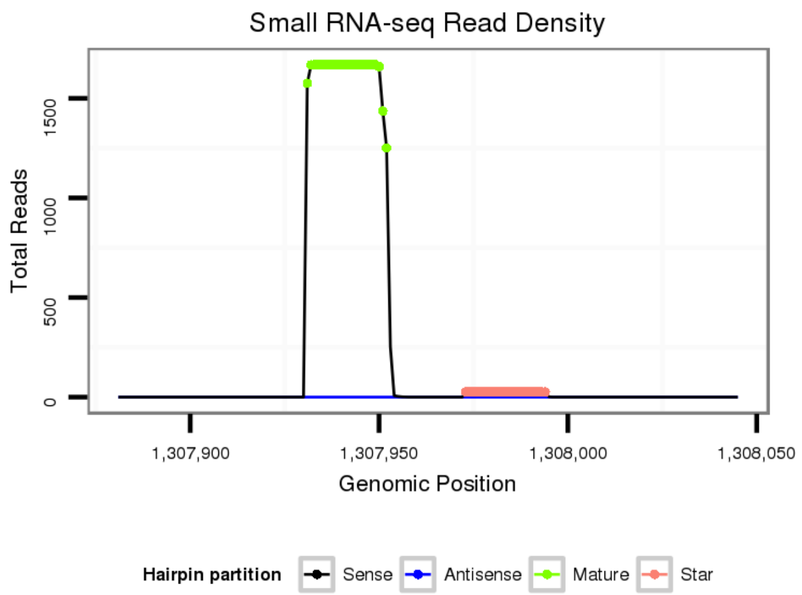
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.ptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

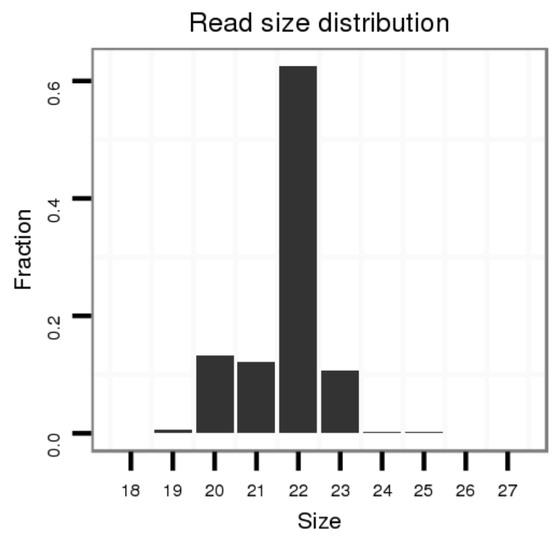
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_46	**scaffold_6308:1307931-1307995 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

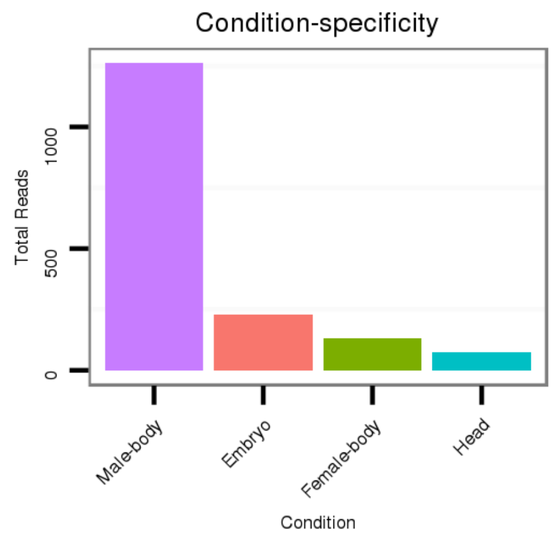
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AACTATTTGTGCAATGGGTCCATAGTAAAAATCGAAGTTAAAACATTTGCTTTCGAGGTATTATGTAGTGCTATACGTTTATGTTTCGGTTATCACTACGTTTTAGCTCGTTAACGAAATGCTCTACTGTGCAACAAGAAAATGTGCCCTATAAACAAAGTGTCT	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M060 embryo	M046 female body	V056 head	V041 embryo	V049 head
**********.....(((((..((.((((.((..(((((((((.((..((.....))..))..)).)))))))..))).))))..))..)))))).....**********											
.....TTTCGAGGTATTATGTAGTGCT.....	22	0	1	972.00	972	674	142	70	31	38	17
.....TTTCGAGGTATTATGTAGTGCTC.....	23	1	1	226.00	226	214	2	3	3	0	4
.....TTTCGAGGTATTATGTAGTG.....	20	0	1	223.00	223	201	1	15	4	1	1
.....TTTCGAGGTATTATGTAGTGC.....	21	0	1	183.00	183	128	21	23	2	7	2
.....TTTCGAGGTATTATGTAGTGCTA.....	23	0	1	181.00	181	152	9	8	4	3	5
.....TTTCGAGGTATTATGTAGTGT.....	21	1	1	66.00	66	65	0	1	0	0	0
.....TTCGAGGTATTATGTAGTGCTA.....	22	0	1	65.00	65	53	1	4	2	3	2
.....TTTCGAGGTATTATGTAGTGCTT.....	23	1	1	49.00	49	39	2	5	2	0	1
.....TTTCGAGGTATTATGTAGTGCC.....	22	1	1	39.00	39	0	39	0	0	0	0
.....TCACTACGTTTTAGCTCGTTAA.....	22	0	1	24.00	24	22	1	0	1	0	0
.....TTCGAGGTATTATGTAGTGCT.....	21	0	1	23.00	23	13	1	9	0	0	0
.....TTTCGAGGTATTATGTAGTGA.....	21	1	1	20.00	20	20	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTC.....	20	1	1	16.00	16	13	0	2	1	0	0
.....TTTCGAGGTATTATGTAGTGCTCC.....	24	2	1	14.00	14	12	0	1	0	0	1
.....TTTCGAGGTATTATGTAGT.....	19	0	1	10.00	10	6	1	1	2	0	0
.....TTCGAGGTATTATGTAGTGCTC.....	22	1	1	6.00	6	6	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGCTAT.....	24	0	1	4.00	4	4	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGCTAA.....	24	1	1	3.00	3	3	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGG.....	21	1	1	3.00	3	3	0	0	0	0	0
.....TCACTACGTTTTAGCTCGTTAAA.....	23	1	1	3.00	3	3	0	0	0	0	0
.....TTCGAGGTATTATGTAGTGC.....	20	0	1	2.00	2	0	0	2	0	0	0
.....TCACTACGTTTTAGCTCGTTAACC.....	24	1	1	2.00	2	1	1	0	0	0	0
.....TCACTACGTTTTAGCTCGTTAAC.....	23	0	1	2.00	2	2	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGCTG.....	23	1	1	2.00	2	2	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGCTCCT.....	25	3	1	2.00	2	2	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGCTATA.....	25	0	1	2.00	2	2	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGAC.....	22	2	1	2.00	2	0	2	0	0	0	0
.....TTTCGAGGTATTATGTAGTGCA.....	22	1	1	2.00	2	2	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....TTCGAGGTATTATGTAGTGCTAC.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TCACTACGTTTTAGCTCGTTAAAA.....	24	2	1	1.00	1	0	0	1	0	0	0
.....TTCGAGGTATTATGTAGTGCTATAC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TTTCGAGGTATTATGTAGC.....	19	1	1	1.00	1	1	0	0	0	0	0
.....TTCGAGGTATTATGTAGTGCTATC.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGCTATAA.....	26	1	1	1.00	1	1	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGCTCA.....	24	2	1	1.00	1	0	0	0	1	0	0
.....TTCGAGGTATTATGTAGTGCTT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....CGAGGTATTATGTAGTGCTATC.....	22	1	1	1.00	1	1	0	0	0	0	0
.....GAGGTATTATGTAGTGCT.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGCTTG.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGTA.....	22	2	1	1.00	1	1	0	0	0	0	0
.....TTCGAGGTATTATGTAGTGCTATTTT.....	26	3	1	1.00	1	1	0	0	0	0	0
.....TTCGAGGTATTATGTAGTG.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TCGAGGTATTATGTAGTGCT.....	20	0	1	1.00	1	0	0	1	0	0	0
.....TTTCGAGGTATTATGTAGTGCTTA.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGCTAC.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TTCGAGGTATTATGTAGTGT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGCTATC.....	25	1	1	1.00	1	1	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGTCT.....	23	3	1	1.00	1	1	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGCTATC.....	25	1	1	1.00	1	1	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGTCT.....	23	3	1	1.00	1	1	0	0	0	0	0
.....TCACTACGTTTTAGCTCGTTA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CACTACGTTTTAGCTCGTTAAA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTCA.....	21	2	1	1.00	1	1	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTCT.....	21	2	1	1.00	1	0	1	0	0	0	0
.....TCACTACGTTTTAGCTCGTTAAT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TTTCGAGGTATTATGTAGTGCTATT.....	25	1	1	1.00	1	0	0	1	0	0	0
.....TTTCGAGGTATTATGTAGTGCTATACG.....	27	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1307881-1308045 +	dmo_46	AACTATTTGTGCAATGGGTCCATAGTAAAAATCGAAGTTAAAACATTTGCTTTCGAGGTATTATGTAGTGCTATACGTTTATGTTTCGGTTATCACTACGTTTTAGCTCGTTAACGAAATGCTCTACTGTGCAACAAGAAAATGTGCCCTATAAACAAAGTGTCT

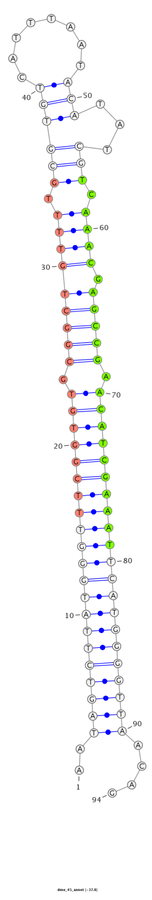
Generated: 09/08/2015 at 08:03 PM

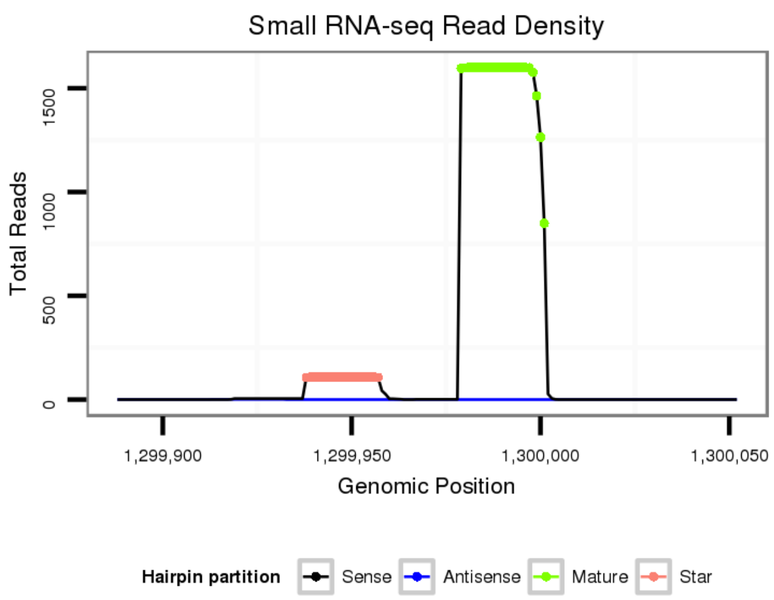
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

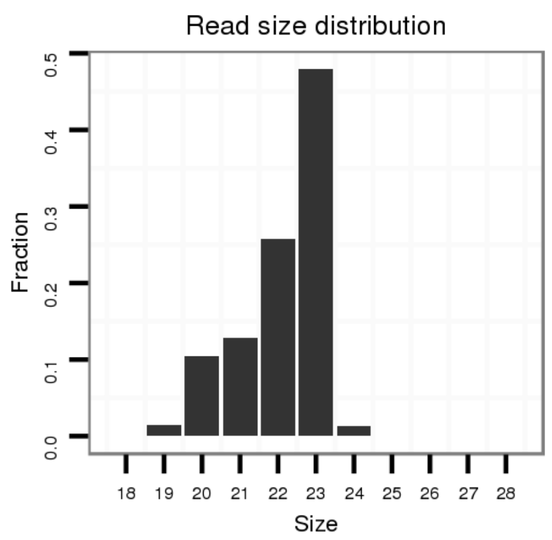
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_45	**scaffold_6308:1299938-1300002 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

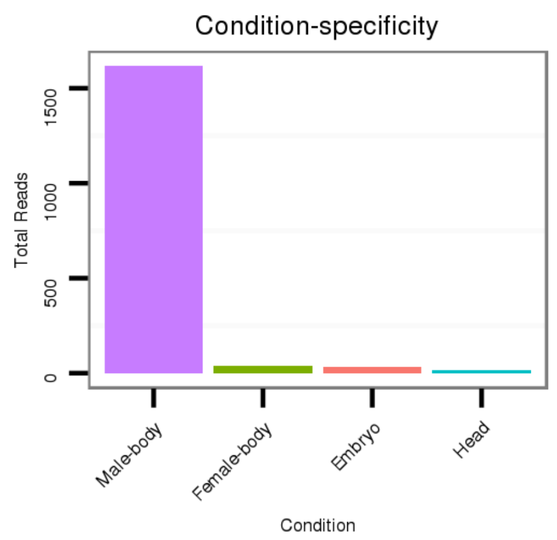
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [DmojGI10984-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GGAAAATTTCTATAGTGAGATCAATTGACGTTTGAAATAGTCTTATGGGTTTCGGTGTGCGGCTGTTTTGCGTGTCATTTAATACATATCGTCAAACGAGCCGAACATCGAAATTCATGGGGTTAACAGCGCCTTTTAAAAGTGTTTTCTAATATATATAGCGAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V056 head	V049 head	V041 embryo
**********..(((((((((((((((((((((.(((((((((.((((((........)))...))).)))))).)))))).)))))))))))))))))....**********											
.....TCAAACGAGCCGAACATCGAAAT.....	23	0	1	817.00	817	785	8	16	5	2	1
.....TCAAACGAGCCGAACATCGAAA.....	22	0	1	415.00	415	398	9	6	1	1	0
.....TCAAACGAGCCGAACATCGAA.....	21	0	1	200.00	200	194	3	2	1	0	0
.....TCAAACGAGCCGAACATCGA.....	20	0	1	113.00	113	107	2	1	3	0	0
.....TCAAACGAGCCGAACATCGAAAC.....	23	1	1	96.00	96	91	1	1	3	0	0
.....TCAAACGAGCCGAACATCGAAAA.....	23	1	1	65.00	65	62	1	0	2	0	0
.....TTCGGTGTGCGGCTGTTTTG.....	20	0	1	63.00	63	59	4	0	0	0	0
.....TCAAACGAGCCGAACATCGAAATC.....	24	1	1	38.00	38	38	0	0	0	0	0
.....TTCGGTGTGCGGCTGTTTTGCG.....	22	0	1	22.00	22	18	2	2	0	0	0
.....TCAAACGAGCCGAACATCG.....	19	0	1	22.00	22	15	5	0	0	2	0
.....TCAAACGAGCCGAACATCGAAATT.....	24	0	1	21.00	21	20	0	1	0	0	0
.....TTCGGTGTGCGGCTGTTTTGC.....	21	0	1	16.00	16	12	3	1	0	0	0
.....TCAAACGAGCCGAACATCGAAATA.....	24	1	1	7.00	7	7	0	0	0	0	0
.....TCAAACGAGCCGAACATCGAAATG.....	24	1	1	7.00	7	7	0	0	0	0	0
.....TTCGGTGTGCGGCTGTTTTGCGCC.....	24	2	1	6.00	6	5	1	0	0	0	0
.....TCAAACGAGCCGAACATCGAAACC.....	24	2	1	6.00	6	6	0	0	0	0	0
.....TCAAACGAGCCGAACATCGAAAAA.....	24	2	1	5.00	5	5	0	0	0	0	0
.....TCAAACGAGCCGAACATCGAAATTC.....	25	0	1	5.00	5	5	0	0	0	0	0
.....TTCGGTGTGCGGCTGTTTTGCGTC.....	24	1	1	4.00	4	4	0	0	0	0	0
.....TTGAAATAGTCTTATGGGT.....	19	0	1	4.00	4	3	1	0	0	0	0
.....TTCGGTGTGCGGCTGTTTTGT.....	21	1	1	3.00	3	3	0	0	0	0	0
.....TTCGGTGTGCGGCTGTTTTGCGC.....	23	1	1	3.00	3	3	0	0	0	0	0
.....AAACGAGCCGAACATCGAAAT.....	21	0	1	3.00	3	2	0	1	0	0	0
.....TCAAACGAGCCGAACATCGAAAG.....	23	1	1	2.00	2	2	0	0	0	0	0
.....TCAAACGAGCCGAACATCGAAATAA.....	25	2	1	2.00	2	1	1	0	0	0	0
.....TTCGGTGTGCGGCTGTTTT.....	19	0	1	2.00	2	1	1	0	0	0	0
.....TCAAACGAGCCGAACATCGAC.....	21	1	1	2.00	2	2	0	0	0	0	0
.....TCAAACGAGCCGAACATCGCC.....	21	2	1	2.00	2	2	0	0	0	0	0
.....TTCGGTGTGCGGCTGTTTTT.....	20	1	1	2.00	2	1	0	0	0	1	0
.....TTCGGTGTGCGGCTGTTTTGCGTGTC.....	26	0	1	2.00	2	2	0	0	0	0	0
.....CAAACGAGCCGAACATCGAAAT.....	22	0	1	2.00	2	1	1	0	0	0	0
.....TCAAACGAGCCGAACATCGAAACA.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TTTGAAATAGTCTTATGGGT.....	20	0	1	1.00	1	0	0	1	0	0	0
.....TCAAACGAGCCGAACATCGAAACCA.....	25	3	1	1.00	1	1	0	0	0	0	0
.....TCAAACGAGCCGAACATCGAAT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TTCGGTGTGCGGCTGTTTTGCGG.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TCAAACGAGCCGAACATCGAAATCA.....	25	2	1	1.00	1	1	0	0	0	0	0
.....TCAAACGAGCCGAACATCGT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....TCAAACGAGCCGAACATC.....	18	0	1	1.00	1	0	0	0	0	1	0
.....TTCGGTGTGCGGCTGTTTTGCGTG.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TTCGGTGTGCGGCTGTTTTA.....	20	1	1	1.00	1	1	0	0	0	0	0
.....TAATACATATCGTCAAACGAGCCGAACA.....	28	0	1	1.00	1	1	0	0	0	0	0
.....TCGGTGTGCGGCTGTTTTGC.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TCAAACGAGCCGAACATCGAAATTCA.....	26	0	1	1.00	1	1	0	0	0	0	0
.....TCAAACGAGCCGAACATCGAAATAT.....	25	2	1	1.00	1	1	0	0	0	0	0
.....TTCGGTGTGCGGCTGTTTTGCGTGT.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TTCGGTGTGCGGCTGTTTTGA.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TTCGGTGTGCGGCTGTTTA.....	19	1	1	1.00	1	1	0	0	0	0	0
.....TTCGGTGTGCGGCTGTTTTGA.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TTCGGTGTGCGGCTGTTTA.....	19	1	1	1.00	1	1	0	0	0	0	0
.....CAAACGAGCCGAACATCGAAATC.....	23	1	1	1.00	1	0	1	0	0	0	0
.....TCGGTGTGCGGCTGTTTTG.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TCAAACGAGCCGAACATCGAAC.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TTCGGTGTGCGGCTGTTTTC.....	20	1	2	1.00	2	2	0	0	0	0	0
.....TTCGGTGTGCGGCTGTTTTTG.....	21	2	2	0.50	1	1	0	0	0	0	0
.....TTCGGTGTGCGGCTGTTAA.....	19	2	4	0.25	1	1	0	0	0	0	0

Anti-sense strand reads

CCTTTTAAAGATATCACTCTAGTTAACTGCAAACTTTATCAGAATACCCAAAGCCACACGCCGACAAAACGCACAGTAAATTATGTATAGCAGTTTGCTCGGCTTGTAGCTTTAAGTACCCCAATTGTCGCGGAAAATTTTCACAAAAGATTATATATATCGCTA	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body
**********..(((((((((((((((((((((.(((((((((.((((((........)))...))).)))))).)))))).)))))))))))))))))....**********						
.....ACTGCAAACTTTATCAGAAT.....	20	0	1	1.00	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1299888-1300052 +	dmo_45	GGAAAATTTCTATAGTGAGATCAATTGACGTTTGAAATAGTCTTATGGGTTTCGGTGTGCGGCTGTTTTGCGTGTCATTTAATACATATCGTCAAACGAGCCGAACATCGAAATTCATGGGGTTAACAGCGCCTTTTAAAAGTGTTTTCTAATATATATAGCGAT

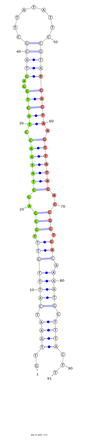
Generated: 09/08/2015 at 08:03 PM

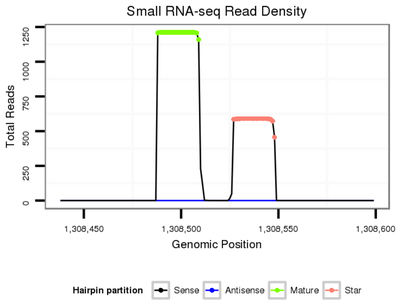
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

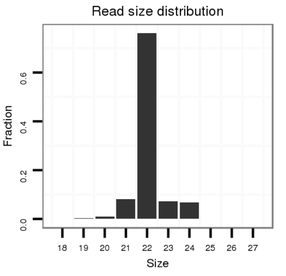
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_31	**scaffold_6308:1308488-1308549 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

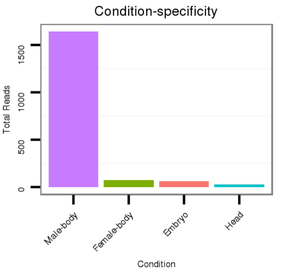
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

mature	star
1. dmo_32 scaffold_6308:1308226-1308247 + 2. dmo_31 scaffold_6308:1308488-1308509 +	1. dmo_32 scaffold_6308:1308265-1308286 + 2. dmo_31 scaffold_6308:1308527-1308548 +

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	V041 embryo	V049 head
TTGATATATAACTTCCAGCTATAGCAAAAATCTAAGTTAAATCATTTGTTTGCGAGCTATAACCTAGTGGAGTACGCTTATATTCCGTATCACTAAGTTATAGACCGCTGACAAAATGCTTTACTTTGCAAAAGGAAAATCGGAAAAACTATCAACTATGAA											
**********..((((.(((((((((.(((..(((((((.(((((..(((((.(((((.........)))))))))).)))))))..)))).)))).)))))...**********											
.....TGCGAGCTATAACCTAGTGGAG	22	0	2	929.50	1859	1801	27	0	15	8	8
.....TCACTAAGTTATAGACCGCTGA	22	0	2	430.50	861	734	54	46	9	13	5
.....TGCGAGCTATAACCTAGTGGAGTA	24	0	2	115.50	231	209	10	5	1	5	1
.....TGCGAGCTATAACCTAGTGGAGT	23	0	2	109.00	218	163	14	28	5	4	4
.....TCACTAAGTTATAGACCGCTG	21	0	2	96.00	192	170	16	1	3	2	0
.....TGCGAGCTATAACCTAGTGGA	21	0	4	46.25	185	155	16	6	5	0	3
.....ATCACTAAGTTATAGACCGCTGA	23	0	2	17.00	34	29	1	3	0	1	0
.....ATCACTAAGTTATAGACCGCTG	22	0	2	14.50	29	27	0	0	1	0	1
.....TCACTAAGTTATAGACCGCTGT	22	1	2	11.00	22	22	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTT	24	1	2	9.50	19	19	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAT	25	1	2	9.00	18	17	0	0	0	0	1
.....TCACTAAGTTATAGACCGCTGAA	23	1	2	8.50	17	16	0	1	0	0	0
.....TCACTAAGTTATAGACCGCT	20	0	2	8.50	17	12	4	1	0	0	0
.....TCACTAAGTTATAGACCGCTGAT	23	1	2	7.50	15	14	0	1	0	0	0
.....TGCGAGCTATAACCTAGTGGAT	22	1	4	7.25	29	27	0	2	0	0	0
.....TGCGAGCTATAACCTAGTGGAGC	23	1	2	6.50	13	1	0	12	0	0	0
.....TATCACTAAGTTATAGACCGCTG	23	0	2	6.00	12	11	0	1	0	0	0
.....TATCACTAAGTTATAGACCGCTGA	24	0	2	6.00	12	11	0	0	0	0	1
.....TGCGAGCTATAACCTAGTGGAGTAA	25	1	2	4.50	9	9	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGG	20	0	4	4.50	18	15	3	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGCC	23	2	4	4.25	17	15	1	0	1	0	0
.....TCACTAAGTTATAGACCGC	19	0	2	3.00	6	0	1	5	0	0	0
.....ATCACTAAGTTATAGACCGCT	21	0	2	2.50	5	5	0	0	0	0	0
.....TATCACTAAGTTATAGACCGCT	22	0	2	2.50	5	5	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTGAGC	24	2	2	2.00	4	3	0	0	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTCT	25	2	2	2.00	4	4	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAAA	26	2	2	2.00	4	4	0	0	0	0	0
.....GCGAGCTATAACCTAGTGGAG	21	0	2	2.00	4	2	2	0	0	0	0
.....TGCGAGCTATAACCTAGTG	19	0	5	1.80	9	7	1	0	0	0	1
.....TGCGAGCTATAACCTAGTGGAGTAC	25	0	2	1.50	3	3	0	0	0	0	0
.....ATCACTAAGTTATAGACCGCTGT	23	1	2	1.50	3	3	0	0	0	0	0
.....ATCACTAAGTTATAGACCGC	20	0	2	1.50	3	0	0	3	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTCA	25	2	2	1.50	3	2	0	0	1	0	0
.....ACTAGTTATAGACCGCTGA	20	0	2	1.50	3	1	2	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTT	24	1	2	1.50	3	2	0	1	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTACG	26	0	2	1.50	3	3	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTGAG	23	1	2	1.50	3	3	0	0	0	0	0
.....CACTAAGTTATAGACCGCTG	20	0	2	1.50	3	0	3	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAT	25	1	2	1.50	3	3	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAAT	22	1	4	1.50	6	6	0	0	0	0	0
.....TTGCGAGCTATAACCTAGTGGA	22	0	4	1.25	5	4	0	0	1	0	0
.....TCACTAAGTTATAGACCGCTGTC	23	2	2	1.00	2	2	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTACGC	27	0	2	1.00	2	2	0	0	0	0	0
.....GCGAGCTATAACCTAGTGGAGT	22	0	2	1.00	2	0	2	0	0	0	0
.....CACTAAGTTATAGACCGCTGA	21	0	2	1.00	2	0	2	0	0	0	0
.....TCACTAAGTTATAGACCGCTGTTT	24	3	2	1.00	2	2	0	0	0	0	0
.....ATCACTAAGTTATAGACCGCTGAA	24	1	2	1.00	2	2	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTGTAT	24	3	2	1.00	2	2	0	0	0	0	0
.....TATCACTAAGTTATAGACCG	20	0	2	1.00	2	2	0	0	0	0	0
.....TATCACTAAGTTATAGACCGCTGT	24	1	2	1.00	2	2	0	0	0	0	0
.....CGAGCTATAACCTAGTGGAG	20	0	2	1.00	2	2	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAGT	26	2	2	1.00	2	2	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTGT	23	1	2	1.00	2	2	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTGG	22	1	2	1.00	2	1	0	0	0	1	0
.....TAAGTTATAGACCGCTGACA	20	0	2	1.00	2	2	0	0	0	0	0
.....TGTTTGCGAGCTATAACCTAG	21	0	5	0.80	4	4	0	0	0	0	0
.....TTATAGACCGCTGACAAAATGC	22	0	3	0.67	2	0	0	2	0	0	0
.....TGTTTGCGAGCTATAACCTAGTG	23	0	5	0.60	3	2	0	0	0	1	0
.....TGCGAGCTATAACCTAGTGGAGTTA	25	2	2	0.50	1	1	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTTC	22	2	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTCG	25	2	2	0.50	1	1	0	0	0	0	0
.....ATCACTAAGTTATAGACCGCTGTCT	24	2	2	0.50	1	1	0	0	0	0	0
.....ATCACTAAGTTATAGACCGCTGATC	25	2	2	0.50	1	1	0	0	0	0	0
.....TATCACTAAGTTATAGACCGCTGAA	25	1	2	0.50	1	0	1	0	0	0	0
.....TATCACTAAGTTATAGACCGCTT	23	1	2	0.50	1	1	0	0	0	0	0
.....TATCACTAAGTTATAGACCGCTTTT	25	3	2	0.50	1	0	1	0	0	0	0
.....TCACTAAGTTATAGACCGCTTG	22	2	2	0.50	1	1	0	0	0	0	0
.....TCACTAAGTTATAGACCG	18	0	2	0.50	1	1	0	0	0	0	0
.....GTATCACTAAGTTATAGACCGT	22	1	2	0.50	1	0	1	0	0	0	0
.....TCACTAAGTTATAGACCGCTCT	22	2	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTG	24	1	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAA	26	2	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAG	26	2	2	0.50	1	1	0	0	0	0	0
.....GCGAGCTATAACCTAGTGGAGTA	23	0	2	0.50	1	0	1	0	0	0	0
.....TCACTAAGTTATAGACCGCTGTA	23	2	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAC	26	2	2	0.50	1	1	0	0	0	0	0
.....ATCACTAAGTTATAGACCGCTGAC	24	0	2	0.50	1	0	1	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGG	23	1	2	0.50	1	1	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTCTTG	24	3	2	0.50	1	1	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTCGT	23	3	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAAA	27	3	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAGC	26	2	2	0.50	1	1	0	0	0	0	0
.....AAGTTATAGACCGCTGAT	18	1	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTTAT	26	3	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTATCA	27	3	2	0.50	1	1	0	0	0	0	0
.....GAGCTATAACCTAGTGGAG	19	0	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTTA	25	2	2	0.50	1	1	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTTTA	23	3	2	0.50	1	1	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTGA	22	1	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTATAT	27	3	4	0.50	2	2	0	0	0	0	0
.....TGTTTGCGAGCTATAACCTAGTG	23	1	5	0.40	2	2	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGCA	21	1	4	0.25	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGCTA	23	2	4	0.25	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGCG	21	1	4	0.25	1	1	0	0	0	0	0
.....TTGCGAGCTATAACCTAGTGG	21	0	4	0.25	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGCTC	22	2	4	0.25	1	1	0	0	0	0	0
.....TGTTTGCGAGCTATAACCTAGT	22	0	5	0.20	1	0	0	1	0	0	0
.....TTGCGAGCTATAACCTAGTG	20	0	5	0.20	1	0	1	0	0	0	0

Anti-sense strand reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V056 head	V110 male body
AACTATATATTGAAGGTCGATATCGTTTTTAGATTCAATTTAGTAAACAAACGCTCGATATTGGATCACCTCATGCGAATATAAGGCATAGTGATTCAATATCTGGCGACTGTTTTACGAAATGAAACGTTTTCCTTTTAGCCTTTTGTAGTTGATACTT								
**********..((((.(((((((((.(((..(((((((.(((((..(((((.(((((.........)))))))))).)))))))..)))).)))).)))))...**********								
.....TGCGAGCTATAACCTAGTGGAG	22	0	2	929.50	1859	1801	15	8
.....TCACTAAGTTATAGACCGCTGA	22	0	2	430.50	861	734	9	13
.....TGCGAGCTATAACCTAGTGGAGTA	24	0	2	115.50	231	209	1	5
.....TGCGAGCTATAACCTAGTGGAGT	23	0	2	109.00	218	163	5	4
.....TCACTAAGTTATAGACCGCTG	21	0	2	96.00	192	170	3	2
.....TGCGAGCTATAACCTAGTGGA	21	0	4	46.25	185	155	5	0
.....ATCACTAAGTTATAGACCGCTGA	23	0	2	17.00	34	29	0	1
.....ATCACTAAGTTATAGACCGCTG	22	0	2	14.50	29	27	1	0
.....TCACTAAGTTATAGACCGCTGT	22	1	2	11.00	22	22	0	0
.....TGCGAGCTATAACCTAGTGGAGTT	24	1	2	9.50	19	19	0	0
.....TGCGAGCTATAACCTAGTGGAGTAT	25	1	2	9.00	18	17	0	0
.....TCACTAAGTTATAGACCGCTGAA	23	1	2	8.50	17	16	0	1
.....TCACTAAGTTATAGACCGCT	20	0	2	8.50	17	12	1	0
.....TCACTAAGTTATAGACCGCTGAT	23	1	2	7.50	15	14	0	1
.....TGCGAGCTATAACCTAGTGGAT	22	1	4	7.25	29	27	0	2
.....TGCGAGCTATAACCTAGTGGAGC	23	1	2	6.50	13	1	0	12
.....TATCACTAAGTTATAGACCGCTG	23	0	2	6.00	12	11	0	1
.....TATCACTAAGTTATAGACCGCTGA	24	0	2	6.00	12	11	0	0
.....TGCGAGCTATAACCTAGTGGAGTAA	25	1	2	4.50	9	9	0	0
.....TGCGAGCTATAACCTAGTGG	20	0	4	4.50	18	15	0	0
.....TGCGAGCTATAACCTAGTGGAGCC	23	2	4	4.25	17	15	0	1
.....TCACTAAGTTATAGACCGC	19	0	2	3.00	6	0	5	0
.....ATCACTAAGTTATAGACCGCT	21	0	2	2.50	5	5	0	0
.....TATCACTAAGTTATAGACCGCT	22	0	2	2.50	5	5	0	0
.....TCACTAAGTTATAGACCGCTGAGC	24	2	2	2.00	4	3	1	0
.....TGCGAGCTATAACCTAGTGGAGTCT	25	2	2	2.00	4	4	0	0
.....TGCGAGCTATAACCTAGTGGAGTAAA	26	2	2	2.00	4	4	0	0
.....GCGAGCTATAACCTAGTGGAG	21	0	2	2.00	4	2	2	0
.....TGCGAGCTATAACCTAGTG	19	0	5	1.80	9	7	1	0
.....TGCGAGCTATAACCTAGTGGAGTAC	25	0	2	1.50	3	3	0	0
.....ATCACTAAGTTATAGACCGCTGT	23	1	2	1.50	3	3	0	0
.....ATCACTAAGTTATAGACCGC	20	0	2	1.50	3	0	3	0
.....TGCGAGCTATAACCTAGTGGAGTCA	25	2	2	1.50	3	2	0	1
.....ACTAGTTATAGACCGCTGA	20	0	2	1.50	3	1	2	0
.....TGCGAGCTATAACCTAGTGGAGTT	24	1	2	1.50	3	2	0	1
.....TGCGAGCTATAACCTAGTGGAGTACG	26	0	2	1.50	3	3	0	0
.....TCACTAAGTTATAGACCGCTGAG	23	1	2	1.50	3	3	0	0
.....CACTAAGTTATAGACCGCTG	20	0	2	1.50	3	0	3	0
.....TGCGAGCTATAACCTAGTGGAGTAT	25	1	2	1.50	3	3	0	0
.....TGCGAGCTATAACCTAGTGGAAT	22	1	4	1.50	6	6	0	0
.....TTGCGAGCTATAACCTAGTGGA	22	0	4	1.25	5	4	0	1
.....TCACTAAGTTATAGACCGCTGTC	23	2	2	1.00	2	2	0	0
.....TGCGAGCTATAACCTAGTGGAGTACGC	27	0	2	1.00	2	2	0	0
.....GCGAGCTATAACCTAGTGGAGT	22	0	2	1.00	2	0	2	0
.....CACTAAGTTATAGACCGCTGA	21	0	2	1.00	2	0	2	0
.....TCACTAAGTTATAGACCGCTGTTT	24	3	2	1.00	2	2	0	0
.....ATCACTAAGTTATAGACCGCTGAA	24	1	2	1.00	2	2	0	0
.....TCACTAAGTTATAGACCGCTGTAT	24	3	2	1.00	2	2	0	0
.....TATCACTAAGTTATAGACCG	20	0	2	1.00	2	2	0	0
.....TATCACTAAGTTATAGACCGCTGT	24	1	2	1.00	2	2	0	0
.....CGAGCTATAACCTAGTGGAG	20	0	2	1.00	2	2	0	0
.....TGCGAGCTATAACCTAGTGGAGTAGT	26	2	2	1.00	2	2	0	0
.....TCACTAAGTTATAGACCGCTGT	23	1	2	1.00	2	2	0	0
.....TCACTAAGTTATAGACCGCTGG	22	1	2	1.00	2	1	0	0
.....TAAGTTATAGACCGCTGACA	20	0	2	1.00	2	2	0	0
.....TGTTTGCGAGCTATAACCTAG	21	0	5	0.80	4	4	0	0
.....TTATAGACCGCTGACAAAATGC	22	0	3	0.67	2	0	0	2
.....TGTTTGCGAGCTATAACCTAGTG	23	0	5	0.60	3	2	0	0
.....TGCGAGCTATAACCTAGTGGAGTTA	25	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTTC	22	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTCG	25	2	2	0.50	1	1	0	0
.....ATCACTAAGTTATAGACCGCTGTCT	24	2	2	0.50	1	1	0	0
.....ATCACTAAGTTATAGACCGCTGATC	25	2	2	0.50	1	1	0	0
.....TATCACTAAGTTATAGACCGCTGAA	25	1	2	0.50	1	0	1	0
.....TATCACTAAGTTATAGACCGCTT	23	1	2	0.50	1	1	0	0
.....TATCACTAAGTTATAGACCGCTTTT	25	3	2	0.50	1	0	1	0
.....TCACTAAGTTATAGACCGCTTG	22	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCG	18	0	2	0.50	1	1	0	0
.....GTATCACTAAGTTATAGACCGT	22	1	2	0.50	1	0	1	0
.....TCACTAAGTTATAGACCGCTCT	22	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTG	24	1	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTAA	26	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTAG	26	2	2	0.50	1	1	0	0
.....GCGAGCTATAACCTAGTGGAGTA	23	0	2	0.50	1	0	1	0
.....TCACTAAGTTATAGACCGCTGTA	23	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTAC	26	2	2	0.50	1	1	0	0
.....ATCACTAAGTTATAGACCGCTGAC	24	0	2	0.50	1	0	1	0
.....TGCGAGCTATAACCTAGTGGAGG	23	1	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTCTTG	24	3	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTCGT	23	3	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTAAA	27	3	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTAGC	26	2	2	0.50	1	1	0	0
.....AAGTTATAGACCGCTGAT	18	1	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTTAT	26	3	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTATCA	27	3	2	0.50	1	1	0	0
.....GAGCTATAACCTAGTGGAG	19	0	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTTA	25	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTTTA	23	3	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTGA	22	1	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTATAT	27	3	4	0.50	2	2	0	0
.....TGTTTGCGAGCTATAACCTAGTG	23	1	5	0.40	2	2	0	0
.....TGCGAGCTATAACCTAGTGCA	21	1	4	0.25	1	1	0	0
.....TGCGAGCTATAACCTAGTGGCTA	23	2	4	0.25	1	1	0	0
.....TGCGAGCTATAACCTAGTGGCG	21	1	4	0.25	1	1	0	0
.....TTGCGAGCTATAACCTAGTGG	21	0	4	0.25	1	1	0	0
.....TGCGAGCTATAACCTAGTGCTC	22	2	4	0.25	1	1	0	0
.....TGTTTGCGAGCTATAACCTAGT	22	0	5	0.20	1	0	1	0
.....TTGCGAGCTATAACCTAGTG	20	0	5	0.20	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1308438-1308599 +	dmo_31	TTGATATATAACTTCCAGCTATAGCAAAAATCTAAGTTAAATCATTTGTTTGCGAGCTATAACCTAGTGGAGTACGCTTATATTCCGTATCACTAAGTTATAGACCGCTGACAAAATGCTTTACTTTGCAAAAGGAAAATCGGAAAAACTATCAACTATGAA

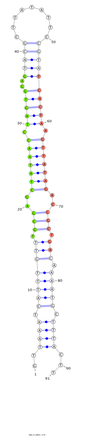
Generated: 09/08/2015 at 08:06 PM

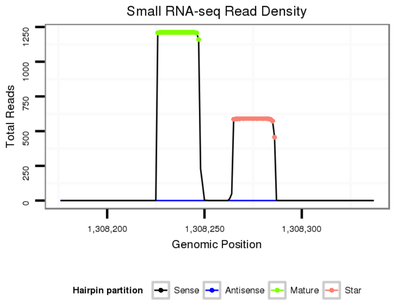
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	1
rescue.confident	1
rescue.candidate	0

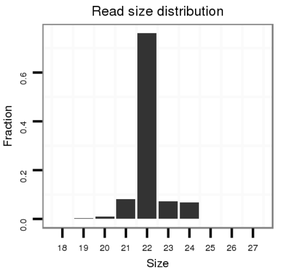
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_32	**scaffold_6308:1308226-1308287 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

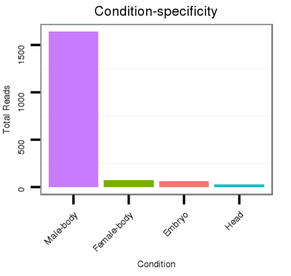
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

mature	star
1. dmo_32 scaffold_6308:1308226-1308247 + 2. dmo_31 scaffold_6308:1308488-1308509 +	1. dmo_32 scaffold_6308:1308265-1308286 + 2. dmo_31 scaffold_6308:1308527-1308548 +

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATTCAATTTACAATCGGTCTATTGCAAAAATCTAAGTTAAATCATTTGTTTGCGAGCTATAACCTAGTGGAGTACGCTTATATTCCGTATCACTAAGTTATAGACCGCTGACAAAATGCTTTACTTTGCAAAAGGAAAATTGAAACAACTATATATACAAAG	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V056 head	V041 embryo	V049 head
********************************..((((.(((((((((.(((..(((((((.(((((..(((((.(((((.........)))))))))).)))))))..)))).)))).)))))...********************************..(((((.(((((((((.(((..(((((((.(((((..(((((.(((((.........)))))))))).)))))))..)))).)))).)))))...********************************..(((((.(((((((((.(((..(((((((.(((((..(((((.(((((.........)))))))))).)))))))..)))).)))).)))))...********************************..(((((.(((((((((.(((..(((((((.(((((..(((((.(((((.........)))))))))).)))))))..)))).)))).)))))...********************************										
.....TGCGAGCTATAACCTAGTGGAG.....	22	0	2	929.50	1859	1801	27	0	15	8	8
.....TCACTAAGTTATAGACCGCTGA.....	22	0	2	430.50	861	734	54	46	9	13	5
.....TGCGAGCTATAACCTAGTGGAGTA.....	24	0	2	115.50	231	209	10	5	1	5	1
.....TGCGAGCTATAACCTAGTGGAGT.....	23	0	2	109.00	218	163	14	28	5	4	4
.....TCACTAAGTTATAGACCGCTG.....	21	0	2	96.00	192	170	16	1	3	2	0
.....TGCGAGCTATAACCTAGTGGA.....	21	0	4	46.25	185	155	16	6	5	0	3
.....ATCACTAAGTTATAGACCGCTGA.....	23	0	2	17.00	34	29	1	3	0	1	0
.....ATCACTAAGTTATAGACCGCTG.....	22	0	2	14.50	29	27	0	0	1	0	1
.....TCACTAAGTTATAGACCGCTGT.....	22	1	2	11.00	22	22	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTC.....	24	1	2	9.50	19	19	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTA.....	25	1	2	9.00	18	17	0	0	0	0	1
.....TCACTAAGTTATAGACCGCT.....	20	0	2	8.50	17	12	4	1	0	0	0
.....TCACTAAGTTATAGACCGCTGAA.....	23	1	2	8.50	17	16	0	1	0	0	0
.....TCACTAAGTTATAGACCGCTGAT.....	23	1	2	7.50	15	14	0	1	0	0	0
.....TGCGAGCTATAACCTAGTGGAT.....	22	1	4	7.25	29	27	0	2	0	0	0
.....TGCGAGCTATAACCTAGTGGAGC.....	23	1	2	6.50	13	1	0	12	0	0	0
.....TATCACTAAGTTATAGACCGCTG.....	23	0	2	6.00	12	11	0	1	0	0	0
.....TATCACTAAGTTATAGACCGCTGA.....	24	0	2	6.00	12	11	0	0	0	0	1
.....TGCGAGCTATAACCTAGTGGAGTAA.....	25	1	2	4.50	9	9	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGG.....	20	0	4	4.50	18	15	3	0	0	0	0
.....TGCGAGCTATAACCTAGTGGACC.....	23	2	4	4.25	17	15	1	0	1	0	0
.....TCACTAAGTTATAGACCGC.....	19	0	2	3.00	6	0	1	5	0	0	0
.....TATCACTAAGTTATAGACCGCT.....	22	0	2	2.50	5	5	0	0	0	0	0
.....ATCACTAAGTTATAGACCGCT.....	21	0	2	2.50	5	5	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAAA.....	26	2	2	2.00	4	4	0	0	0	0	0
.....GCGAGCTATAACCTAGTGGAG.....	21	0	2	2.00	4	2	2	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTCC.....	25	2	2	2.00	4	4	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTGATC.....	24	2	2	2.00	4	3	0	0	1	0	0
.....TGCGAGCTATAACCTAGTG.....	19	0	5	1.80	9	7	1	0	0	0	1
.....TCACTAAGTTATAGACCGCTGAG.....	23	1	2	1.50	3	3	0	0	0	0	0
.....CACTAAGTTATAGACCGCTG.....	20	0	2	1.50	3	0	3	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTACG.....	26	0	2	1.50	3	3	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAT.....	25	1	2	1.50	3	3	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTT.....	24	1	2	1.50	3	2	0	1	0	0	0
.....ATCACTAAGTTATAGACCGCTGT.....	23	1	2	1.50	3	3	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAC.....	25	0	2	1.50	3	3	0	0	0	0	0
.....ATCACTAAGTTATAGACCGC.....	20	0	2	1.50	3	0	3	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTCA.....	25	2	2	1.50	3	2	0	0	1	0	0
.....ACTAAGTTATAGACCGCTGA.....	20	0	2	1.50	3	1	2	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAT.....	22	1	4	1.50	6	6	0	0	0	0	0
.....TTGCGAGCTATAACCTAGTGGA.....	22	0	4	1.25	5	4	0	0	1	0	0
.....TCACTAAGTTATAGACCGCTGT.....	22	1	2	1.00	2	1	0	0	0	1	0
.....TGCGAGCTATAACCTAGTGGAGTAT.....	26	2	2	1.00	2	2	0	0	0	0	0
.....ATCACTAAGTTATAGACCGCTGT.....	23	1	2	1.00	2	2	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTGTT.....	23	2	2	1.00	2	2	0	0	0	0	0
.....ATCACTAAGTTATAGACCGCTGAA.....	24	1	2	1.00	2	2	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTGTTT.....	24	3	2	1.00	2	2	0	0	0	0	0
.....TATCACTAAGTTATAGACCGCTGT.....	24	1	2	1.00	2	2	0	0	0	0	0
.....CGAGCTATAACCTAGTGGAG.....	20	0	2	1.00	2	2	0	0	0	0	0
.....GCGAGCTATAACCTAGTGGAGT.....	22	0	2	1.00	2	0	2	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTACGC.....	27	0	2	1.00	2	2	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTGAA.....	24	3	2	1.00	2	2	0	0	0	0	0
.....TAAGTTATAGACCGCTGACA.....	20	0	2	1.00	2	2	0	0	0	0	0
.....TATCACTAAGTTATAGACCG.....	20	0	2	1.00	2	2	0	0	0	0	0
.....CACTAAGTTATAGACCGCTGA.....	21	0	2	1.00	2	0	2	0	0	0	0
.....TGTTTGCGAGCTATAACCTAG.....	21	0	5	0.80	4	4	0	0	0	0	0
.....TTATAGACCGCTGACAAAATGC.....	22	0	3	0.67	2	0	0	2	0	0	0
.....TGTTTGCGAGCTATAACCTAGTG.....	23	0	5	0.60	3	2	0	0	0	1	0
.....AAGTTATAGACCGCTGAT.....	18	1	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAA.....	26	2	2	0.50	1	1	0	0	0	0	0
.....GCGAGCTATAACCTAGTGGAGTA.....	23	0	2	0.50	1	0	1	0	0	0	0
.....TATCACTAAGTTATAGACCGCTT.....	23	1	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAAG.....	26	2	2	0.50	1	1	0	0	0	0	0
.....TATCACTAAGTTATAGACCGCTTTT.....	25	3	2	0.50	1	0	1	0	0	0	0
.....TCACTAAGTTATAGACCGCTTTA.....	23	3	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAAAA.....	27	3	2	0.50	1	1	0	0	0	0	0
.....ATCACTAAGTTATAGACCGCTGAC.....	24	0	2	0.50	1	0	0	1	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTATC.....	26	2	2	0.50	1	1	0	0	0	0	0
.....GAGCTATAACCTAGTGGAG.....	19	0	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAGC.....	26	2	2	0.50	1	1	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTGTA.....	23	2	2	0.50	1	1	0	0	0	0	0
.....ATCACTAAGTTATAGACCGCTGTT.....	24	2	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTATCA.....	27	3	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTTT.....	25	2	2	0.50	1	1	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTGT.....	22	1	2	0.50	1	1	0	0	0	0	0
.....ATCACTAAGTTATAGACCGCTGATC.....	25	2	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTTAT.....	26	3	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTTA.....	25	2	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTCG.....	25	2	2	0.50	1	1	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTCT.....	22	2	2	0.50	1	1	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTTG.....	22	2	2	0.50	1	1	0	0	0	0	0
.....TCACTAAGTTATAGACCG.....	18	0	2	0.50	1	1	0	0	0	0	0
.....GTATCACTAAGTTATAGACCGT.....	22	1	2	0.50	1	0	1	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGC.....	23	1	2	0.50	1	1	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTGTTG.....	24	3	2	0.50	1	1	0	0	0	0	0
.....TATCACTAAGTTATAGACCGCTGAA.....	25	1	2	0.50	1	0	1	0	0	0	0
.....TCACTAAGTTATAGACCGCTCGT.....	23	3	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTG.....	24	1	2	0.50	1	1	0	0	0	0	0
.....TCACTAAGTTATAGACCGCTTC.....	22	2	2	0.50	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGAGTAAT.....	27	3	4	0.50	2	2	0	0	0	0	0
.....TGTTTGCGAGCTATAACCTAGTG.....	23	1	5	0.40	2	2	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGCTC.....	22	2	4	0.25	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGACA.....	23	2	4	0.25	1	1	0	0	0	0	0
.....TTGCGAGCTATAACCTAGTGG.....	21	0	4	0.25	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGC.....	21	1	4	0.25	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGGT.....	21	1	4	0.25	1	1	0	0	0	0	0
.....TGTTTGCGAGCTATAACCTAGT.....	22	0	5	0.20	1	0	0	1	0	0	0
.....TTGCGAGCTATAACCTAGTG.....	20	0	5	0.20	1	0	1	0	0	0	0

Anti-sense strand reads

TAAGTTAAATGTTAGCCAGATAACGTTTTTAGATTCAATTTAGTAAACAAACGCTCGATATTGGATCACCTCATGCGAATATAAGGCATAGTGATTCAATATCTGGCGACTGTTTTACGAAATGAAACGTTTTCCTTTTAACTTTGTTGATATATATGTTTC	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V056 head	V110 male body
********************************..((((.(((((((((.(((..(((((((.(((((..(((((.(((((.........)))))))))).)))))))..)))).)))).)))))...********************************..(((((.(((((((((.(((..(((((((.(((((..(((((.(((((.........)))))))))).)))))))..)))).)))).)))))...********************************..(((((.(((((((((.(((..(((((((.(((((..(((((.(((((.........)))))))))).)))))))..)))).)))).)))))...********************************								
.....TGCGAGCTATAACCTAGTGGAG.....	22	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTGA.....	22	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTA.....	24	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGT.....	23	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTG.....	21	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGA.....	21	2	4	0.50	1	1	0	0
.....ATCACTAAGTTATAGACCGCTGA.....	23	2	2	0.50	1	1	0	0
.....ATCACTAAGTTATAGACCGCTG.....	22	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTGT.....	22	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTC.....	24	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTA.....	25	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGG.....	20	2	4	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGACC.....	23	2	4	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGC.....	19	2	2	0.50	1	1	0	0
.....TATCACTAAGTTATAGACCGCT.....	22	2	2	0.50	1	1	0	0
.....ATCACTAAGTTATAGACCGCT.....	21	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTAAA.....	26	2	2	0.50	1	1	0	0
.....GCGAGCTATAACCTAGTGGAG.....	21	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTCC.....	25	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTGATC.....	24	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTG.....	19	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTGAG.....	23	2	2	0.50	1	1	0	0
.....CACTAAGTTATAGACCGCTG.....	20	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTACG.....	26	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTAT.....	25	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTT.....	24	2	2	0.50	1	1	0	0
.....ATCACTAAGTTATAGACCGCTGT.....	23	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTGTT.....	23	2	2	0.50	1	1	0	0
.....ATCACTAAGTTATAGACCGCTGAA.....	24	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTGTTT.....	24	2	2	0.50	1	1	0	0
.....TATCACTAAGTTATAGACCGCTGT.....	24	2	2	0.50	1	1	0	0
.....CGAGCTATAACCTAGTGGAG.....	20	2	2	0.50	1	1	0	0
.....GCGAGCTATAACCTAGTGGAGT.....	22	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTACGC.....	27	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTGAA.....	24	2	2	0.50	1	1	0	0
.....TAAGTTATAGACCGCTGACA.....	20	2	2	0.50	1	1	0	0
.....TATCACTAAGTTATAGACCG.....	20	2	2	0.50	1	1	0	0
.....CACTAAGTTATAGACCGCTGA.....	21	2	2	0.50	1	1	0	0
.....TGTTTGCGAGCTATAACCTAG.....	21	2	5	0.50	1	1	0	0
.....TTATAGACCGCTGACAAAATGC.....	22	2	3	0.50	1	1	0	0
.....TGTTTGCGAGCTATAACCTAGTG.....	23	2	5	0.50	1	1	0	0
.....AAGTTATAGACCGCTGAT.....	18	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTAA.....	26	2	2	0.50	1	1	0	0
.....GCGAGCTATAACCTAGTGGAGTA.....	23	2	2	0.50	1	1	0	0
.....TATCACTAAGTTATAGACCGCTT.....	23	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTAAG.....	26	2	2	0.50	1	1	0	0
.....TATCACTAAGTTATAGACCGCTTTT.....	25	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTTTA.....	23	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTAAAA.....	27	2	2	0.50	1	1	0	0
.....ATCACTAAGTTATAGACCGCTGAC.....	24	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTATC.....	26	2	2	0.50	1	1	0	0
.....GAGCTATAACCTAGTGGAG.....	19	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTAGC.....	26	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTGTA.....	23	2	2	0.50	1	1	0	0
.....ATCACTAAGTTATAGACCGCTGTT.....	24	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTATCA.....	27	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTTT.....	25	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTGT.....	22	2	2	0.50	1	1	0	0
.....ATCACTAAGTTATAGACCGCTGATC.....	25	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTTAT.....	26	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTTA.....	25	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTCG.....	25	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTCT.....	22	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTTG.....	22	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCG.....	18	2	2	0.50	1	1	0	0
.....GTATCACTAAGTTATAGACCGT.....	22	2	2	0.50	1	0	1	0
.....TGCGAGCTATAACCTAGTGGAGC.....	23	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTGTTG.....	24	2	2	0.50	1	1	0	0
.....TATCACTAAGTTATAGACCGCTGAA.....	25	2	2	0.50	1	0	1	0
.....TCACTAAGTTATAGACCGCTCGT.....	23	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTG.....	24	2	2	0.50	1	1	0	0
.....TCACTAAGTTATAGACCGCTTC.....	22	2	2	0.50	1	1	0	0
.....TGCGAGCTATAACCTAGTGGAGTAAT.....	27	2	4	0.50	2	2	0	0
.....TGTTTGCGAGCTATAACCTAGTG.....	23	2	5	0.40	2	2	0	0
.....TGCGAGCTATAACCTAGTGCTC.....	22	2	4	0.25	1	1	0	0
.....TGCGAGCTATAACCTAGTGGACA.....	23	2	4	0.25	1	1	0	0
.....TTGCGAGCTATAACCTAGTGG.....	21	2	4	0.25	1	1	0	0
.....TGCGAGCTATAACCTAGTGGC.....	21	2	4	0.25	1	1	0	0
.....TGCGAGCTATAACCTAGTGGT.....	21	2	4	0.25	1	1	0	0
.....TGTTTGCGAGCTATAACCTAGT.....	22	2	5	0.20	1	0	0	0
.....TTGCGAGCTATAACCTAGTG.....	20	2	5	0.20	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1308176-1308337 +	dmo_32	ATTCAATTTACAATCGGTCTATTGCAAAAATCTAAGTTAAATCATTTGTTTGCGAGCTATAACCTAGTGGAGTACGCTTATATTCCGTATCACTAAGTTATAGACCGCTGACAAAATGCTTTACTTTGCAAAAGGAAAATTGAAACAACTATATATACAAAG

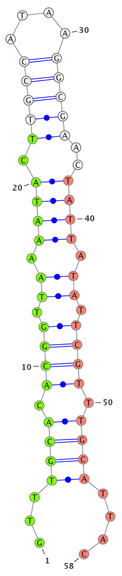
Generated: 09/08/2015 at 08:07 PM

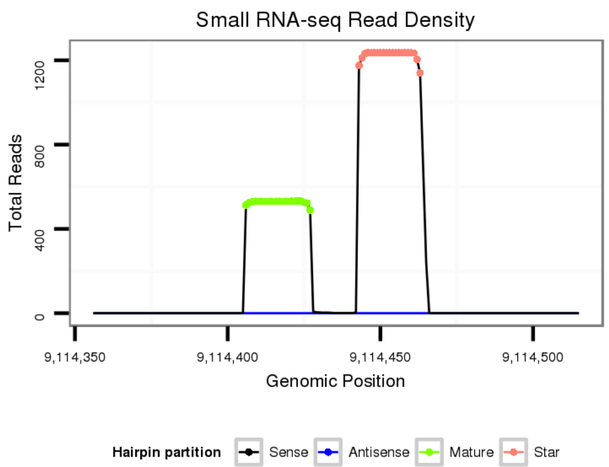
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	1
rescue.confident	1
rescue.candidate	0

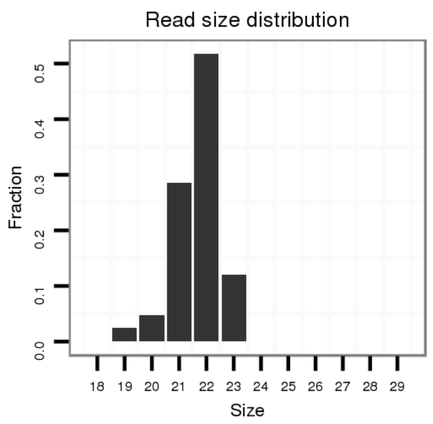
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_717	**scaffold_6473:9114406-9114465 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

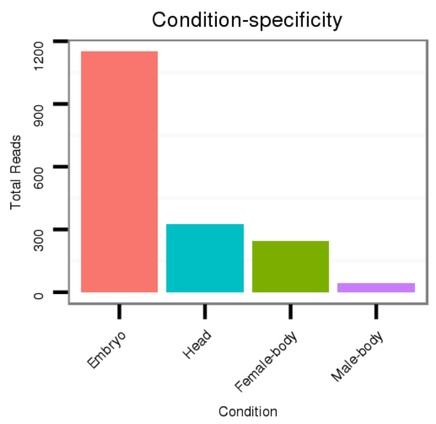
Legend: mature star mismatch in alignment mismatch in read

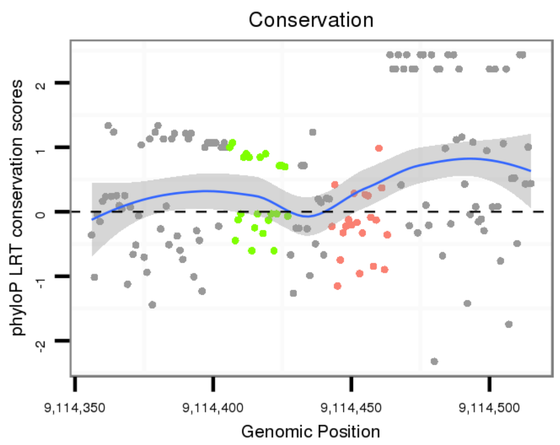
Predicted structure











dmo_717_annot | 14.9 |

Show Alternate Folds

Flybase annnotation

intron [DmojGI15720-in]; CDS [DmojGI15720-cds]; CDS [DmojGI15720-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATGACGATGACAACGCCAACGCCGATGATGATGTTGACAGGGAATTCGAGGTTTGCACACGGTTAAAATACTTGCCATAAGGCGAACTATTATATTCGTTTGCATTACAGGTGGAGGCGATTGTAGGTCACAAGTCGAAGAACGGCGAGTCGTTTTTCCT **********...((((.((((.((.((((.(((((....)))))..))))).)).)))).))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V056 head	V041 embryo	V049 head	V110 male body
.....GTTTGCACACGGTTAAAATACT.....	22	0	1	466.00	466	287	44	49	52	15	19
.....TATTATATTCGTTTGCATTAC.....	21	0	1	440.00	440	266	65	41	29	28	11
.....TATTATATTCGTTTGCATTACA.....	22	0	1	429.00	429	244	48	60	38	35	4
.....TATTATATTCGTTTGCATTACAG.....	23	0	1	208.00	208	105	17	22	36	24	4
.....TATTATATTCGTTTGCATTA.....	20	0	1	63.00	63	22	20	8	2	8	3
.....GTTTGCACACGGTTAAAATACC.....	22	1	1	51.00	51	51	0	0	0	0	0
.....ATTATATTCGTTTGCATTACAGT.....	23	1	1	47.00	47	39	0	1	5	1	1
.....TTATATTCGTTTGCATTACAGT.....	22	1	1	42.00	42	29	6	3	2	0	2
.....GTTTGCACACGGTTAAAATAC.....	21	0	1	32.00	32	26	6	0	0	0	0
.....TATTATATTCGTTTGCATT.....	19	0	1	31.00	31	5	7	13	1	5	0
.....ATTATATTCGTTTGCATTACAG.....	22	0	1	19.00	19	7	6	1	2	2	1
.....TTATATTCGTTTGCATTACAG.....	21	0	1	13.00	13	1	5	3	2	1	1
.....ATTATATTCGTTTGCATTACA.....	21	0	1	12.00	12	5	4	1	0	2	0
.....TTATATTCGTTTGCATTACAGC.....	22	1	1	9.00	9	8	0	0	1	0	0
.....ATTATATTCGTTTGCATTACAGC.....	23	1	1	8.00	8	8	0	0	0	0	0
.....TTTGCACACGGTTAAAATACT.....	21	0	1	8.00	8	2	6	0	0	0	0
.....TTATATTCGTTTGCATTACA.....	20	0	1	7.00	7	1	1	3	1	1	0
.....GTTTGCACACGGTTAAAAT.....	19	0	1	6.00	6	0	2	1	0	2	1
.....TATTATATTCGTTTGCATTACAGT.....	24	1	1	6.00	6	6	0	0	0	0	0
.....TATTATATTCGTTTGCATTACAGC.....	24	1	1	5.00	5	5	0	0	0	0	0
.....TATTATATTCGTTTGCATTACT.....	22	1	1	4.00	4	0	0	1	2	1	0
.....TTGCACACGGTTAAAATACT.....	20	0	1	4.00	4	4	0	0	0	0	0
.....ATTATATTCGTTTGCATTAC.....	20	0	1	4.00	4	1	3	0	0	0	0
.....TATTATATTCGTTTGCATTACAT.....	23	1	1	4.00	4	1	0	1	0	2	0
.....TGCACACGGTTAAAATACT.....	19	0	1	3.00	3	2	0	0	0	0	1
.....ATTATATTCGTTTGCATTACAGA.....	23	1	1	3.00	3	2	1	0	0	0	0
.....GTTTGCACACGGTTAAAATA.....	20	0	1	3.00	3	1	2	0	0	0	0
.....CTATTATATTCGTTTGCATTACA.....	23	0	1	3.00	3	2	0	1	0	0	0
.....TATTATATTCGTTTGCATTACAC.....	23	1	1	3.00	3	3	0	0	0	0	0
.....TTTGCACACGGTTAAAATAC.....	20	0	1	2.00	2	0	2	0	0	0	0
.....GTTTGCACACGGTTAAAATACTT.....	23	0	1	2.00	2	1	1	0	0	0	0
.....TTATATTCGTTTGCATTACAGA.....	22	1	1	2.00	2	0	1	0	0	1	0
.....TATATTCGTTTGCATTACA.....	19	0	1	2.00	2	2	0	0	0	0	0
.....TTATATTCGTTTGCATTAC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TATTATATTCGTTTGCATTG.....	20	1	1	1.00	1	0	0	0	0	1	0
.....ATATTCGTTTGCATTACAGC.....	20	1	1	1.00	1	1	0	0	0	0	0
.....GTTTGCACACGGTTAAAATACTTG.....	24	0	1	1.00	1	0	1	0	0	0	0
.....TATATTCGTTTGCATTAC.....	18	0	1	1.00	1	0	1	0	0	0	0
.....TATTATATTCGTTTGCATTAA.....	21	1	1	1.00	1	0	0	0	0	1	0
.....TTTGCACACGGTTAAAATACTGC.....	23	2	1	1.00	1	0	0	0	0	1	0
.....TATTATATTCGTTTGCATTACC.....	22	1	1	1.00	1	0	0	0	0	1	0
.....TATATTCGTTTGCATTACAG.....	20	0	1	1.00	1	0	1	0	0	0	0
.....AAATACTTGCCATAAGGCGAACTATT.....	26	0	1	1.00	1	0	1	0	0	0	0
.....GTTTGCACACGGTTAAAATACTTGCCAT.....	28	0	1	1.00	1	1	0	0	0	0	0
.....GTTTGCACACGGTTAAAATACTTGC.....	25	0	1	1.00	1	0	1	0	0	0	0
.....GTTTGCACACGGTTAAAATACTTGCCATA.....	29	0	1	1.00	1	0	1	0	0	0	0
.....TATTATATTCGTTTGCAT.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TATTATATTCGTTTGCATTACAGA.....	24	1	1	1.00	1	0	1	0	0	0	0
.....TATTATATTCGTTTGCATTACCT.....	23	2	1	1.00	1	0	0	0	1	0	0
.....TTTGCACACGGTTAAAATACTT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TGCACACGGTTAAAATACTC.....	20	1	1	1.00	1	1	0	0	0	0	0
.....GTTTGCACACGGTTAAAATACTG.....	23	1	1	1.00	1	0	0	0	1	0	0
.....ATTATATTCGTTTGCATTACAAT.....	23	2	1	1.00	1	1	0	0	0	0	0
.....ATTATATTCGTTTGCATTA.....	19	0	1	1.00	1	0	1	0	0	0	0
.....ATTATATTCGTTTGCATTACATT.....	23	2	1	1.00	1	0	0	1	0	0	0
.....TATTATATTCGTTTGCATA.....	19	1	2	0.50	1	0	0	1	0	0	0

Anti-sense strand reads

TACTGCTACTGTTGCGGTTGCGGCTACTACTACAACTGTCCCTTAAGCTCCAAACGTGTGCCAATTTTATGAACGGTATTCCGCTTGATAATATAAGCAAACGTAATGTCCACCTCCGCTAACATCCAGTGTTCAGCTTCTTGCCGCTCAGCAAAAAGGA **********...((((.((((.((.((((.(((((....)))))..))))).)).)))).))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V049 head
.....AGGTGGAGGCGATTGTAGGTCACAAGTCGAAGAACGGCGAGTCGTTTTTCCT	44	0	1	466.00	466	287	44	49
.....AGGTGGAGGCGATTGTAGGTCACAAGTCGAAGAACGGCGAGTCGTTTTTCCT	44	0	1	466.00	466	287	44	49

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:9114356-9114515 +	dmo_717	ATGACGATGACAAC------GCCAACGCCGATGATGATGTTG---ACAGGGAATTCGAGGTT----------TGCACACGGTTAAAATAC----------T---------TGCCATAAGGCGAACTATTAT---ATTC----------GTTTGCATTACAGGTGGAGGCGATTGTAGGTCACAAGTCGAAGAACGGCGAGTCGTTTTTCCT
droVir3	scaffold_12726:1048300-1048454 _	dvi_1873	AGGACGATGACAAT------AT------AGAT---------------GCCGAATTCGAGGTACACAAAATATTA-GC----TGCACCGGCTGACA---------------AATT---------GCTTATTT-------AAACAAATTTCATTTG----------AATTGCATAACAGGTTGAGGCCATTGTGGCCATAAGACCAAGCGGGCGAATCGTATTTCCT
droGri2	scaffold_14853:10002475-10002627 -		AGGAGAAGACGACAC------A-----ACGACGAGAAGTGGGAGGCAGAATTGAGGTAAGCT----ATTT-GC----------ATTTGCAGGAGAAT----AAGACGATTTTATTATTG-------AA----------TGTATCTAGGTGGAGGCCATCGTGGGTCACAAGACCAAGAACGGAGAATCTATTTTCCT
droWil2	scf2_1100000004909:7203628-7203787 +		TAGCGATGGGGGA------GAAGAACGGAAGCAGAAGATG---AAAGGAATTGAGGTTTGTC----ATTA-GT----------TTTCGAA-----ACAAATCA--------GTTTTTTAAGTCAAGTGCTCTCTT----------TTAAAAGGTGGAAGCCATTGTTGGTCATAAGACGATAAATGCGTCTCGTACTTCTT
dp5	XL_grouple:4445183-4445387 +	dps_2682	CTATCGATGACGAATCCTTAGCTAAGTCCGATGACGATTTG---ACAC----------AAAGCAGCAAGATGCCGACACAGAGTTGGAGTAGGAAGTGAGTGATAGAG-----TG-GGACA--------GTCGCTCTGCGTTAGAGTTTGCTTTAACCTAAAAAAATCTGTAAATTTCTAGGTGGACGCCATTCTTGGCCACAGGACGGTGCGTGGCGCCTCCTATTTTCT
droPer2	scaffold_17:1387278-1387483 +		CTGTCGATGACGAAATCCTTAGCTAAGTCCGATGACGATTTG---ACAC----------AAAGCAGCAAGATGTCGACACAGAGTTGGAGTAGGAAGTGAGTAAGTGATAGAG-----TAAAGACA--------GTCGCTCTGCGTTAGAGTTTGCTTTAACCTAAAAAAATCTGTAAATTTCTAGGTGGACGCCATTATTGGCCACAAGAAGGTGCGCGGCGCCTCCTATTTTCT
droAna3	scaffold_13248:1824923-1824978 +		---
droBip1	scf7180000395544:37352-37407 -		---
droKik1	scf7180000302592:1540195-1540267 +		TAA---
droEle1	scf7180000490996:231476-231563 +		AT---
droRho1	scf7180000779333:759428-759479 -		---
droBia1	scf7180000301760:3547210-3547265 -		---
droTak1	scf7180000415210:498587-498642 +		---
droEug1	scf7180000409271:601223-601274 -		---

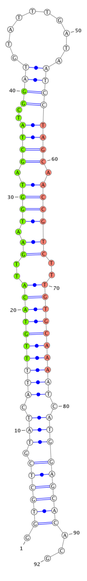
Generated: 09/08/2015 at 07:00 PM

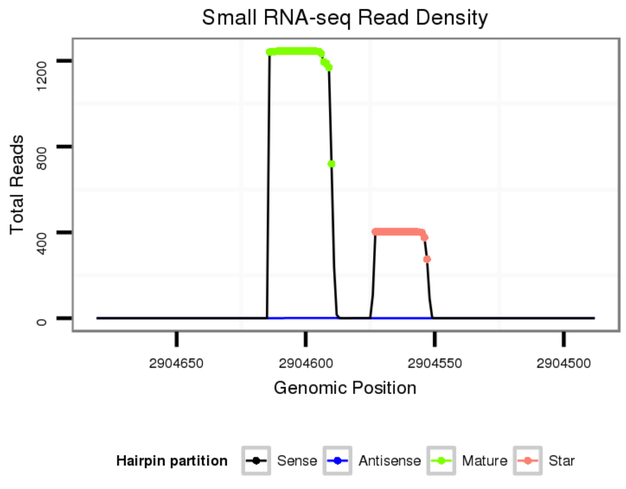
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

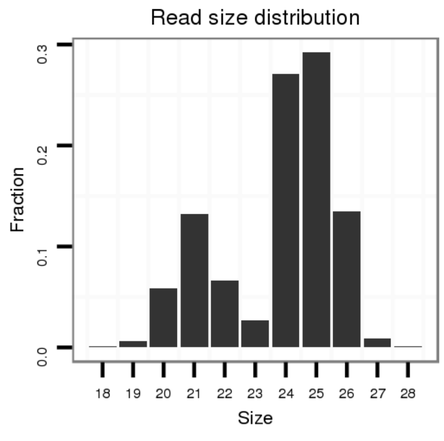
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_203	**scaffold_6328:2904538-2904631 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

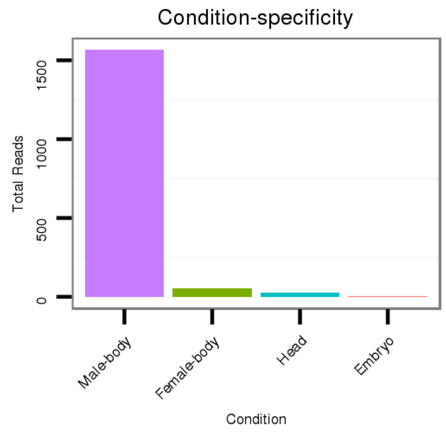
Legend: mature star mismatch in alignment mismatch in read

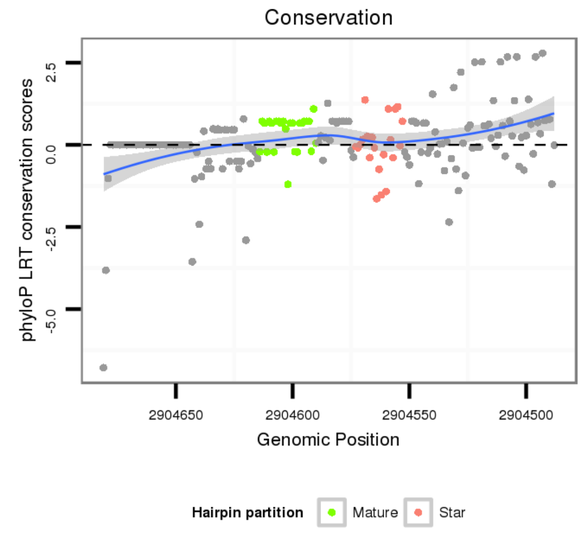
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TCATTCAAATGCAGTTGAATTCACGCAAAGTTCTTTGAGAATCGAGGAGAGCGGTGCTCGTATCATTTTGTACATTGAATGGTAGCTATCGGATGTATTTGATAATCCTAGCAACCGTCTTTGTGCAAAATCATGGAGCACACGAGCAGCAAAATGATAATGATATAATAATGATAATGCGAATGATAATAAGA **********.(((((((.(((.((((((((((..((.((((.((((..((((.........))))))))).))))))..))))))))))..)))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head	V049 head	M060 embryo	V041 embryo
.....TTGTACATTGAATGGTAGCTATCGG.....	25	0	1	481.00	481	474	5	1	0	1	0
.....TTGTACATTGAATGGTAGCTATCG.....	24	0	1	446.00	446	436	3	3	4	0	0
.....TTGTACATTGAATGGTAGCTATCGGA.....	26	0	1	221.00	221	212	3	2	2	2	0
.....TAGCAACCGTCTTTGTGCAAA.....	21	0	1	149.00	149	133	12	2	2	0	0
.....TAGCAACCGTCTTTGTGCAA.....	20	0	1	71.00	71	64	6	0	1	0	0
.....TAGCAACCGTCTTTGTGCAAAA.....	22	0	1	66.00	66	58	5	2	1	0	0
.....TTGTACATTGAATGGTAGCTA.....	21	0	1	38.00	38	35	1	2	0	0	0
.....CTAGCAACCGTCTTTGTGCAAA.....	22	0	1	35.00	35	31	4	0	0	0	0
.....CTAGCAACCGTCTTTGTGCAA.....	21	0	1	30.00	30	29	1	0	0	0	0
.....TTGTACATTGAATGGTAGCTATCGT.....	25	1	1	23.00	23	23	0	0	0	0	0
.....TTGTACATTGAATGGTAGCTATCGGAA.....	27	1	1	23.00	23	23	0	0	0	0	0
.....CTAGCAACCGTCTTTGTGCAAAA.....	23	0	1	22.00	22	20	1	1	0	0	0
.....TTGTACATTGAATGGTAGCTATC.....	23	0	1	19.00	19	16	3	0	0	0	0
.....CTAGCAACCGTCTTTGTGCA.....	20	0	1	16.00	16	13	3	0	0	0	0
.....TTGTACATTGAATGGTAGCTATCGTC.....	26	2	1	15.00	15	14	1	0	0	0	0
.....TTGTACATTGAATGGTAGCTATCGGAT.....	27	0	1	14.00	14	14	0	0	0	0	0
.....TTGTACATTGAATGGTAGCTATCGGC.....	26	1	1	12.00	12	11	1	0	0	0	0
.....TTGTACATTGAATGGTAGCTATCGGT.....	26	1	1	10.00	10	10	0	0	0	0	0
.....TTGTACATTGAATGGTAGCT.....	20	0	1	10.00	10	10	0	0	0	0	0
.....TTGTACATTGAATGGTAGCTAT.....	22	0	1	8.00	8	6	2	0	0	0	0
.....TAGCAACCGTCTTTGTGCA.....	19	0	1	7.00	7	4	2	0	1	0	0
.....TTGTACATTGAATGGTAGCTATCGGAAA.....	28	2	1	4.00	4	4	0	0	0	0	0
.....TTGTACATTGAATGGTAGCTATCGC.....	25	1	1	4.00	4	3	0	0	1	0	0
.....TTGTACATTGAATGGTAGCTATCGA.....	25	1	1	3.00	3	2	0	1	0	0	0
.....CTAGCAACCGTCTTTGTGC.....	19	0	1	3.00	3	2	1	0	0	0	0
.....TTGTACATTGAATGGTAGCTATCT.....	24	1	1	2.00	2	2	0	0	0	0	0
.....TTGTACATTGAATGGTAGCTATCTC.....	25	2	1	2.00	2	2	0	0	0	0	0
.....TTGTACATTGAATGGTAGCTATCGGATC.....	28	1	1	2.00	2	2	0	0	0	0	0
.....TAGCAACCGTCTTTGTGCAAAT.....	22	1	1	2.00	2	2	0	0	0	0	0
.....TTGTACATTGAATGGTAGCTATCC.....	24	1	1	2.00	2	2	0	0	0	0	0
.....TTGTACATTGAATGGTAGCTATCGGATG.....	28	0	1	2.00	2	2	0	0	0	0	0
.....TAGCAACCGTCTTTGTGCAAAAT.....	23	0	1	2.00	2	2	0	0	0	0	0
.....TTGTACATTGAATGGTAGCTC.....	21	1	1	1.00	1	0	1	0	0	0	0
.....CTAGCAACCGTCTTTGTGCAC.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TTGTACATTGAATGGTAG.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TACATTGAATGGTAGCTATCGG.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TTGTACATTGAATGGTAGCTATTC.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TGTACATTGAATGGTAGCTATCG.....	23	0	1	1.00	1	0	1	0	0	0	0
.....TAGCAACCGTCTTTGTGCAAG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TAGCAACCGTCTTTGTGCATG.....	21	2	1	1.00	1	0	0	0	1	0	0
.....TTGTACATTGAATGGTAGC.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TTGTACATTGAATGGTAGCTATCGGG.....	26	1	1	1.00	1	0	0	0	0	0	1
.....TGATAATCCTAGCAACCGTCTTTGTG.....	26	0	1	1.00	1	0	1	0	0	0	0
.....CTAGCAACCGTCTTTGTGCAAAAT.....	24	0	1	1.00	1	0	1	0	0	0	0
.....TAGCAACCGTCTTTGTGCAATT.....	22	2	1	1.00	1	1	0	0	0	0	0
.....TAGCAACCGTCTTTGTGCAAAAA.....	23	1	1	1.00	1	0	1	0	0	0	0
.....TACATTGAATGGTAGCTATCG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TTGTACATTGAATGGTAGCTT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....CTAGCAACCGTCTTTGTGCAAAAAA.....	25	2	1	1.00	1	1	0	0	0	0	0
.....ATTGAATGGTAGCTATCG.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TTGTACATTGAATGGTAGCTATCTT.....	25	2	1	1.00	1	1	0	0	0	0	0
.....TAGCAACCGTCTTTGTGCAAATC.....	23	2	1	1.00	1	1	0	0	0	0	0
.....TGTACATTGAATGGTAGCTATCGGA.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TTGTACATTGAATGGTAGCTATCGGAAT.....	28	2	1	1.00	1	1	0	0	0	0	0
.....CTAGCAACCGTCTTTGTGCAAAATCT.....	26	1	1	1.00	1	1	0	0	0	0	0
.....TAGCAACCGTCTTTGTGCAC.....	20	1	1	1.00	1	0	1	0	0	0	0
.....TTGTACATTGAATGGTAGCTATCGGTC.....	27	2	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

AGTAAGTTTACGTCAACTTAAGTGCGTTTCAAGAAACTCTTAGCTCCTCTCGCCACGAGCATAGTAAAACATGTAACTTACCATCGATAGCCTACATAAACTATTAGGATCGTTGGCAGAAACACGTTTTAGTACCTCGTGTGCTCGTCGTTTTACTATTACTATATTATTACTATTACGCTTACTATTATTCT **********.(((((((.(((.((((((((((..((.((((.((((..((((.........))))))))).))))))..))))))))))..)))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V049 head
.....TAACTTACCATCGATAGCCTA.....	21	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6328:2904488-2904681 -	dmo_203	TCATTCAAATGCAGTTGAATTCACGCAAAGTTCTTTGAGAATCGAGGAGAGCGGTGCTCGTATCATTTTGTACATTGAATGGTAGCTATCGGATGTATTTGATAAT----------CCTAGCAACCGTCTTTGTGCAAAATCATGGAGCACACGAG---C---AGCAAAA----------TGATAATGAT--ATA----------ATAATGATAATGCGAATGATAATAAGA
droVir3	scaffold_13042:912378-912496 -	dvi_185	TGA----------GAAGCGCATAGAGAGGCGGCAATATCATATTGTACATTGAACGGTAGCTATCGGATGTATTTGATAAT----------CCTAGCAACCGTCTTTGTGCAAAACGATGTGGCACAGATT---C---------------------------AACATAA
droGri2	scaffold_15081:2048219-2048334 -		GTG----------CCTA----------TATCAATCTGAACTTTGA-GGGCTGCTATTGGATGTATTTGATAAT----------CCTAGCAACCACCATCGTCACATTGATGCGGCACACAAT---C---------------------------ACA---AATAATTACAAAATAATAA--
droWil2	scf2_1100000003148:747-800 -		ATG----------AGA----------GA-CAAAA----------CAATAATAATA-ATA----------ATAATAATAATAATAATAATAA
dp5	Unknown_singleton_3905:292-339 +		AAT----------AA----------T-----TA----------TAATAATAATA-ATA----------AAAATAATAATAATAAAATAAGA
droPer2	scaffold_36:275281-275323 +		AA----------T-----TGCTGAGAATA-TTA----------GTAATAATAGTAGCAATAATAATAATT
droAna3	scaffold_13266:18390601-18390668 +		AAA----------TGACGA----------T----------GAAGA----------CGAGGATGAGGA----------TGAGGAAGATA-ATG----------AGGAGGAAGATGAAGATGATGAAAACG
droBip1	scf7180000396735:1662313-1662389 +		TGA----------GGAAGA----------C----------GATGAAGG----------CGACG---AAGATGAAGATAA----------TGAAGATGAAG-ATG----------AAGATGACAATGATAAGGATAATGAAG
droKik1	scf7180000302476:2277506-2277573 -		CAT----------GGAGTA----------TT----------T----------CG---GTAAGATAAATTA----------TAATAATAATA-ATA----------ATAATAATAATAATAATAATAAA
droFic1	scf7180000453535:5506-5549 -		CAT----------AGTAAT----------GAAA----------ATAATGATAATGATAATTATAATAAA
droEle1	scf7180000490478:10231-10306 -		TAA----------TGTA----------TGATT----------A----------T----------GATGA----------TTATGATGATTATGATG----------TATTATGATG-ATT----------ATGATGATTATGATGATGATGATGATG
droRho1	scf7180000776936:32961-33004 -		AA----------A----------TAATAATAATA-ATA----------ATAATAATAATAATAATAATAAA
droBia1	scf7180000302430:15944-15990 -		GCA----------A----------TA----------ATAATGATAATAATAATAACAATAAA
droTak1	scf7180000414393:263835-263896 -		AAA----------AT----------AATGATAATAATAATAAAATGATAAAA-ATG----------ATAATAATGATAGTAATGATAATAATG
droEug1	scf7180000409676:103755-103837 +		TAC----------AAA----------TCAA----------AATGTAAACAAAGAATAA----------TAATAATA-TTATAATAAAAATAATAATAATTAATAATATTA
dm3	chr4:1241571-1241665 +		TAA----------TAATCA----------TA----------ATAAT-------CATAATAAT-GATAATAATCATAATA----------ATCATAATAATATTA----------TAATAATCATA-ATA----------ATCATAATAATCATAATAATCATAATA
droSim2	4:53449-53520 -		AAA----------AGTA----------TTAAG----------AAT---------AAAAA----------TAATAACAATAA----CGATA-AAATA-AAA----------ATAACAATAATAAATAATAATAATA
droSec2	scaffold_28:196669-196768 +		GTA----------GATA----------TC----------GTCAGAAT-------CTT-GTATA-GATGGTATGTATGTTGGCTCAA----------AAAAAAAAAAAA----------TAATAATAATA-ATA----------ATAATAATAATAATAATAATAACA
droYak3	v2_chr3L_random_080:1652-1739 -		CGT----------TAATT----------TTTCA----------AAAG-------GAG-GGAGATGTA-GT----------ATATA---GGA-ACATAATAA----------TTATAATAATA-ATA----------ATAATAATAATAATAATAATAAA
droEre2	scaffold_4855:122527-122584 -		GCA----------TAATAA----------T----------AAATAA----------TAATAACAATA-ATA----------ATAATAATAATAATAATAATAAA

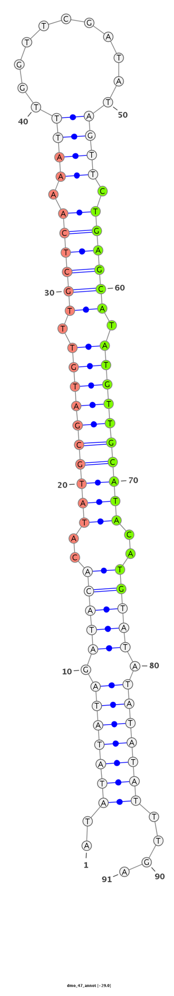
Generated: 09/08/2015 at 08:03 PM

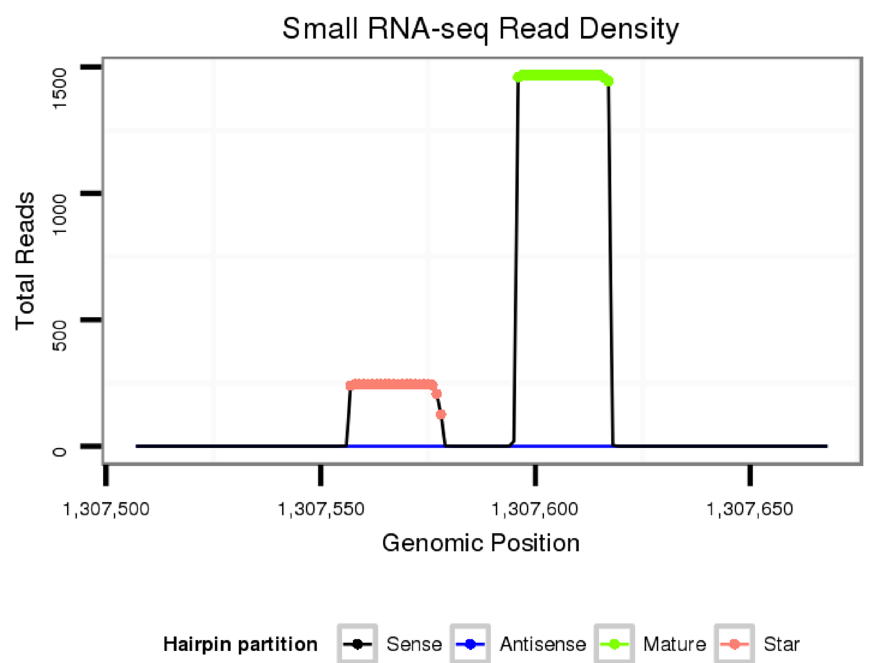
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	3
rescue.candidate	0

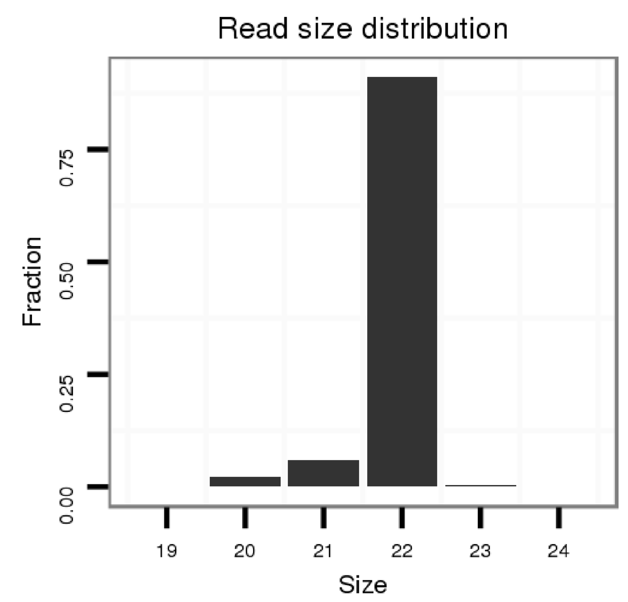
ID: dmo_47	Coordinate: scaffold_6308:1307557-1307618 +	Confidence: confident	Class: Testes-restricted	Genomic Locale: intergenic	[View on UCSC Genome Browser {Cornell Mirror}]

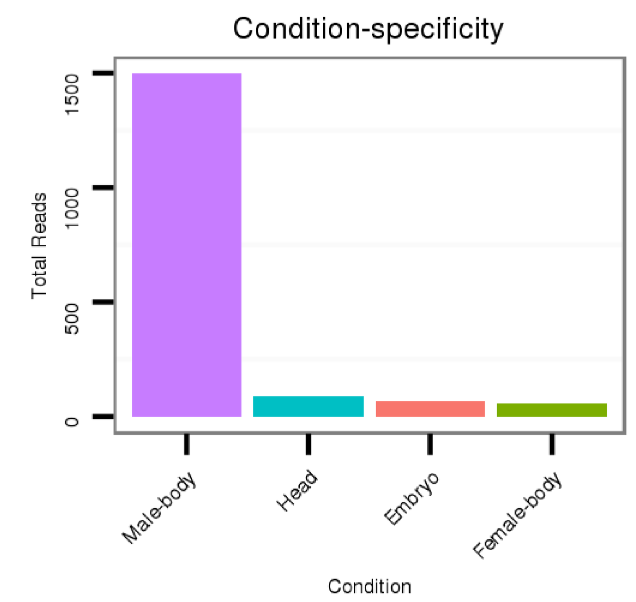
Legend: mature star mismatch in alignment mismatch in read

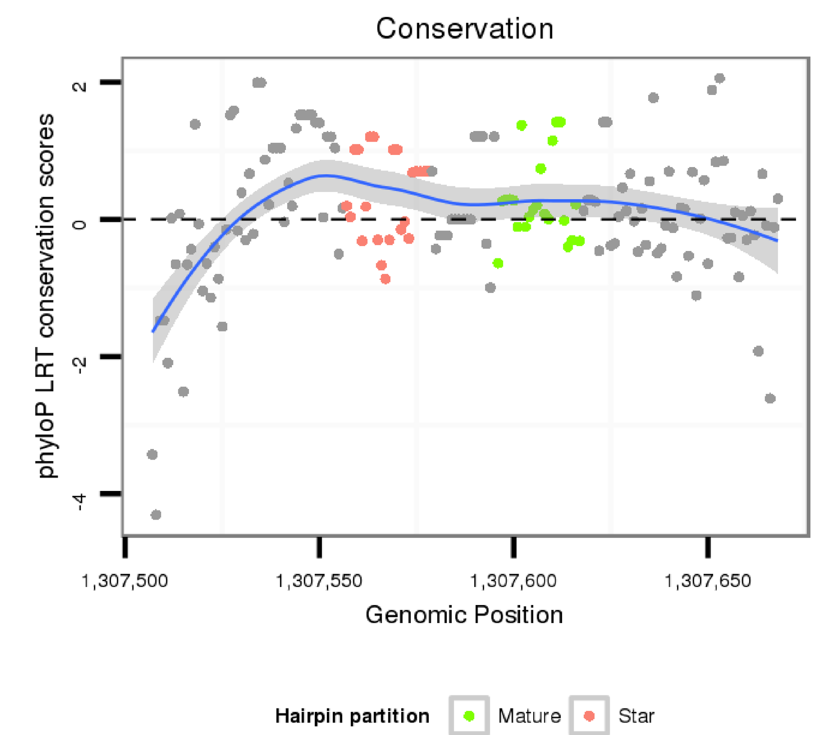
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GTTTAGCATCCAAGTGTAGAATATAATATACATACATATATATAGATACACATATGCGATGTTTGCTCAAAATTTGGTTCGATATAGTTCTGAGCATATGTTGCATACATGTATATATATATTTGAGCATCACTGATTGTCTCTATATTGATTGATTCGCGT ***********************************..(((((((.(((((..(((((((((.((((((.((((..........)))).)))))).))))))))))..))))).)))))))....***********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	V056 head	M046 female body	M060 embryo	V041 embryo	V049 head
....CTGAGCATATGTTGCATACATG...	22	0	1	1429.00	1429	1284	51	26	13	30	25
....CATATGCGATGTTTGCTCAAAA..	22	0	1	121.00	121	95	1	14	7	3	1
....CATATGCGATGTTTGCTCAAA...	21	0	1	79.00	79	59	4	7	5	3	1
....CATATGCGATGTTTGCTCAA..	20	0	1	34.00	34	32	0	2	0	0	0
....CTGAGCATATGTTGCATACATC...	22	1	1	13.00	13	12	0	1	0	0	0
....TCTGAGCATATGTTGCATACAT..	22	0	1	9.00	9	5	0	0	2	2	0
....TCTGAGCATATGTTGCATACA...	21	0	1	8.00	8	7	1	0	0	0	0
....TGAGCATATGTTGCATACATG...	21	0	1	8.00	8	5	0	3	0	0	0
....CTGAGCATATGTTGCATACATT...	22	1	1	6.00	6	3	0	0	1	0	2
....CTGAGCATATGTTGCATACATGC..	23	1	1	5.00	5	5	0	0	0	0	0
....CATATGCGATGTTTGCTCA...	19	0	1	4.00	4	1	2	0	0	1	0
....CATATGCGATGTTTGCTCAAAAA...	23	1	1	4.00	4	4	0	0	0	0	0
....ATATGCGATGTTTGCTCAAAA..	21	0	1	4.00	4	2	0	2	0	0	0
....CTGAGCATATGTTGCATACAT..	21	0	1	4.00	4	2	1	1	0	0	0
....TCTGAGCATATGTTGCATACATG...	23	0	1	3.00	3	1	0	0	1	1	0
....CTGAGCATATGTTGCATACATGT..	23	0	1	3.00	3	3	0	0	0	0	0
....CTGAGCATATGTTGCATACATGA..	23	1	1	3.00	3	2	1	0	0	0	0
....ATATGCGATGTTTGCTCAAA...	20	0	1	2.00	2	0	0	2	0	0	0
....TTCTGAGCATATGTTGCATACATC...	24	1	1	2.00	2	2	0	0	0	0	0
....CTGAGCATATGTTGCATACA...	20	0	1	2.00	2	1	0	0	1	0	0
....CTGAGCATATGTTGCATACATGG..	23	1	1	2.00	2	1	0	1	0	0	0
....TCTGAGCATATGTTGCATACATC...	23	1	1	2.00	2	2	0	0	0	0	0
....CATATGCGATGTTTGCTCAT..	20	1	1	1.00	1	1	0	0	0	0	0
....CATATGCGATGTTTGCTCAAT...	21	1	1	1.00	1	1	0	0	0	0	0
....CTGAGCATATGTTGCATACATGTC...	24	1	1	1.00	1	1	0	0	0	0	0
....CATATGCGATGTTTGCTCAAAATT..	24	0	1	1.00	1	1	0	0	0	0	0
....CATATGCGATGTTTGCTCCC..	20	2	1	1.00	1	1	0	0	0	0	0
....CTGAGCATATGTTGCATACATGTA...	24	0	1	1.00	1	1	0	0	0	0	0
....CTGAGCATATGTTGCATACATAA..	23	2	1	1.00	1	1	0	0	0	0	0
....CTGAGCATATGTTGCATACAC..	21	1	1	1.00	1	0	0	0	1	0	0
....CTGAGCATATGTTGCATACATCC..	23	2	1	1.00	1	1	0	0	0	0	0
....CTGAGCATATGTTGCATACATA...	22	1	1	1.00	1	0	0	0	0	0	1
....CACATATGCGATGTTTGCTCAA..	22	0	1	1.00	1	0	0	0	1	0	0
....TTCTGAGCATATGTTGCATACA...	22	0	1	1.00	1	0	0	1	0	0	0
....TCTGAGCATATGTTGCATACAA..	22	1	1	1.00	1	0	0	1	0	0	0
....CATATGCGATGTTTGCTCTC..	20	2	1	1.00	1	1	0	0	0	0	0
....CATATGCGATGTTTGCTCC...	19	1	1	1.00	1	0	0	1	0	0	0
....CATATGCGATGTTTGCTTT...	19	2	4	0.25	1	1	0	0	0	0	0
....ATACATGTATATATATATTT......................................	20	0	6	0.17	1	0	0	1	0	0	0

Anti-sense strand reads

CAAATCGTAGGTTCACATCTTATATTATATGTATGTATATATATCTATGTGTATACGCTACAAACGAGTTTTAAACCAAGCTATATCAAGACTCGTATACAACGTATGTACATATATATATAAACTCGTAGTGACTAACAGAGATATAACTAACTAAGCGCA ***********************************..(((((((.(((((..(((((((((.((((((.((((..........)))).)))))).))))))))))..))))).)))))))....***********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1307507-1307668 +	dmo_47	GTTTAGCATCCA--AGTG-----T--AGAATAT----------AATAT------------------------ACATACA----------TATATATAGATACA--CATATGCGATGTTTGCTCAAAATTTGGTTCGATATAGTTCTGAGCAT--ATGTTGCATACATG--------TATATATATATTT----GAGCATCACTGATTGTCTCTATATTGATTGATTCGC----GT
droVir3	scaffold_13047:4542862-4542998 +		GCTAAGCATTCA--ATT------CA-T----------AAGTTTAACATACACATAT------------ATATATTT----ATA----TCCATATATATATAT---ATATATTTAAGTAAATGTGCAAAGCATATATATATTATATTGTAT--TATAATCTACTATATAGATTTATATGT----AT
droGri2	scaffold_14830:1298197-1298354 +		TGTGG-CAC-CATTAGCC-----C-AATAATATAT--------GCATGTATTTAT------------GTATGTAT----GTA----TGTA-----------T--GTATGTAC--------ATATGTATAGCT--CGTAATTATGTTT--GTAAGTAA--ATACGCA--------TATAAATGCGCATATAAGCACGTAATTAAAACTGACAATATTACATGTTCTGT----CT
droWil2	scf2_1100000004852:154942-155092 +		CAGCT-G-----------A-------AGGATGT----AAGT--TACATTCATTTAC-CAT----------ATGTAC----ATA----CATA-----------C--ATATGTAC--------A-ATGTATGGTAAATTTAATCATTTTTTTGGGTACATATGTACCTAATATG----AGCGTGCA--GTGT----GAAAATCGTAGATTGTTAAAATATT----------GCTCTAAA
dp5	3:19703026-19703089 -		ATATA-CAT-A-TA-------------------------------------TATGTATA------------------------------TATATA----TA--TATA------------------------------------TCTATGCGTTGATTGCACAAAATGCAA--TTTG----AT
droPer2	scaffold_15:496490-496593 -		AAAGA-AAC-CA--AATT-----C--AAAATAT----------ATATGTA----TGTATATAT------ATATAT-----ATA--TATA-----------TGTATATATAT--GT-------------AT----ATATATATATGTATATTTATATATATATATATATAT----AT
droKik1	scf7180000302344:690234-690365 +		AA------------------------------------TAT------------------------ATATACA----------CATATATATATAA---TATAAACGACTTTTTTT--AAAACTAAAATAAGAAGTAACGTTTTTTAATCAACTATCGCATGCATCTGTCTCCGTGCCTATCGATAC----AAG------------------CATCGTTCATCGTGC----CT
droEle1	scf7180000490996:135881-135971 +		TAGTC-C----------AAATCT--TC-----ACTC--CATATATATATATATAT----------ATATAT------ATA--TATATATATA------T---ATATATATATATATATATATATATATATACGTAA----AC
droRho1	scf7180000770833:673-808 +		ATATA-CAT-A-TA----------------------------------TACATATA--TACAT----A--------TATACATA-----------T--ATACATAT----ATACATATATAC-ATA--T--ATACATATATACAT---ATA-TACATATATA--------CATATATACATAT----ATACATATATACATATATACATATATACATATATAC----AT
dm3	chrU:6539367-6539523 +		ACATAATATACA--TATA-----T--ACA-T----------ATATACATGTATACATATA--TACAT----A--------TATACATA-----------T-----ATACATGTATACATATATAC-ATA--T--ATACATATATACAT---ATA-TACATATATA--------CATATATACATAT----ATACATGTATACATATATACATATATACATATATAC----AT
droSim2	x:4908920-4908923 -		GCAT---
droSec2	scaffold_34:432893-432963 +		TTCCG-CGC-C-TTGGC-AAATTT-T-------AAGT--AACATATATATAC-------------AAATATAT----ATA----TATA--TATATATATATAT----AT
droYak3	X:17900248-17900311 +		GTTTT-TCC-A-CTGGC-GC-T-C-CATCATCAATGCAAGTATAATAT------------------------ATATATA----------TATATATATATATA--TA--
droEre2	scaffold_4820:10143729-10143866 +		ATATA-CAT-A-CA---------------------------------TACATATACATACAT----A---------CATACATA-----------C--ATATGTAC----ATACATATATAC-ATA--C--ATACTTACATACAT---ACA-TACATACTTA--------CATACATACATAT----GTACATACATACATATTTACATACATACATACATAC----AT

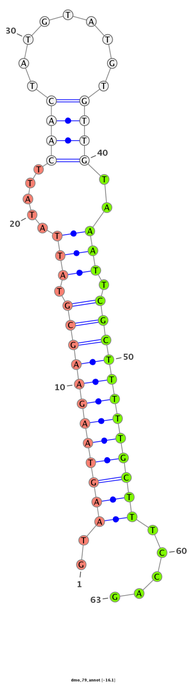
Generated: 09/08/2015 at 08:04 PM

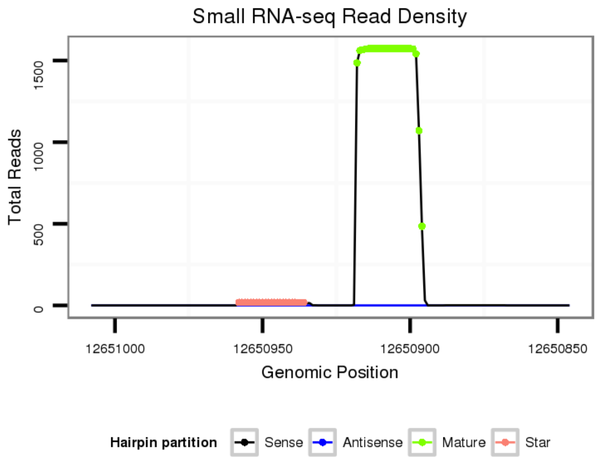
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

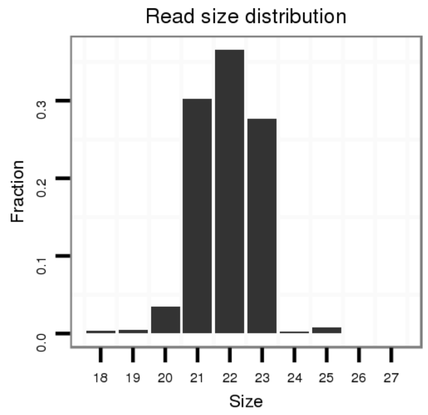
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_79	**scaffold_6500:12650896-12650958 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

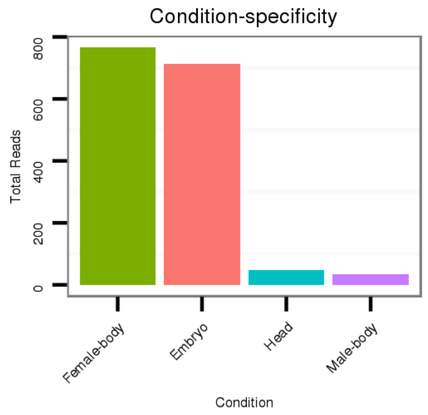
Legend: mature star **mismatch in alignment** mismatch in read

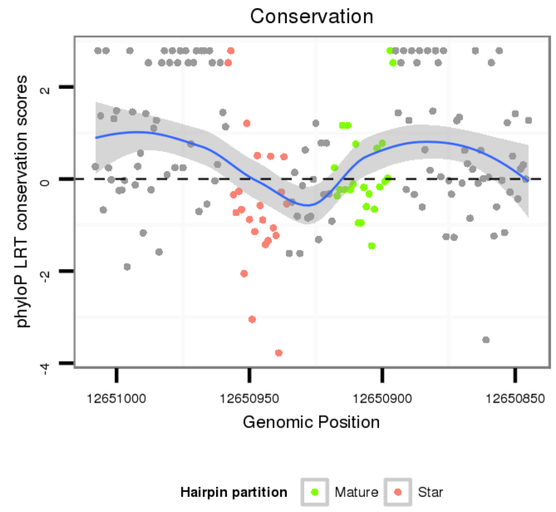
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI11683-in]; CDS [DmojGI11683-cds]; CDS [DmojGI11683-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTACAGCGAGGTGAACAGCTCAAGGGACGTAGACTGTGTGATTACCTCAAGTAAGTAAGAAGCGTATTATATTCAACTATGTATGTGTTGTAAATTCGCTTTTTGCTTTCCAGTTGAGGTAGAACAAATGCTCCAGACAGAGGAACAAACGCTGCAGCAATTC **********..((((((((((((.(((.....((((.........))))))..))).))))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V041 embryo	V110 male body	V056 head	V049 head
.....TAAATTCGCTTTTTGCTTTCCA.....	22	0	1	554.00	554	343	134	39	18	11	9
.....TAAATTCGCTTTTTGCTTTCC.....	21	0	1	441.00	441	155	250	18	7	8	3
.....TAAATTCGCTTTTTGCTTTCCAG.....	23	0	1	428.00	428	171	187	52	2	10	6
.....TAAATTCGCTTTTTGCTTTCCAGT.....	24	0	1	30.00	30	9	16	2	1	1	1
.....AAATTCGCTTTTTGCTTTCCA.....	21	0	1	30.00	30	27	3	0	0	0	0
.....TAAATTCGCTTTTTGCTTTC.....	20	0	1	27.00	27	15	9	1	1	0	1
.....AAATTCGCTTTTTGCTTTCC.....	20	0	1	26.00	26	26	0	0	0	0	0
.....TAAATTCGCTTTTTGCTTTCCAGC.....	24	1	1	22.00	22	14	8	0	0	0	0
.....AAATTCGCTTTTTGCTTTCCAG.....	22	0	1	17.00	17	16	1	0	0	0	0
.....GTAAGTAAGAAGCGTATTATATTCA.....	25	0	1	13.00	13	0	1	6	5	1	0
.....TAAATTCGCTTTTTGCTTTCCAA.....	23	1	1	8.00	8	6	2	0	0	0	0
.....TAAATTCGCTTTTTGCTTTCCC.....	22	1	1	7.00	7	2	5	0	0	0	0
.....TAAATTCGCTTTTTGCTTTCCAC.....	23	1	1	5.00	5	0	5	0	0	0	0
.....GTAAGTAAGAAGCGTATTATATT.....	23	0	1	3.00	3	2	1	0	0	0	0
.....GTAAATTCGCTTTTTGCTTTCCAG.....	24	0	1	3.00	3	2	0	1	0	0	0
.....TAAATTCGCTTTTTGCTTTCCAGA.....	24	1	1	3.00	3	0	2	0	0	0	1
.....TAAATTCGCTTTTTGCTTTCCAAA.....	24	2	1	3.00	3	3	0	0	0	0	0
.....TAAATTCGCTTTTTGCTTTCCT.....	22	1	1	3.00	3	1	2	0	0	0	0
.....ATTCGCTTTTTGCTTTCC.....	18	0	1	3.00	3	1	2	0	0	0	0
.....TAAATTCGCTTTTTGCTTTCCAAAA.....	25	3	1	3.00	3	3	0	0	0	0	0
.....TTCGCTTTTTGCTTTCCAG.....	19	0	1	2.00	2	0	2	0	0	0	0
.....AATTCGCTTTTTGCTTTCCAG.....	21	0	1	2.00	2	2	0	0	0	0	0
.....TAAATTCGCTTTTTGCTTT.....	19	0	1	2.00	2	0	2	0	0	0	0
.....TTCGCTTTTTGCTTTCCAGC.....	20	1	1	2.00	2	2	0	0	0	0	0
.....AAATTCGCTTTTTGCTTTC.....	19	0	1	2.00	2	2	0	0	0	0	0
.....TAAATTCGCTTTTTGCTTTCCG.....	22	1	1	1.00	1	0	1	0	0	0	0
.....TTCGCTTTTTGCTTTCCAGA.....	20	1	1	1.00	1	1	0	0	0	0	0
.....GTAAGTAAGAAGCGTATTATATTCC.....	25	1	1	1.00	1	0	0	0	1	0	0
.....TAAATTCGCTTTTTGCTTTCCAGG.....	24	1	1	1.00	1	1	0	0	0	0	0
.....AATTCGCTTTTTGCTTTCCAGT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....ATTCGCTTTTTGCTTTCCA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....AAATTCGCTTTTTGCTTT.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TCGCTTTTTGCTTTCCAG.....	18	0	1	1.00	1	0	1	0	0	0	0
.....GTAAGTAAGAAGCGTATTATATTCAAC.....	27	0	1	1.00	1	1	0	0	0	0	0
.....GTAAGTAAGAAGCGTATTAT.....	20	0	1	1.00	1	0	0	0	1	0	0
.....GTAAGTAAGAAGCGTATTATATTCAACA.....	28	1	1	1.00	1	1	0	0	0	0	0
.....GTAAATTCGCTTTTTGCTTTCCAGC.....	25	1	1	1.00	1	1	0	0	0	0	0
.....AAATTCGCTTTTTGCTTTCCG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....AAATTCGCTTTTTGCTTTCCAA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TAAATTCGCTTTTTGCTTTCCAT.....	23	1	1	1.00	1	0	0	0	0	1	0
.....ATTCGCTTTTTGCTTTCCAG.....	20	0	1	1.00	1	0	1	0	0	0	0
.....AATTCGCTTTTTGCTTTCC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....AGAACAAATGCTCCAGACAGA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GTAAATTCGCTTTTTGCTTTCCA.....	23	0	1	1.00	1	0	1	0	0	0	0
.....GTAAGTAAGAAGCGTATTATATTC.....	24	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

GATGTCGCTCCACTTGTCGAGTTCCCTGCATCTGACACACTAATGGAGTTCATTCATTCTTCGCATAATATAAGTTGATACATACACAACATTTAAGCGAAAAACGAAAGGTCAACTCCATCTTGTTTACGAGGTCTGTCTCCTTGTTTGCGACGTCGTTAAG **********..((((((((((((.(((.....((((.........))))))..))).))))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V049 head	V056 head
.....AATTCGCTTTTTGCTTTCCAG.....	21	0	1	2.00	2	2	0	0	0	0	0
.....AAATTCGCTTTTTGCTTTCC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....AAATTCGCTTTTTGCTTTCCAA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TAAATTCGCTTTTTGCTTTCCAT.....	23	1	1	1.00	1	0	0	0	0	1	0
.....ATTCGCTTTTTGCTTTCCAG.....	20	0	1	1.00	1	0	1	0	0	0	0
.....AATTCGCTTTTTGCTTTCC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....AGAACAAATGCTCCAGACAGA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GTAAATTCGCTTTTTGCTTTCCA.....	23	0	1	1.00	1	0	1	0	0	0	0
.....GTAAGTAAGAAGCGTATTATATTC.....	24	0	1	1.00	1	0	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6500:12650845-12651008 -	dmo_79	CTACAGCGAGGTGAACAGCTCAAGGGACGTAGACTGTGTGATTACCTCAAGTAAGTA----------AG--AA----------GCGTATTATATTCAACT----ATGTATG--TGTTG---TAAATTCGC-TTTTTGCTTTCCAGTTGAGGTAGAACAAATGCTCCAGACAGAGGAACAAACGCTGCAGCAATTCG
droVir3	scaffold_12963:2485213-2485372 -		CTACAGTGAAGTCAATGGCTGTAGGGATGTGGATTGTGTGATTACCTCGAGTAAGTG----------AG--AC----------CAGCGTTCTTTCCGGCTCATACCGTTTG--------TCAATTGTTTCTTTCGGCCCGCAGTTGAAGTGGAGCAAATGCTCAAGCAGAGGAACAAACGCTACAGCAATTCG
droGri2	scaffold_15252:2094809-2094976 -		CTACAGCGAAGTAAGCAGCTCACGGGATGTGGACTGTGTAATTAGTGCAAGTGAGTG----------A----AA--TC----------AGATGCTTCCTTGGG-GGAATTTCAGTGG---ACGATTCTAAT--TGTGTTGTGCTTGCAGTTGAGGTGGAGCAAATGCTTCAGGGCGAGGAGCAAACCTTGCAACAATTCG
droWil2	scf2_1100000004521:6738006-6738162 -		CTACAGCGAAGTCAATGGTTCACGTGATGTGGATTGTGTAATTACCTCAAGTATGTA-A----------G----AA--GA----------AGGCCCAGAAGGGAATGTTTTTTTCAA--------GTTTTTATCTTTCAGTTGAAGTGGAACAAATGCTAATGGAAGATGAACGGCTCGTTGTCACAGCATG
dp5	4_group4:6422431-6422604 +		CTACAGTGAAGTGAATGAATGGCGGGATGTGGACTGTGTTATTAGTTCAGGTCAGTGGATCATGGAAGCGAACAAA--ATGAAAAACTAAAACAAATTAA----------TAATTTCAA---------TTTCTTATACTTGTAGTTGAGGTGGAACAAATGTTGAACGAAGATGAACGGTCACTTCCGAGCACG
droPer2	scaffold_16:439362-439535 -		CTACAGTGAAGTGAATGAATGGCGGGATGTGGACTGTGTTATTAGTTCAGGTCAGTGGATCATGGAAGCGAACAAA--ATGAAAAACTAAAACAAATTAA----------TAATTTCAA---------TTTCTTATACTTGTAGTTGAGGTGGAACAAATGTTGAACGAAGATGAACGGTCACTTCCGAGCACG
droAna3	scaffold_13258:489145-489297 -		TTTCAGCGAGGTAAATGCTTCGGGTGACGTGGACTGCGTGATTAGTTCAGGTTGTAT----------A----A--CT----------AAACATGTGGGCGTATAAAA---AATT--------TATTACTTTCTTTGCAGTTGAAGTGGAGCAAATGTTGCTCGAAGTTGACCAAACTTTAACGGCCCAAG
droBip1	scf7180000394860:25258-25411 -		TTTTAGTGAGGCAAATGCGTGGCGAGACGTGGACTGTGTTATAAGTTCAGGTTTCAT----------A----AA--TA----------AAATATTTAATCTTTAGAAAA-ATTT--A--------TATTTTTTTTTTTGCAGTTGAAGTGGAGCAAATGTTGCTTGAAGATTGACCAAACTTTATCGGCCCAAG
droKik1	scf7180000302644:48367-48525 -		CTTCAGCGAGGTGAATGAGTCTCGAGATGTTGACTGTGTTAATTAGTTCAGGTTGCGA----------TTGT----------GATGTGTTGTATGAGCTGAGATTGATG--------TA----GATACTCCTATTCTTGCAGTTGAGATTGAACAGATGTTGACAGAGGATGAGCACCGTTTGGCGCAGCACG
droFic1	scf7180000454176:30477-30633 +		CTTTAATGAAGTAAACAATGTCGAGATGTGGACTGCGTAATAAGATCAGGTTGTGG----------A----AG--AA----------AGCTATGACATTTTAATTTAAGTTATA--------TTTTCCTTTCCATTAGTTGAGGTAGACAGATGCTGGATGAAGCGCGAGAGGACGTTGTCAGAGTATG
droEle1	scf7180000490342:19643-19798 -		CTTAAACGAACAGAACAAGTCACGGGACGTGGACTGTGTTATTAGATCAGGTAGGTG----------AG--GC----------AATCATGACATTCGAGTTGTCATCTGTA--------TATTACCTTTGCAGTCGAAGTGGAACAAATGCTGACCGAGGATGAGCGTAGACTGTCGCAACAGG
droRho1	scf7180000778195:8326-8478 +		CTTTAACGAAAAGAACAATCTCAGGGACGTGGACTGTGTAATCAGAGCAGGTTGTTA----------T--TC----------AATC--ATGATTTGTCTTGTGATCAATA--------TACCTTCTTTTGCAGTCGAGGTGGAACAGATGCTGACCGAGGAAGAGCGGAGTCTGTCGCAATACG
droBia1	scf7180000301527:16439-16597 -		TTTCAGCAAAGTGAACAATGCACAGGACGTGGACTGTGTAATCAGAGCAGGTACTGAGATA----------T----AC--AT----------AGCCATAAGATTTTACTTGAGAATATAGTG--------TA--ACTTGTATGTAGTTGAGGTTGAAAAGATGTTGACCGAGGACCAGCGAAGACTGCGCAGTAGG
droTak1	scf7180000415510:45581-45735 +		CTTTAACAAGCGAACACGCACGAGACGTGGACTGTGTAATCACATCAGGTAGAAC----------G----AC--GC----------AAACATTACATTGGAGATAAGATTGATG--------TA--ACTCTTCTGCAGTTGAGGTGGAGGAGATGTTGACCGAGCACAAGAGGAGATTGGCGCAATTGTA
droEug1	scf7180000409515:18495-18650 -		CTTTAGCAAAACCAATAACTCACGCGACGTGGATTGTGTTATTAGTCAGGTTATTT----------G----GG--TC----------AAGAC----------CAGTGTGTTTATTAAATAATAATGCTAGTTTTATAGTTGAGGTGGACAGATGCTTACTGAGGACGAACGTAGATTGACGGAGTAGG
dm3	chr2R:19435-19592 +		TTTCAGCAAGGCAAATAACTCACGCGACGTAGACTGTGTAATCAGTTCAGGTAATTGA----------G----AG--CC----------AAAAGTACAATTTGAGCTAATAATAA-A--------TAATATATCTTTGCAGTTGAGGTGGAACAGTTGCTTAGTGAGGCTCAGCAGCCGCTGTCGCAGTAGG
droSim2	2r:13042-13200 +	dsi_27890	TTTCAGCAAGGCAAATAACTCACGCGACGTAGACTGTGTAATCAGTTCAGGTTGTTGA----------G----AG--CC----------AAACGTACAATTTGAGCTAATAATTAATA--------TAATATATCTTTGCAGTTGAGGTGGAACAATTGCTGAGTGAGCTCAGCGTCCGCTATCGCAGTAGG
droSec2	scaffold_184:26297-26455 -		TTTCAGCAAGGCAAATAACTCACGCGACGTAGACTGTGTAATCAGTTCAGGTTGTTGA----------G----AG--CC----------AAACGTACAATTTGAGCTAATAATTAATA--------TAATATATCTTTGCAGTTGAGGTGGAACAGTTGCTGAGTGAGCTCAGCGGACCGCTATCGCAGTAGG
droYak3	chr2h:157833-157989 -		TTTTAGCAAGACAAATAACTCACGCGACGTAGACTGTGTTATCAGTTCAGGTTGTGA----------A----AG--CC----------AAAACTACAATATGAGCTAATAATTAATA--------TAATGCATCTTTGCAGTTGAGGTGGAACAGTTGCTGGGTGAGGCGCAGCGGACGCTGTCAGAGTTCG
droEre2	scaffold_4845:1055411-1055567 -		TTTCAGCACGGCGAAATAACTCACGTGACGTAGACTGTGTAATTAGTTCAGGTTGTGA----------G----AG--CC----------AAAAATACTATTGCAGATAATATGAATG--------TAAATATATTTTGCAGTTGAAGTGGAACAGTTGCTAAGTGAGTCCCAGCGGACGCTGCGCAGTAGG

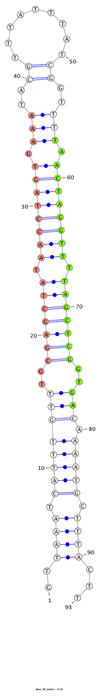
Generated: 09/08/2015 at 07:01 PM

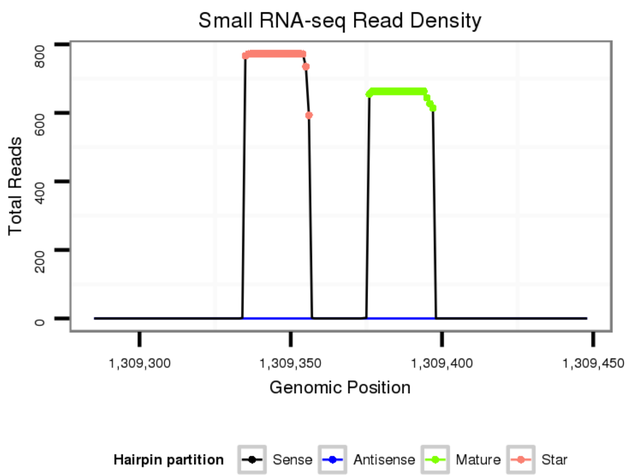
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

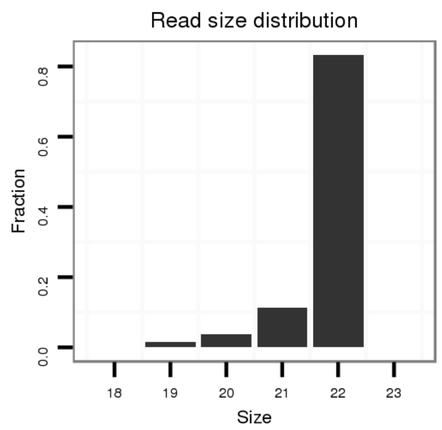
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_48	**scaffold_6308:1309335-1309398 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

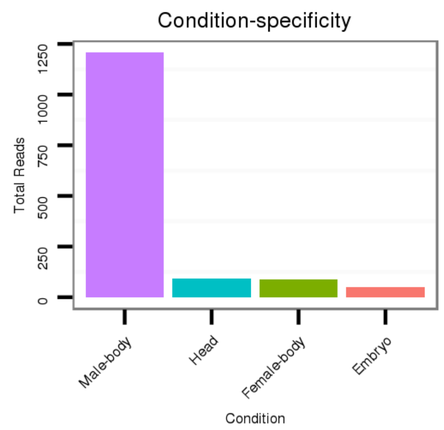
Legend: mature star mismatch in alignment mismatch in read

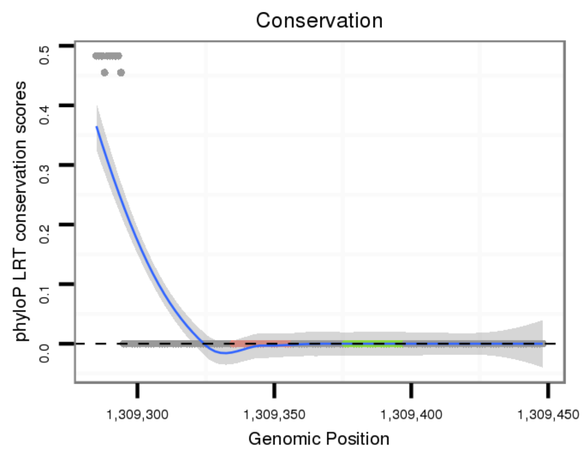
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATTCAATTTGCAATCGGTCTATAGCAAAAATCTAAGTTAAATCATTTGTTTGCGAGCTATAACCTAGTGAAATACGTTTATTTATCGGTTTTAACTAGGTTTTAGCTCGGTGACAAAATGCTTTACTTTGCAACAGAAAAATCGGGAAAACTATCATCGATATC **********..((((.(((((((((..(((((((.(((((((((.(((..((.....)).)..)))..)))))))).)))))))..)))..)))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head	V049 head	V041 embryo	M060 embryo
.....TAACTAGGTTTTAGCTCGGTGA.....	22	0	1	608.00	608	470	43	40	21	26	8
.....TGCGAGCTATAACCTAGTGAAA.....	22	0	1	585.00	585	556	12	8	4	1	4
.....TGCGAGCTATAACCTAGTGAA.....	21	0	1	141.00	141	116	10	7	3	2	3
.....TAACTAGGTTTTAGCTCGGTGT.....	22	1	1	62.00	62	61	1	0	0	0	0
.....TGCGAGCTATAACCTAGTGAAAA.....	23	1	1	40.00	40	36	3	0	0	0	1
.....TGCGAGCTATAACCTAGTGA.....	20	0	1	36.00	36	22	6	3	3	2	0
.....TAACTAGGTTTTAGCTCGG.....	19	0	1	18.00	18	17	1	0	0	0	0
.....TAACTAGGTTTTAGCTCGGT.....	20	0	1	16.00	16	16	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTG.....	21	0	1	11.00	11	5	2	0	1	2	1
.....TAACTAGGTTTTAGCTCGGTGAG.....	23	1	1	10.00	10	8	1	1	0	0	0
.....TAACTAGGTTTTAGCTCGGTGC.....	22	1	1	9.00	9	9	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGAAC.....	22	1	1	8.00	8	8	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTGAA.....	23	1	1	8.00	8	7	0	0	0	0	1
.....TAACTAGGTTTTAGCTCGGTGTT.....	23	2	1	7.00	7	7	0	0	0	0	0
.....AACTAGGTTTTAGCTCGGTGA.....	21	0	1	6.00	6	0	6	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTGTA.....	23	2	1	6.00	6	6	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTT.....	21	1	1	4.00	4	4	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTGAT.....	23	1	1	4.00	4	3	1	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTGATC.....	24	2	1	4.00	4	4	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGG.....	20	1	1	3.00	3	3	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGAAAG.....	23	1	1	3.00	3	3	0	0	0	0	0
.....GCGAGCTATAACCTAGTGAAA.....	21	0	1	3.00	3	0	3	0	0	0	0
.....TGCGAGCTATAACCTAGTGAG.....	21	1	1	3.00	3	3	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTC.....	21	1	1	3.00	3	3	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTTG.....	22	2	1	2.00	2	2	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGAAAT.....	23	0	1	2.00	2	2	0	0	0	0	0
.....TTGCGAGCTATAACCTAGTGAAA.....	23	0	1	2.00	2	2	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTTT.....	22	2	1	2.00	2	2	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTGTTC.....	24	3	2	2.00	4	4	0	0	0	0	0
.....TGCGAGCTATAACCTAGTG.....	19	0	5	1.80	9	7	1	0	1	0	0
.....TTAACTAGGTTTTAGCTCGGTG.....	22	0	1	1.00	1	0	0	0	0	1	0
.....CGAGCTATAACCTAGTGAAA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TTAACTAGGTTTTAGCTCGGTGT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTGATG.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TTTAACTAGGTTTTAGCTCGGT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGAAAAG.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGA.....	20	1	1	1.00	1	1	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTGAAC.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTGC.....	22	1	1	1.00	1	0	0	0	0	1	0
.....TAACTAGGTTTTAGCTCGGTGACC.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGAAATAG.....	25	1	1	1.00	1	1	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTAT.....	22	2	1	1.00	1	1	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTCT.....	22	2	1	1.00	1	1	0	0	0	0	0
.....TGCGAGCTATAACCTAGTGAAT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....GCGAGCTATAACCTAGTGA.....	19	0	1	1.00	1	0	1	0	0	0	0
.....GCGAGCTATAACCTAGTGAA.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TGCGAGCTATAACCTAGTGAAAC.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTGATT.....	24	2	1	1.00	1	1	0	0	0	0	0
.....AACTAGGTTTTAGCTCGGTG.....	20	0	1	1.00	1	0	1	0	0	0	0
.....AACTAGGTTTTAGCTCGG.....	18	0	1	1.00	1	0	1	0	0	0	0
.....TGCGAGCTATAACCTAGTGAAG.....	22	1	3	1.00	3	2	0	0	0	1	0
.....TGTTTGCGAGCTATAACCTAG.....	21	0	5	0.80	4	4	0	0	0	0	0
.....TAACTAGGTTTTAGCTCGGTTTA.....	23	3	3	0.67	2	2	0	0	0	0	0
.....TGTTTGCGAGCTATAACCTAGTG.....	23	0	5	0.60	3	2	0	0	0	1	0
.....TAACTAGGTTTTAGCTCGTGA.....	21	3	5	0.40	2	2	0	0	0	0	0
.....TGTTTGCGAGCTATAACCTAGTC.....	23	1	5	0.40	2	2	0	0	0	0	0
.....TACGTTTATTTATCGGTTTC.....	20	1	3	0.33	1	1	0	0	0	0	0
.....TGTTTGCGAGCTATAACCTAGT.....	22	0	5	0.20	1	0	0	0	0	0	1
.....TTGCGAGCTATAACCTAGTG.....	20	0	5	0.20	1	0	1	0	0	0	0
.....TAACTAGGTTTTAGCTCGTGT.....	21	3	8	0.13	1	1	0	0	0	0	0

Anti-sense strand reads

TAAGTTAAACGTTAGCCAGATATCGTTTTTAGATTCAATTTAGTAAACAAACGCTCGATATTGGATCACTTTATGCAAATAAATAGCCAAAATTGATCCAAAATCGAGCCACTGTTTTACGAAATGAAACGTTGTCTTTTTAGCCCTTTTGATAGTAGCTATAG **********..((((.(((((((((..(((((((.(((((((((.(((..((.....)).)..)))..)))))))).)))))))..)))..)))))...**********	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_6308:1309285-1309448 +	dmo_48	ATTCAATTTGCAATCGGTCTATAGCAAAAATCTAAGTTAAATCATTTGTTTGCGAGCTATAACCTAGTGAAATACGTTTATTTATCGGTTTTAACTAGGTTTTAGCTCGGTGACAAAATGCTTTACTTTGCAACAGAAAAATCGGGAAAACTATCATCGATATC
droVir3	scaffold_12970:9420573-9420582 -		ATTCAATTTG----------

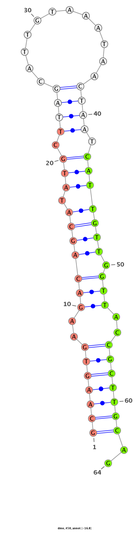
Generated: 09/08/2015 at 08:03 PM

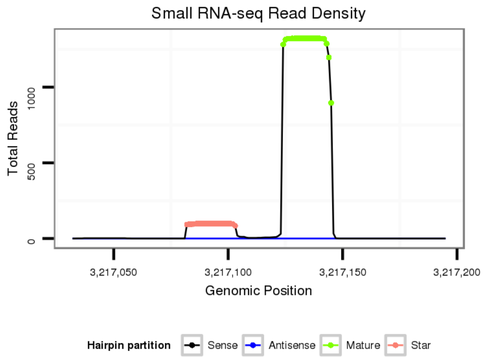
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

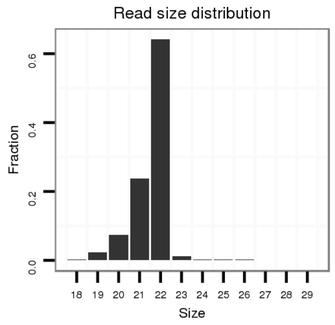
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_450	**scaffold_6308:3217082-3217145 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

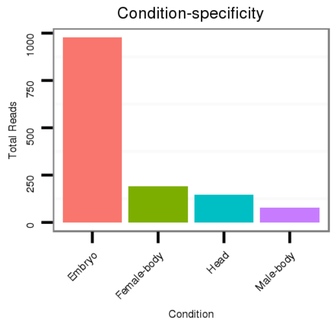
Legend: mature star mismatch in alignment mismatch in read

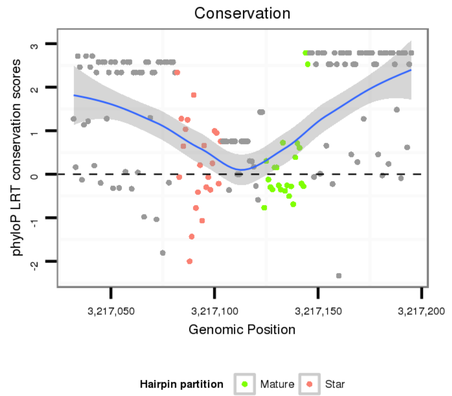
Predicted structure











Show Alternate Folds

Flybase annotation

intron [DmojGI11213-in]; CDS [DmojGI11213-cds]; CDS [DmojGI11213-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CCACTGAGCAGGACATTGAAACCCATTTCGGAGCCATTGGCATAATAAAGGCAAGTAGGCAAGTGACATGTAAATAACTAATCATTGTTGGTTACCGCTTGCAGAAGGATAAGCGCACCATGAAGCCAAAGATTTGGCTGTACAAGAACAAGGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V041 embryo	M046 female body	V110 male body	V056 head	V049 head
**********(((((((..(((((((.(((.((((.....)))).)))))))..)))..)))))))..**********											
.....CATTGTTGGTTACCGCTTGCAGT.....	23	1	1	1089.00	1089	655	80	144	131	46	33
.....CATTGTTGGTTACCGCTTGCAG.....	22	0	1	824.00	824	362	245	87	54	53	23
.....CATTGTTGGTTACCGCTTGCA.....	21	0	1	288.00	288	110	88	42	13	23	12
.....CATTGTTGGTTACCGCTTGCAGC.....	23	1	1	158.00	158	156	0	1	0	0	1
.....CATTGTTGGTTACCGCTTGC.....	20	0	1	83.00	83	40	10	14	3	12	4
.....GCAAGTGAAGACAGCATATGCT.....	22	0	1	68.00	68	59	2	4	1	1	1
.....CATTGTTGGTTACCGCTTGCAGA.....	23	0	1	31.00	31	14	10	2	2	2	1
.....CATTGTTGGTTACCGCTTG.....	19	0	1	28.00	28	1	1	17	1	2	6
.....CATTGTTGGTTACCGCTTGCAA.....	22	1	1	26.00	26	19	3	4	0	0	0
.....ATTGTTGGTTACCGCTTGCAG.....	21	0	1	22.00	22	2	9	5	0	3	3
.....CATTGTTGGTTACCGCTTGCAGTT.....	24	2	1	21.00	21	13	0	7	0	1	0
.....ATTGTTGGTTACCGCTTGCAGT.....	22	1	1	20.00	20	5	0	10	2	1	2
.....GCAAGTGAAGACAGCATATGCC.....	22	1	1	13.00	13	13	0	0	0	0	0
.....CATTGTTGGTTACCGCTTGCAC.....	22	1	1	13.00	13	11	0	1	0	1	0
.....CATTGTTGGTTACCGCTTGCAA.....	22	1	1	12.00	12	4	0	4	0	1	3
.....GCAAGTGAAGACAGCATATGC.....	21	0	1	11.00	11	7	1	0	2	0	1
.....TCATTGTTGGTTACCGCTTGCAG.....	23	0	1	10.00	10	7	2	1	0	0	0
.....ATTGTTGGTTACCGCTTGCA.....	20	0	1	10.00	10	2	3	4	0	0	1
.....CATTGTTGGTTACCGCTTGA.....	20	1	1	7.00	7	1	0	0	2	2	2
.....GCAAGTGAAGACAGCATATGCTT.....	23	0	1	5.00	5	0	0	2	3	0	0
.....GTTGGTTACCGCTTGCAGT.....	19	1	1	4.00	4	1	0	1	2	0	0
.....ATTGTTGGTTACCGCTTGCAG.....	22	1	1	4.00	4	4	0	0	0	0	0
.....TAGCATTGTAAATAACTAAT.....	20	0	1	4.00	4	1	1	1	0	1	0
.....CATTGTTGGTTACCGCTTGCG.....	21	1	1	4.00	4	2	1	0	0	0	1
.....TCATTGTTGGTTACCGCTTGCAGT.....	24	1	1	3.00	3	2	1	0	0	0	0
.....CATTGTTGGTTACCGCTTGCAGG.....	23	1	1	3.00	3	3	0	0	0	0	0
.....GCAAGTGAAGACAGCATATG.....	20	0	1	3.00	3	2	0	1	0	0	0
.....TCATTGTTGGTTACCGCTTGC.....	21	0	1	3.00	3	1	0	2	0	0	0
.....CATTGTTGGTTACCGCTTGCAGAAA.....	25	1	1	3.00	3	2	0	1	0	0	0
.....TTGTTGGTTACCGCTTGCAG.....	20	0	1	3.00	3	3	0	0	0	0	0
.....ATCATTGTTGGTTACCGCTTG.....	21	0	1	3.00	3	0	0	1	0	2	0
.....GCAAGTGAAGACAGCATATGCTTAGC.....	26	0	1	3.00	3	3	0	0	0	0	0
.....CATTGTTGGTTACCGCTTGCAGTC.....	24	2	1	3.00	3	3	0	0	0	0	0
.....CATTGTTGGTTACCGCTTGCAGAT.....	24	1	1	2.00	2	1	1	0	0	0	0
.....TTGTTGGTTACCGCTTGCA.....	19	0	1	2.00	2	2	0	0	0	0	0
.....TTGTTGGTTACCGCTTGC.....	18	0	1	2.00	2	1	0	1	0	0	0
.....ATCATTGTTGGTTACCGCTTGCAG.....	24	0	1	2.00	2	1	1	0	0	0	0
.....GCAAGTGAAGACAGCATATGCTTAGCA.....	27	0	1	2.00	2	0	0	2	0	0	0
.....CATTGTTGGTTACCGCTTGCACC.....	23	2	1	2.00	2	2	0	0	0	0	0
.....CAAGTGAAGACAGCATATGCT.....	21	0	1	2.00	2	1	0	1	0	0	0
.....GTGAAGACAGCATATGCTT.....	19	0	1	2.00	2	0	0	2	0	0	0
.....CATTGTTGGTTACCGCTTGCG.....	21	1	1	2.00	2	2	0	0	0	0	0
.....ATCATTGTTGGTTACCGCTTGCAGC.....	25	1	1	2.00	2	2	0	0	0	0	0
.....TCATTGTTGGTTACCGCTTGCAGC.....	24	1	1	2.00	2	2	0	0	0	0	0
.....CATTGTTGGTTACCGCTTGCATT.....	23	2	1	2.00	2	2	0	0	0	0	0
.....ATCATTGTTGGTTACCGCTTGC.....	22	0	1	2.00	2	2	0	0	0	0	0
.....TTGTTGGTTACCGCTTGCAGC.....	21	1	1	1.00	1	1	0	0	0	0	0
.....ATCATTGTTGGTTACCGCTTGCAG.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TCATTGTTGGTTACCGCTTGCAG.....	23	1	1	1.00	1	1	0	0	0	0	0
..ACTGAGCAGGACATTGAAACCCAT.....	24	0	1	1.00	1	0	0	1	0	0	0
.....TAATCATTGTTGGTTACCGCTTGCAG.....	26	0	1	1.00	1	1	0	0	0	0	0
.....CATTGTTGGTTACCGCTTGA.....	20	1	1	1.00	1	0	0	0	1	0	0
.....GCAAGTGAAGACAGCATATGCTTA.....	24	0	1	1.00	1	0	0	1	0	0	0
.....GTTGGTTACCGCTTGCAG.....	18	0	1	1.00	1	0	1	0	0	0	0
.....CATTGTTGGTTACCGCTTGCAGCT.....	24	2	1	1.00	1	0	0	1	0	0	0
.....AATCATTGTTGGTTACCGCTT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TAATCATTGTTGGTTACCGCTTGCAGT.....	27	1	1	1.00	1	0	0	0	1	0	0
.....AAATAACTAATCATTGTTGGTTACCGCT.....	29	0	1	1.00	1	0	0	1	0	0	0
.....CATTGTTGGTTACCGCTTGCAGTTT.....	25	3	1	1.00	1	1	0	0	0	0	0
.....CTAATCATTGTTGGTTACCGCTTGC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....GTTGGTTACCGCTTGCAGC.....	19	1	1	1.00	1	1	0	0	0	0	0
.....ATCATTGTTGGTTACCGCTTGCA.....	23	0	1	1.00	1	0	1	0	0	0	0
.....AGTGAAGACAGCATATGCTTAGC.....	23	0	1	1.00	1	0	0	1	0	0	0
.....ATTGTTGGTTACCGCTTGCAG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....CATTGTTGGTTACCGCTTGCATG.....	23	2	1	1.00	1	0	0	0	0	0	1
.....TGAAGACAGCATATGCTTAGC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....CATTGTTGGTTACCGCTTA.....	19	1	1	1.00	1	0	0	0	0	1	0
.....TGTTGGTTACCGCTTGCAGT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....CATTGTTGGTTACCGCTTTT.....	20	2	1	1.00	1	0	0	0	0	0	1
.....CATTGTTGGTTACCGCTTGCACT.....	23	2	1	1.00	1	0	0	0	1	0	0
.....CATTGTTGGTTACCGCTTGCAGAA.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TGGTTACCGCTTGCAGAAG.....	19	0	1	1.00	1	1	0	0	0	0	0
.....ATAACTAATCATTGTTGGTTACCGC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TAACTAATCATTGTTGGTTACCGCT.....	25	0	1	1.00	1	0	0	1	0	0	0
.....CATTGTTGGTTACCGCTTGCT.....	21	1	1	1.00	1	0	0	0	0	0	1
....GAGCAGGACATTGAAACCC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....ATTGTTGGTTACCGCTTTT.....	19	2	2	0.50	1	0	0	1	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:3217032-3217195 +	dmo_450	CCACTGAGCAGGACATTGAAACCCATTTCGGAGCCATTGGCATAATAAAGGCAAGTGA----------A-GA-CA-----G---CA-----TA----TGCTTAGCATTGTAAATAACTAATCATTGTTGGTTA--------C------C---GCTTGCAGAAGGATAAGCGCACCATGAAGCCAAAGATTTGGCTGTACAAGAACAAGGA	
droVir3	scaffold_12472:263764-263941 -		CCACAGAGCAGGACATTGAGAGTCATTCGGTGCCATTGGCATTATAAAGGCAAGTGT----------A--G--C--CCA----T----C-----TTACCATCATGATTCATTTTCGTGCATTGTGCCTAAT----------A-AGATTATTATTTTTC--------C------A---TATTATAGAAGGACAAGCGCACCATGAACCAAAGATTTGGTTGTATAAGAATTAAGGA	
droGri2	scaffold_15203:4719893-4720067 +		CAACAGAGCAGGACATGAGAGTCATTCGGTGCCATTGGCATTATCAAGGTAACGTA----------A--G--C--CCA----GAAT--TCGTTATTC--AAA---TC----------AATTTCGTGCATGTTTGTAATATGGTAAATGT----------T-GG--------C------AATT---TTTATAGAAAGACGCACCATGAAACCAAAGATTTGGTTGTATCAAGAATTAAGGA	
droWil2	scf2_1100000004909:6538393-6538561 +		CCACAGAGCAGACATTGAAAGTCATTTGGTGCCATTGGCATAATAAAGGTTTGTAT----------A--G--C--------G----T--TTCGTAGTTGGA-CAACCAATTTGGATTCTTTTT----------GGTAATAATTTATA----------A--------A------AATT---TTTCAGAAAGATAAGCGCAGTATGAAACCAAAGATTTGGTTGTATAAGAATTAAGA	
dp5	XL_group1c10412167-10412359 -		CCACAGAGCAGACATTGAGAGCATTTCGGTGCCATTGGCATCATCAAGGCAAGTAT----------A-TGT-CC-------G---GA-----TATCGA----------TGGAATCCCGA----A---TCGTCAAA--AGTCTGGGCAGGAGTTCTAAT----------A-TAATCAATCAAACCCT--------C------A---AATTGCAGAAGGATAAGCGCAGAATGAAGCCAAAGATTTGGCTATACAAGAACAAGGA	
droPer2	scaffold_69:107321-107524 +		CCACAGAGCAGACATGAGAGTCATTTCGGTGCCATTGGCATCATCAAGGCAAGTAT----------A-TGT-CC-------G---GA-----TATGGA----------TGGAATCCCGAAGCCCATCCCCATCGTCACA--AGTCTGGACAGGAGTTCTAAT----------A-TAATCAATCAAACCCT--------C------A---AATTGCAGAAGGATAAGCGCAGAATGAAGCCAAAGATTTGGCTCTACAAGAACAAGGA	
droAna3	scaffold_13137:1193212-1193376 -		CAACAGAGCAGGATATTGAGAGTCATTTTGGAGCTATTGGCATCATAAAGGCAAGTAT----------A-TATTT-------G---GTTTTTATG------------GAATT----------AT----------A-TTTCATAATGCAAAATATT--------TACACCGT---TATTTTAGAAAGACAAGCGCACATGAAGCCAAAGATTTGGCTCTATAAGAATTAAGA	
droBip1	scf7180000394930:2399-2596 +		CAACAGAGCAGGATATTGAGAGTCATTTCGGAGCTATTGGCATAATAAAGGCAAGTCTTTTTTTTTTTTTTTTTTTTTTGGTATAA-GATTAGTCATA---TA----------GCAT----------TTTTTTTT----------ACAAAATATTTTCTTTTGTATTCCCA---AATTTCAGAAAGACAAGCGCACATGAAGCCAAAGATTTGGCTGTATAAGAACAAGGA	
droKik1	scf7180000302696:1025750-1025827 +		TAAGCGAACAT----------C-----T-----C--G--C-----C----T-----C----------C----TT----------TTT----------TTGT--------G------GCT---TTGCAGAAGGACAAGCGCACCATGAAGCCAAATTTGGCTGTACAAGAATAAGGA	
droFic1	scf7180000453495:459264-459427 +		CCACAGAGCAGGATATTGAGAGTCATTTGGAGCTATTGGCATTATCAAGGTAAGTTG----------A-CT-GT-------G---G---CAAGG-AAA---ATC-A----------TGTTTAGAATT---AAATTTAAAATTTA------TTA--------A------ACT---TTTGTAGAAGGACAAGCGCAACCATGAAGCCAAAGATTTGGCTGTACAAGAACAAGGA	
droEle1	scf7180000491182:94869-95050 -		CCACAGAGCAGGACATTGAAAGTCATTCGGAGCCATTGGCATAATAAAGGCAAGTCA----------A--G--C--TCATC---GACT---GTCCCAACAGGC-GACAAGCC-GTTTTGACCATTCCTTTTTCCTACC---TTGTA----------TTTA--------G------ACT---CAACAGAAGGACAAGCGCACGTATGAAGCCAAAGATTTGGCTGTACAAGAACAAGGA	
droRho1	scf7180000778073:9795-9972 +		CCACAGAGCAGGATATTGAGAGTCATTCGGAGCTATTGGCATAATAAGGCAAGTAA----------A--G--C--TCATA---GACT---GTCCTCACAGGCGGC-CAGCTCTTTTGACCACTGGTTTCTTTTGTAC----------TTTA--------G------GCT---CAACAGAAGGACAAGCGCAGCATGAAGCCAAAGATTTGGCTGTACAAGAACAAGGA	
droBia1	scf7180000302126:820398-820570 -		CCACAGAGCAGGATATTGAGACCCATTTGGAGCCATTGGCATTATCAAGGTAAGTTT----------A--G--C--TCGG---GAAT---GTCTTTATG--TAGA---TAT-ATTTGAACCCTTCTTTCTCT-TCCT----CCA----------TTG--------C------GCT---TAACAGAAGGACAAACGCACCATGAAGCCAAGATTTGGCTGTACAAGAACAAGGA	
droTak1	scf7180000415289:248363-248415 +		C----------A--G--C--------A---G---C--------C----------C----------C----------A--------G------A---G---C-------AGAAGGACAAGCGCAGCATGAAGCCAAGATTTGGCTGTACAAGAACAAGGA	
droEug1	scf7180000409008:1423766-1423935 -		CCACAGAGCAGGATATTGAAACACATTCGGAGCTATTGGCATATTATCAAGGCAAGTCA----------A--G--C--TA---GGATT---GTCTTCCTAG-AAA---TCC-ATTTTAATCTT-CTT-CCTTTTATT----TTA----------TTTA--------G------AAT---TTTATAGAAAGACAAGCGCAGCATGAAGCCTAAGATTTGGCTGTACAAGAACAAGGA	
dm3	chrX:16186094-16186277 +		CCACCGAGCAGGACATTGAGACACATTTGGAGCAATTGGCATCATCAAGGCAAGTAG----------A--G--C--TA---ATG-TATTTTATGTATCTG--TAGC---TAC-GTTTTAACCTTTGTATCTTTCTATTCCTTTGCA----------ACT--------C------ATCTAACAACAGAAAGACAAGCGCAGCATGAAGCCAAGATTTGGCTGTACAAGAACAAGGA	
droSim2	x:15305970-15306158 +		CCACCGAGCAGGACATTGAGACTCATTTGGAGCCATTGGCATCATCAAGGCAAGTAG----------A--G--C--TA---ATG-CATTTTAGGTCTCTG--TAGC---TAC-GTTTTAACCATTGTATCTTTGTATCCCTTTGCAACTTTGGAATC----------A--------C------A---CCAACAACAGAAAGACAAGCGCAGCATGAAGCCAAGATTTGGCTGTACAAGAACAAGGA	
droSec2	scaffold_17:12974-13157 +		CCACCGAGCAGGACATTGAGACTCATTTGGAGCCATTGGCATCATCAAGGCAAGTAG----------A--G--C--TA---ATG-TATTTTAGGTCTCTG--TAGC---TAC-GTTTTAACCTTTGTATCTTTGTATCCCATTGCA----------A--------C------ACCCAACAACAGAAAGACAAGCGCAGCATGAAGCCAAGATTTGGCTGTACAAGAACAAGGA	
droYak3	X:10331751-10331930 +		CCACCGAGCAGGATATTGAAACTCATTTGGAGCCATTGGCATCATCAAGGCAAGTAG----------A--G--C--TCATC---ACATT---ATCCGTCTG--TAGA---CAC-GTTTTAACATTTGAATCGTTCTATCCTTTTCA----------A--------C------ACT---AACAGAAAGATAAGCGCAGCATGAAGCCAAGATTTGGCTGTACAAGCACAAGGA	
droEre2	scaffold_4690:10901501-10901682 -		CCACCGAGCAGGATATTGAGAGTCATTTGGAGCAATTGGCATCATCAAGGCAAGTAA----------A--G--C--ACATGATG-CATC---ATGTGTATG--TCGA---AAC-GTTTTAACCTTTGTATCTTTGTATCCCATTGCA----------A--------C------ATT---AACAGAAAGACAAGCGCAGCATGAAGCCAAGATTTGGCTGTACAAGAACAAGGA	

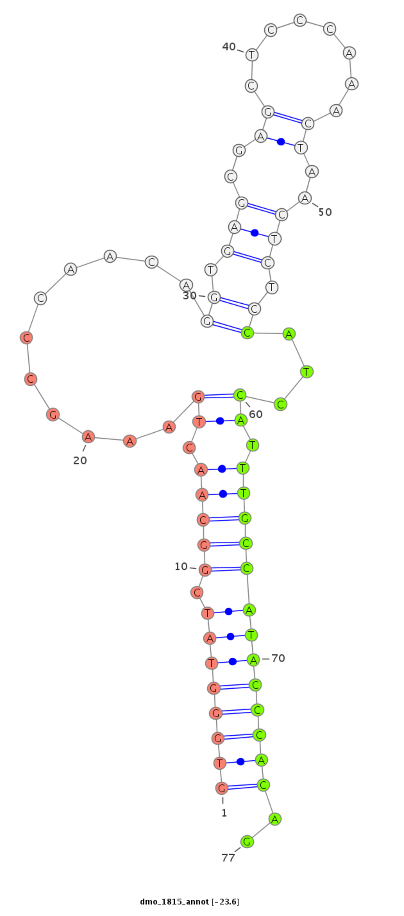
Generated: 09/08/2015 at 07:01 PM

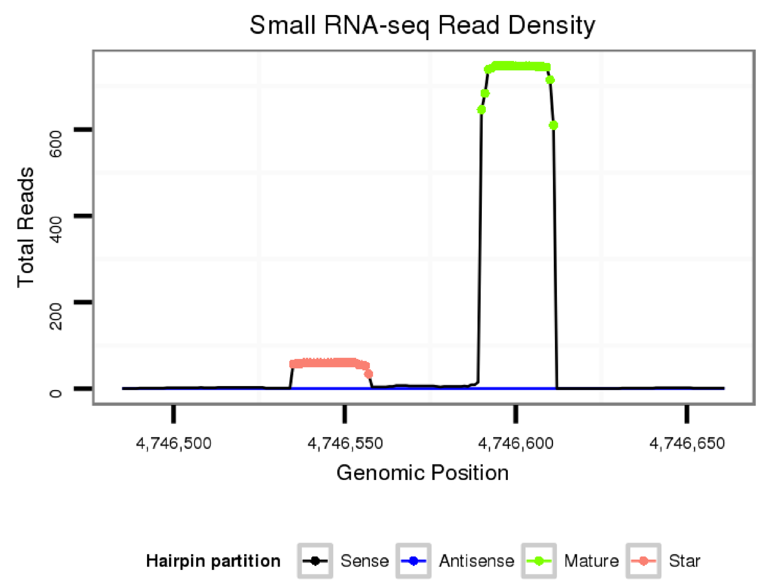
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

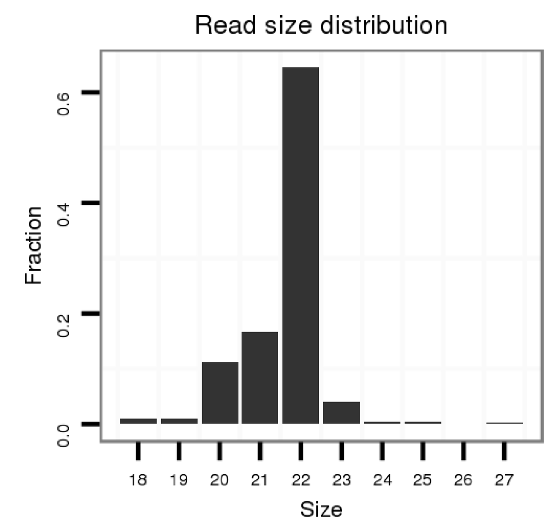
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1815	**scaffold_6540:4746535-4746611 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

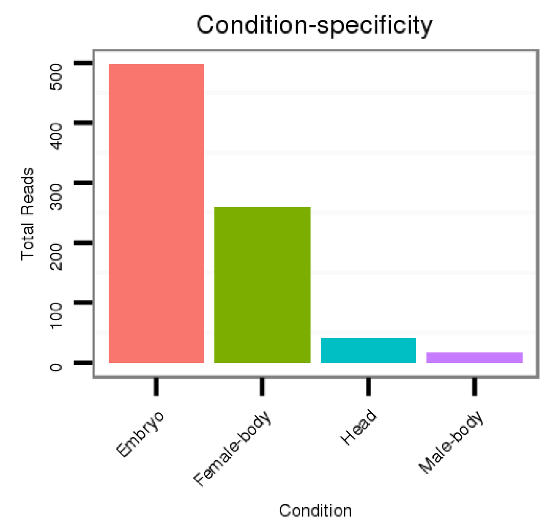
Legend: mature star mismatch in alignment mismatch in read

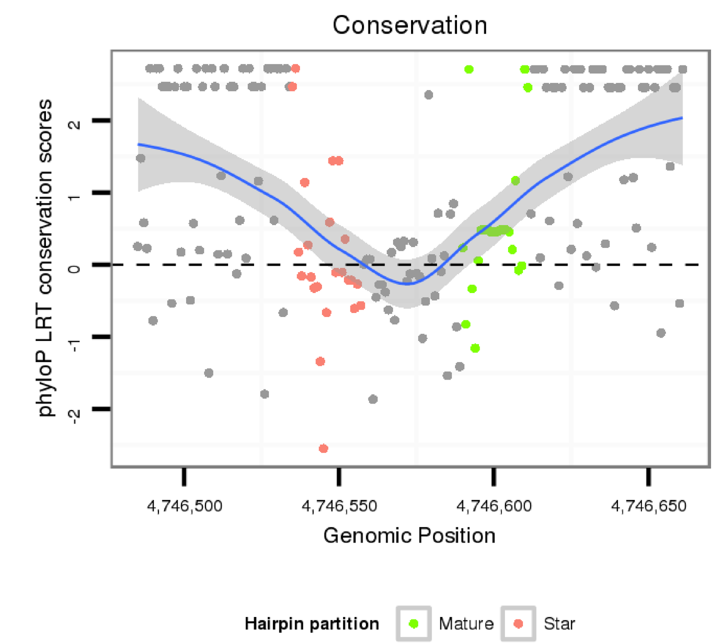
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI24013-in]; CDS [Dmoj\GI24013-cds]; CDS [Dmoj\GI24013-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CTAATCATGGGCGTGGCGCTGCTGACGCTGGCGCTCTGGGCATACATCAGGTGGGTATCGGCAACTGAAAGCCCAACAGGTGAGCGAGCTCCCAAACTAACTCTCCATCCATTTGCCATACCCACAGGTATAGCGGCGAGCTGAGCGATTTCGGCGGAAAGCTGGATGAGTTTGCAA **(((((((.(((((.((..........((.(((..((........))..))).))...)).)))))))))))))..**	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V041 embryo	V056 head	V049 head	V110 male body
....CATCCATTTGCCATACCCACAG..	22	0	1	505.00	505	308	135	40	11	10	1
....CATCCATTTGCCATACCCACAGT...	23	1	1	320.00	320	219	17	36	28	14	6
....CATCCATTTGCCATACCCACA...	21	0	1	98.00	98	48	42	2	4	1	1
....TCCATTTGCCATACCCACAGT...	21	1	1	93.00	93	41	19	13	13	6	1
....CATCCATTTGCCATACCCACAGA...	23	1	1	56.00	56	39	13	4	0	0	0
....TCCATTTGCCATACCCACAG..	20	0	1	55.00	55	25	22	2	2	3	1
....CATCCATTTGCCATACCCACAGC...	23	1	1	47.00	47	47	0	0	0	0	0
....ATCCATTTGCCATACCCACAG..	21	0	1	32.00	32	8	22	0	1	1	0
....GTGGGTATCGGCAACTGAAAGCC..	23	0	1	28.00	28	15	2	1	2	0	8
....CATCCATTTGCCATACCCAC..	20	0	1	28.00	28	16	11	0	1	0	0
....ATCCATTTGCCATACCCACAGT...	22	1	1	25.00	25	13	8	3	1	0	0
....GTGGGTATCGGCAACTGAAAGC...	22	0	1	19.00	19	12	1	0	3	0	3
....CATCCATTTGCCATACCCACAC..	22	1	1	16.00	16	15	1	0	0	0	0
....TCCATTTGCCATACCCACAGC...	21	1	1	12.00	12	12	0	0	0	0	0
....TCCATTTGCCATACCCACAGA...	21	1	1	10.00	10	3	7	0	0	0	0
....CATTTGCCATACCCACAGT...	19	1	1	6.00	6	4	0	1	0	1	0
....ATCCATTTGCCATACCCACA...	20	0	1	6.00	6	1	5	0	0	0	0
....CATTTGCCATACCCACAG..	18	0	1	6.00	6	1	4	0	1	0	0
....CCATCCATTTGCCATACCCACAGT...	24	1	1	6.00	6	6	0	0	0	0	0
....ATCCATTTGCCATACCCACAC..	21	1	1	6.00	6	3	3	0	0	0	0
....ATCCATTTGCCATACCCACAGC...	22	1	1	5.00	5	5	0	0	0	0	0
....CATCCATTTGCCATACCCACAA..	22	1	1	5.00	5	2	3	0	0	0	0
....CCATCCATTTGCCATACCCACAG..	23	0	1	4.00	4	4	0	0	0	0	0
....CTCCATCCATTTGCCATACCCACAG..	25	0	1	4.00	4	0	4	0	0	0	0
....GTGGGTATCGGCAACTGAA..	19	0	1	4.00	4	0	3	0	0	0	1
....ATCCATTTGCCATACCCACAGA...	22	1	1	4.00	4	0	4	0	0	0	0
....TCCATTTGCCATACCCACAGTA..	22	2	1	3.00	3	3	0	0	0	0	0
....CCATTTGCCATACCCACAGT...	20	1	1	3.00	3	0	2	1	0	0	0
....CCATTTGCCATACCCACAG..	19	0	1	3.00	3	2	1	0	0	0	0
....GTGGGTATCGGCAACTGAAAGCCC...	24	0	1	2.00	2	1	0	0	0	0	1
....GTGGGTATCGGCAACTGAAAG..	21	0	1	2.00	2	0	1	0	0	0	1
....CATCCATTTGCCATACCCACACT...	23	2	1	2.00	2	2	0	0	0	0	0
....TCCATTTGCCATACCCACAGTC..	22	2	1	1.00	1	0	0	0	0	0	1
....ATCCATTTGCCATACCCACACT...	22	2	1	1.00	1	1	0	0	0	0	0
....CATCCATTTGCCATACCCACACA...	23	2	1	1.00	1	1	0	0	0	0	0
....CCATCCATTTGCCATACCCAC..	21	0	1	1.00	1	1	0	0	0	0	0
.............TGGCGCTGCTGACGCTGGCGCTCTGGGCA...	29	0	1	1.00	1	1	0	0	0	0	0
....AACAGGTGAGCGAGCTCCC..	19	0	1	1.00	1	1	0	0	0	0	0
....GGTGAGCGAGCTCCCAAACTAACTCTC..	27	0	1	1.00	1	0	1	0	0	0	0
....TCCATTTGCCATACCCACAGAA..	22	2	1	1.00	1	1	0	0	0	0	0
....TGGGTATCGGCAACTGAAAGCC..	22	0	1	1.00	1	1	0	0	0	0	0
....ATCCATTTGCCATACCCACAT..	21	1	1	1.00	1	1	0	0	0	0	0
....ATCCATTTGCCATACCCACAGTA..	23	2	1	1.00	1	1	0	0	0	0	0
....TGAGCGAGCTCCCAAACTAACTCT...	24	0	1	1.00	1	0	0	1	0	0	0
....CCATTTGCCATACCCACAGA...	20	1	1	1.00	1	1	0	0	0	0	0
....AACAGGTGAGCGAGCTCC...	18	0	1	1.00	1	1	0	0	0	0	0
....CATCCATTTGCCATACCCA...	19	0	1	1.00	1	1	0	0	0	0	0
....GATTTCGGCGGAAAGCTGGAT..........	21	0	1	1.00	1	0	0	0	0	0	1
....ATTTGCCATACCCACAGT...	18	1	1	1.00	1	1	0	0	0	0	0
....CCATTTGCCATACCCACAGC...	20	1	1	1.00	1	1	0	0	0	0	0
....CCATCCATTTGCCATACCCACA...	22	0	1	1.00	1	0	1	0	0	0	0
....TCCATTTGCCATACCCACACT...	21	2	1	1.00	1	0	1	0	0	0	0
....GTGGGTATCGGCAACTGA...	18	0	1	1.00	1	0	1	0	0	0	0
....CCATCCATTTGCCATACC...	18	0	1	1.00	1	1	0	0	0	0	0
....TCCATCCATTTGCCATACCCACAG..	24	0	1	1.00	1	1	0	0	0	0	0
.....CATGGGCGTGGCGCTGCTG...	19	0	1	1.00	1	0	1	0	0	0	0
....CTCTCCATCCATTTGCCATAC..	21	0	1	1.00	1	0	1	0	0	0	0
....TCCATTTGCCATACCCACAC..	20	1	1	1.00	1	1	0	0	0	0	0
....GGTATCGGCAACTGAAAGCC..	20	0	1	1.00	1	1	0	0	0	0	0
....ACTGAAAGCCCAACAGGTGAG...	21	0	1	1.00	1	0	0	1	0	0	0
............................TGGCGCTCTGGGCATACATCAG...	22	0	1	1.00	1	0	0	1	0	0	0
.......................GACGCTGGCGCTCTGGGCA...	19	0	1	1.00	1	0	1	0	0	0	0
....ATCCATTTGCCATACCCACAGAA..	23	2	1	1.00	1	0	1	0	0	0	0
....TGAGCGAGCTCCCAAACTAAC..	21	0	1	1.00	1	0	1	0	0	0	0
....TGAGCGAGCTCCCAAACTAACTC..	23	0	1	1.00	1	0	0	0	1	0	0
..............GGCGCTGCTGACGCTGGCGCTCTGGGT..	27	1	1	1.00	1	0	1	0	0	0	0
....ATCCATTTGCCATACCCACACAA..	23	3	1	1.00	1	0	1	0	0	0	0
....AACTAACTCTCCATCCATTTG..	21	0	1	1.00	1	0	1	0	0	0	0
....GAAAGCTGGATGAGTTTGCAA	21	0	1	1.00	1	0	0	0	0	0	1
....GGTATCGGCAACTGAAAGCCCAACAGG...	27	0	1	1.00	1	1	0	0	0	0	0
....GTGGGTATCGGCAACTGAAA...	20	0	1	1.00	1	1	0	0	0	0	0
....CATTTGCCATACCCACAGC...	19	1	2	0.50	1	1	0	0	0	0	0
....ATTTGCCATACCCACAGC...	18	1	3	0.33	1	1	0	0	0	0	0

Anti-sense strand reads

GATTAGTACCCGCACCGCGACGACTGCGACCGCGAGACCCGTATGTAGTCCACCCATAGCCGTTGACTTTCGGGTTGTCCACTCGCTCGAGGGTTTGATTGAGAGGTAGGTAAACGGTATGGGTGTCCATATCGCCGCTCGACTCGCTAAAGCCGCCTTTCGACCTACTCAAACGTT **(((((((.(((((.((..........((.(((..((........))..))).))...)).)))))))))))))..**	Read size	# Mismatch	Hit Count	Total Norm	Total	V041 embryo	V056 head	M046 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:4746485-4746661 +	dmo_1815	CTAATCATGGGCGTGGCGCTGCTGACGCTGGCGCTCTGGGCATACATCAGGTGGGTATCGGCA--ACTGAAAGCCCAACAGGTGAG------CGAGCTCCC--------------A----AACTAA---CT-----CTCCATCCATTTGCCATACCCACAGGTATAGCGGCGAGCTGAGCGATTTCGGCGGAAAGCTGGATGAGTTTGCAA
droVir3	scaffold_13047:750738-750910 +	dvi_68	CTGGTCATGGGTGTAGCGTTGCTGACGCTGGCACTCTGGGCGTACATTAGGTGGGTATCGGCA--ACTGAAAACTCAATA----AC------TGAGCTTCC--------------A----AACTAA---TT-----CTCAATCCATTTGCCATACCCACAGATATAGCGGTGAGTTGAGCGACTTGGTGGCAAGCTGGACGAATTTGCAA
droGri2	scaffold_14906:5563611-5563770 -		CTGGTCATGGGTGTGGCGCTGCTAACACTGGCACTCTGGGCCTACATAAGGTGACTCTCCA--ATA-------------------------------------ACT------CT---TGGCTA---AACATAATCACTA----AACCGA---TT--C---CATATTC----------GTATAGATATAGCGGCGAGCTGAGCGACTTGGTGGCAAGCTGGACGACTTTGCCA
droWil2	scf2_1100000004902:9643172-9643331 -		CTGGTTATGGGCGTGGCCCTACTGACCCTTGCCCTGTGGTCTTACATTAGGTAAGAGTTAA---T---CGAAT--------------------------GTTCGTAT-------------------------AAACATTT--ATTGAATTGG---CT--G---CTTTTATT----------TTACAGATACAGCGGTGAGTTGAGCGACTTGGTGGCAAGCTGGATGACTTTGCCA
dp5	2:1779221-1779388 -		CTGGTGATGGGCGTAGCCCTGCTGACGCTTGCACTCTGGGCGTACATCAGGTAAGAGCATTC---GTAAA--------------------------ACCCGAAA-------------------------AAAGATTTCCCATCCAACTGA---GAGTCTCCTCGATCCA----------TTACAGGTACAGCGGCGAGTTGAGCGATTTCGGTGGCAAATTGGATGAGTTTGCCA
droPer2	scaffold_7:1932990-1933157 -		CTGGTGATGGGCGTAGCCCTGCTGACGCTTGCACTCTGGGCGTACATCAGGTAAGAGCATTC---GTAAA--------------------------ACCCGAAA-------------------------AGAGATTTCCCATCCAACTGA---GAGTCTCCTCGATCCA----------TTACAGGTACAGCGGCGAGTTGAGCGATTTCGGTGGCAAATTGGATGAGTTTGCCA
droAna3	scaffold_13340:4715779-4715938 -		CTTGTGATGGGCGTGGCGCTGCTAACGCTGGCCCTATGGGCTTACATCAGGTAAGATTAAGAA--A--TAACCTTTGTAGAAATATATCCT----AAG---AAAC--C---ATTATCAT----------TTACAGATACAGTGGCGAGCTGAGCGACTTGGCGGCAAGTTGGATGACTTTGCAA
droBip1	scf7180000396359:474012-474176 +		CTTGTGATGGGAGTGGCGTTGCTAACGCTAGCTCTATGGGCATACATCAGGTAAGTTTAAAAA--A-------------------------------------A----TACT--TATTGTTAAAAA---AATATTAAA----ACTTAC---CTCCA---CTTCTCCT----------TTACAGATACAGTGGAGAGCTGAGCGACTTGGTGGCAAGCTGGACGACTTCGCAA
droKik1	scf7180000302388:1746441-1746626 -		CTGGTCATGGGCGTGGCTCTGCTCACGCTGGCTTTGTGGGCCTATATCAGGTGAGTGTAGTAC----ATTTTTTGATCGGACTTATGTCTCTACCTCCTACTTG-----ACTCC--TTG--TGACTGA--CC---AATA---T---CTTTCAT----------TTTCAGATATAGCGGCGAGCTGAGTGACTTGGCGGCAAGTTGGATGATTTTGCCA
droFic1	scf7180000454106:1853720-1853875 -		TTGGTTATGGGAGTCGCTCTGCTCACGCTGGCTTTGTGGGCCTACATTAGGTATGTTCTTATA--TGG------CT---ACGTTA--GACGATCA-----CT----AAT---CATT---T---AATTTCCT----------CTTTAGATATAGTGGCGAACTGAGCGACTTGGTGGCAAGTTGGATGACTTTGCCA
droEle1	scf7180000491194:509212-509290 +		AC---TCACT----ATC---GATC--T---CATTTCCA----------TTTCAGATATAGCGGCGAGCTGAGCGATTTCGGTGGCAAGTTGGATGAGTTTGCCA
droRho1	scf7180000779488:553376-553587 +		CTGGTCATGGGAGTGGCGCTGCTTACATTGGCTCTGTGGGCCTACATCAGGTAGGTTATTTT--GA--------------GGGGAGCCATTACAT--------TTT-----------------TCTTAAAAATAGGGCAAGGTCTGGCCATTAGTTGTTAATCCGGTGGTTTCACA------------------TTGCT----ATT---TATC--T---CTTTTTTA----------TTATAGATACAGCGGCGAGCTGAGCGATTTTGGTGGCAAGTTGGATGATTTTGCCA
droBia1	scf7180000302402:4234745-4234800 +		CTGGTCATGGGTGTGGCACTGCTGACGCTGGCTCTGTGGGCCTACATCAGGTGGGT---
droTak1	scf7180000415310:684862-685088 -		CTGGTCATGGGTGTGGCGCTGCTCACGCTGGCTCTGTGGGCCTACATAAGGTGGGTTTAGATA--GGGATTACATAGCGTGACGGGTTGCACTTCTATTGTTCCCCACTCAAAGCTATATTACCTTTTGAAAATTGG----------TAACTGAAACTAAATGCAAATACTC--TA--C--CCTCTCTA----------TTTTAGATATAGCGGCGAGCTGAGTGACTTGGCGGCAAGTTGGATGACTTTGCTA
droEug1	scf7180000409881:182755-182963 +		CTGATTATGGGTGTGGCGCTGCTAACGCTGGCTCTGTGGGCCTATATCAGGTAAGTTCTATT--GGAAAATACTCT--TTGAGAAATTGCAATTT--------TTC-----------------ACTGAGAAAAAAGTTAATTGTTTAGAATTAATTGATTATTTAAATACCC---T--A--TATCTTCA----------TTTCAGATATAGCGGTGAGCTTAGTGACTTGGGGGCAAGTTGGATGACTTTGCAA
dm3	chr3R:20459043-20459204 +		CTGGTTATGGGTGTGGCGCTTCTAACGCTGGCTCTGTGGGCCTACATTAGGTAGGTTGATTTAGCT--TGAGCTTTTGATGATAATTTTGCC----AAC---GATG--T---TTTATCAA----------TTCCAGATATAGCGGAGAGCTCAGCGACTTTGGCGGCAAGTTGGATGACTTTGCAA
droSim2	3r:19988183-19988344 +		TTGATCATGGGTGTGGCGCTTCTAACGCTGGCTCTGTGGGCTTACATTAGGTAGGTTGATGCAGCT--TGAGCTTTTGATGATAATCTTGCC----AAC---GATC--A---CTTTTCCA----------TTCCAGATATAGCGGAGAGCTCAGCGATTTTGGCGGCAAGTTGGATGACTTTGCAA
droSec2	scaffold_0:20793428-20793589 +		TTGATCATGGGTGTGGCGCTTCTAACGCTGGCTCTGTGGGCTTACATTAGGTAGGTTGATGCAGCT--TGAGCTTTTGATGATAATCTTGCC----AAC---GATC--A---CTTTTCCA----------TTCCAGATATAGCGGAGAGCTCAGCGACTTTGGCGGCAAGTTGGATGACTTTGCAA
droYak3	3R:26038688-26038849 -		CTGGTCATGGGTGTGGCGCTGCTCACGCTGGCTCTGTGGGCCTACATCAGGTAGGTTGATAA--C---TGAGTTTTGGTTGAGAATCTTGCC----AACTAA---CTTTA--CTTTTGAA----------TTGCAGATATAGCGGAGAGCTCAGTGACTTTGGCGGCAAGTTGGATGACTTTGCAA
droEre2	scaffold_4820:7599484-7599645 -		CTGGTCATGGGTGTGGCGCTACTCACGCTGGCTCTGTGGGCTTACATCAGGTAGGTTGATAA--T---TGAGCTCTGGATGATAATCTTGCC----AACTAA---CTCTT--CTTTTGAA----------TTGCAGATATAGCGGAGAGCTCAGTGACTTTGGCGGCAAGTTGGATGACTTTGCTA

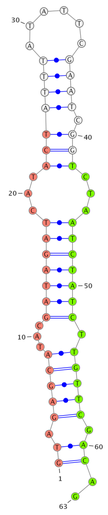
Generated: 08/18/2015 at 04:02 PM

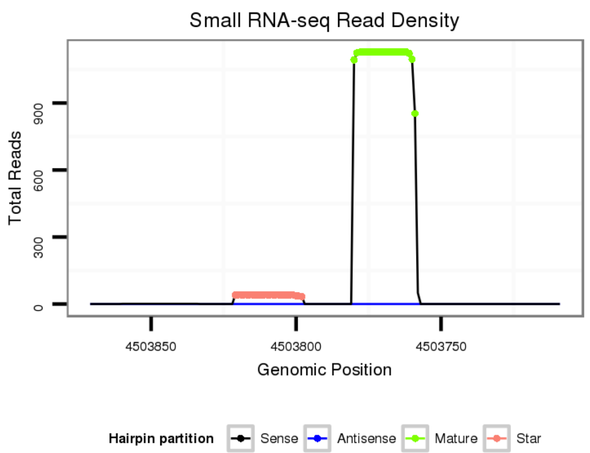
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

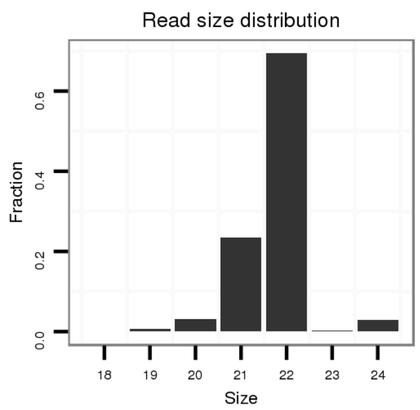
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_593	**scaffold_6359:4503759-4503821 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

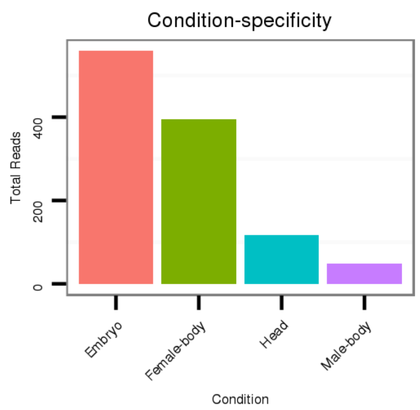
Legend: mature star mismatch in alignment mismatch in read

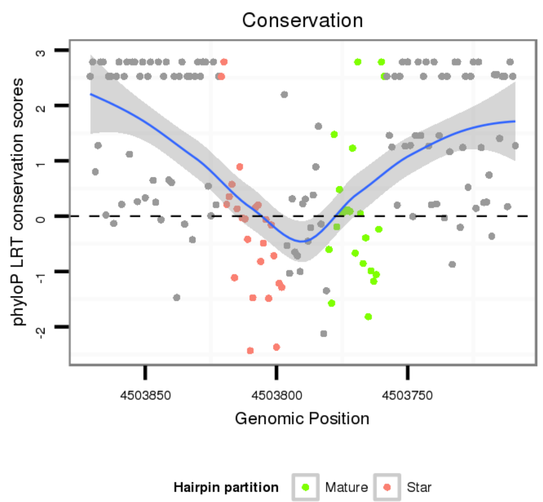
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI21426-in]; CDS [DmojGI21426-cds]; CDS [DmojGI21426-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTACTACGCCGTGCAGAACGACGATCTGGAGCGCGTGGCCGAGATATTGGGTAGAGCATACGATAGATCATACTATTTATATTCGAATCGGTCTAATCTATCTTGTTCGACAGCCGCCGACTACAATGTAATGACGCGCATGCGTGAATTTCTGAATGGTACC	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V041 embryo	V056 head	V110 male body	V049 head
**********((.((((((...(((((((...(((((((.....))))).)))...)))))))..)))))).))..**********											
.....TCTAATCTATCTTGTTCGACAG.....	22	0	1	777.00	777	121	277	274	44	29	32
.....TCTAATCTATCTTGTTCGACAGT.....	23	1	1	246.00	246	173	22	14	14	15	8
.....TCTAATCTATCTTGTTCGACA.....	21	0	1	235.00	235	72	78	37	22	15	11
.....TCTAATCTATCTTGTTCGACAGC.....	23	0	1	49.00	49	47	2	0	0	0	0
.....GTAGAGCATACGATAGATCATACT.....	24	0	1	33.00	33	26	0	3	0	4	0
.....TCTAATCTATCTTGTTCGAC.....	20	0	1	26.00	26	16	9	0	0	0	1
.....CTAATCTATCTTGTTCGACAG.....	21	0	1	24.00	24	0	23	0	1	0	0
.....TCTAATCTATCTTGTTCGACAGA.....	23	1	1	19.00	19	15	3	1	0	0	0
.....TCTAATCTATCTTGTTCGACAC.....	22	1	1	19.00	19	15	3	1	0	0	0
.....TCTAATCTATCTTGTTCGA.....	19	0	1	6.00	6	2	0	0	4	0	0
.....CTAATCTATCTTGTTCGACA.....	20	0	1	6.00	6	0	6	0	0	0	0
.....CTAATCTATCTTGTTCGACAGT.....	22	1	1	6.00	6	4	2	0	0	0	0
.....TCTAATCTATCTTGTTCGACAA.....	22	1	1	6.00	6	0	6	0	0	0	0
.....GTAGAGCATACGATAGATCATACC.....	24	1	1	4.00	4	4	0	0	0	0	0
.....GTAGAGCATACGATAGATCAT.....	21	0	1	4.00	4	0	0	1	1	1	1
.....GTAGAGCATACGATAGATCATAC.....	23	0	1	3.00	3	3	0	0	0	0	0
.....TAATCTATCTTGTTCGACAGT.....	21	1	1	3.00	3	0	3	0	0	0	0
.....TCTAATCTATCTTGTTCGACAGTT.....	24	2	1	2.00	2	1	1	0	0	0	0
.....TAATCTATCTTGTTCGACAG.....	20	0	1	2.00	2	0	1	1	0	0	0
.....TCTAATCTATCTTGTTCGACAT.....	22	1	1	2.00	2	0	0	2	0	0	0
.....TCTAATCTATCTTGTTCGACAGAA.....	24	2	1	1.00	1	0	1	0	0	0	0
.....AATCTATCTTGTTCGACAGT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....AATCTATCTTGTTCGACA.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TCTAATCTATCTTGTTCGACAGTA.....	24	2	1	1.00	1	0	1	0	0	0	0
.....CTAATCTATCTTGTTCGACAGC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....GTAGAGCATACGATAGATCATA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TAATCTATCTTGTTCGACA.....	19	0	1	1.00	1	0	0	1	0	0	0
.....CTAATCTATCTTGTTCGACAGA.....	22	1	1	1.00	1	0	1	0	0	0	0
.....TCTAATCTATCTTGTTCGACATT.....	23	2	1	1.00	1	1	0	0	0	0	0
.....CTAATCTATCTTGTTCGA.....	18	0	1	1.00	1	0	1	0	0	0	0
...........TGCAGAACGACGATCTGGAGCGCGTGG.....	27	0	1	1.00	1	0	0	0	0	0	1
.....TCTAATCTATCTTGTTCGACT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TCTAATCTATCTTGTTCGACAAA.....	23	2	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

CATGATGCGGCACGTCTTGCTGCTAGACCTCGCGCACCGGCTCTATAACCCATCTCGTATGCTATCTAGTATGATAAATATAAGCTTAGCCAGATTAGATAGAACAAGCTGTCGGCGGCTGATGTTACATTACTGCGCGTACGCACTTAAAGACTTACCATGG	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_6359:4503709-4503871 -	dmo_593	GTACTACGCCGTGCAGAACGACGATCTGGAGCGCGTGGCCGAGATATTGGGTAGA----------GCA----TACGATAGAT----CAT-----A----------CTATTTAT--------ATTCGAAT---------CGG------TCTAATC-TATCT---TG---T-TCGACAGCCGCCGACTACAATGTAATGACGCGCATGCGTGAATTTCTGAATGGTACC
droVir3	scaffold_12928:6294639-6294805 -		GTACTACGCCGTGCAGAACGATGATCTGGAGCGTGTGCCGAGATTCTCGGTAAGAGTCTGG----------AGTATCCTTT---CTGTACT--TCTGCT----------CAACGT--T----T----AATT--------T-----CG----ATCATT---CG---A-CGAACAGCTGCCGACTACAATGTGCTGACGCGTATGCGTGAATTCCTAAATGGCACC
droGri2	scaffold_14853:5111518-5111698 -		GTACTACGCCGTGCAGAATGATGATCTGGAGCGTGTCGCCGAGATACTGGGTAAGCCTTTGC---C----TC-CCA----TTCCACAGTTGAA-GC-TTAGCC----------AACCT--T----T----AAATCTCTCTCTTT-CTCT---C------A---TT---CTCTGT-GTCGCAGCTGGTGACTATGATGTTGTCGACGCGCGATGCGTGAATACCTAAATGGTACC
droWil2	scf2_1100000004909:9940414-9940589 -		GTACTATGCCGTCAGAACGATGATCTTGAGCGTGTGGCTGAGATATTGGGTAAGATTTAA----C------------------C----CCCAGAGAGATACAGAGAGAGAGAGAGAGAGAGAATCA-----TGTCATT--------GTTT-ATTC---T------A---CT---T---T---TTTAGCTGCCGATTATAATGTGCTACGGCCATGCGTGAATATC----TGGTACC
dp5	XL_group1a:548360-548521 +		GTACTATGGCGTGCAGAACGACGATCTGGAGCGGTTGCCGAGATTCTAGGTGAGTCTCTAGTGCTCTAGTG-A----------AGATCT----C----------CCA-----TGCTACT--------CCAT-CTGC---T------A---CT---CC---T-CGGACAGCTGGCGACTTCAATGTGCTGACACGCATCCGGGAGTACTTGAATGGTACC
droPer2	scaffold_26:157872-158033 +		GTACTATGGCGTGCAGAACGACGATCTGGAGCGGTTGCCGAGATTCTAGGTGAGTCTCTAGTGCTCTAGTG-A----------AGATCT----C----------CCA-----TGCTACT--------CCAT-CTGC---T------A---CT---CC---T-CGGACAGCTGGCGACTTCAATGTGCTGACACGCATCCGGGAGTACTTGAATGGTACC
droAna3	scaffold_12929:1687240-1687396 -		GTACTATGCCGTTCAGAACGATGATCTCGAAAGGTGGCCGAGATTCTAGGTACTGGTCT----TCCAG-GAGCA----CTTAACAGTAA----------------------CCCTTTCT----------AAT----------CC------C------A---TT---T---T-GTTCGACGCTGCCGACTTCAATGTGTTAACTCCCATCAGGAGTACTCAATGGAACC
droBip1	scf7180000396543:152803-152959 -		GTACTATGGCGTTCAGAACGATGATCTCGAACGGTGGCCAGAGATTCTAGGTACTGGCTC----TCCAG-G-C---T----------AGATCT----T----------AAA-----TGT---AT--------CCCATCT---T---C-ATTACAGCTGCCGACTTTAATGTGTTGACTCCCATCAGGGACTACTCTGAATGGAACC
droKik1	scf7180000302610:367332-367490 +		GTACTATGCCGTGCAGAACGATGATCTAGAGCGAGTGGCTGAGATTTTGGGTAAGCTGATAATGTT----TC-C---A----------AGCTCT----A----------AAA-----TGT---AT--------CCTTAT-TTAT---T------A---CT---TATTT---C-TGTACAGCTGCCGACTTCAATGTGCTGACCCCATTCGGGAGTACCTGAATGGCACCA
droFic1	scf7180000453927:560310-560478 +		GTACTATGGCGTGCAGAATGACGATCTGGAGCGGTGGCGGAGATTTTGGGTGAGCTATC----C------GCA----CTACATATACATATGTA----T----------T----------CTTATTCCT---------ATTCTAAT----------GG------CT---ACG---AA---T---C---T-TGCCAGCTTCCGACTTCAATGTGCTGACCCCATTCGGGAGTACCTGAATGGCACC
droEle1	scf7180000491011:1124750-1124918 +		GTACTATGGCGTGCAGAACGATGACCTGGAGCGCGTGGCAGAGATTCTGGGTGCGTTTTTGC---T------GCA----CT--GC----------A----------TCACCT--T----C----TAATCCCTGTAATT-CCTCTAATCCTTATG---TT----A---C-TGGCCAGCTGCCGACTTCAATGTGCTGACCCCATTCGGGAGTACCTGAATGGCACC
droRho1	scf7180000779506:909994-910145 +		GTTCTACGGCGTGCAGAACGATGATTGGAGCGCGTGGCAGAGATTCTGGGTGAGTTTGTT----------GGT--CTCATATCTGTA----------TCCTTACT---------TA----------TGG------T------A---TT---AT---T-TGACTAGCTGCCGACTTCAATGTGCTGACCCCATCGGGAGTACCTTAATGGCACC
droBia1	scf7180000301760:1086586-1086751 +		GTACTACGCCGTGCAGAATGATGATTGGAGCGGTGGCGGAGATTCTGGGTGAGTTGGTCC----------GA----TTCCCCTTTATATTTG----G----------CTGTACT---------CAT-GTGC---TATTTGTG---TT----T---T-GGATAGCTGCCGACTTCAATGTGCTGACCCCATTCGGGAGTACTTGAACGGCACC
droTak1	scf7180000415179:73725-73886 +		GTACTATGGCGTGCAGAACGATGATTGTGGAAGGGTGGCGGAGATTCTGGGTGAGTTTGTTTTGAC---TG-C---A----------AATGCT----C----------CTATCTAT--------CTTTTAATT---------T-----CC-----CCGTTT---TC---C-CGATAGCTGCCGACTTCAATGTGCTGACCCCATTCGGGAGTACTTGAACGGCACC
droEug1	scf7180000409277:450883-451045 +		GTTTTATGGCGTGCAAAACGATGACCTAGACCGTGTGCCGAGATTCTGGGTGAGTGATT----------GCA----CTTCACAAATAAGCGCA----C----------CTTTTCT---TT--CATGA---------ACTTT---T-----TG---TT---T---TTGGAGCAGCTGCCGACTTTAATGTGCTTACCCCATTCGTGAGTACTTGAATGGCACC
dm3	chrX:144977-145132 +		GTACTATGGAGTCCAAAACGATGACTTGGAGCGTGTAGCGGAGATTCTGGGTAAGTTTGCT----T------GCA----CTCGGCATTT----T----------A----------AC---------GATATAA----------AGG------CTTAATG---CT---T---T---T-GGAATAGCTGCCGACTTCAACGTGCTGACTCCATACGGGAGTACTTAAATGGCACC
droSim2	x:82501-82656 +		GTACTATGGAGTCCAAAACGATGACTTGGAGCGTGTAGCGGAGATTCTGGGTAATTTGTT----T------GCA----CTCGGCATTT----T----------A----------AC---------GTTATAA----------AGG------CTTAATG---CT---T---T---T-GGAACAGCTGCCGACTTCAACGTGCTGACTCCTATACGGGAGTACCTAAATGGCACC
droSec2	scaffold_10:16740-16895 +		GTACTATGGAGTCCAAAACGATGACTTGGAGCGTGTAGCGGAGATTCTGGGTAAGTTTGTT----T------GCA----CTCGGCATTT----T----------A----------AC---------GTTATAA----------AGG------CTTAATG---CT---T---T---T-GGAACAGCTGCCGACTTCAACGTGCTGACTCCTATACGGGAGTACCTAAATGGCACC
droYak3	X:84867-85022 +		GTACTATGGCGTCCAAAACGATGACTTGGAGCGCGTAGCGGAGATTCTGGGTATGTTTGTT----T------GCA----CTCAACAGTT----T----------A----------AT---------CTTATAA----------AGG------TTAATG---CT---T---T---T-GAAATTAGCTGCTGACTTCAACGTGCTGACTCCATACGGGAATACTTAAATGGCACC
droEre2	scaffold_4644:85909-86063 +		GTACTACGCAGTCCAAAACGATGACTTGGAGCGCGTAGCGGAGATTCTGGGTAAGTTTGTT----T------GCA----CTCGACATTT----T----------A----------AT---------CTTTA-AA----------AGG------TCTAATG---CT---T---T---T-GGAATAGCTGCCGACTTCAACGTGCTGACTCCATACGGGAGTACTTAAATGGCACC

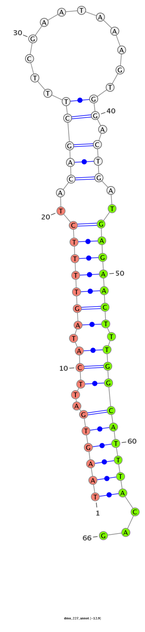
Generated: 09/08/2015 at 06:07 PM

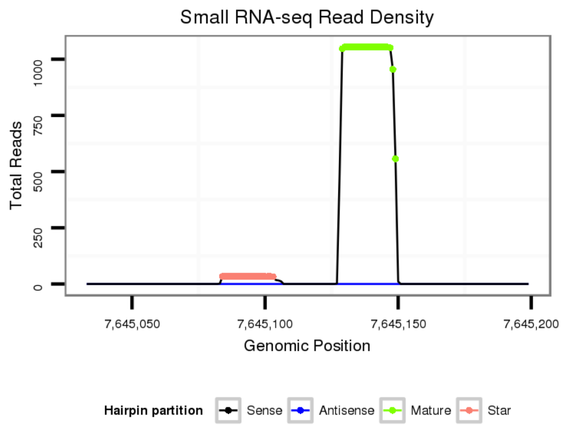
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

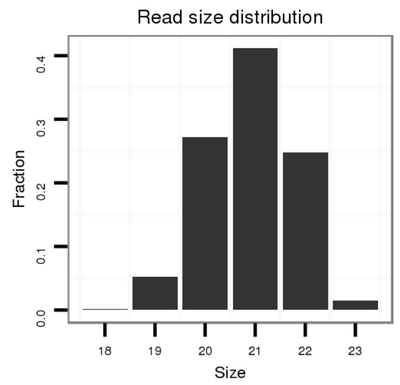
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_227	**scaffold_6473:7645083-7645149 +**	**confident**	**5p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

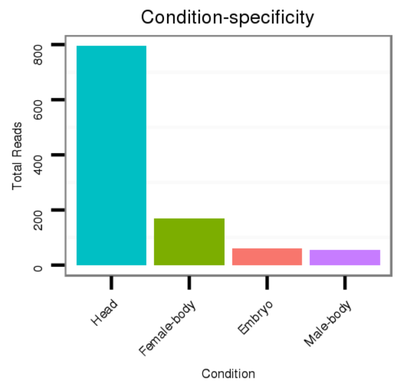
Legend: mature star mismatch in alignment mismatch in read

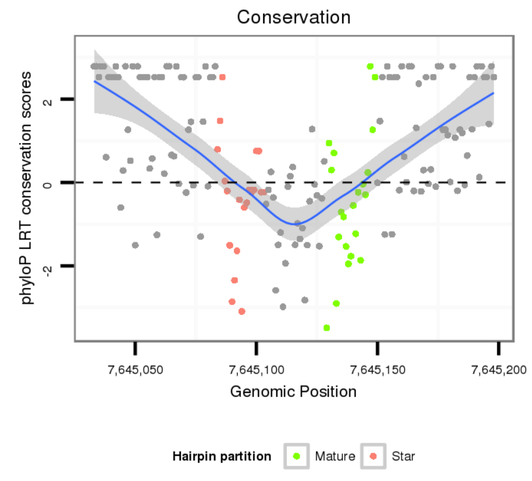
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI15657-in]; CDS [Dmoj\GI15657-cds]; CDS [Dmoj\GI15657-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CATGTACGCCACGCTGCTCTGGGGACGACCCAAGCTGCCGGTGCCCGTGGGTAAGTGATTCATAGTTTTCTACAGCTTTCGAATAAAGTGGACTGATGAGAACTTTGGCATTTACAGCCACCTCGCCGAGCAAGACCACGTCCAAGGTGAACGCCTCGGACAGCATG **********(((((((..(((.(((((((..(((((.....)))).)))).))))))).)))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head	V049 head	M046 female body	M060 embryo	V110 male body	V041 embryo
.....TGAGAACTTTGGCATTTACAGT.....	22	1	1	372.00	372	144	76	44	42	62	4
.....TGAGAACTTTGGCATTTACAG.....	21	0	1	276.00	276	121	93	42	5	14	1
.....ATGAGAACTTTGGCATTTACAG.....	22	0	1	265.00	265	105	64	42	28	18	8
.....TGAGAACTTTGGCATTTACA.....	20	0	1	228.00	228	125	67	26	0	10	0
.....ATGAGAACTTTGGCATTTACA.....	21	0	1	166.00	166	76	39	31	10	10	0
.....TGAGAACTTTGGCATTTAC.....	19	0	1	49.00	49	28	14	7	0	0	0
.....ATGAGAACTTTGGCATTTAC.....	20	0	1	47.00	47	20	18	5	2	2	0
.....ATGAGAACTTTGGCATTTACAGT.....	23	1	1	34.00	34	8	3	2	12	9	0
.....TAAGTGATTCATAGTTTTCT.....	20	0	1	15.00	15	6	8	1	0	0	0
.....TAAGTGATTCATAGTTTTCTACA.....	23	0	1	12.00	12	3	1	6	1	0	1
.....TGAGAACTTTGGCATTTACAGA.....	22	1	1	8.00	8	1	2	1	4	0	0
.....TGAGAACTTTGGCATTTACAGC.....	22	0	1	7.00	7	0	0	0	7	0	0
.....GAGAACTTTGGCATTTACA.....	19	0	1	4.00	4	1	0	3	0	0	0
.....ATGAGAACTTTGGCATTTACAGC.....	23	0	1	3.00	3	0	0	0	3	0	0
.....GAGAACTTTGGCATTTACAG.....	20	0	1	3.00	3	1	0	2	0	0	0
.....TGAGAACTTTGGCATTTACAGTT.....	23	2	1	3.00	3	1	0	2	0	0	0
.....GAGAACTTTGGCATTTACAGT.....	21	1	1	2.00	2	0	0	2	0	0	0
.....GATGAGAACTTTGGCATTTACAG.....	23	0	1	2.00	2	0	0	1	0	0	1
.....GTAAGTGATTCATAGTTTTCTAC.....	23	0	1	2.00	2	0	0	0	2	0	0
.....ATGAGAACTTTGGCATTTACAC.....	22	1	1	2.00	2	1	0	0	1	0	0
.....TAAGTGATTCATAGTTTTCTAC.....	22	0	1	2.00	2	0	0	1	1	0	0
.....TGAGAACTTTGGCATTTACAT.....	21	1	1	2.00	2	1	1	0	0	0	0
.....TAAGTGATTCATAGTTTTCTA.....	21	0	1	2.00	2	0	0	2	0	0	0
.....TGAGAACTTTGGCATTTACC.....	20	1	1	2.00	2	1	1	0	0	0	0
.....ATGAGAACTTTGGCATTTACAGA.....	23	1	1	2.00	2	0	0	0	1	0	1
.....ATGAGAACTTTGGCATTTA.....	19	0	1	2.00	2	1	1	0	0	0	0
.....ATGAGAACTTTGGCATTTACTC.....	22	2	1	1.00	1	1	0	0	0	0	0
.....TGAGAACTTTGGCATTTACAC.....	21	1	1	1.00	1	0	1	0	0	0	0
.....TGAGAACTTTGGCATTTACACT.....	22	2	1	1.00	1	1	0	0	0	0	0
.....ATGAGAACTTTGGCATTTACACT.....	23	2	1	1.00	1	0	0	0	1	0	0
.....ATGAGAACTTTGGCATTT.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TGAGAACTTTGGCATTTACAA.....	21	1	1	1.00	1	0	0	1	0	0	0
.....TGAGAACTTTGGCATTTACT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....ATGAGAACTTTGGCATTTACAGTT.....	24	2	1	1.00	1	0	0	0	1	0	0
.....ATGAGAACTTTGGCATTTACAT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TAAGTGATTCATAGTTTTC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....GAGAACTTTGGCATTTACAGC.....	21	0	1	1.00	1	0	0	0	1	0	0
.....TGAGAACTTTGGCATTTACATT.....	22	2	1	1.00	1	0	1	0	0	0	0
.....TGAGAACTTTGGCATTTA.....	18	0	1	1.00	1	0	1	0	0	0	0
.....ATGAGAACTTTGGCATTTACC.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TGAGAACTTTGGCATTTACAGAT.....	23	2	1	1.00	1	1	0	0	0	0	0
.....TGAGAACTTTGGCATTTT.....	18	1	4	1.00	4	4	0	0	0	0	0
.....TGAGAACTTTGGCATTTAA.....	19	1	2	0.50	1	1	0	0	0	0	0
.....TGAGAACTTTGGCATTTACAGTTT.....	24	3	2	0.50	1	1	0	0	0	0	0
.....ATGAGAACTTTGGCATTTAA.....	20	1	2	0.50	1	1	0	0	0	0	0

Anti-sense strand reads

GTACATGCGGTGCGACGAGACCCCTGCTGGGTTCGACGGCCACGGGCACCCATTCACTAAGTATCAAAAGATGTCGAAAGCTTATTTCACCTGACTACTCTTGAAACCGTAAATGTCGGTGGAGCGGCTCGTTCTGGTGCAGGTTCCACTTGCGGAGCCTGTCGTAC **********(((((((..(((.(((((((..(((((.....)))).)))).))))))).)))))))...**********						V110 male body	M060 embryo
.....TGAGAACTTTGGCATTTACAGT.....	22	1	1	372.00	372	62	4
.....TGAGAACTTTGGCATTTACAG.....	21	0	1	276.00	276	14	1
.....ATGAGAACTTTGGCATTTACAG.....	22	0	1	265.00	265	18	8
.....TGAGAACTTTGGCATTTACA.....	20	0	1	228.00	228	10	0
.....ATGAGAACTTTGGCATTTACA.....	21	0	1	166.00	166	10	0
.....TGAGAACTTTGGCATTTAC.....	19	0	1	49.00	49	0	0
.....ATGAGAACTTTGGCATTTAC.....	20	0	1	47.00	47	2	0
.....ATGAGAACTTTGGCATTTACAGT.....	23	1	1	34.00	34	9	0
.....TAAGTGATTCATAGTTTTCT.....	20	0	1	15.00	15	0	0
.....TAAGTGATTCATAGTTTTCTACA.....	23	0	1	12.00	12	0	1
.....TGAGAACTTTGGCATTTACAGA.....	22	1	1	8.00	8	4	0
.....TGAGAACTTTGGCATTTACAGC.....	22	0	1	7.00	7	0	0
.....GAGAACTTTGGCATTTACA.....	19	0	1	4.00	4	0	0
.....ATGAGAACTTTGGCATTTACAGC.....	23	0	1	3.00	3	3	0
.....GAGAACTTTGGCATTTACAG.....	20	0	1	3.00	3	0	0
.....TGAGAACTTTGGCATTTACAGTT.....	23	2	1	3.00	3	0	0
.....GAGAACTTTGGCATTTACAGT.....	21	1	1	2.00	2	0	0
.....GATGAGAACTTTGGCATTTACAG.....	23	0	1	2.00	2	1	0
.....GTAAGTGATTCATAGTTTTCTAC.....	23	0	1	2.00	2	0	0
.....ATGAGAACTTTGGCATTTACAC.....	22	1	1	2.00	2	0	0
.....TAAGTGATTCATAGTTTTCTAC.....	22	0	1	2.00	2	0	0
.....TGAGAACTTTGGCATTTACAT.....	21	1	1	2.00	2	0	0
.....TAAGTGATTCATAGTTTTCTA.....	21	0	1	2.00	2	0	0
.....TGAGAACTTTGGCATTTACC.....	20	1	1	2.00	2	0	0
.....ATGAGAACTTTGGCATTTACAGA.....	23	1	1	2.00	2	0	1
.....ATGAGAACTTTGGCATTTA.....	19	0	1	2.00	2	0	0
.....ATGAGAACTTTGGCATTTACTC.....	22	2	1	1.00	1	0	0
.....TGAGAACTTTGGCATTTACAC.....	21	1	1	1.00	1	0	0
.....TGAGAACTTTGGCATTTACACT.....	22	2	1	1.00	1	0	0
.....ATGAGAACTTTGGCATTTACACT.....	23	2	1	1.00	1	0	0
.....ATGAGAACTTTGGCATTT.....	18	0	1	1.00	1	0	0
.....TGAGAACTTTGGCATTTACAA.....	21	1	1	1.00	1	0	0
.....TGAGAACTTTGGCATTTACT.....	20	1	1	1.00	1	0	0
.....ATGAGAACTTTGGCATTTACAGTT.....	24	2	1	1.00	1	0	0
.....ATGAGAACTTTGGCATTTACAT.....	22	1	1	1.00	1	0	0
.....TAAGTGATTCATAGTTTTC.....	19	0	1	1.00	1	0	0
.....GAGAACTTTGGCATTTACAGC.....	21	0	1	1.00	1	0	0
.....TGAGAACTTTGGCATTTACATT.....	22	2	1	1.00	1	0	0
.....TGAGAACTTTGGCATTTA.....	18	0	1	1.00	1	0	0
.....ATGAGAACTTTGGCATTTACC.....	21	1	1	1.00	1	0	0
.....TGAGAACTTTGGCATTTACAGAT.....	23	2	1	1.00	1	0	0
.....TGAGAACTTTGGCATTTT.....	18	1	4	1.00	4	0	0
.....TGAGAACTTTGGCATTTAA.....	19	1	2	0.50	1	0	0
.....TGAGAACTTTGGCATTTACAGTTT.....	24	3	2	0.50	1	0	0
.....ATGAGAACTTTGGCATTTAA.....	20	1	2	0.50	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:7645034-7645199 +	dmo_227	ATGTACGCCACGCTGCTCTGGGGACGACCCAAGCTGCCGGTGCCCGTGGGTAAGTGATTCAT-AGTTTTCTACAG--CTT-TCG----AA----------T---------A--------AAGTGGACTGATG----------A-----GAA-CTT----TGGCATTTACAGCCACCTCGCCGAGCAAGACCACGTCCAAGGTGAACGCCTCGGACAGCATG
droVir3	scaffold_12970:4637544-4637703 +		ATGTACGCCACACTGCTATGGGGACGCCCAAGCTGCCAGTGCCGATGGGTAAGTGAGATTAAA---------G--GTT-GTG----TGT----------GCA----------E---------E--------CATGAGATTAATG----------AT-----TCCTT----TGGCATTTGAAGCTACATCGCCTAGCAAGTGCGGCGCCAAGGTGAACGCCTCGGATAGCATG
droGri2	scaffold_15203:10655308-10655480 -		ATGTACGCCACACTGCTCTGGGGTGGCGCAAGCTGCCAGTGCCCATGGGTAAGTGAATTAT-TG---------GATCT--GG----AGA----------GCG--AA------TC--------E------GGGCGAATTGATG----------ACTGACTCCATTC-----GCATT----TCGCATTTGCAGGTAGTCGCCAATAAGTGCAACGACCAAGGTGAGCGCCACGGATAGCATG
droWil2	scf2_1100000004515:1915285-1915461 -		ATGTATGCCACATTACTGTGGGGANGACCCAAGCTACGAGTGCAATTGGTAAGTAATTTAG-TC---------AGTCAGTCA----GG----------GTC--AG------TG-AG----TT------G-AAAGAA-----E----ATT----TC------AAT----A-TTGAATTGCATTTTGTGTCAAAGCAGGCAACTCGCCAACAATGCACGGCCAAAGTGAGTGCCTCGGATAGCGTG
dp5	XL_groupla:8166858-8167017 -		ATGTATGCCACGTTGCTGTGGGGTGGCCCAAGCTACGAACACCCATGGGTAAGTGCCGGCACTG---------GTG-AG----GG----------E----GGG-A------GATGAGATGCATC----------ATAATAATCCTT----GTCTTTGTGCAGCCAGCATCACCGAATAAA---ACAACAAAGACCAGCACCTCGGACAGCATG
droPer2	scaffold_15:526331-526494 -		ATGTACGCCACGTTGCTGTGGGGTGGCCCAAGCTGCCAACACCCATGGGTAAGTGCCGGCAGCC---------AC-TGG----GG----------T-GAGGGGG-A------GATGAGATGCATC----------ATATTAATCCTT----GTTTTTGTGCAGCCAGCATCACCGAATAAA---ACAACAAAGACCAGCACCTCGGACAGCATG
droAna3	scaffold_13117:1988447-1988604 +		ATGTACGCCACTCTGCTCTGGGGANGCCCAAGCTTCCGGTTGCAATAGGTAAGGACACCCA----------TTT-ATAGT----GG----------AGC---CACTAGA-G------CAGTAACTAAATTGG--TCATC----------E----------E---E----AACCCAGCCACTTCTCCGAACAAGTCCACCACCAAGCCAGTGCGCACGGACAGCATG
droBip1	scf7180000396425:79173-79329 -		ATGTACGCCAGTCTGCTCTGGGGANGACCCAAGCTGCCAGTGCGATAGGTAAGGAAA----TAGCACTCATGGG--CCC-TTG----AA----------E----------T--------GGTGACTAACATG----------ACCACAA---E---E-----ACTCAGCCACTTCTCCGAACAAGTCCGCGACAAAGGCCAGTGGGACGGACAGCATG
droKik1	scf7180000302698:1109321-1109510 +		ATGTACGCCACCCTGCTCTGGGGACGACCCAAGTTGCCAGTGCCCATAGGTAAGGCTCTAAG-GG---------A--T--TTC----T-TAATAAATTAATATTAATATTTAATATTATAATAAATGAT----------E----AA-E---------ATTA----------AAT---E-TCTAATTTCC----TACCCCCGTAGCCACCTCTGCCAACAAATGCACGACCAAGGCCAGTGCGCAACGGACAGCATG
droFic1	scf7180000454072:2562865-2563047 +		ATGTACGCCACCTTGCTGTGGGGACGCCCAAACTGCCGGTGCCAATTGGTAAGCTCGGGAGCAG---------CTC-GGSAT----GG----------E----------E----CG-A------TGTGATACTCATCCTTACAATCCAATCCATATTCCCATCC-----E---ACGTT----CCATTTCCACAGCCACCTCGCCGAACAAGTGCACGACCAAGGCGAGTGGAACGGACAGCATG
droEle1	scf7180000491001:906201-906366 +		ATGTACGCCACTTGTTATGGGGACGTCCCAAGTTGCCGGTTGCAATTGGTTAGTAAAGGACGAT---------TTT-TAACT-CAAA----------E----------T--------GTACGTATCCAAT----------ATCTGATAATGC----TTTTCGCCACAGCCACTTCACGAACAAGTGCACGACCAAGGCGAGCGGAACGGACAGCATG
droRho1	scf7180000779976:729821-729980 +		ATGTACGCCACTTTGTTCTGGGGACGACCTAAGTTGCCGGTTGCAATTGGTAGGTTAAAAGATAT---------TTT-CTTGC----GG----------CGA----------E----CA-A------TATACTATTATTA----------T-----E-GCTGT----ACCCTTATCCAGCCACTTCCCGAACAAGTGCGACGACCAAGGCGAGTGGAACGGACAGCATG
droBia1	scf7180000302069:275493-275652 +		ATGTACGCCACTTTGCTGTGGGGACGTCCCAAATTGCCAGTTGCAATTGGTAAGTTGTGTTGAGG---------G--TCC-TTG----AAT----------GGTCTAA-----CC--------E------GCAGGGATT----G----------E----------E---E----TCTTCE---TTATCTCCACAGCCACTTCCCGAACAAGTGCGACGACCAAGGCGAGTGGAACAGACAGCATG
droTak1	scf7180000415289:590646-590809 +		ATGTACGCCACCTTGCTATGGGGACGTCCTAAGTTGCCAGTTGCAATTGGTAAGTTTGGATTTG---------TAAAGGAATTAGTAT----------G----------E----------GT--------GCACAGATT-----E-----ATT----------E----------E---E---TTAAGA-CAT----ATTCCTATTAGCCACTTCCCGAATAAATGCGACCACCAAGGCGAGTGGAACGGACAGCATG
droEug1	scf7180000409095:588545-588697 -		ATGTACGCCACTTTGATATGGGGACGTCCCAAGTTGCCAGTTGCAATTGGTAAGTTATTAAG-AG---------TCC-TCA----AA----------E----------E----------E-------AGGATATCAAGT----------E----------E----------E---E---CAA----TTTCGTGCACAGCCACTTCTCCGAACAAGTGCAACGACCAAGGCCAGTGGGACGGACAGCATG
dm3	chrX:5549430-5549591 -		ATGTACGCCACTTTGATATGGGGTGGTGCCCAAGTTACCAGTTGCCATTGGTAAGTTTCGAAAAAG---------TAC-TAAAT----GG----------E----------E----------T-------AAGTGGATTTATTT----------E----------E----------E---E---ATCGAAAGCGTTG----TCCTTTGCCACACCAGCATCGCCGAGTAAATCGGCAACGCAAGGCGAGTGGGAACGGACAGCATG
droSim2	x:5183899-5184060 -		ATGTACGCCACTTTGATATGGGGACGTCCCAAGTTACCAGTTGCCATTGGTGAGTTTCAAAAAG---------TAC-TAAAG----GG----------E----------E----------T-------AAGTGGATTTCATT----------E----------E----------E---E---ATCGAAAGCGTTG----TCCTTTGCCACACCAGCATCGCCGAATAAATCGGCAACGCAAGGCGAGTGGGAACGGACAGCATG
droSec2	scaffold_4:1208273-1208434 +		ATGTACGCCACTTTGATATGGGGACGTCCCAAGTTACCAGTTGCCATTGGTGAGTTTCGAAAGAG---------TAC-TAAAG----GG----------E----------E----------T-------AAGTGGATTTCATT----------E----------E----------E---E---ATCGAAAGCGTTG----ACCTTTGCCACACCAGCATCGCCGAATAAATCGGCAACGCAAGGCGAGTGGGAACGGACAGCATG
droYak3	X:2919548-2919712 +		ATGTACGCCACTTTGATATGGGGACGTCCCAAGTTGCCGGTTGCAATTGGTAAGAATTGAAACAG---------TAC-TGG----AA----------E----------E----CAGT--------ATGTGGATTTATTA----------E----------E----------E---E---ATCGAAATCTCCG----CACTTCGCACAGCAAACATCGCCGAATAAATCGGCAACGCAAGGCGAGTGGGTACGGACAGCATG
droEre2	scaffold_4690:2901916-2902082 -		ATGTACGCCACTTTGATATGGGGACGTCCCAAGTTGCCAGTTGCCAATTGGGTAAGTTCTTGACTAC---------TTC-TGTAA----GG----------CA----------E----------E----ATG-A------AAGTGGATTTAGTC----------E----------E----------E---E---GACGAGTCCTTG----TCCTCGCACAGCAAGTTCGCCGAATAAATCGGCAACGAAGGCGAGTGGGTACGGACAGCATG

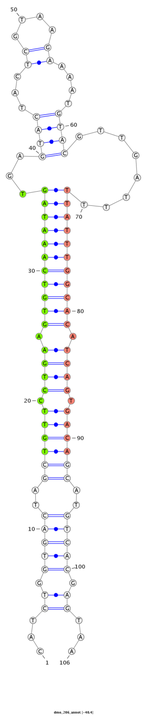
Generated: 09/08/2015 at 06:07 PM

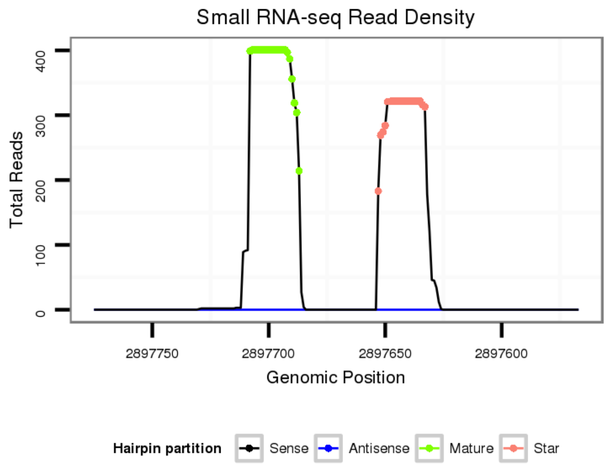
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

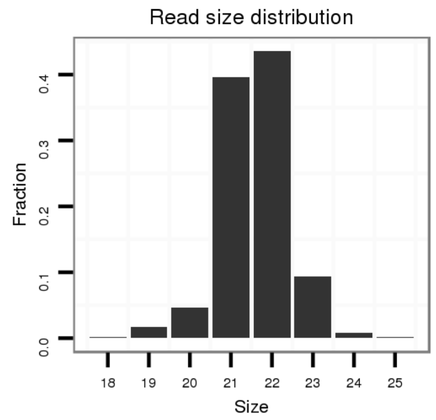
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_206	**scaffold_6328:2897617-2897725 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

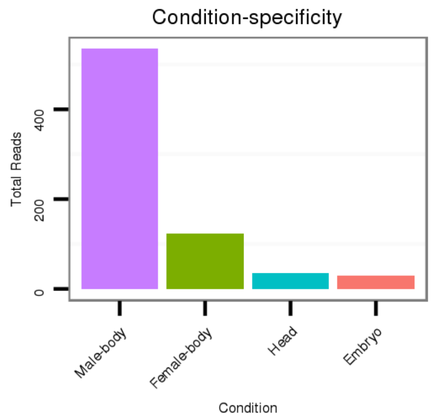
Legend: mature star mismatch in alignment mismatch in read

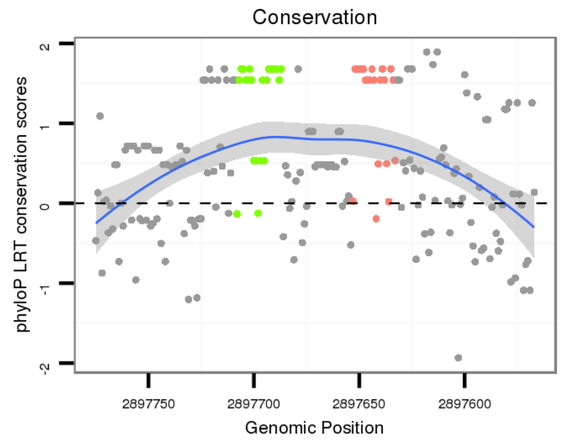
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CCGCTCACAATCGGCAATATCGATTTGGGCGGTCATCGATAGACAATGCGCGCATCTGGTGACTAGCTGTTCCTGAAGTGTCAAATAGTGAGTACTACTCGTAAGAAAATGTACGTTGATTTTTATTTGGCACATCAGTGACAGCATGTCACGAGTAATTGCACAACGACCAGAGCCGATAACGACGGCGATCGCGATTATTGTGCTAT **********...((.((((((..(((((((.((((.((((((((((((...((((...((....))....))))).....)))))))))))).)))).)))))))..))))))..))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V056 head	V049 head	V041 embryo
.....TGTTCCTGAAGTGTCAAATAGTG.....	23	1	1	202.00	202	191	5	1	3	2	0
.....TGTTCCTGAAGTGTCAAATAGT.....	22	0	1	186.00	186	174	5	0	5	1	1
.....TTATTTGGCACATCAGTGACA.....	21	0	1	123.00	123	82	26	2	6	7	0
.....TGTTCCTGAAGTGTCAAATAG.....	21	0	1	88.00	88	79	4	1	4	0	0
.....TATTTGGCACATCAGTGACAGC.....	22	0	1	45.00	45	23	13	7	0	1	1
.....AGCTGTTCCTGAAGTGTCAAAT.....	22	0	1	37.00	37	35	0	0	1	1	0
.....AGCTGTTCCTGAAGTGTCAAA.....	21	0	1	31.00	31	28	2	0	0	1	0
.....TATTTGGCACATCAGTGACAG.....	21	0	1	29.00	29	6	20	1	2	0	0
.....TTATTTGGCACATCAGTGACAG.....	22	0	1	27.00	27	6	19	0	1	1	0
.....TGTTCCTGAAGTGTCAAATAGTCT.....	24	2	1	27.00	27	27	0	0	0	0	0
.....TTATTTGGCACATCAGTGACAGC.....	23	0	1	26.00	26	9	5	11	0	0	1
.....TGTTCCTGAAGTGTCAAATAGTG.....	23	0	1	23.00	23	23	0	0	0	0	0
.....TATTTGGCACATCAGTGACAGT.....	22	1	1	19.00	19	16	2	0	0	1	0
.....TGTTCCTGAAGTGTCAAATAGTT.....	23	1	1	18.00	18	18	0	0	0	0	0
.....TTGGCACATCAGTGACAGCATG.....	22	0	1	16.00	16	10	5	0	1	0	0
.....TATTTGGCACATCAGTGACAGCT.....	23	1	1	12.00	12	8	3	1	0	0	0
.....TTGGCACATCAGTGACAGCAT.....	21	0	1	11.00	11	3	7	1	0	0	0
.....AGCTGTTCCTGAAGTGTCAA.....	20	0	1	10.00	10	9	0	0	1	0	0
.....TATTTGGCACATCAGTGACA.....	20	0	1	10.00	10	6	4	0	0	0	0
.....TTGGCACATCAGTGACAGCATGT.....	23	0	1	9.00	9	9	0	0	0	0	0
.....TTATTTGGCACATCAGTGACAGT.....	23	1	1	9.00	9	3	5	1	0	0	0
.....TGTTCCTGAAGTGTCAAATA.....	20	0	1	8.00	8	8	0	0	0	0	0
.....AGCTGTTCCTGAAGTGTCAAATT.....	23	1	1	7.00	7	5	0	0	2	0	0
.....TGTTCCTGAAGTGTCAAATAGTTC.....	24	2	1	6.00	6	4	2	0	0	0	0
.....AGCTGTTCCTGAAGTGTCAAATA.....	23	0	1	5.00	5	4	1	0	0	0	0
.....TTATTTGGCACATCAGTGA.....	19	0	1	5.00	5	4	0	0	1	0	0
.....TTTGGCACATCAGTGACAGCATG.....	23	0	1	5.00	5	1	4	0	0	0	0
.....TGTTCCTGAAGTGTCAAATAGTGA.....	24	0	1	4.00	4	4	0	0	0	0	0
.....AGCTGTTCCTGAAGTGTCAAATC.....	23	1	1	4.00	4	4	0	0	0	0	0
.....TTGGCACATCAGTGACAGCATGA.....	23	1	1	3.00	3	3	0	0	0	0	0
.....TGTTCCTGAAGTGTCAAATAGTTT.....	24	2	1	3.00	3	3	0	0	0	0	0
.....TGTTCCTGAAGTGTCAAATAGTGT.....	24	1	1	3.00	3	3	0	0	0	0	0
.....AGCTGTTCCTGAAGTGTCA.....	19	0	1	3.00	3	2	0	0	1	0	0
.....TGTTCCTGAAGTGTCAAATAGTCC.....	24	2	1	3.00	3	2	1	0	0	0	0
.....AGCTGTTCCTGAAGTGTCAAATTT.....	24	2	1	2.00	2	1	1	0	0	0	0
.....ATTTGGCACATCAGTGACA.....	19	0	1	2.00	2	0	2	0	0	0	0
.....GCTGTTCCTGAAGTGTCAAATA.....	22	0	1	2.00	2	2	0	0	0	0	0
.....ATTTGGCACATCAGTGACAGC.....	21	0	1	2.00	2	1	0	1	0	0	0
.....TTATTTGGCACATCAGTGT.....	19	1	1	2.00	2	2	0	0	0	0	0
.....TGTTCCTGAAGTGTCAAATAGC.....	22	1	1	2.00	2	2	0	0	0	0	0
.....TTTGGCACATCAGTGACAGCATGT.....	24	0	1	2.00	2	2	0	0	0	0	0
.....TTATTTGGCACATCAGTGAC.....	20	0	1	2.00	2	1	1	0	0	0	0
.....GGCACATCAGTGACAGCATG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....ATTTGGCACATCAGTGACAG.....	20	0	1	1.00	1	0	1	0	0	0	0
.....CTGTTCCTGAAGTGTCAAATAG.....	22	0	1	1.00	1	1	0	0	0	0	0
.....AGCTGTTCCTGAAGTGTCAAC.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TGTTCCTGAAGTGTCAAATAGTGC.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TGTTCCTGAAGTGTCAAATAGTA.....	23	1	1	1.00	1	1	0	0	0	0	0
.....ATGCGCGCATCTGGTGACTAGC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TATTTGGCACATCAGTGACAGCG.....	23	1	1	1.00	1	0	0	0	1	0	0
.....TTATTTGGCACATCAGTGACAT.....	22	1	1	1.00	1	0	1	0	0	0	0
.....TTATTTGGCACATCAGTGACTT.....	21	1	1	1.00	1	0	1	0	0	0	0
.....TTGGCACATCAGTGACAGCATC.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TTCCTGAAGTGTCAAATAGTC.....	21	1	1	1.00	1	0	1	0	0	0	0
.....TTGGCACATCAGTGACAGC.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TGTTCCTGAAGTGTCAAATAA.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TTTGGCACATCAGTGACAGCATGTC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....GTTCCTGAAGTGTCAAATAG.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TTTGGCACATCAGTGACAGCA.....	21	0	1	1.00	1	0	0	1	0	0	0
.....TTGGCACATCAGTGACAGCATGTTC.....	25	2	1	1.00	1	1	0	0	0	0	0
.....ACTAGCTGTTCCTGAAGTGTCA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TGTTCCTGAAGTGTCAAATAGTGCCA.....	25	3	1	1.00	1	1	0	0	0	0	0
.....TGTTCCTGAAGTGTCAAATAGTGCG.....	24	2	1	1.00	1	1	0	0	0	0	0
.....AGCTGTTCCTGAAGTGTCAAATCT.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TATTTGGCACATCAGTGA.....	18	0	1	1.00	1	0	0	0	1	0	0
.....TATTTGGCACATCAGTGAC.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TTTATTTGGCACATCAGTGACAGCT.....	25	1	1	1.00	1	1	0	0	0	0	0
.....TGTTCCTGAAGTGTCAAATAGTTCT.....	25	3	1	1.00	1	1	0	0	0	0	0
.....TTTGGCACATCAGTGACAGCT.....	21	1	1	1.00	1	0	1	0	0	0	0
.....TTTGGCACATCAGTGACAGC.....	20	0	1	1.00	1	0	0	1	0	0	0
.....TTGGCACATCAGTGACAGCATGTTT.....	25	2	1	1.00	1	0	0	0	1	0	0
.....GTTCCTGAAGTGTCAAATAGT.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TGCGCGCATCTGGTGACTAGC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....AGCTGTTCCTGAAGTGTCAAATAT.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TGTTCCTGAAGTGTCAAATAGA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TGTTCCTGAAGTGTCAAATAGTCTC.....	25	3	1	1.00	1	1	0	0	0	0	0
.....TTATTTGGCACATCAGTGACAGCT.....	24	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

GGCGAGTGTTAGCCGTTATAGCTAAACCCGCCAGTAGCTATCTGTTACGCGCGTAGACCACTGATCGACAAGGACTTCACAGTTTATCACTCATGATGAGCATTCTTTTACATGCAACTAAAAATAAACCGTGTAGTCACTGTCGTACAGTGCTCATTAACGTGTTGCTGGTCTCGGCTATTGCTGCCGCTAGCGCTAATAACACGATA **********...((.((((((..(((((((.((((.((((((((((((...((((...((....))....))))).....)))))))))))).)))).)))))))..))))))..))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V049 head	M046 female body	V110 male body
Show Alignment With Reads								

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6328:2897567-2897775 -	dmo_206	CCGCTCACAATCGGCAATATCGAT----------TTGGGCGGTCATCGATAGACAATGCGCGCATCTGGTGACTAGCTGTTCCTGAAGTGTCAAATAGTGAGTACTACTCGTAAGAAAATGTACGTTGATTTTTATTTGGCACATCAGTGACAGCATGTCACGAGTAATTGCACAACGA-CCAGAGCCGATAACGACGGCGATCGCG---------ATTATTGTGCTAT----
droVir3	scaffold_13042:902951-903167 -	dvi_45	ACGATAACGATA-ACAATAACGAT----------AACTTAAGCGATAA-CGATA-ACGATAAGCGCATCTGGTGACTAGCCGTTCCTGAAGTGTCAAATAGTACGTACTACTCGTAAGAAAATGTACGTTGATTTTTATTTGGCACATCAGTGACAGCATGTACGAGTAATTGCACAACAG-CCACAGCCGGAGAC------AGATCCGGAGACAGATGAGTCTTGGATGATAACG
droGri2	scaffold_15081:2041139-2041289 -	dgr_20	ACGG-ACGG----GCAACAGCATTCGTGGCGGGGAATCTGAGTG---------AGCCGGAGGATGCATCTGGTAACTAGCCGTTCCTGTGTACCCAAATAGTTCGTAGCACG------------------ATTGTTATTTGGCACATCAGTGACTGCTGGTTAACGGTGAGCGCACAACAA-CC---
droWil2	scf2_1100000004909:7960783-7960897 +	dwi_143	----------GGGTCTTGTGACGGGCAGTTCCTGAAGTGTCAAATAGTAGAGTACACTGATAA----------TTAGTATCTATTTGGCAGCTCAGTAACAGCCTTTTACAATTAAATGCAAATGCCGGCGAGAGC----------
droAna3	scaffold_13417:2460889-2461001 -	dan_75	C----------GCGTCCCGTGACGGGCAGTTCCTGAACTGTCAAATAGTGGACGGCATA----------AA-CATATTTGGCACGTCAGTAACAGCCTGTTACAAGTCAGCGCACGACCA-GCATTACCGGCCAC----------
droBip1	scf7180000395874:32867-33015 -		C----------GGGTCCCGTGACGGGCAGTTCCTGAACTGTCAAATAGTGGACGGCATA----------AA-CATATTTGGCACGTCAGTAACAGCCTGTTACAAGACAGCGCACGACCA-GCATACCGGCCACCTCGATGGAAGCGTACAGGGATCAGTTTTGGTCGAC----
droKik1	scf7180000302517:1186181-1186284 +		----------GGGTCCCGTGACAGGCAGTTCCTGAAGTGTCAAATAGTGGATGACATG----------AG-AATATTTGGCACGCCAGAGACAGCCTGTTACTGGGCAGCGAACGACCC---ATGCCG----------
droEre2	scaffold_4690:10368787-10368850 -		ATGCACCA----------C----------TAAGGCGACGACCA-ACGGCACCAATGATGCGCGCGATAGCG----------ATCATACCGACAC----

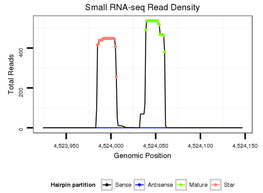
Generated: 09/08/2015 at 08:04 PM

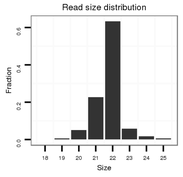
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	4
rescue.candidate	1

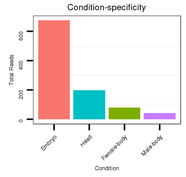
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2939	**scaffold_6680:4523974-4524097 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

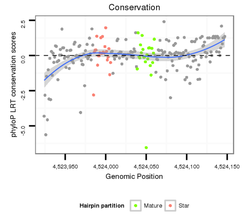
Legend: mature star one mature bp aligns w/ mismatch in read

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
(CAG)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

						M060	V041	V049	V056	M046	V110
										female	
Read #	Hit	Total				embryo	embryo	head	head	body	male
size	Mismatch	Count	Norm	Total							body
22	0	1	293.00	293		199	68	8	11	7	0
22	0	1	200.00	200		78	33	23	30	17	19
21	0	2	84.00	168		56	17	35	22	29	9
21	0	1	69.00	69		18	10	18	17	4	2
22	0	1	67.00	67		43	10	3	2	6	3
22	0	1	45.00	45		25	11	2	4	1	2
23	0	1	43.00	43		43	0	0	0	0	0
21	0	1	32.00	32		28	3	0	0	1	0
20	0	2	25.00	50		13	5	9	5	17	1
24	0	1	16.00	16		8	4	1	1	1	1
21	0	1	15.00	15		2	0	7	2	3	1
20	0	3	13.33	40		0	0	15	19	5	1
21	0	1	11.00	11		3	1	1	3	1	2
22	0	1	8.00	8		2	3	2	1	0	0
22	0	1	8.00	8		8	0	0	0	0	0
21	0	2	7.50	15		1	4	2	3	4	1
23	0	1	6.00	6		4	0	1	0	0	1
23	1	2	5.50	11		2	0	4	3	0	2
25	0	1	5.00	5		3	0	0	1	0	1
20	0	1	5.00	5		1	1	2	1	0	0
22	1	2	5.00	10		0	3	4	2	1	0
20	0	2	4.50	9		0	1	2	0	4	2
21	0	1	4.00	4		1	0	0	1	2	0
23	1	1	4.00	4		4	0	0	0	0	0
19	0	2	3.50	7		2	0	0	0	3	0
23	0	1	3.00	3		0	3	0	0	0	0
23	0	1	3.00	3		2	0	0	1	0	0
24	2	2	3.00	6		3	0	1	1	1	0
23	0	1	2.00	2		2	0	0	0	0	0
24	1	1	2.00	2		0	0	2	0	0	0
22	0	1	2.00	2		1	0	0	0	1	0
23	1	1	2.00	2		0	0	0	2	0	0
21	1	2	2.00	4		1	0	1	1	1	0

Anti-sense strand reads

						M060
Read #	Hit	Total				embryo
size	Mismatch	Count	Norm	Total		
22	0	19	0.05	1	1	

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dmo	scaffold_6680:4523974-4524097 +	dmo_2939	
droVir	scaffold_13049:8203718-8203926 -		
droGri	scaffold_13110:6529187-		
droWil	scaffold_11000000045111:2852284-		
dp5	Unknown_singleton_18271:3655-		
droPer	scaffold_31250687:2326457 -		
droAna	scaffold_13337:3643582-		
droBip	scaffold_20003396411:501456-		
droKik	scaffold_20003392419:437854-		
droFic	scaffold_20003453829:1511054-		
droEle	scaffold_20003491011:1493532-		
droRho	scaffold_20003776529:4793580-47734		
droBia	scaffold_20003391723:2647393-		
droTak	scaffold_20003414393:2824514-2826		
droEug	scaffold_20003419894:3366-3554 -		
dse	chr21:2934447-2934624 -		
droSim	CH480484:2604840-		
droSec	scaffold_20184151:1683443 -		
droTak	KB742828:1927252 -		
droEre	scaffold_4690:1353871-		

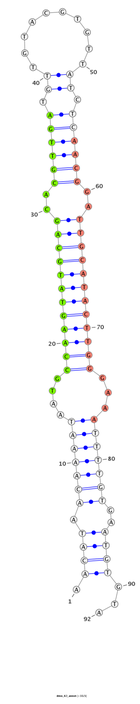
Generated: 08/18/2015 at 04:41 PM

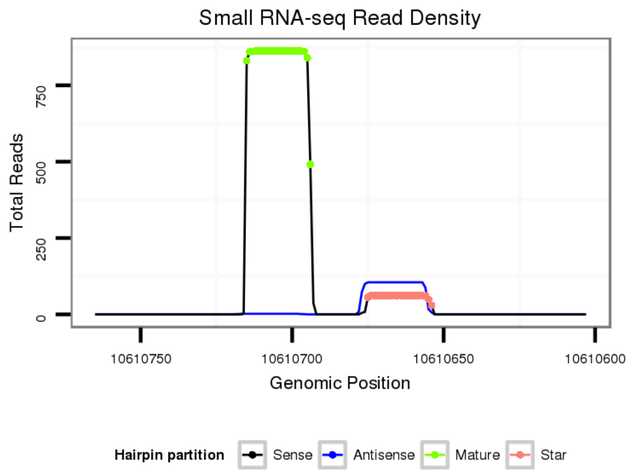
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mat	0
crit.hpf	1
crit.total	1
crit.mfe	0
crit.sig1	1
crit.sig2	1
crit.freq	0
crit.frac	0
rescue.mfe	0
rescue.dominant	0
rescue.significant	0
rescue.confident	0
rescue.candidate	0

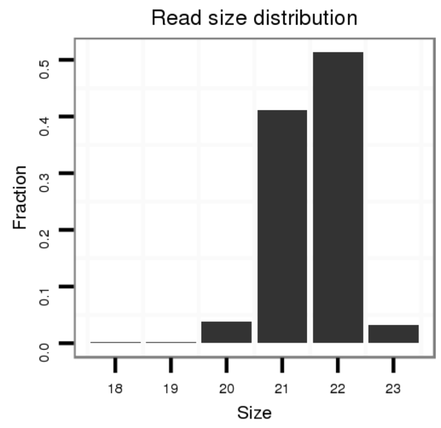
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_62	**scaffold_6500:10610653-10610715 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

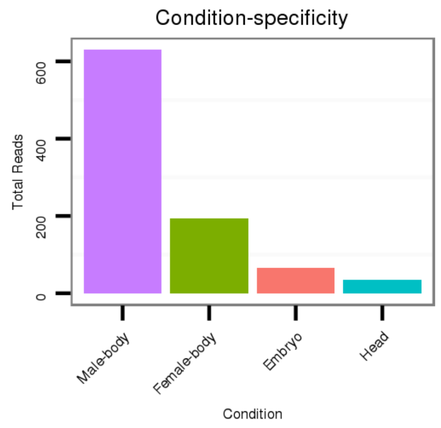
Legend: mature star mismatch in alignment mismatch in read

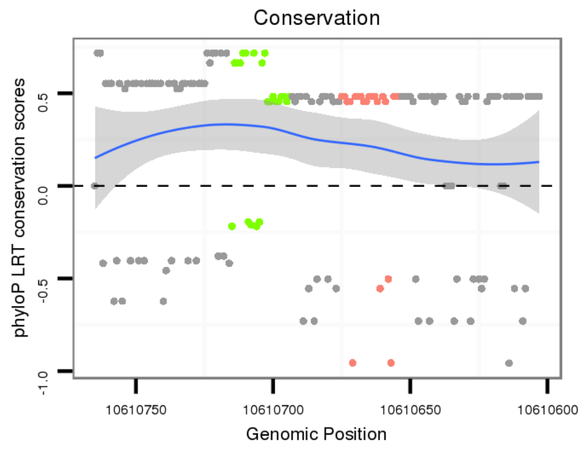
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TAATATTTTAGCAAATCACAATTAACAATAGCAAAAACATAACAAAATAATGCCAAGTATGCAGCACGTTGATGTTGTACGTGTTATCTCAACGGATTGCATACTTGGGAAATTTTGTGAATGTGTATTATGTTGCTGATGTGCATAAAAACTTATGTTAATA	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V041 embryo	V049 head	V056 head
..........(((((.(((((((....(((((((((((..(((((((.((.........)).)))))))..)))))))))))...)))))))..)))))...**********												
.....TGCCAAGTATGCAGCACGTTGA.....	22	0	1	436.00	436	285	91	21	19	10	10
.....TGCCAAGTATGCAGCACGTTG.....	21	0	1	342.00	342	254	73	2	2	6	5
.....TGCCAAGTATGCAGCACGTTGAT.....	23	0	1	29.00	29	25	2	1	0	0	1
.....AACGGATTGCATACTTGGGAAA.....	22	0	1	25.00	25	14	2	7	2	0	0
.....TGCCAAGTATGCAGCACGTT.....	20	0	1	20.00	20	18	1	0	0	0	1
.....TGCCAAGTATGCAGCACGTTGATC.....	24	1	1	18.00	18	18	0	0	0	0	0
.....AACGGATTGCATACTTGGGAA.....	21	0	1	16.00	16	5	4	7	0	0	0
.....GCCAAGTATGCAGCACGTTGA.....	21	0	1	15.00	15	6	9	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGAA.....	23	1	1	11.00	11	10	1	0	0	0	0
.....GCCAAGTATGCAGCACGTTGAT.....	22	0	1	8.00	8	6	0	2	0	0	0
.....TGCCAAGTATGCAGCACGTTGAC.....	23	1	1	7.00	7	5	2	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGT.....	22	1	1	7.00	7	5	1	1	0	0	0
.....AACGGATTGCATACTTGGGA.....	20	0	1	6.00	6	3	1	2	0	0	0
.....GCCAAGTATGCAGCACGTTG.....	20	0	1	6.00	6	0	6	0	0	0	0
.....AACGGATTGCATACTTGGGAAT.....	22	1	1	5.00	5	5	0	0	0	0	0
.....ACGGATTGCATACTTGGGAAA.....	21	0	1	4.00	4	4	0	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGATT.....	24	1	1	4.00	4	3	0	1	0	0	0
.....ACGGATTGCATACTTGGGAT.....	20	1	1	4.00	4	4	0	0	0	0	0
.....TCAACGGATTGCATACTTGGGA.....	22	0	1	4.00	4	3	0	0	0	0	1
.....AACGGATTGCATACTTGGGAAAA.....	23	1	1	3.00	3	3	0	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGAAA.....	24	2	1	3.00	3	2	0	0	0	0	1
.....GCCAAGTATGCAGCACGTTGATC.....	23	1	1	2.00	2	2	0	0	0	0	0
.....CAACGGATTGCATACTTGGGA.....	21	0	1	2.00	2	2	0	0	0	0	0
.....AACGGATTGCATACTTGGGAT.....	21	1	1	2.00	2	2	0	0	0	0	0
.....ACGGATTGCATACTTGGGAA.....	20	0	1	2.00	2	1	1	0	0	0	0
.....CAACGGATTGCATACTTGGGAT.....	22	1	1	2.00	2	2	0	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGG.....	22	1	1	2.00	2	2	0	0	0	0	0
.....CCAAGTATGCAGCACGTTGATT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....GCCAAGTATGCAGCACGTTGATT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGAAAA.....	25	3	1	1.00	1	0	0	1	0	0	0
.....TGCCAAGTATGCAGCACGTTT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TGCCAAGTATGCAGCACGT.....	19	0	1	1.00	1	0	1	0	0	0	0
.....AACGGATTGCATACTTGGGAAAT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....CAAGTATGCAGCACGTTGA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGC.....	22	1	1	1.00	1	0	1	0	0	0	0
.....ATGCCAAGTATGCAGCACGTTGA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TCAACGGATTGCATACTTGGGCCT.....	24	3	1	1.00	1	1	0	0	0	0	0
.....AACGGATTGCATACTTGGGTT.....	21	2	1	1.00	1	1	0	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGTC.....	23	2	1	1.00	1	0	1	0	0	0	0
.....TGCCAAGTATGCAGCACG.....	18	0	1	1.00	1	0	1	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGAAC.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGATAA.....	25	2	1	1.00	1	0	1	0	0	0	0
.....ACGGATTGCATACTTGGGAAAA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....ACGGATTGCATACTTGGGATG.....	21	2	1	1.00	1	1	0	0	0	0	0
.....CAAGTATGCAGCACGTTG.....	18	0	1	1.00	1	0	1	0	0	0	0
.....GCCAAGTATGCAGCACGTTGAC.....	22	1	1	1.00	1	0	1	0	0	0	0
.....CCAAGTATGCAGCACGTTGA.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TCAACGGATTGCATACTTGGG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGTAA.....	24	3	1	1.00	1	1	0	0	0	0	0
.....AACGGATTGCATACTTGGGAAAAA.....	24	2	1	1.00	1	1	0	0	0	0	0
.....ACGGATTGCATACTTGGGAAT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....ACGGATTGCATACTTGGGATC.....	21	2	1	1.00	1	1	0	0	0	0	0
.....CAACGGATTGCATACTTGGGAA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....ATGCCAAGTATGCAGCACGTT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....AACGGATTGCATACTTGGTCC.....	21	3	2	0.50	1	1	0	0	0	0	0

Anti-sense strand reads

ATTATAAAATCGTTTAGTGTTAATTGTTATCGTTTTTGTATTGTTTTATTACGGTTCATACGTCGTGCAACTACAACATGCACAATAGAGTTGCCTAACGTATGAACCCTTTAAAACACTTACACATAATACAACGACTACACGTATTTTTGAATACAATTAT	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	V049 head	M060 embryo	V056 head	V041 embryo
**********.(((((.(((((((....(((((((((((..(((((((.((.........)).)))))))..)))))))))))...)))))))..)))))...**********												
.....AGTTGCCTAACGTATGAACCCT.....	22	0	1	55.00	55	34	9	4	4	3	1
.....GTTGCCTAACGTATGAACCCT.....	21	0	1	15.00	15	11	3	1	0	0	0
.....GAGTTGCCTAACGTATGAACCC.....	22	0	1	9.00	9	5	4	0	0	0	0
.....GTTGCCTAACGTATGAACCCTT.....	22	0	1	9.00	9	6	3	0	0	0	0
.....AGTTGCCTAACGTATGAACCC.....	21	0	1	7.00	7	7	0	0	0	0	0
.....TTGCCTAACGTATGAACCCTTT.....	22	0	1	5.00	5	4	1	0	0	0	0
.....GTTGCCTAACGTATGAACCC.....	20	0	1	2.00	2	0	2	0	0	0	0
.....AGTTGCCTAACGTATGAACCCT.....	23	1	1	2.00	2	2	0	0	0	0	0
.....TTACGGTTCATACGTCGTGCAA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TTTTGCCTAACGTATGAACCC.....	21	2	1	1.00	1	0	0	0	0	1	0
.....TATTACGGTTCATACGTCGTGC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....AGTTGCCTAACGTATGAACCCTTT.....	24	0	1	1.00	1	1	0	0	0	0	0
.....GTTGCCTAACGTATGAACCCTTT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....AGTTGCCTAACGTATGAACCCTT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....AATTACGGTTCATACGTCGTGCAA.....	24	1	1	1.00	1	0	0	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6500:10610603-10610765	dmo_62	TAATATTTTAGCAAATCACAATTAACAATAGCAAAAACATAACAAAAT-A-----ATGCCAAGTATGCAGCACGTTGATGTTGTACGTGTTATCTCAACGGATTGCATACTTGGGAAATTTTGTGAATGTGTATTATGTTGCTGATGTGCATAAAAACTTATGTTAATA-------
droVir3	scaffold_12723:4640718-4640849 -	dvi_207	-AAA----------ACAAAAT-ATAAATTTGCCAAGTATGCAGCACGTTGATGTTTTTCTCGTTGTCACAACGCATTGCATACATGACAAATTTTGCTAATTGTATT---TCTGCTTGTAAACATAA--AGTAATTATAATAGCACTTA
droGri2	scaffold_15203:4252192-4252254 +		-AATATTGCATCAGATTATAATTAAATACAGCAAGAATATAACAAGAGA-----AAGCCAACACAACA-----------

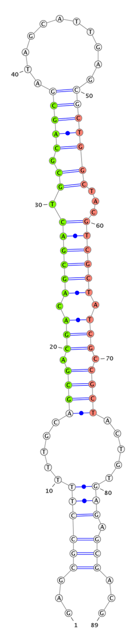
Generated: 09/08/2015 at 08:04 PM

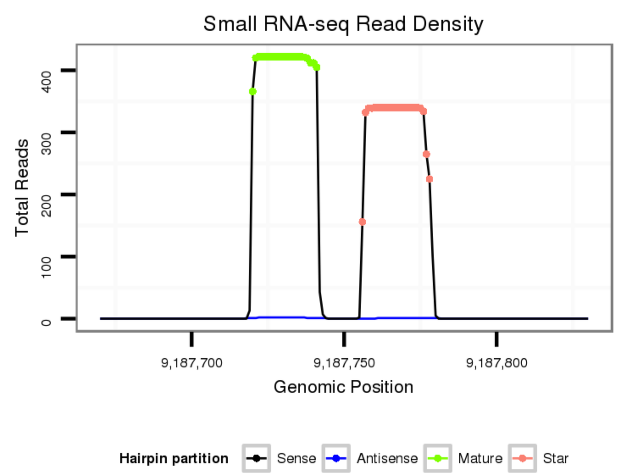
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

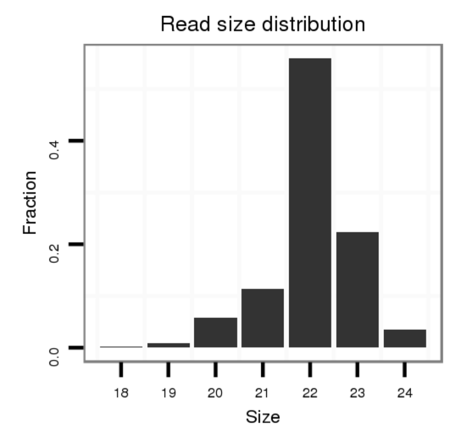
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_73	**scaffold_6473:9187720-9187780 +**	**confident**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

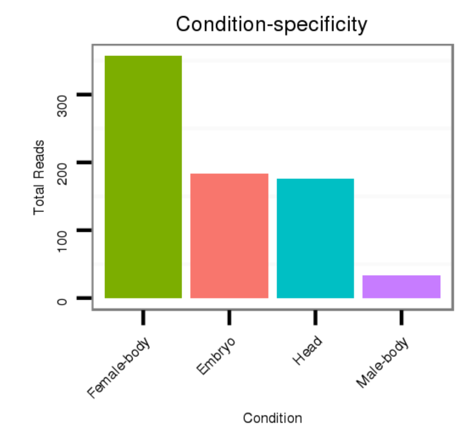
Legend: mature star mismatch in alignment mismatch in read

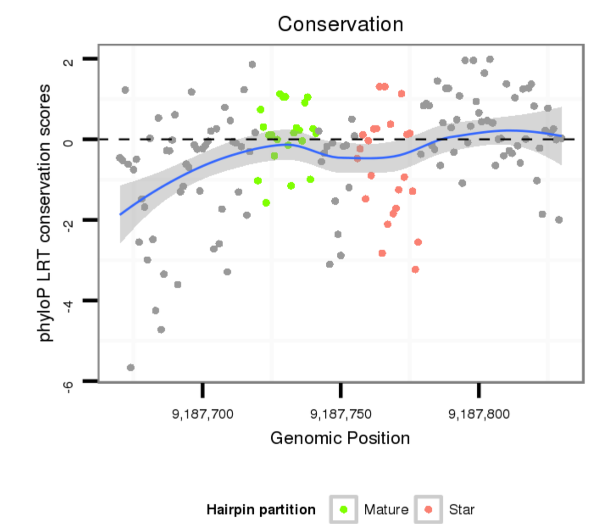
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dmoj\GI15727-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AGCGTCATTTTCTACTGCGGCTATGACAAATTGCTGAGCGCCTTTTTGCAGCGACGACAGCGACTGCGCAGCGATAGCATTGAGCGCTGGCTACGTCGCTATCGCCGCTACTGTGAGAGCGACGACAACAACAACAATATCGCCGAGTGTGAGTCAGCGTC	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V056 head	V049 head	V110 male body	V041 embryo
**********************************...((((((.....((((.(((.((((((.((.(((((..........)))))))...)))))).))).)))).....))).)))...*************************************											
...GCGACGACAGCGACTGCGCAGC...	22	0	1	326.00	326	160	124	14	14	6	8
...CTGGCTACGTCGCTATCGCCGCT...	23	0	1	76.00	76	40	8	12	6	8	2
...TGGCTACGTCGCTATCGCCGCTA...	23	0	1	73.00	73	28	4	21	15	3	2
...TGGCTACGTCGCTATCGCCGCT...	22	0	1	44.00	44	24	9	2	7	2	0
...TGGCTACGTCGCTATCGCCG...	20	0	1	34.00	34	4	0	12	14	4	0
...CTGGCTACGTCGCTATCGCCG...	21	0	1	34.00	34	9	1	9	12	2	1
...CGACGACAGCGACTGCGCAGC...	21	0	1	24.00	24	16	5	1	2	0	0
...CGACGACAGCGACTGCGCAGCG...	22	0	1	23.00	23	13	7	0	0	1	2
...CTGGCTACGTCGCTATCGCCGC...	22	0	1	20.00	20	13	1	3	3	0	0
...CTGGCTACGTCGCTATCGCCGCTA...	24	0	1	19.00	19	6	1	4	4	4	0
...TGGCTACGTCGCTATCGCCGC...	21	0	1	19.00	19	10	2	3	4	0	0
...GCGACGACAGCGACTGCGCAGCG...	23	0	1	13.00	13	10	1	0	1	1	0
...AGCGACGACAGCGACTGCGCAGC...	23	0	1	11.00	11	3	6	1	0	0	1
...GCGACGACAGCGACTGCGC...	19	0	1	7.00	7	7	0	0	0	0	0
...CTGGCTACGTCGCTATCGCCGCC...	23	1	1	6.00	6	0	6	0	0	0	0
...CTGGCTACGTCGCTATCGCCGCTT...	24	1	1	6.00	6	4	1	0	1	0	0
...TGGCTACGTCGCTATCGCCGCTAC...	24	0	1	5.00	5	0	2	2	1	0	0
...GCGACGACAGCGACTGCGCAGCGT...	24	1	1	5.00	5	0	0	1	0	4	0
...GCGACGACAGCGACTGCGCAG...	21	0	1	5.00	5	3	0	0	0	2	0
...CTGGCTACGTCGCTATCGCC...	20	0	1	5.00	5	1	0	2	2	0	0
...GGCTACGTCGCTATCGCCGCTA...	22	0	1	4.00	4	4	0	0	0	0	0
...CGACGACAGCGACTGCGCAGCGA...	23	0	1	4.00	4	2	1	0	1	0	0
...CGACGACAGCGACTGCGCAGCGT...	23	1	1	3.00	3	0	0	0	0	3	0
...TGGCTACGTCGCTATCGCCGCC...	22	1	1	3.00	3	0	3	0	0	0	0
...GGCTACGTCGCTATCGCCGCT...	21	0	1	3.00	3	2	0	1	0	0	0
...TGGCTACGTCGCTATCGCCGCTT...	23	1	1	3.00	3	1	1	0	1	0	0
...CTGGCTACGTCGCTATCGCCGCTC...	24	1	1	2.00	2	0	0	1	0	1	0
...TGGCTACGTCGCTATCGCCGCTAA...	24	1	1	2.00	2	1	0	0	1	0	0
...CGACGACAGCGACTGCGCAG...	20	0	1	2.00	2	1	0	0	1	0	0
...CTACGTCGCTATCGCCGCTA...	20	0	1	1.00	1	0	0	1	0	0	0
...TGGCTACGTCGCTATCGCCGCTTA...	24	2	1	1.00	1	0	0	0	1	0	0
...GCTGGCTACGTCGCTATCGCCG...	22	0	1	1.00	1	0	0	1	0	0	0
...TGGCTACGTCGCTATCGC...	18	0	1	1.00	1	0	0	1	0	0	0
...TGGCTACGTCGCTATCGCCGCTATC...	25	2	1	1.00	1	0	0	1	0	0	0
...GCTGGCTACGTCGCTATCGCCGC...	23	0	1	1.00	1	1	0	0	0	0	0
...GCGACGACAGCGACTGCGCAGCGA...	24	0	1	1.00	1	1	0	0	0	0	0
...CTGGCTACGTCGCTATCGCCGCTTT...	25	2	1	1.00	1	1	0	0	0	0	0
...TGGCTACGTCGCTATCGCCGCGT...	23	2	1	1.00	1	0	0	1	0	0	0
...AGCGACGACAGCGACTGCG...	19	0	1	1.00	1	0	1	0	0	0	0
...GCGACGACAGCGACTGCGCAGCT...	23	1	1	1.00	1	0	1	0	0	0	0
...GCGACGACAGCGACTGCGCAGCC...	23	1	1	1.00	1	0	1	0	0	0	0
...GACGACAGCGACTGCGCAGCGA...	22	0	1	1.00	1	1	0	0	0	0	0
...CGACGACAGCGACTGCGCAGCGC...	23	1	1	1.00	1	0	0	1	0	0	0
...TGGCTACGTCGCTATCGCCGCTAT...	24	1	1	1.00	1	1	0	0	0	0	0
...CGACGACAGCGACTGCGCAGCGAT...	24	0	1	1.00	1	0	1	0	0	0	0
...GCGACGACAGCGACTGCGCAGT...	22	1	1	1.00	1	0	1	0	0	0	0
...GACGACAGCGACTGCGCAGC...	20	0	1	1.00	1	0	0	0	0	0	1
...CTGGCTACGTCGCTATCGCCGTC...	23	2	1	1.00	1	0	0	0	0	1	0
...TGGCTACGTCGCTATCGCCGCTG...	23	1	1	1.00	1	0	0	1	0	0	0
...AGCGACGACAGCGACTGC...	18	0	1	1.00	1	0	1	0	0	0	0
...AGCGACGACAGCGACTGCGCAGT...	23	1	1	1.00	1	0	1	0	0	0	0
...GCGACGACAGCGACTGCG...	18	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

TCGCAGTAAAAGATGACGCCGATACTGTTTAACGACTCGCGGAAAAACGTCGCTGCTGTCGCTGACGCGTCGCTATCGTAACTCGCGACCGATGCAGCGATAGCGGCGATGACACTCTCGCTGCTGTTGTTGTTGTTATAGCGGCTCACACTCAGTCGCAG	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V049 head	M060 embryo	V110 male body
*************************************...((((((.....((((.(((.((((((.((.(((((..........)))))))...)))))).))).)))).....))).)))...**********************************									
...CTGCTGTCGCTGACGCGTCGCTA...	23	0	1	1.00	1	1	0	0	0
...GTCGCTGCTGTCGCTGACGC...	20	0	1	1.00	1	1	0	0	0
...ATGCAGCGATAGCGGCGATGA...	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_6473:9187670-9187830 +	dmo_73	AG-----CGTCATTTTCTACTGCG---GCTATGA-CAA-----ATTGCT---GAGCGCCTTTT---TGCA------GC---G---A---CGA---CAGCGACTGCGCAGCGATAGCATTGAG---CGCTGGCTACGTCGC----TATC---G---CCGCT----ACTGT---G-----A---GAGCGACG-ACAACAA---CAACAATATCG---CCGAGT---GTGAGT---CAG---CGTC
droVir3	scaffold_12726:978100-978263 -		AG-----CGTCATTTGCTTCTTTG---GCTATGA-CAA-----ATTACT---GAGCGCCTTTTTGCA--TA------GCAG--CCA------GC---G---T---CGA---CAGCGACTGCGCAGCGTCGCTATTGAG---CGCTGGCTGCGACGC----TATC---G---CCGGC----TCTGC---G-----A---GA-GCCACAG---CAACAGCAGCG---CTGAGC---GTGAGT---CAG---CGCT
droGri2	scaffold_14853:1378501-1378642 +		GG-----CAGCAGCTACTGCTGCG---GCTGCGT-CAA-----TT-GCT---GGA---GCTGCTTCA------AC---G---C---CGG---CAGCTGCTAC--TAAGATGGCTGGTTT---CGCT---G---GCA--AG---CGACTGCAATTG---CCGCGGGCCAACAACAATGT-G---CCCAGTGTGATTA---TGC---TGC---CG--
droWil2	scf2_1100000004909:5002701-5002877 +		AG-----CGCCAACATCGACAACG---ACCACGA-CGAC--AACT-GCA---GCACCAAC---TACA------AC---GACTACAACAACAGCAGCAACGACAACAACCACAGAA-----CCAAC---A---ACGACAACG---ACGGCTGCA-ACAACAACT---A---C-C--GCTGCAA---CGACG-----A---CA-ACAACA---GCAG--CAACGACAACAACCACA---GAAC---CAA---CGAC
dp5	4_group1:4366200-4366370 +		AG-----CATCACCAGCAACAATTGAGCATGTATGGTCAGGCAATG---GGCCAGCA-GCA---GCA---GCAACCACAGCCAACGCAGCAG---CAAC---AAGTGGT---TGTGC---CAGCAGTGGCGGCAC---AGCC---GC---AACCGCCAGTGGCA-----ACAA---C---ACAACAA---CAGCAGCAGCAACA-ACAAGT---GC---A---GCAG---CAG---CACC
droPer2	scaffold_46:341470-341620 +		AG-----CGCTACTCTCTGCTGAG---GCCTTAACAG---AGCCCT---GTT---AGCGC---TACTCTTTGCCAGACTTAAC---G---GT-CATTGAA---TGCTGCTCGTGTCGCATCGTATC---G---TGTCC----TCTGC---AGCCGAAGAGAGACCAACTAGCCAGCAGTTGAA---GCAG---CAG---TA--
droAna3	scaffold_12903:688433-688611 +		TG-----CGTGGCTT-TCTCACCA---GCTATGA-CAA-----ATCGTT---G-GCT---CAAT---G---G---CT---G---T-T--TC---TGCAGCAGCA-ACAACAACAACAGCAGCAGCAAC---ACCGACGCCATCACTCAGCGATCGCCATGCGAGCTTATCTGAAAAGAGCGGGAAAAAGAGCGTCGGCAAAGAGAGTAGTTGATCGTGAAT---CAG---CG--
droBip1	scf7180000395916:21481-21656 -		TG-----CGCGGCTT-TCTCACCA---GCTATGA-CAA-----ATCGTT---G-GCT---CAAT---G---G---CT---G---T-T--TC---TGCAGCAGCA-GCAACAACAACCACACCAGCAAC---ACCGACGCCATAACTCAACGATCGCCATGCGAGCTTATCTGAAAAGAGCGGGAAAAAGAGCGGCGGCAAAGAGA---GCTGATCGTGAAT---CAG---CG--
droKik1	scf7180000302677:1059974-1060126 -		AG-----CATCAGCAACAG--GCG---GCAGTGG-CTGCCCATC---AGCA------GCAACAACAGCAGCTGCAGCAGCAGCAGCAATTGCTGCAGTTGTCCAT-----CCAAC---AG---GCGGCTC---ATCACCATCA-GCAG---G-AG--CAGCAC---CGTC---AA---CAGC---AGCAGCAG--CAGCA---A---CAC---CAGC
droFic1	scf7180000453903:228814-228976 -		AG-----CAGCGCTG-CTTCTGCT---GT-ACAG-CAGC--A-ATTGCT---GCC---ACCGCC---TGGTACCTATCAATACCAAC---AGGTGGCGGCAATACCGTT---G---TCGTTGCCGTGCGTCATCAACAG---CA---G---T-T--GC---AACAGCAGCA-GCAGCAA---CAACAACAGCA---ACTGG---CCCT---ACAC---CAG---CAAC
droEle1	scf7180000491011:109282-109440 -		AA-----CATCAGCAACAACTGCG---GCGGCAA-CAGC--AATG-GCA---GCA---GCAGCAGCG------AC---AGCAGCAAC---ATCTGCGGCAACAACGGGGAG---CAGC---G---GCAGCGGCA---GCGGCAGCG-GCAG---T-AGTACA---ACC---A---CA-ACGGCG---GCAA--CCACAACAGCAACCTGT---GTGA---CAG---CAGC
droRho1	scf7180000776808:11995-12133 -		AT-----CGCCATGA-TGATGATG---GTGATGC-GAAT--ATTG-GCA---GCACGAG---TGCA------AC---A---G---CAA---CAGCAACAG---CAAAAGCAACGGCAACTGTA---G---AA-CAACAGCAACCCC---AA---CTAT---AACAGCAA---TAACA---A---CAG---CAAC
droBia1	scf7180000302428:7570243-7570378 +		GC-----TGCAGTTA-C---AA-----ATTGCT---GCAAACAAGTTTTGGGAA---AACGTTGCGTCGCCGCC---AGCGCC---T---CAGT---CG---CTTT---CACT---A---A---GCCC---GC---AGCCGCCGCACTTG---A-C--ACT---GCCACAA---TAACAGCAGCA---ACAA---CTGC---GA---CAG---CA--
droTak1	scf7180000415762:329283-329425 -		CA-----ACTC-CGATGGCA---GCTACAA-CCG-----ATCACT---GAACTCAAACTCCCA---GG---G---A---G---GAGGAGGAGTAGGAGGCGGATCTGGAGCCAGC---A---A---CT---A---T-C--GCTCCGG---CCGC---AA---CTAC---GAGAACGG---CAATG---G---GAGCAACGGCCCACCGTCACGTT
droEug1	scf7180000405770:877-1007 -		AG-----CGCAATGACAACAGCG---GCAGTGA-CAA-----AA-GCGGCCGCGACA--AC---AGCG------GC---AGCGACAAC---A---GC---GGCAGCGACAA---CAGC---G---GCAGCG-ACAA---C-AA--CGGCAG---CGAC---A-----A---CAACGGCAGCAA---CAA---A---GCGG---CAG---CAAC
dm3	chrX:19047572-19047709 -		GAGTGTGCGTGGCTT-TCTCACCG---CCTATGA-CAA-----ATCGTT---CAGCTT---GTGGCTGTGGCACCA-GCAACAACAACAGCGACAACAACCACCGA---TCAACGGT---TATCGGC---GAAGGAGAGCG---CGTGACTCAGTTGTTGGCG---TTGT
droSim2	x:13038431-13038593 -		AA-----CGCAACTGCGCGGCG---GCAACAT-CGA-----CC-TCAACCTCAGCA--ACAT--C-TGCGG--CGGCAACGGCAGCAGCG------AC---AGC---AGCAACATCTGCGTCCACAACG---GC---T---ACGGCGGCG-GCGG---GGAGTA---G-T--AAT---ACAACAA---CAACAACGGCG---GCAA---CCACAACAGCAAC---CTGT
droSec2	scaffold_8:1336892-1337029 -		GTGTGTGCGTGGCTT-TCTCACCG---CCTATGA-CAA-----ATCGTT---CAGCTT---GTGGCTGTGGCACCA-GCAACAACAACAGCGACAACAACCACCGA---TCAACGGT---TATCGGC---GAAGGAGAGCG---CGTGACTCAGTTGTTGGCG---TTGT
droYak3	2L:2082171-2082322 -		AG-----CGGCGCCGACGACGTCG---ACGTCAT-CGA-----ATCGCG---TAGCCCAGGC---C---ATGCTGCTGATGTCGACGTCGCAGCAGCAGCAGCAGTGGCAGCAACATCAGTG---GCAGCA-ACAG---C-AA--CTGCAG---CAGC---AG---CAAC---AGCAG-CAG---CAACA---A---CAG---CAGC
droEre2	scaffold_4929:9839575-9839720 +		AG-----CATCACTGGCGCCGGT---AC-GCAT-CAA-----TT-GCA---GCGCG---CGACGGCAGCCAGCGGAGGCG---GAGC---TGGTGCTGGGGGCGTGGCAG---GCGCCTC---GACAGCAGCG-GCAG---T-TACACTCCAG---CAAC---AT---CAGC---ATCAGCAG---CAACA---A---CAG---CAGC

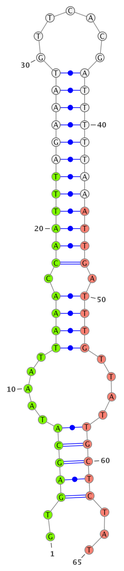
Generated: 09/08/2015 at 07:33 PM

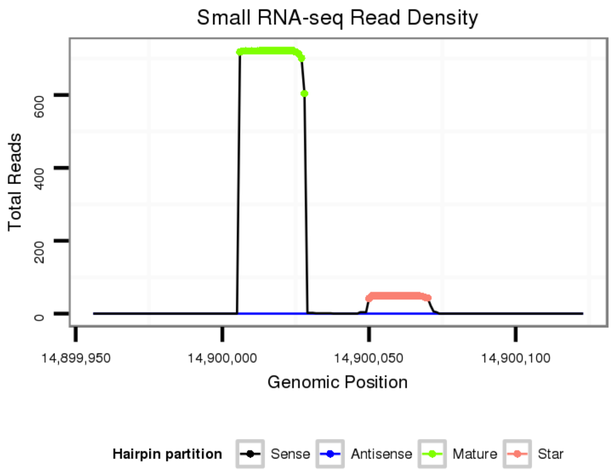
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

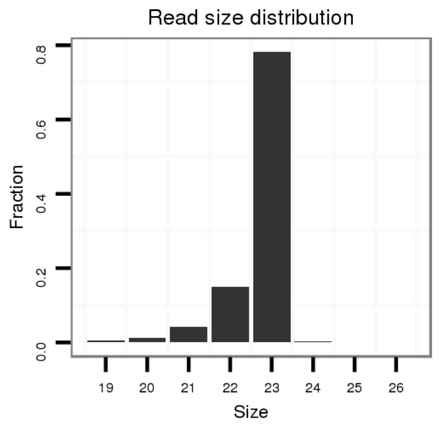
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_63	**scaffold_6496:14900006-14900073 +**	**confident**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

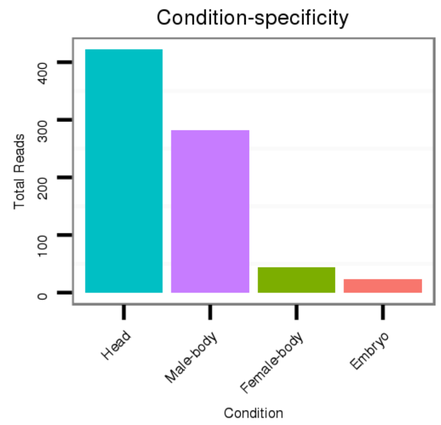
Legend: mature star mismatch in alignment mismatch in read

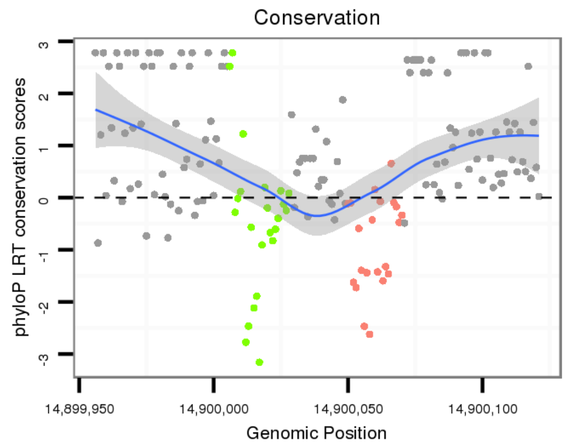
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI20712-in]; CDS [Dmoj\GI20712-cds]; CDS [Dmoj\GI20712-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTCTCGCATCGGTGGACACAACCAAGGCGGACATAGATACCCAAATGGAGGTGAGCATAAATTAAACCAATTTAGAAATGTTCACGATTTTTAAATTGATTTGTTATTGCTCTATCAGAAATGTGAGACAACAATGAAATCATCGAAGCCCTATGCCGCGCCCACGGA	Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head	V110 male body	V049 head	M046 female body	M060 embryo	V041 embryo
**********..(((((.....((((.(((((((((((((.......)))))))))))).))))....)))))...**********											
.....GTGAGCATAAATTAAACCAATTT.....	23	0	1	600.00	600	239	250	80	21	5	5
.....GTGAGCATAAATTAAACCAATT.....	22	0	1	96.00	96	48	22	16	10	0	0
.....ATTGATTTGTTATTGCTCTAT.....	21	0	1	17.00	17	8	3	2	1	3	0
.....ATTGATTTGTTATTGCTCTATC.....	22	0	1	15.00	15	3	3	2	0	7	0
.....GTGAGCATAAATTAAACCAAT.....	21	0	1	12.00	12	5	2	2	3	0	0
.....GTGAGCATAAATTAAACCAA.....	20	0	1	5.00	5	2	1	1	1	0	0
.....GTGAGCATAAATTAAACCAATTC.....	23	1	1	4.00	4	3	0	0	0	1	0
.....TTGATTTGTTATTGCTCTAT.....	20	0	1	4.00	4	3	0	0	0	0	1
.....GTGAGCATAAATTAAACCA.....	19	0	1	4.00	4	2	0	2	0	0	0
.....ATTGATTTGTTATTGCTCTATCAG.....	24	0	1	3.00	3	1	0	0	1	1	0
.....ATTGATTTGTTATTGCTCTATT.....	22	1	1	2.00	2	0	0	1	0	1	0
.....TGAGCATAAATTAAACCAATTT.....	22	0	1	2.00	2	0	0	0	2	0	0
.....TAAATTGATTTGTTATTGCTCT.....	22	0	1	2.00	2	1	0	0	1	0	0
.....TGAGCATAAATTAAACCAATT.....	21	0	1	1.00	1	0	0	0	1	0	0
.....TAAATTGATTTGTTATTGCTC.....	21	0	1	1.00	1	0	0	0	0	1	0
.....ATTGATTTGTTATTGCTCTATCA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GTGAGCATAAATTAAACCAATTTAGA.....	26	0	1	1.00	1	0	1	0	0	0	0
.....TTGATTTGTTATTGCTCTATC.....	21	0	1	1.00	1	0	0	0	1	0	0
.....TTGATTTGTTATTGCTCTATCA.....	22	0	1	1.00	1	0	0	1	0	0	0
.....GTGAGCATAAATTAAACCAATTA.....	23	1	1	1.00	1	0	1	0	0	0	0
.....TAAATTGATTTGTTATTGCTCTA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....ATTGATTTGTTATTGCTCTA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....ATTGATTTGTTATTGCTCT.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TTGATTTGTTATTGCTCTATCAG.....	23	0	1	1.00	1	0	0	0	1	0	0
.....TAAATTAAACCAATTTAGAAATGTT.....	25	0	1	1.00	1	0	0	0	1	0	0
.....GTGAGCATAAATTAAACCAATTTC.....	24	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6496:14899956-14900121 +	dmo_63	TTCTCGCATCGGTGGACACAACCAAGGCGGACATAGATACCCAAA-TGGAGGTGAGCATAAAT-----TAA--A----------CCAAT----------TTAGAAATGTTCACGATTT--TTAA----------ATTGATTTG-TTAT-TGCTCTATCAGAAATGTGAGACA---ACAATGAAATCATCGAAGCCCTATGCCGCGCCCACG
droVir3	scaffold_12875:11984543-11984696 -		TCCTTGCATCGGTAGACACAAGTAAAAGTGATATGGACTGTCAAA-TAGAGGTAAGCGAGCACAATCA-AATT-----GC--ATTACCACT----------TTA----------A--------------AACTATT-T-ACATTATTTAGAAATGTGAAACA---ACAATAAAATCATCAAAAACTCCTGGA-CGGCGCTCA
droGri2	scaffold_15245:11805212-11805296 -		TACTTGCCTCAGTGGACACAACTAAACGGCTAAGATACCCAAT-TAGAGGTAAGT--AAACGATAAACTTT-AAATATTATCGATT
droWil2	scf2_1100000004514:1131530-1131688 -		TTATTGTATCCGTGAATACAACAAAACTGATAGAGATTCCCAAG-TTGAGGTAACTTTACTT-----------A-----------AGATACATGATG--ATAAACATAA---------ATTACATAA-----------------GTATAT-A-ATTTTTTCTAGAAATGTGAATCT---ACAAATAAATCATCAAAACCTTATGTACCTGCGAAT
droPer2	scaffold_2:1984838-1985022 +		TACTTGTATCAATTAATCCAACTAAGAGTGAAAGAGAAACTGAAACCTGAGGTATTTTGG-----------------------AATATTATTTAGTAATTAGATT-GAA---------AGTTGTTCATATACATATATGCATGTACATAT----GTACCTCTAT-TCCTTTCCTAGAAATGTGAAGCG---ACAGATAAACTATCAAAGTCCGGTGTACCTGCAACA
droAna3	scaffold_13266:5713158-5713316 +		TTCTTGTATCAATTAATACCACTAAGAAGAAAGAGAACGGAAA-CTGAGGTGGTGTTCC-----T-ATTT-----GC--ATTTCTAATTA-----AAT----------------ACCTTTAA----------------------GCCGT-----GTTT-TTTCTTTCTAGAAATGTGAACT---TCTGATAAACTATCTAAACCGGTGTACCTGCAACT
droBip1	scf7180000396372:327252-327410 +		TTCTTGTATCAATTAATACGACTAAGAACGAAAGAGAACGGAAA-CTGAGGTGGATTTACTT-----------A-----AC--TTTTCCAATTAGGTATCTTAATT-CTA---------GC-----------------------TCATT-CTTTTGCTTCTAGAAATGTGAACT---TCTGATAAACTATCTAAACCGGTGTACCTGCAACT
droKik1	scf7180000302355:430932-431096 +		TTCTAGTATCAATTAATACAACTAAGGGCGACAGAGAGCCCGAAA-CTGAGGTAAGTTATTAA-----------A-----TCCA-GTT-----------CCACTTACT---------GCTAACTAGACAAA----------------------GCGTTGG---CTTT-CCCCCACACAGAAATGTGAAACCACAACAGATAAACTATCAAATCCGGTGTACCTGCAACA
droFic1	scf7180000453858:1583356-1583512 +		TACTGGTATCAATTAACAGCACTAAGAGCGACAGAGAGTTGAAA-CTGAGGTGGTCCCCTACC-----CT--T-----------TTTTGAGTCTTTTCTT---------GCTAACAA----------------------CTCGAA-T-CTCTTTCTTAGAAATGCGAAAGC---ACAGATAAACTAACGAAATCCGGTGTACCTGCAACA
droEle1	scf7180000491214:5236644-5236810 -		TACTTGTATCAATTAATACGACTAAGAACGACAGAGAAGGTCAAA-CTGAGGTATGTCCCCAA-----AAA--C-------TCTCACAACACTA----TTGTCCACTG-------------------TCCCTAT--CTA-CCTGTTCTTGCTTCTTTTAGAAATGTGAAGC---ACAGATAAACTAACAAAATCCGGTGTACCTGCAACA
droRho1	scf7180000766026:24183-24338 +		TACTTGTATCAATTAATACGACTAAGAACGACAGAGAAGGTGAAG-CTGAGGTAGGTTCCCC-----AAA--C-----------C-------TTAACCACTAATTTTGCTAACTA----------------------CTTGCT-C-GCTTTCTCAGAAATGTGAAGC---ACAGATAAACTAACAAAATCCGGTGTACCTGCAACA
droBia1	scf7180000302143:374601-374758 +		TCCTTGTATCAATTAATACGACTAAGAACGACAGAGAAGGTCAAA-CTGAGGTAGGTGTTATC-----T-C---------GTGCCCCCG--ATAA-----GACTGCT---------CTAAG----------------------TGATATCC-C-TAATCCCTAGAAATGCGAAAGC---ACAGATAAACTAACAAAATCCGGTGTACCTGCAACA
droTak1	scf7180000415878:970853-971011 +		TACTTGTATCAATTAATACTACTAAGAACGACAGAGAAGGTCAAA-CTGAGGTGGGTCATTAT------TAA--TTTAGGTACCCCTTATAG----------------------TAAT----------------------ATTACTTCC-CCGT-ACTTCCCTCAGAAATGTGAACC---ACAGATAAACTAACAAAATCCGGTGTACCTGCAACA
droEug1	scf7180000409464:220091-220247 +		TACTTGTATCTATTAATACTACTAAGAACGACAGAGAAGGTCGAAA-CTGAGGTAGGTCACTAACG-----AA--C-----------AT-CAGACGTTTTTGTT---------GCTAAC----------------------TACTTTCG-G-TACTTCCCCAGAAATGTGAAACC---ACAGATAAACTAACAAAATCCGGTGTACCTGCAACA
dm3	chr2R:19847554-19847712 +		TCCTCGTCTCGATCAACAGCACCAAGGGTGACAGAGATGGTCATG-CTGAGGTGGTTGC-----------A-----------TGCCGAGAGTGGGCGAGGTAATCACTA---------AC-----------------------TTACTTCC-G-ATCTTCCCCAGAAATGCGAAAGCTCCTCAGACAAACTAACAAAATCCGGTGTACCTGCAACA
droSim2	2r:20348257-20348415 +	dsi_9305	TCCTCGTCTCGATCAACAGCACCAAGGGTGACAGAGAGGTTGATG-CTGAGGTGGTTGC-----------A-----------TGCCGAGAGTGGGCAAGGTAGTCACTA---------AC-----------------------TTACTTCC-G-ATCTTCCCCAGAAATGCGAGAGCTCCTCAGACAAACTAACAAAATCCGGTGTACCTGCAACA
droSec2	scaffold_9:3131448-3131606 +		TCCTCGTCTCGATCAACAGCACCAAGGGTGACAGAGAGGTTGATG-CTGAGGTGGTTGC-----------A-----------TGCCGAGAGTGGGCAAGGTAGTCACTA---------AC-----------------------TTACTTCC-G-ATCTTCCCCAGAAATGCGAGAGCTCCTCAGACAAACTAACAAAATCCGGTGTACCTGCAACA
droYak3	2R:19825256-19825420 +		TCCTCGTTTCAATCAACAGCACCAAGAGTGATAGAGAAGGTCATG-CTGAGGTGGGTACCAACG-----C-ACCA---CCTACCGCCAAGAGTA---------AACCCAGTAAT----------------------GTGTGTATATCC-G-ATCTTCCCCAGAAATGCGAGAGCC---TCAGACAAACTAACAAAATCCGGTGTACCTGCAACA
droEre2	scaffold_4845:21220411-21220581 +		TCCTCGTTTCAATCAACAGCACTAAGAGTGACAGAGAAGGTCATG-CTGAGGTGGGTACCAAA-----CAC--C--------TACCGAGAGATGCGG----GTAATCACTA---------ACCCAGTAAT----------------------GTGCTTGCCTCC-G-ATCTTCCACAGAAATGCGAGAGCC---TCAGACAAACTAACAAAATCCGGTGTACCTGCAACA

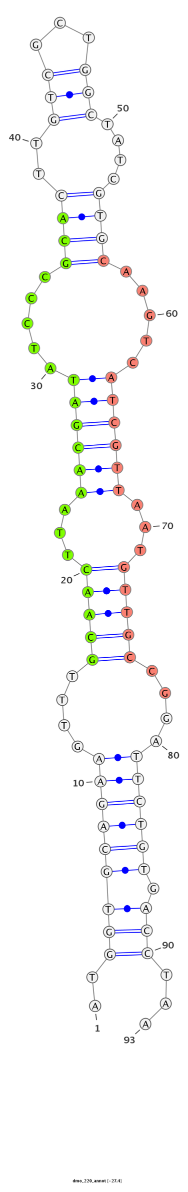
Generated: 09/08/2015 at 10:36 PM

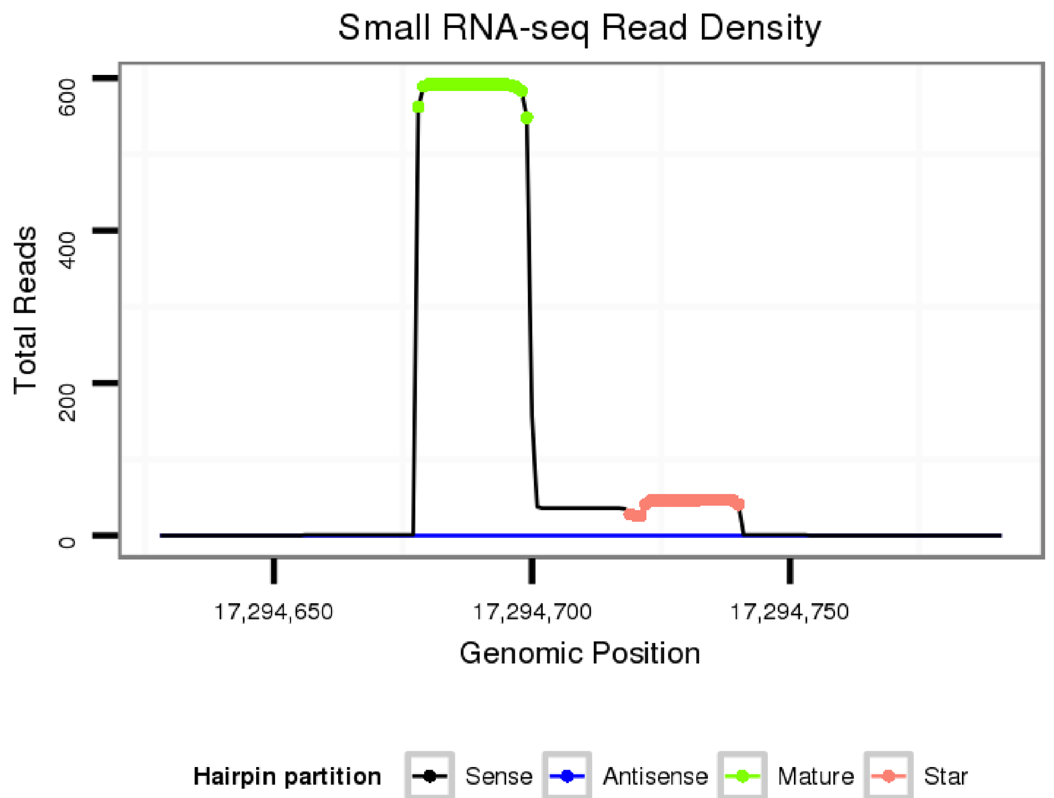
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

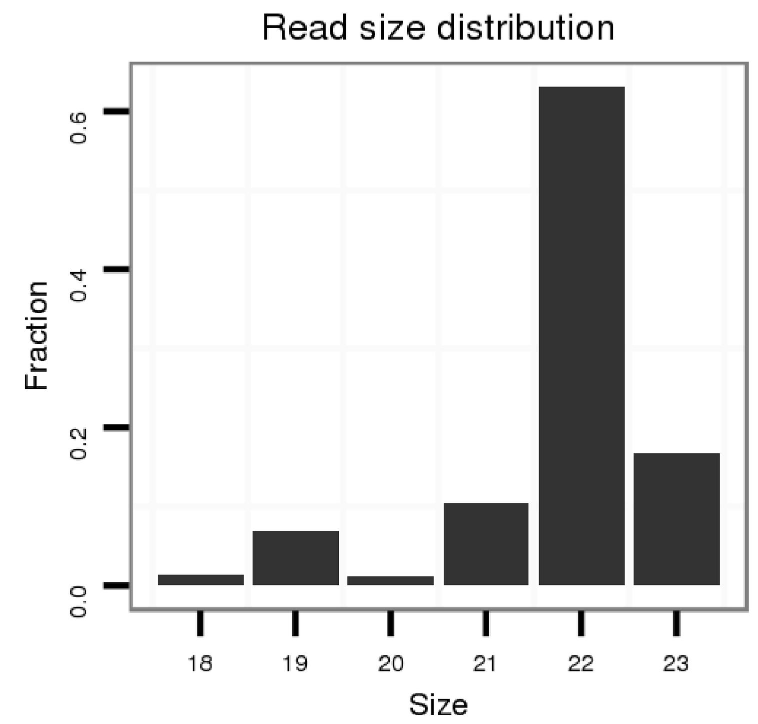
ID: dmo_220	Coordinate: scaffold_6680:17294678-17294741 +	Confidence: confident	Class: Canonical miRNA	Genomic Locale: intergenic	[View on UCSC Genome Browser {Cornell Mirror}]

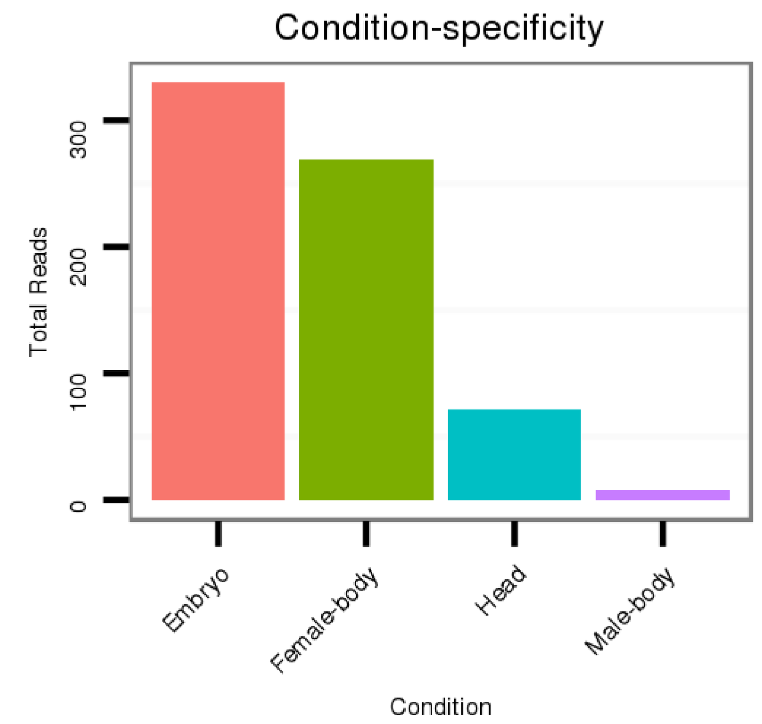
Legend: mature star mismatch in alignment mismatch in read

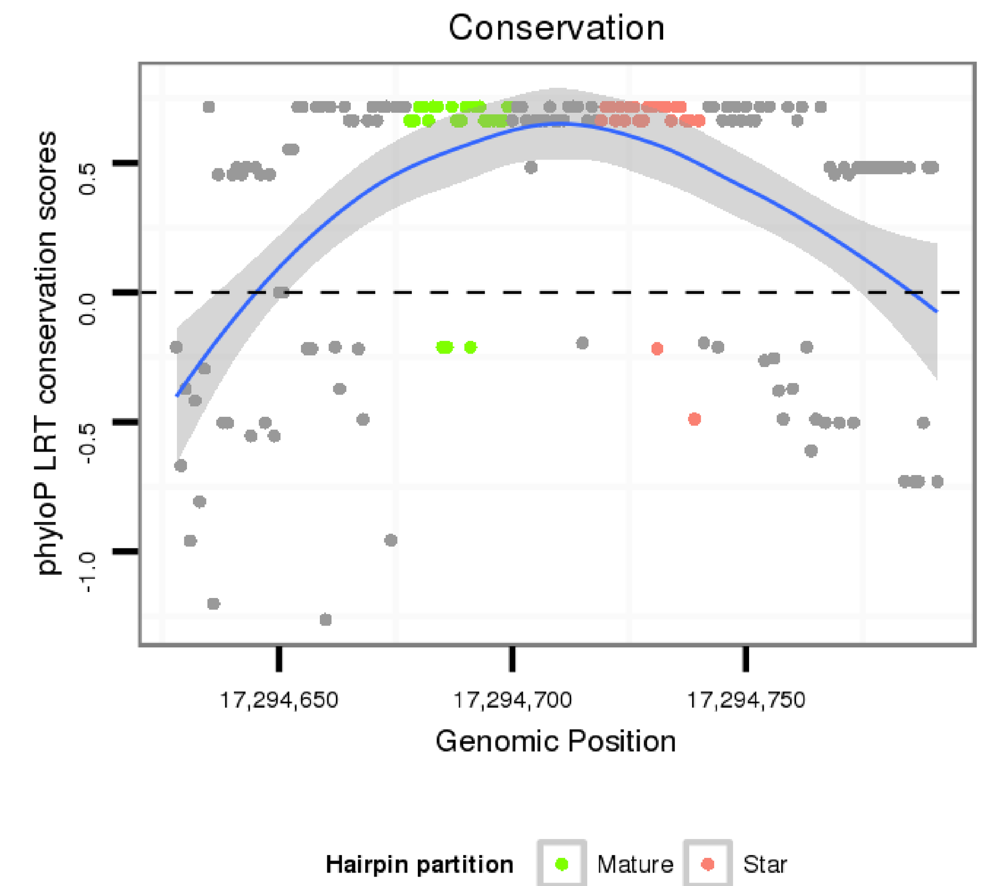
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dmo_221 scaffold_6680:17294294-17294315 + 2. dmo_220 scaffold_6680:17294678-17294699 +	1. dmo_221 scaffold_6680:17294335-17294356 + 2. dmo_220 scaffold_6680:17294719-17294740 +

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATTAACGAACCGGTGATACACTAAATATTAAACATATGGTGCAGAAGTTTGCAACTTAAACGATATCCCGCACTTGTCGCTGGCTATCGTGCAAGTCATCGTTAATGTTGCCGGATTCTGTGACCTAAGACAACAAGCAATGAACATTAAAAATATGAGCTAAG ***********************************..((((((((....(((((...((((((.....((((..(((...)))....))))......))))))...)))))....)))))).)))...***********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head	M046 female body	V049 head	V110 male body	M060 embryo	V041 embryo
....GCAACTTAAACGATATCCCGCA..	22	0	2	402.00	804	28	364	18	8	360	26
....GCAACTTAAACGATATCCCGCAC...	23	0	2	113.50	227	3	50	1	1	170	2
....GCAACTTAAACGATATCCCGC...	21	0	2	38.50	77	4	21	2	0	50	0
....CTTGTCGCTGGCTATCGTG...	19	0	1	30.00	30	8	0	10	2	4	6
....CAACTTAAACGATATCCCGCA..	21	0	2	20.00	40	0	38	1	0	1	0
....CAAGTCATCGTTAATGTTGCCG...	22	0	2	18.00	36	11	7	14	0	3	1
....GTCATCGTTAATGTTGCCG...	19	0	2	15.50	31	1	30	0	0	0	0
....CAACTTAAACGATATCCCGCAC...	22	0	2	6.00	12	0	9	1	0	2	0
....GCAACTTAAACGATATCCCG..	20	0	2	5.50	11	3	3	2	2	1	0
....CAAGTCATCGTTAATGTTGCC..	21	0	2	5.00	10	3	0	3	0	4	0
....TCATCGTTAATGTTGCCG...	18	0	2	5.00	10	3	7	0	0	0	0
....ACTTGTCGCTGGCTATCGTGC..	21	0	1	4.00	4	0	0	0	0	2	2
....GCAACTTAAACGATATCCCGCAT...	23	1	2	4.00	8	2	6	0	0	0	0
....GCAACTTAAACGATATCCCGCAA...	23	1	2	3.50	7	0	1	0	1	5	0
....CTTGTCGCTGGCTATCGTT...	19	1	1	3.00	3	1	0	2	0	0	0
....GCAACTTAAACGATATCC..	18	0	2	2.50	5	0	1	0	0	4	0
....GCAACTTAAACGATATCCCGCACC..	24	1	2	2.00	4	0	1	0	0	3	0
....GCAACTTAAACGATATCCC...	19	0	2	2.00	4	0	0	0	0	4	0
....AAGTCATCGTTAATGTTGCCG...	21	0	2	2.00	4	0	3	1	0	0	0
....CAAGTCATCGTTAATGTTGCCT...	22	1	2	2.00	4	1	0	2	0	1	0
....AACTTAAACGATATCCCGCACT..	22	0	2	2.00	4	2	0	0	0	2	0
....AACTTAAACGATATCCCGCAC...	21	0	2	1.50	3	0	1	0	0	2	0
....CAAGTCATCGTTAATGTTGC...	20	0	2	1.50	3	1	0	1	1	0	0
....CAACTTAAACGATATCCCGC...	20	0	2	1.50	3	0	3	0	0	0	0
....GCAACTTAAACGATATCCCGCC..	22	1	2	1.50	3	0	0	2	0	1	0
....CTTGTCGCTGGCTATCGT..	18	0	1	1.00	1	0	0	1	0	0	0
....TTGTCGCTGGCTATCGTG...	18	0	1	1.00	1	1	0	0	0	0	0
............................TAAACATATGGTGCAGAAGTTT..	22	0	1	1.00	1	0	0	0	0	1	0
....AAGTCATCGTTAATGTTGCCGT..	22	1	2	1.00	2	0	0	0	0	1	1
....CAAGTCATCGTTAATGTTGCCC...	22	1	2	1.00	2	0	0	1	0	1	0
....GCAAGTCATCGTTAATGTTGCCC...	23	1	2	1.00	2	0	0	0	0	2	0
....TGTTGCCGGATTCTGTGACCT......................................	21	0	2	1.00	2	1	0	1	0	0	0

Anti-sense strand reads

TAATTGCTTGGCCACTATGTGATTTATAATTTGTATACCACGTCTTCAAACGTTGAATTTGCTATAGGGCGTGAACAGCGACCGATAGCACGTTCAGTAGCAATTACAACGGCCTAAGACACTGGATTCTGTTGTTCGTTACTTGTAATTTTTATACTCGATTC ***********************************..((((((((....(((((...((((((.....((((..(((...)))....))))......))))))...)))))....)))))).)))...***********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head	V049 head	M060 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6680:17294628-17294791 +	dmo_220	ATTAACGAACCGGTGATACACTAAATAT-----------TAAAC---A--TATGGTGCAGAAGTTTGCAACTTAAACGATATCCCGCACTTGTCGCTGGCTATCGTGCAAGTCATCGTTAATGTTGCCGGATTCTGTGACCTAAGACAACAAGCA-ATGAACATTAAA--AATATGAGCTAAG
droVir3	scaffold_13049:22675497-22675662 +	dvi_17	AGCTTGGAGCTAGTGAAACGCA----AT-----------TAAAGATAA--TGTGGTTCAGAAATTTGCAACTTAAACGATATCCCGCACTTGTCGCTGGCTATCGTGCAAGTCATCGTTAATGTTGCCGGATTCTGTGACCTTAAAAAGCAACAAAGTGGACGTTAAAAGAATATTATACAAT
droGri2	scaffold_15110:20857832-20857970 -	dgr_466	GTTCACTAC--------------ATATAAAAATGTAATATAATATAAGCCATGGAGCAGAATTTTGCAACTTGGACGACATCCCGCACTTG-CGCTGGCTATTGTGCAAGTCATCGTTTATGTTGCGGAATCCTGTGACCTTAACCAACAGCCA--------------------------------

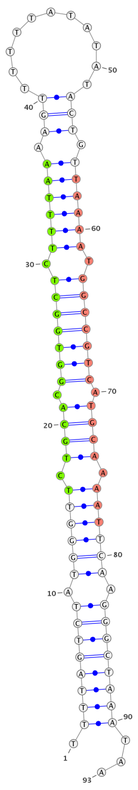
Generated: 09/08/2015 at 07:38 PM

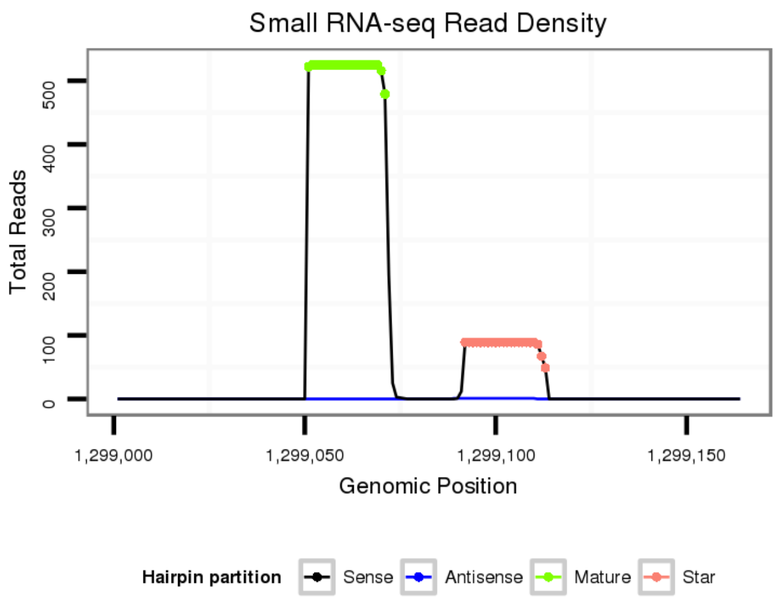
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	3
rescue.candidate	2

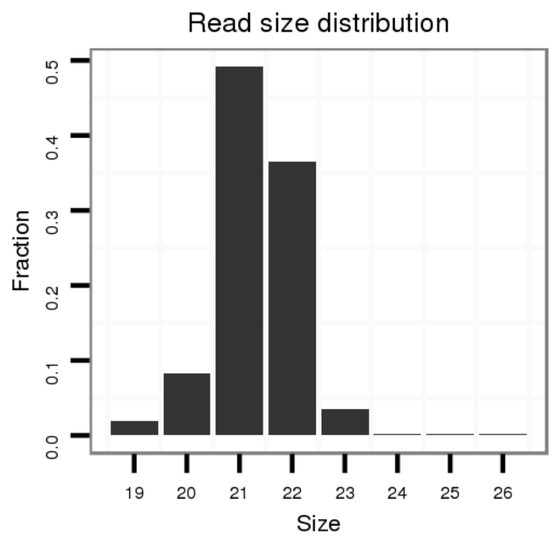
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_64	**scaffold_6308:1299051-1299114 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

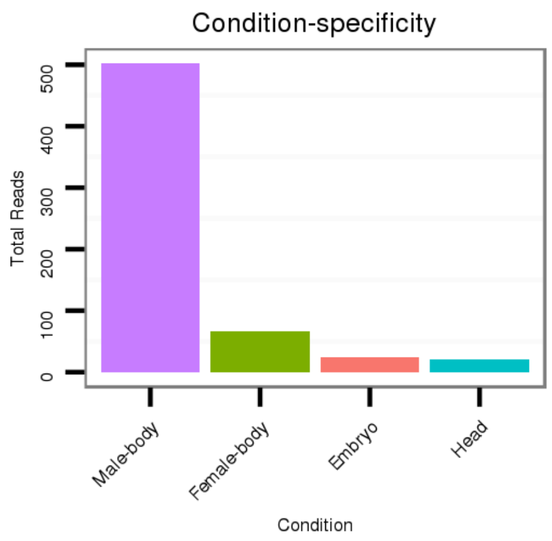
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [DmojGI10984-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AGAAAATTTGTATAGTACCTGCCAGCAAAGGAAATTTTTAGTCTATGGGTTCTGCACGGTGGCTCTTTTAAAAGTTTTTTATATATACTGTTAAAATGGCCGTCATGCAAAATTCAAGGGCTAAATAAGCAACGAAACGTGCAGAAACCCAATTCTTTATACAG **********.(((((((((.(((((((.((((.(((((((.(((((((.(((...........))).)))))))..)))))))..))))..)))))))..)))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V041 embryo	V056 head	V049 head	M060 embryo
..........TCTGCACGGTGGCTCTTTTAA..........	21	0	1	283.00	283	234	27	8	7	4	3
..........TCTGCACGGTGGCTCTTTTAAA..........	22	0	1	168.00	168	145	8	9	2	2	2
..........TAAAATGGCCGTCATGCAAAAT..........	22	0	1	49.00	49	36	11	0	1	0	1
..........TCTGCACGGTGGCTCTTTTA..........	20	0	1	37.00	37	27	7	1	1	0	1
..........TCTGCACGGTGGCTCTTTTAAAA..........	23	0	1	22.00	22	20	2	0	0	0	0
..........TAAAATGGCCGTCATGCAAA..........	20	0	1	13.00	13	12	1	0	0	0	0
..........TAAAATGGCCGTCATGCAAAA..........	21	0	1	12.00	12	7	5	0	0	0	0
..........TCTGCACGGTGGCTCTTTT..........	19	0	1	9.00	9	4	3	0	1	1	0
..........TCTGCACGGTGGCTCTTTTAC..........	21	1	1	8.00	8	7	0	0	0	1	0
..........TCTGCACGGTGGCTCTTTTC..........	20	1	1	7.00	7	7	0	0	0	0	0
..........TCTGCACGGTGGCTCTTTTAAAC..........	23	1	1	6.00	6	5	0	0	1	0	0
..........TTAAAATGGCCGTCATGCAAAA..........	22	0	1	6.00	6	6	0	0	0	0	0
..........TTAAAATGGCCGTCATGCAAA..........	21	0	1	5.00	5	4	0	0	0	1	0
..........TAAAATGGCCGTCATGCAAAAA..........	22	1	1	5.00	5	5	0	0	0	0	0
..........TCTGCACGGTGGCTCTTTTT..........	20	1	1	5.00	5	3	1	0	0	1	0
..........TCTGCACGGTGGCTCTTTTAT..........	21	1	1	4.00	4	3	0	0	0	1	0
..........TAAAATGGCCGTCATGCAAAATC..........	23	1	1	3.00	3	3	0	0	0	0	0
..........TAAAATGGCCGTCATGCAA..........	19	0	1	3.00	3	3	0	0	0	0	0
..........TCTGCACGGTGGCTCTTTTAAC..........	22	1	1	2.00	2	2	0	0	0	0	0
..........TAAAATGGCCGTCATGCAAAT..........	21	1	1	2.00	2	2	0	0	0	0	0
..........CTGCACGGTGGCTCTTTTAAA..........	21	0	1	2.00	2	0	2	0	0	0	0
..........TCTGCACGGTGGCTCTTTTAAAAA..........	24	1	1	2.00	2	2	0	0	0	0	0
..........GTTAAAATGGCCGTCATGCAAA..........	22	0	1	1.00	1	1	0	0	0	0	0
..........TCTGCACGGTGGCTCTTTTAAATC..........	24	2	1	1.00	1	1	0	0	0	0	0
..........TAAAATGGCCGTCATGCAAATC..........	22	2	1	1.00	1	1	0	0	0	0	0
..........TCTGCACGGTGGCTCTTTTAAAAGTT..........	26	0	1	1.00	1	1	0	0	0	0	0
..........TCTGCACGGTGGCTCTTTTAAAAAA..........	25	2	1	1.00	1	0	1	0	0	0	0
..........TCTGCACGGTGGCTCTTTTAAAAG..........	24	0	1	1.00	1	1	0	0	0	0	0
..........TCTGCACGGTGGCTCTTTTTG..........	21	2	1	1.00	1	1	0	0	0	0	0
..........TCTGCACGGTGGCTCTTTTCC..........	21	2	1	1.00	1	1	0	0	0	0	0
..........TCTGCACGGTGGCTCTTTTAATC..........	23	2	1	1.00	1	0	1	0	0	0	0
..........TCTGCACGGTGGCTCTTTTAAAAGT..........	25	0	1	1.00	1	1	0	0	0	0	0
..........TAAAATGGCCGTCATGCAAAAAA..........	23	2	1	1.00	1	1	0	0	0	0	0
..........CTGCACGGTGGCTCTTTTAA..........	20	0	1	1.00	1	0	1	0	0	0	0
..........TAAAATGGCCGTCATGCAAAACC..........	23	2	1	1.00	1	1	0	0	0	0	0
..........TCTGCACGGTGGCTCTTTTATC..........	22	2	1	1.00	1	1	0	0	0	0	0
..........TAAAATGGCCGTCATGCAAAAC..........	22	1	1	1.00	1	1	0	0	0	0	0
..........TCTGCACGGTGGCTCTTTTAG..........	21	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

TCTTTTAAACATATCATGGACGGTCGTTTCCTTTAAAAATCAGATACCCAAGACGTGCCACCGAGAAAATTTTCAAAAAATATATATGACAATTTTACCGGCAGTACGTTTTAAGTTCCCGATTTATTCGTTGCTTTGCACGTCTTTGGGTTAAGAAATATGTC **********.(((((((((.(((((((.((((.(((((((.(((((((.(((...........))).)))))))..)))))))..))))..)))))))..)))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body
..........ACAATTTTACCGGCAGTACGTT..........	22	0	1	1.00	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1299001-1299164 +	dmo_64	AGAAAATTTGTATAGTACCTGCCAGCAAAGGAAATTTTTAGTCTATGGGTTCTGCACGGTGGCTCTTTTAAAAGTTTTTTATATATACTGTTAAAATGGCCGTCATGCAAAATTCAAGGGCTAAATAAGCAACGAAACGTGCAGAAACCCAATTCTTTATACAG

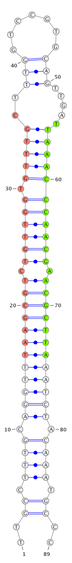
Generated: 09/08/2015 at 08:04 PM

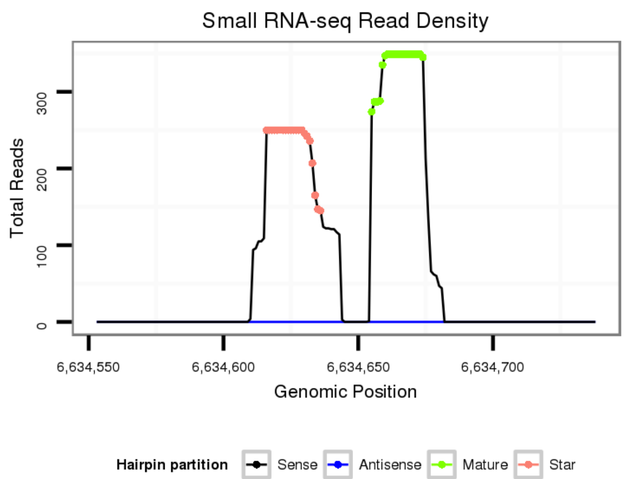
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

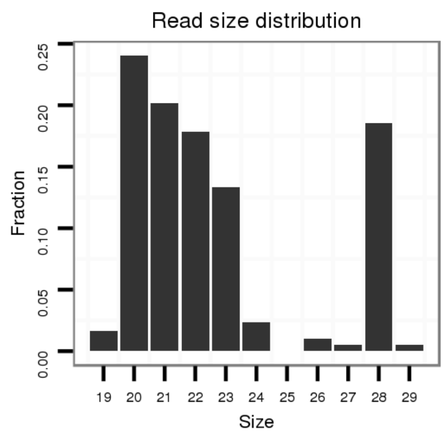
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3127	**scaffold_6540:6634603-6634688 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

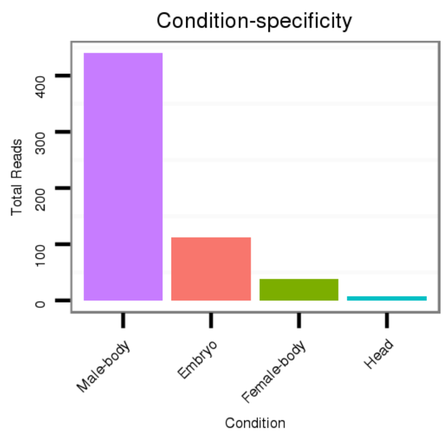
Legend: mature star **mismatch in alignment** mismatch in read

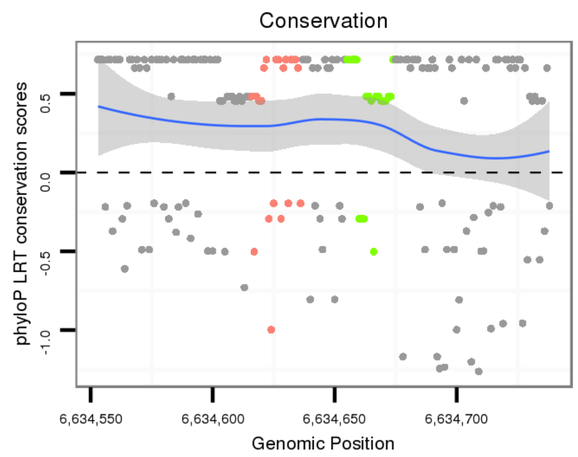
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTTAATATTTGGAAACACGTCGTCAATTTGTAATTTGAATTTTTTGTGTTGCCTTTGCAGGTTTAAGCGTCTGTTGGTGTTTGCTTTGGTCCGTGCAGTTGATTAAACCCAACGAACGCTTAAATCTACAAATGCCCAGCAGGCAGCACTCAAACTGCGGGAATATTTAGTGAACGATGTGAGTGT **..((.((((.((((((((((((.((((((.((((((..(((.......)))).....)))))))))))).))))))))))))).))))..**	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M060 embryo	M046 female body	V041 embryo	V056 head	V049 head
.....TTAAACCCAACGAACGCTTA.....	20	0	1	132.00	132	122	3	5	0	2	0
.....TAAGCGTCTGTTGGTGTTTGCTTTGGTC.....	28	0	1	111.00	111	63	48	0	0	0	0
.....TTAAACCCAACGAACGCTTAA.....	21	0	1	76.00	76	62	4	10	0	0	0
.....TTAAACCCAACGAACGCTTAAA.....	22	0	1	62.00	62	48	6	4	3	0	1
.....AGGTTTAAGCGTCTGTTGGTGTT.....	23	0	1	42.00	42	40	1	1	0	0	0
.....ACCCAACGAACGCTTAAATCTAC.....	23	0	1	32.00	32	5	21	4	2	0	0
.....AGGTTTAAGCGTCTGTTGGTGT.....	22	0	1	21.00	21	18	1	0	2	0	0
.....TAAGCGTCTGTTGGTGTTTGC.....	21	0	1	15.00	15	14	0	1	0	0	0
.....ACCCAACGAACGCTTAAATCT.....	21	0	1	12.00	12	2	6	2	0	1	1
.....AGGTTTAAGCGTCTGTTGGTGTTT.....	24	0	1	11.00	11	10	0	0	0	0	1
.....CCCAACGAACGCTTAAATCTAC.....	22	0	1	10.00	10	1	7	2	0	0	0
.....AGGTTTAAGCGTCTGTTGGTGTTTC.....	25	1	1	7.00	7	6	1	0	0	0	0
.....TAAACCCAACGAACGCTTAAA.....	21	0	1	6.00	6	5	0	1	0	0	0
.....AGGTTTAAGCGTCTGTTGGTG.....	21	0	1	6.00	6	6	0	0	0	0	0
.....GTTTAAGCGTCTGTTGGTGTTT.....	22	0	1	5.00	5	4	0	0	1	0	0
.....AGGTTTAAGCGTCTGTTGG.....	19	0	1	4.00	4	2	0	1	0	1	0
.....AGGTTTAAGCGTCTGTTGGT.....	20	0	1	4.00	4	4	0	0	0	0	0
.....TTAAACCCAACGAACGCTTT.....	20	1	1	4.00	4	4	0	0	0	0	0
.....AGGTTTAAGCGTCTGTTGGTGTTC.....	24	1	1	4.00	4	4	0	0	0	0	0
.....TAAGCGTCTGTTGGTGTTTGCTTTGGTC.....	26	0	1	4.00	4	3	0	1	0	0	0
.....AGGTTTAAGCGTCTGTTGGTGTC.....	23	1	1	4.00	4	3	1	0	0	0	0
.....CAGGTTTAAGCGTCTGTTGGTGT.....	23	0	1	4.00	4	4	0	0	0	0	0
.....TAAACCCAACGAACGCTTAAAT.....	22	0	1	4.00	4	1	1	2	0	0	0
.....TTAAACCCAACGAACGCTT.....	19	0	1	3.00	3	2	0	1	0	0	0
.....CCCAACGAACGCTTAAATCTAA.....	22	1	1	3.00	3	2	0	1	0	0	0
.....TAAGCGTCTGTTGGTGTTTGCTTTGGTCC.....	29	0	1	3.00	3	1	2	0	0	0	0
.....TAAGCGTCTGTTGGTGTTTGCTTTGGT.....	27	0	1	3.00	3	3	0	0	0	0	0
.....GGTTTAAGCGTCTGTTGGTGT.....	21	0	1	2.00	2	2	0	0	0	0	0
.....TTAAGCGTCTGTTGGTGTTTGCTCC.....	25	2	1	2.00	2	1	1	0	0	0	0
.....TAAGCGTCTGTTGGTGTTTGCTTTGGC.....	27	1	1	2.00	2	1	1	0	0	0	0
.....ACCCAACGAACGCTTAAATCTA.....	22	0	1	2.00	2	2	0	0	0	0	0
.....GTTTAAGCGTCTGTTGGTGTTTGC.....	24	0	1	2.00	2	2	0	0	0	0	0
.....CCAACGAACGCTTAAATCTAC.....	21	0	1	2.00	2	0	2	0	0	0	0
.....TTAAACCCAACGAACGCTTAAC.....	22	1	1	2.00	2	1	1	0	0	0	0
.....AGGTTTAAGCGTCTGTTGGTGTTTGC.....	26	0	1	2.00	2	2	0	0	0	0	0
.....TTAAACCCAACGAACGCTTAAAC.....	23	1	1	2.00	2	0	2	0	0	0	0
.....TTAAGCGTCTGTTGGTGTTTGC.....	22	0	1	2.00	2	2	0	0	0	0	0
.....CCCAACGAACGCTTAAATCTACG.....	23	1	1	2.00	2	0	2	0	0	0	0
.....TAAGCGTCTGTTGGTGTTT.....	19	0	1	2.00	2	2	0	0	0	0	0
.....GTTTAAGCGTCTGTTGGTGT.....	20	0	1	2.00	2	2	0	0	0	0	0
.....TAAACCCAACGAACGCTTAA.....	20	0	1	2.00	2	1	0	1	0	0	0
.....ACCCAACGAACGCTTAAATCC.....	21	1	1	2.00	2	0	2	0	0	0	0
.....AGGTTTAAGCGTCTGTTGGTGTTA.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TAAACCCAACGAACGCTTAAT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....CCCAACGAACGCTTAAATCTAT.....	22	1	1	1.00	1	0	1	0	0	0	0
.....TAAGCGTCTGTTGGTGTTTGCTTT.....	24	0	1	1.00	1	1	0	0	0	0	0
.....CCCAACGAACGCTTAAATCT.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TAAACCCAACGAACGCTTAAAAA.....	23	2	1	1.00	1	1	0	0	0	0	0
.....TAAGCGTCTGTTGGTGTTTG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....ACCCAACGAACGCTTAAATCTAT.....	23	1	1	1.00	1	0	1	0	0	0	0
.....TTAAGCGTCTGTTGGTGTTTGCT.....	23	0	1	1.00	1	0	1	0	0	0	0
.....TTAAACCCAACGAACGCTTAAAA.....	23	1	1	1.00	1	0	0	1	0	0	0
.....TTAAACCCAACGAACGCTTC.....	20	1	1	1.00	1	1	0	0	0	0	0
.....ACCCAACGAACGCTTAAATCTACC.....	24	1	1	1.00	1	0	1	0	0	0	0
.....CAGGTTTAAGCGTCTGTTGGTGTC.....	24	1	1	1.00	1	1	0	0	0	0	0
.....AGGTTTAAGCGTCTGTTGGTGTTTTTC.....	27	3	1	1.00	1	1	0	0	0	0	0
.....ATTAAACCCAACGAACGCTT.....	20	0	1	1.00	1	0	0	1	0	0	0
.....AGGTTTAAGCGTCTGTTGGTGTTTT.....	25	1	1	1.00	1	1	0	0	0	0	0
.....TAAACCCAACGAACGCTTAAATC.....	23	0	1	1.00	1	1	0	0	0	0	0
.....ACCCAACGAACGCTTAAATCTATC.....	24	2	1	1.00	1	0	0	0	0	1	0
.....GTTTAAGCGTCTGTTGGTGTTTT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....ACCCAACGAACGCTTAAATC.....	20	0	1	1.00	1	0	0	0	0	1	0
.....TAAGCGTCTGTTGGTGTTTGCT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....GTTTAAGCGTCTGTTGGTGTTCAA.....	24	3	1	1.00	1	1	0	0	0	0	0
.....TTAAACCCAACGAACGCTTAAATT.....	24	1	1	1.00	1	0	1	0	0	0	0
.....CCCAACGAACGCTTAAATCTA.....	21	0	1	1.00	1	0	0	1	0	0	0
.....TTAAGCGTCTGTTGGTGTTTG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TTAAACCCAACGAACGCTTAAAG.....	23	1	1	1.00	1	1	0	0	0	0	0
.....AACCCAACGAACGCTTAAA.....	19	0	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

AAATTATAAACCTTTGTGCAGCAGTTAAACATTAAACTTAAAAAACACAACGGAAACGTCCAAATTCGCAGACAACCACAAACGAAACCAGGCACGTCAACTAATTTGGGTTGCTTGCGAATTTAGATGTTTACGGGTCGTCCGTCGTGAGTTTGACGCCCTTATAAATCACTTGCTACACTCACA **..((.((((.((((((((((((.((((((.((((((..(((.......)))).....)))))))))))).))))))))))))).))))..**	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_6540:6634553-6634738 +	dmo_3127	TTTAATATTTGGAAACACGTCGTCAATTTGTAATTTGAATTTTTTGTGT-------TGCCTTTGCAGGTTTAAGCGTCTGTTGGTGTTTGCTTTGGTCCGTGCAGTTGATTAAACCCAACGAACGCTTAAATCTACAAATGCCCAGCAGGCAGCACTCAAACTGCGGGAATATTTAGTGAACG--ATGTGAGTGT
droVir3	scaffold_12855:6286589-6286783 +	dvi_77	TTTGATGTTTGCAAACACTTCGTCAATTTGTAATTTGATTATTTTTTTATTTTTGTGGTTTTGCAGTTTTGAGCGTCGGTTGGTGTTTGGTTTCGTCCGTGCACTTGATTAAACCCAACAAACGCTTAAATTTACAAATGCCCAGTCGCCAGACGTCGAGTTCATGATATATATAGTGAATGTCTTGTGTGCGT
droGri2	scaffold_14906:7794745-7794892 -		TTTGATATTTTCGAACACGTCCTTAATATT-ACATTAAATTATTTTTTT-------T----------GTAAATTTGTATTTGTTTGTGCCACTGCAGTCTATTAAAAAA----------AAATGTACAAAAGGCCAGGATGAGGTCT-AACCTAATGAGGTAAGTAGTGAAAG--------TGC

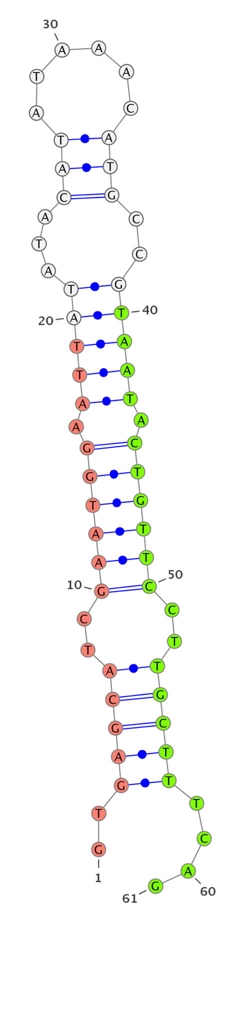
Generated: 09/08/2015 at 08:07 PM

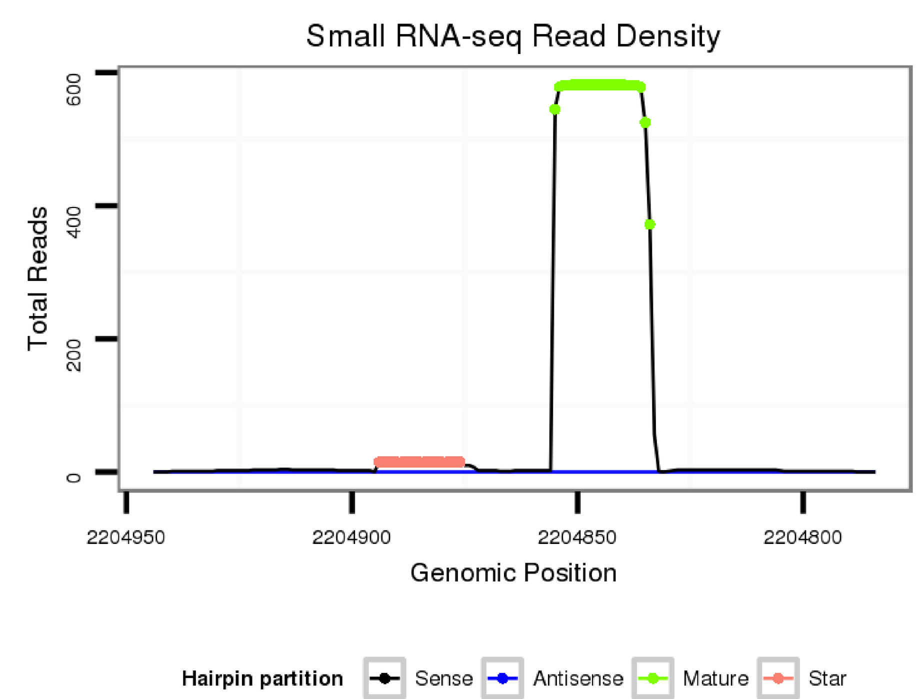
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

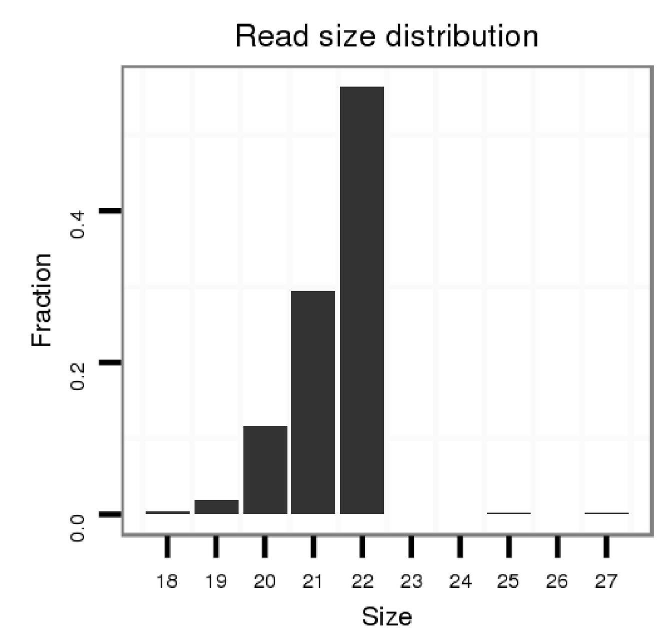
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_638	**scaffold_6473:2204834-2204894 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

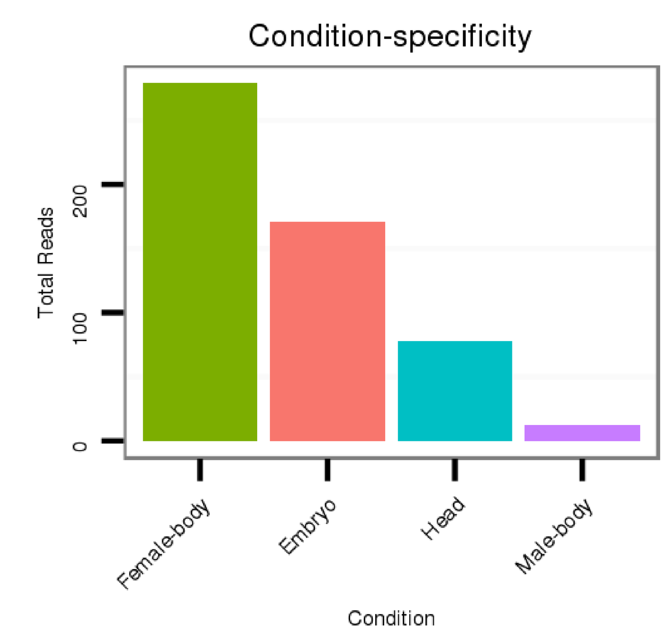
Legend: mature star mismatch in alignment mismatch in read

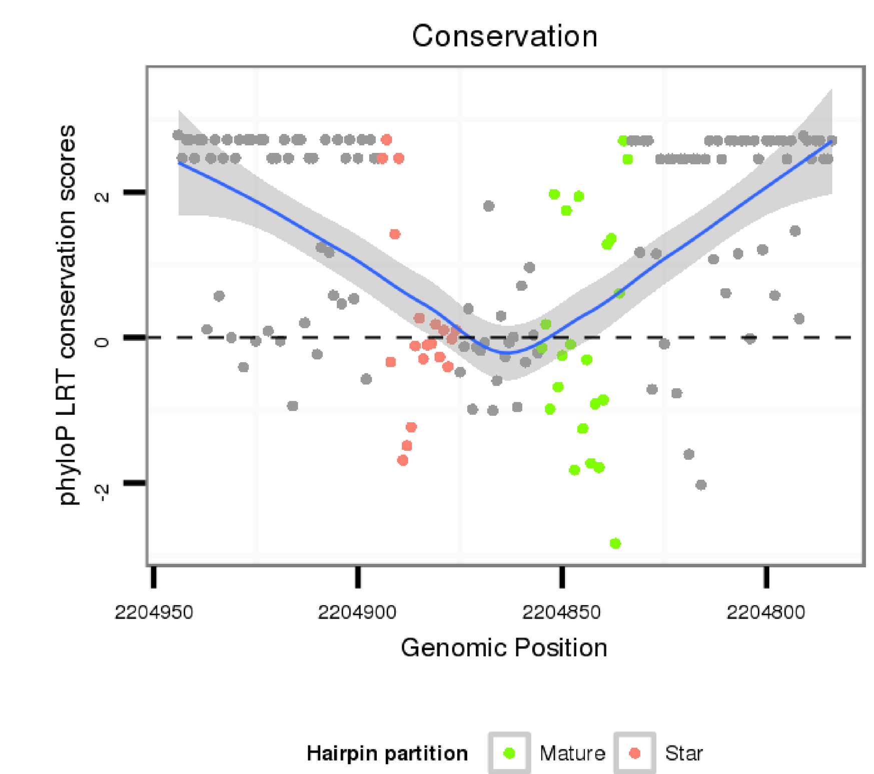
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI15195-in]; CDS [Dmoj\GI15195-cds]; CDS [Dmoj\GI15195-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGATGATACATCACGTCTTCATTGGCACCTTCGGACTGCTGGTCGTAACGGTGAGCATCGAATGGAATTATATACATATAAACATGCCGTAATACTGTTCCTTGCTTTCAGTATATACGCGGAGGCGGACATTGCATCTATAGCTACATGTTCATGATGGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V049 head	V041 embryo	V056 head	V110 male body
..(((((..((((((.(((((...(((......)))..))))).))))))..)))))....											
....TAATACTGTTCCTTGCTTTCAG..	22	0	1	300.00	300	137	99	14	31	17	2
....TAATACTGTTCCTTGCTTTCA...	21	0	1	143.00	143	86	14	14	11	14	4
....TAATACTGTTCCTTGCTTTC..	20	0	1	51.00	51	26	8	8	0	9	0
....TAATACTGTTCCTTGCTTTCAGT...	23	0	1	46.00	46	8	38	0	0	0	0
....TAATACTGTTCCTTGCTTTCAGA...	23	1	1	20.00	20	5	14	1	0	0	0
....AATACTGTTCCTTGCTTTCAG..	21	0	1	12.00	12	9	3	0	0	0	0
....AATACTGTTCCTTGCTTTCA...	20	0	1	10.00	10	9	1	0	0	0	0
....AATACTGTTCCTTGCTTTCAGT...	22	0	1	10.00	10	2	8	0	0	0	0
....AATACTGTTCCTTGCTTTCAGA...	22	1	1	7.00	7	3	2	0	1	0	1
....GTGAGCATCGAATGGAATT..	19	0	1	5.00	5	1	0	1	0	0	3
....TAATACTGTTCCTTGCTTTCAGC...	23	1	1	5.00	5	0	5	0	0	0	0
....GTGAGCATCGAATGGAATTATA...	22	0	1	5.00	5	2	1	0	0	1	1
....GTGAGCATCGAATGGAATTAT..	21	0	1	4.00	4	2	1	0	0	0	1
....TAATACTGTTCCTTGCTTTCAA..	22	1	1	3.00	3	3	0	0	0	0	0
....ATACTGTTCCTTGCTTTCAGA...	21	1	1	2.00	2	2	0	0	0	0	0
....ATACTGTTCCTTGCTTTCAG..	20	0	1	2.00	2	1	1	0	0	0	0
....AATACTGTTCCTTGCTTTCAGC...	22	1	1	2.00	2	1	1	0	0	0	0
....TAATACTGTTCCTTGCTTT...	19	0	1	2.00	2	1	0	0	0	0	1
....AATACTGTTCCTTGCTTTC..	19	0	1	2.00	2	2	0	0	0	0	0
....ATACATATAAACATGCCGT...	19	0	1	1.00	1	1	0	0	0	0	0
....AATACTGTTCCTTGCTTT...	18	0	1	1.00	1	1	0	0	0	0	0
..............GTCTTCATTGGCACCTTCGGACTGCTG..	27	0	1	1.00	1	0	0	0	0	0	1
....AACATGCCGTAATACTGTTCCTTGC..	25	0	1	1.00	1	1	0	0	0	0	0
....ACTGTTCCTTGCTTTCAG..	18	0	1	1.00	1	0	1	0	0	0	0
....TAATACTGTTCCTTGCTTTCAGTA..	24	0	1	1.00	1	0	1	0	0	0	0
.........................CACCTTCGGACTGCTGGTCGTAACGT..	26	1	1	1.00	1	1	0	0	0	0	0
........................GCACCTTCGGACTGCTGGTCGTAACGTAT..	29	3	1	1.00	1	1	0	0	0	0	0
....TAATACTGTTCCTTGCTTTCG...	21	1	1	1.00	1	0	1	0	0	0	0
....GTGAGCATCGAATGGAATTATATACAT..	27	0	1	1.00	1	0	0	0	0	0	1
....TAATACTGTTCCTTGCTTTCAT..	22	1	1	1.00	1	0	0	1	0	0	0
....TACGCGGAGGCGGACATTGCAT........................	22	0	1	1.00	1	1	0	0	0	0	0
....ACGCGGAGGCGGACATTGCATCTA.....................	24	0	1	1.00	1	1	0	0	0	0	0
....GATACATCACGTCTTCATTGGCACCTT..	27	0	1	1.00	1	1	0	0	0	0	0
............................CTTCGGACTGCTGGTCGTAAC..	21	0	1	1.00	1	1	0	0	0	0	0
....ATACGCGGAGGCGGACATTGCATCT......................	25	0	1	1.00	1	1	0	0	0	0	0
....CTATAGCTACATGTTCATG.....	19	0	1	1.00	1	1	0	0	0	0	0
......................TGGCACCTTCGGACTGCTGGTCGTAAC..	27	0	1	1.00	1	1	0	0	0	0	0
....TAATACTGTTCCTTGCTTTCAC..	22	1	1	1.00	1	0	1	0	0	0	0
....TAATACTGTTCCTTGCTTTCAGG...	23	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:2204784-2204944 -	dmo_638	TGATGATACATCACGTCTTCATTGGCACCTTCGGACTGCTGGTCGTAACGGTGAGCAT-------------CGAATGGAATT----------------------AT---------ATAC-----------------------------------AT---------ATA----AACATGCCGTAATAC--TGT---T--------------CC----TTGCTTTCAGTATATACGCGGAGGCGGACATTGCATCTATAGCTACATGTTCATGATGGA
droVir3	scaffold_12932:95677-95829 +		TGATGATACATCACGTATTCATTGGCACCTTCGGACTGCTCGTGGTGACGGTAAGTGTTAAACAAACTT--AAATTCCCCAT----------------------CT---------AATTG---G---T-------C-----ATT----TCTCTTGCAGTATATACGCGGCGGTGGCCATTGCATCTATAGCTATATGTTCATGATGGA
droGri2	scaffold_15203:7453558-7453717 -		TGATGATACATCACGTATTCATTGGCACCTTCGGACTGCTCGTGGTCACGGTGAGTGC-------------TG--------T----GTATTTGTG--ATA-------C--AT---------TCA----TACATT--TTACTAAT-T-C---T-------C-----ATT----GATTTTGCAGTATATACGCGGCGGTGGTCATTGCATCTATAGCTACATGTTCATGATGGA
droWil2	scf2_1100000004401:1112394-1112557 +		TGATGATACATCATGTGTTTATTGGCACTTTCGGTCTGTTGGTAGTTACGGTGAGAAT-------------AAAAA-------------------------AAA---AAT---------GTTTATAAACACCTAAAATATAAGCT--TT----T---T------CAT-----TT----TTAATTGCAGTACATTAGAGGCGGTGGGCATTGCATATACAGTTATATGTTTATGATGGA
dp5	XL_group1a:6883122-6883297 -		TGATGATCCATCACGTCTTTATCGGCACCTTTGGTCTGCTGGTGGTCACGGTAAGGCA-------------------------CACGCACACGCGTACCCATTC---GA-TGCTCAGTCG-----------------------------TACACATAATTCAATG-------------------CAC-T-------------CCT-----CT----TCCTTTACAGTACATTCGTGGTGGTGGCCACTGCATCTATAGCTACATGTTCATGATGGA
droPer2	scaffold_25:407225-407400 +		TGATGATCCATCACGTCTTTATCGGCACCTTTGGTCTGCTGGTGGTCACGGTAAGGCA-------------------------CACGCACACGCGTACCCATTC---GA-TGCTCAGTCG-----------------------------TACACGTAATTCAATG-------------------CCC-T-------------CCT-----CT----TCCTTTGCAGTACATTCGTGGTGGTGGCCACTGCATCTATAGCTACATGTTCATGATGGA
droAna3	scaffold_13335:2454987-2455139 -		TGATGATCCATCACGTTTTCATTGGAACCTTCGGCCTCCTGGTGGTGACGGTAAGGGA---------------------TTA----G--------TCTCCATT-CCA---TG--A--ATA--TAACTAAT-T-C-----------TT-----AC----CCCCTTTCAGTACATCCGTGGCGGCGGCCACTGCATCTACAGCTACATGTTCATGATGGA
droBip1	scf7180000396683:118353-118508 +		TGATGATCCACCACGTCTTCATCGGCACCTTCGGCCTGTTGGTGGTGACGGTAAGGGA---------------------TTA----C--------TCTCCAAG-CAG---TG---------------------------------------ACCAT------------------------TATCTAATA--TTT---------AC-----CT----TCTCCCGCAGTACATCCGCGGTGGTGGCCACTGCATCTACAGCTACATGTTCATGATGGA
droKik1	scf7180000302698:888246-888408 -		TGATGATCCACCATGTCTTTATAGGCACCTTTGGCCTGCTGGTGGTCACGGTAAGTTA-------------AACTT-------------------------TAA---AAA---------CTTTAAGA---C--TTGGG--AAACTGA----T---TTATTTCTCT-----GT----GTCTTTCTAGTACATACGCGGTGGCGGACACTGTATCTACAGCTACATGTTCATGATGGA
droFic1	scf7180000454050:178124-178290 +		TGATGATACACCACGTCTTCATCGGAACCTTTGGCCTGCTGGTGGTGACGGTGAGTGG-------------CAGTTGG----------------------ATTC---GA-TGCTCTTTTG--GTTGCTTTAATCC--TGTATAT--------------CCTGTACTCCTTTCAGTACATTCGCGGCGGCGGCCACTGCATCTACAGCTACATGTTCATGATGGA
droEle1	scf7180000491087:399656-399711 -		T--TGCAGTACATCCGCGGCGGTGGGCACTGCATCTACAGCTACATGTTCATGATGGA
droRho1	scf7180000778808:41252-41342 +		TGATGATACACCACGTCTTTATCGGAACGTTTGGACTGCTGGTGGTGACGGTAAGAGC-------------AAGCCGG----------------------ATAT---GA-TAT---TTATTTATAT-ATG----A---ATA-------
droBia1	scf7180000302126:3119421-3119579 +		TGATGATACACCACGTCTTTATCGGCACATTCGGACTGCTGGTGGTGACGGTGAGAGC---------------------TTT----A----------------T---TATATATATTTAAATGATA----A--ATA-------------T---TCATT--CTT-----CTTG--CTGATTTCAGTACATACGCGGCGGTGGCCACTGCATCTACAGCTACATGTTCATGATGGA
droTak1	scf7180000415394:42851-43012 +		TGATGATTCACCACGTTTTTATCGGTACTTTTGGACTGCTGGTGGTGACGGTATGGGC---------------------TTT----A------------------T---------ATC-------------------------------------TTCTTATAT-T-ATATC-TTTTA--TAACTAATAT-C---T-------T-----ATG----TAAATTTCAGTACATTCGCGGTGGGGGCCACTGCATCTACAGCTACATGTTCATGATGGA
droEug1	scf7180000409230:36967-37132 -		TGATGATACACCACGTCTTTATCGGAACGTTTGGGCTGCTGGTGGTGACGGTAAGAAG-------------AAGTTGGCATT----------------------AT---------AATTG-----------------------------------T---------TGA----TTTATACTATATTGA--TAT---TTA----TTT-----TT----TTCGTTTTAGTACATTCGAGGTGGGGGTCACTGCATCTATAGCTACATGTTCATGATGGA
dm3	chrX:10276093-10276263 +		TGATGATACACCATGTCTTCATCGGAACATTTGGATTGCTGGTGGTGACGGTAAGCCGC----------CCAACTTGGCA---CAT------GCA--ACAACAA---GAT---ATGTA--TAGTTAATA--ATT------GTA----ATATT----CCGATTGCAGTACATTCGCGGTGGCGGTCACTGCATCTACAGCTACATGTTCATGATGGA
droSim2	x:9748876-9749045 +		TGATGATACACCATGTCTTTATCGGAACATTTGGATTGCTGGTGGTGACGGTAAGCAC-------------AACTTGGC-------GCACATGTA--ACAACAA---GAT---ATGTA--TAGCTAATA--ATT------GTT----ATATT----CCGATTGCAGTACATTCGCGGTGGCGGGCACTGCATCTACAGCTACATGTTCATGATGGA
droSec2	scaffold_15:973246-973302 +		TGATGATACACCATGTCTTTATCGGAACATTTGGATTGCTGGTGGTGACGGTAAGCA---
droYak3	X:18850246-18850423 +		TGATGATACACCATGTCTTTATCGGAACCTTTGGATTGCTGGTGGTGACGGTAAGCAC-------------AACTTGCCACCACAT------ACA--ACA-------CAT------------------------------ACATATACC-------------------TATGT----------TTAATA--CCT---AT-GTAC-ATATCTA----ACGATTTCAGTACATACGCGGTGGCGGCCACTGTATCTATAGCTACATGTTCATGATGGA
droEre2	scaffold_4690:4860015-4860172 -		TGATGATACACCACGTCTTTATCGGAACGTTTGGATTGCTGGTGGTGACGGTGAGCGC-------------AACTAGGCA---TAT------GCA--ACA-------TGT------------------------------ACTTCTACT-------------------TATGT----------------------------------ATATT----CCGATTGCAGTACATTCGCGGTGGCGGCCACTGCATCTACAGCTACATGTTTATGATGGA

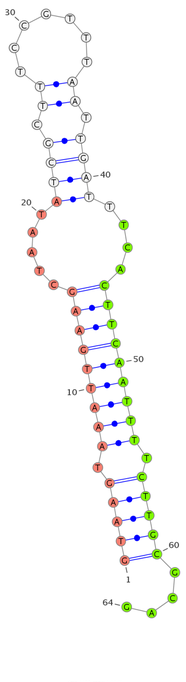
Generated: 09/08/2015 at 10:36 PM

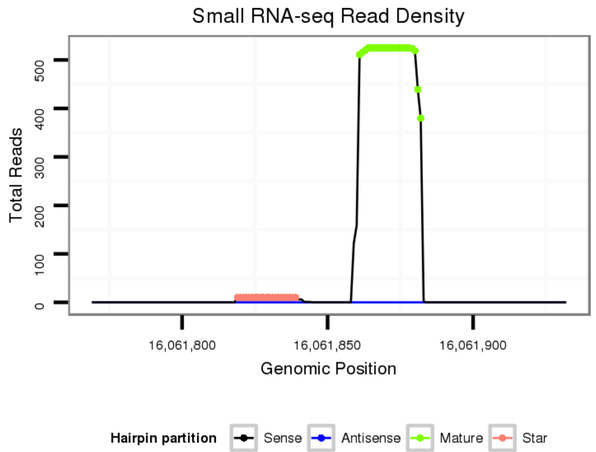
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

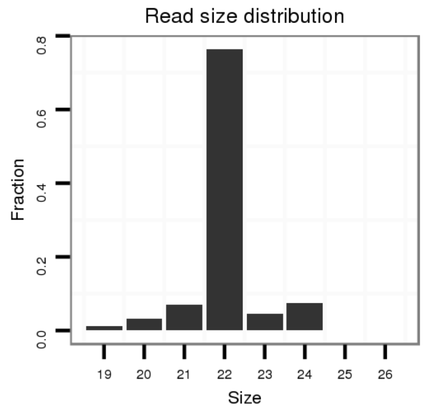
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1180	**scaffold_6496:16061819-16061882 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

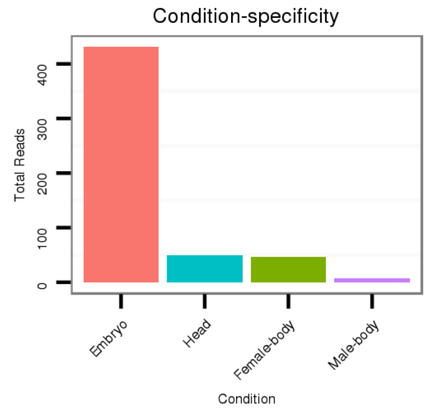
Legend: mature star mismatch in alignment mismatch in read

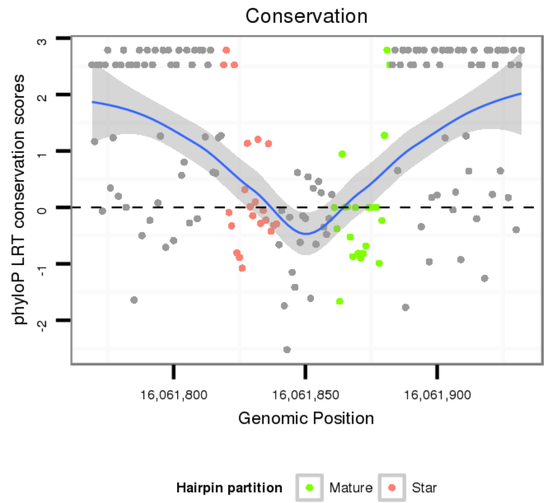
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI20815-in]; CDS [DmojGI20815-cds]; CDS [DmojGI20815-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CGGGCGATCGACAGGGCGTCGTCGTGCTCACCGAATTCGACTATCAAGCGGTAAGTAAATTGAAGCTAATATCGCTTTCCGTTTAATTGATTTCACTTCAATTTTCTTGCGCAGCACCTGAGCAAATCGTTGGAAATACTGAACGAAGCCTATGAGATTGTTCA	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V041 embryo	V049 head	V056 head	V110 male body
**********(((((.(((((((((.....((((.((.......)).)))).....)))))))))).)))))....**********											
.....TCACTTCAATTTTCTTGCGCAG.....	22	0	1	321.00	321	241	22	18	23	16	1
.....TTTCACTTCAATTTTCTTGCGC.....	22	0	1	61.00	61	47	5	3	4	1	1
.....TTTCACTTCAATTTTCTTGCGCAG.....	24	0	1	40.00	40	36	4	0	0	0	0
.....TTCACTTCAATTTTCTTGCGCA.....	22	0	1	25.00	25	15	3	4	0	1	2
.....TCACTTCAATTTTCTTGCGCA.....	21	0	1	18.00	18	11	3	2	0	2	0
.....TTTCACTTCAATTTTCTTGCGCA.....	23	0	1	16.00	16	9	2	2	0	1	2
.....TCACTTCAATTTTCTTGCGC.....	20	0	1	11.00	11	10	1	0	0	0	0
.....TTCACTTCAATTTTCTTGCGC.....	21	0	1	8.00	8	7	1	0	0	0	0
.....TCACTTCAATTTTCTTGCGCAG.....	22	1	1	6.00	6	6	0	0	0	0	0
.....CTTCAATTTTCTTGCGCAG.....	19	0	1	5.00	5	4	1	0	0	0	0
.....CACTTCAATTTTCTTGCGCAG.....	21	0	1	5.00	5	3	2	0	0	0	0
.....GTAAGTAAATTGAAGCTAATATC.....	23	0	1	5.00	5	4	0	1	0	0	0
.....ACTTCAATTTTCTTGCGCAG.....	20	0	1	4.00	4	4	0	0	0	0	0
.....GTAAGTAAATTGAAGCTAATA.....	21	0	1	4.00	4	2	0	2	0	0	0
.....TTTCACTTCAATTTTCTTGCG.....	21	0	1	3.00	3	2	0	0	0	1	0
.....CACTTCAATTTTCTTGCGCAGT.....	22	1	1	3.00	3	3	0	0	0	0	0
.....TCACTTCAATTTTCTTGCGCAGA.....	23	1	1	3.00	3	3	0	0	0	0	0
.....TTCACTTCAATTTTCTTGCGCAG.....	23	0	1	3.00	3	2	0	0	0	0	1
.....TCACTTCAATTTTCTTGCGCAGT.....	23	1	1	2.00	2	2	0	0	0	0	0
.....CACTTCAATTTTCTTGCGCAGA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....ACTTCAATTTTCTTGCGCAC.....	20	1	1	1.00	1	1	0	0	0	0	0
.....TTCACTTCAATTTTCTTGCG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TTTCACTTCAATTTTCTTGC.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TTTCACTTCAATTTTCTTGCGCAGC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TCACTTCAATTTTCTTGCGCAGC.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GTAAGTAAATTGAAGCTAATATCGCT.....	26	0	1	1.00	1	0	1	0	0	0	0
.....TTTCACTTCAATTTTCTTGCGCAGT.....	25	1	1	1.00	1	1	0	0	0	0	0
.....TTTCACTTCAATTTTCTTGCGCAC.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TCACTTCAATTTTCTTGCG.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TTCACTTCAATTTTCTTGCGCT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TCACTTCAATTTTCTTGCGTC.....	21	2	1	1.00	1	0	0	0	0	0	1
.....TTTCACTTCAATTTTCTTGCGCAT.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TCACTTCAATTTTCTTGCCAG.....	21	3	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

GCCCGCTAGCTGTCCCGCAGCAGCACGAGTGGCTTAAGCTGATAGTTCGCCATTCATTTAACTTCGATTATAGCGAAAGGCAAATTAACTAAAGTGAAGTTAAAAGAACGCGTCGTGGACTCGTTTAGCAACCTTTATGACTTGCTTCGGATACTCTAACAAGT	Read size	# Mismatch	Hit Count	Total Norm	Total	V041 embryo	V056 head
**********(((((.(((((((((.....((((.((.......)).)))).....)))))))))).)))))....**********							
.....TTCACTTCAATTTTCTTGCGCAGT.....	25	1	1	1.00	1	1	0
.....TTTCACTTCAATTTTCTTGCGCAC.....	24	1	1	1.00	1	1	0
.....TCACTTCAATTTTCTTGCG.....	19	0	1	1.00	1	1	0
.....TTCACTTCAATTTTCTTGCGCT.....	22	1	1	1.00	1	1	0
.....TCACTTCAATTTTCTTGCGTC.....	21	2	1	1.00	1	0	0
.....TTTCACTTCAATTTTCTTGCGCAT.....	24	1	1	1.00	1	1	0
.....TCACTTCAATTTTCTTGCCAG.....	21	3	20	0.05	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6496:16061769-16061932 +	dmo_1180	CGGGCGATCGACAGGGCGTCGTCGTGCTCACCGAATTCGACTATCAAGCGGTAAGTAAA------TTGAAGCTAATA--TCGCT----------TTCC-GTT---------TAA----------T-TGATTT-CA--------CTTCAATTTTCTTGCGCAGCACCTGAGCAAATCGTTGGAAATACTGAACGAAGCCTATGAGATTGTTCA
droVir3	scaffold_12875:10875638-10875805 -		CGGGTGATCGACAGGGCGTTGTAGTACTCACCGAATTCGACTATCAAGCGGTACGTAGAGCA----CAGG-A-T-TAATTCC----------ATCA-ACT---------TGGCATTCATCAT-----CATT----------------C--C--T-TTAAAT-----CCGGGC----GACAGCACCTGAGCAAATCGCTGGAAATACTAAGCGAAGCTTATGAGATTGTACA
droGri2	scaffold_15245:3978684-3978839 -		CGGGCGATAGACAAGGTGTCGTTGTCCTTACCGAATTCGACTATCAAAAGGTGCGTGTAGATG---------ATTA--TATT----------ATCT-ACT---------TTT---------TTTA---AAC-AA--------C-------C---------CTTATATATTT----GACAGCACCTGAGCAAATCTTTGGAAATACTCAGCGAAGCTTATGAGATTGTCCA
droWil2	scf2_1100000004513:6147062-6147223 +		CGGAGACGCCAGGGAGTTGTCGTCTTCACCGAATTCGATTATCAAGCGGTCAGTTT-------------------A---------GCC-ACTAAAGCCATCTG--AATCAGCATCAACTT--------ATAAACTAA-TG-GACC--C--TT-----------TGCAGCACCTCAGCAAATCAGTGGAGATACTCAGTGAGCCTATGAGATTGTGCA
dp5	3:6686727-6686881 +		CGGCGACGCCAAGGCGTTGTGTGCTAACGGAATTCGACTATCAATCGGTGGGTACAAGAGTTTGAAAGA-ATC--CTCCAGTA---------GCC-AC----------------------TATA----------C--CCT--T-TTCTA-----------------TCCAGCACCTAAGCAAATCTGTTGAGATCCTGAGCGAAGCCTATGAAATTGTCCA
droPer2	scaffold_2:6908796-6908950 +		CGGCGACGCCAAGGCGTTGTGTGCTAACGGAATTCGACTATCAATCGGTGGGTACAAGAGTTTGAAAGA-ATC--CTCCAGTA---------GCC-AC----------------------TATA----------C--CCT--T-TTCCA-----------------TCCAGCACCTAAGCAAATCTGTTGAGATCCTGAGCGAAGCCTATGAAATCGTCCA
droAna3	scaffold_13266:6816673-6816825 -		CGGCGATCGACAAGGTGTATGTGTGCTCACAGAATTCGATTACCAGCGGTATGCAAT------TCCAATGTATTT--CTACAAT---------GCC-ATC---------------------TA-------A--------T-TGAGTTT-TTTTT-----------------TACAGCATCTAAGCAAATCTGTGGAGATCTCAGTGAGGCTACGAGATCGTCCA
droBip1	scf7180000396423:357548-357700 -		CGGTGATCGCCAAGGTTGTAGTGTGCTCACTGAATTCGATTACCAGCGGTATGTAAT------TCCA--------------------------ATG---------TAT-----------TTCA---AAA-ATATTCTTAATG-GTCCT-GGTTT-----------------TACAGCATCTTAGCAACTCGGTGGAGATCTCAGTGAGGCTACGAGATCGTCCA
droKik1	scf7180000302670:87949-88107 -		CGGGCGATCGCCAGGGTGTAGTGTGCTCACAGAGTTCGATTACCAGCGCAGTAAGTA---------C-TAGATTT----------ACGT-GCA---------GAA----------CCTA---TAAAAAACGCTAA-CGTATTCC--CTAT-----------------AACAGCACCTCAGCAACTCCGTAGAGATTCTGAGCGAAGCCTACGAGATCGTCCA
droFic1	scf7180000453948:107435-107595 -		CGGCGATCGCCAGGGCGTGGTGTGCTCACAGAGCTTGACTACCAGCGGTAAGGC---------CCTTATT---------ATTT-ATT---------AAA----------CCCA---AGT-ACTAACTAATGGTAATCT-TCGATC-----------C----ACCAGCATCTTAGCAAATCTGTGGAGATCCTGAGCGAGCCTACGAGATCGTGCA
droEle1	scf7180000491347:181543-181717 -		CGGCGATCGCCAGGGAGTCGTAGTGCTCACGGAGTTCGACTACCAGCGGTAAGCA---------T-TAATCTT----------TGCT-GTT---------CAG----------CCCG---AGC-TTAAGCTTATTCTAACCC-TCCACACACACACACACA----GACAGCACCTCAGCAACTCCGTGGAGATCCTGAGCGAGCCTACGAGATCGTCCA
droRho1	scf7180000779868:10636-10796 -		CGGCGATCGTCAGGGAGTCGTGTGCTTACGGAGTTCGACTACCAGCGGTGAGCA---------T-TTATCC----------TCCT-TTT---------CAA----------TCCG---AGT-ATAAGCTAATTGTATTCCCCACAC-----------------AACAGCACCTTAGCAAGTCCGTGGAGATCTTGAGCGAGCCTATGAAATCGTCCA
droBia1	scf7180000302292:2798170-2798329 +		CGGCGACGCCAGGGTGTGGTGTGCTCACGGAGTTCGACTACCAGCGGTACGAT---------C-TTATCAT----------TCCC-ATT---------CAC----------CCCA---AGG-TTTTGCTAATTTGTACCC-CTAAA-----------------AACAGCACCTCAGCAACTCCGTGGAGATCCTGAGCGAGCCTACGAGATAGTCCA
droTak1	scf7180000412807:116140-116302 -		CGGCGATCGCCAGGGCGTGGTGTGCTCACGGAGTTTGATTACCAAGCGGTGAGCC---------T-TTAATAT----------ACCC-CAA---------TAA----------CCCT---AGA-ATTTGCTAAATGTAACCC-CCGAAT-----------C----TACAGCACCTCAGCAAATCCGTGGAGATCCTGAGCGAGCCTACGAGATAGTCCA
droEug1	scf7180000409672:5362693-5362852 -		CGGGCGATCGCCAAGGCGTGGTGTGCTTACAGAGTTGGACTACCAGCGGTAAGCT---------C-TACATCT----------GCCA-ACT---------CAA----------TACC---AGC-ATTAGCATAATGAAACCC-TTCAA-----------------TATAGCACCTTAGCAAATCCGTTGAGATCTTAAGCGAGGCTATGAGATCGTCCA
dm3	chr2R:3349799-3349966 -		CGGGCGATCGCCAGGGAGTGGTGTGCTCACGGAGCTCGATTACCAGCGCGTAAGGG---------G-TAATCTTGTA----TATTTAAAT-ATT----------TAA----------ATTA---AGC-AATCGCCTATTGTGTACCG-TTGAA-----------------TGCAGCACCTCAGCAAATCGGTGGAGATCCTGAGCGAAGCTACGAGATCGTACA
droSim2	2r:4172991-4173158 -		CGGCGATCGCCAGGGAGTGGTGTGCTCACGGAGCTTGATTACCAGCGCGTAAGGA---------G-CCATCCTTTA----TATTTAAAT-GTT----------TAA----------ATTA---AGC-AATTGCTTATTGTGTACCG-TTGAA-----------------TGCAGCACCTCAGCAACTCGGTGGAGATCCTGAGCGAGCGTACGAGATCGTACA
droSec2	scaffold_1:1007024-1007191 -		CGGCGATCGCCAGGGAGTGGTGTGCTCACGGAGCTTGATTACCAGCGCGTAAGGA---------G-CCATCCTTTA----TATTTAAAT-GTT----------TAA----------ATTA---AGC-AATTGCTTATTGTGTACCG-TTGAA-----------------TGCAGCACCTCAGCAACTCGGTGGAGATCCTGAGCGAGCGTACGAGATCGTACA
droYak3	2L:16028478-16028639 -		CGGAGATCGCCAGGGAGTGGTGTGCTTACGGAGTTGATTACCAGCGCGTAAGAA---------C-CAATCGTTTA---------TAT-ATT----------AAA----------ATCA---TTC-AATTCCTTATTGTGTACCG-TTGAA-----------------TACAGCACCTTAGCAAATCGGTGGAGATTTTAAGCGAAGCGTACGAGATCGTGCA
droEre2	scaffold_4929:19247936-19248103 +		CGGAGATCGCCAGGGAGTGGTGTGCTCACGGAATTCGATTACCAGCGCGTAAGAA---------C-CAATCATATAAGAATAT--GTAT-ATT----------TAA----------ATCA---ATC-AATCGCGTATTGTGTAACCG-TTG-------------------AACAGCACCTCAGCAAATCGGTGGAGATCCTGAGCGAGCGTACGAGATCGTACA

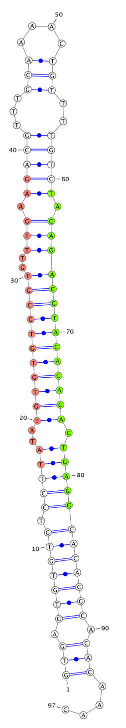
Generated: 09/08/2015 at 07:01 PM

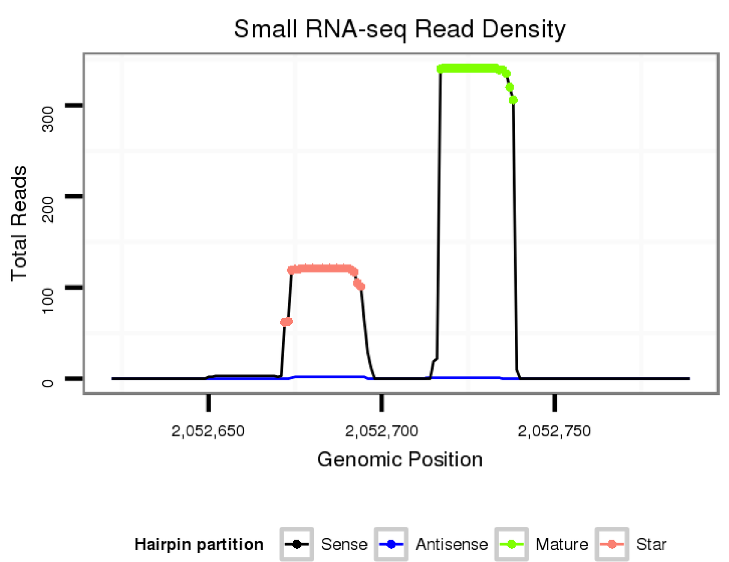
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

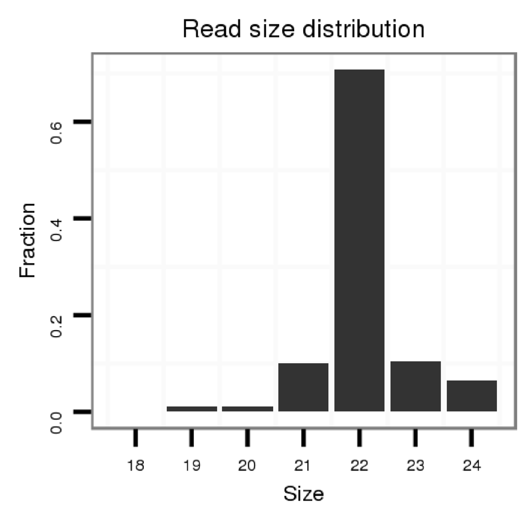
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_80	**scaffold_6359:2052672-2052739 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

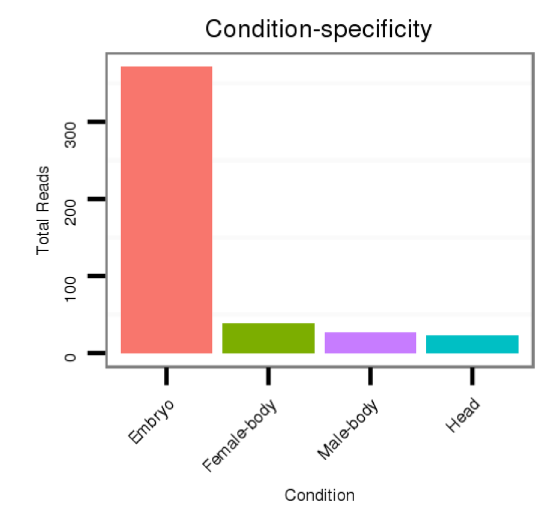
Legend: mature star mismatch in alignment mismatch in read

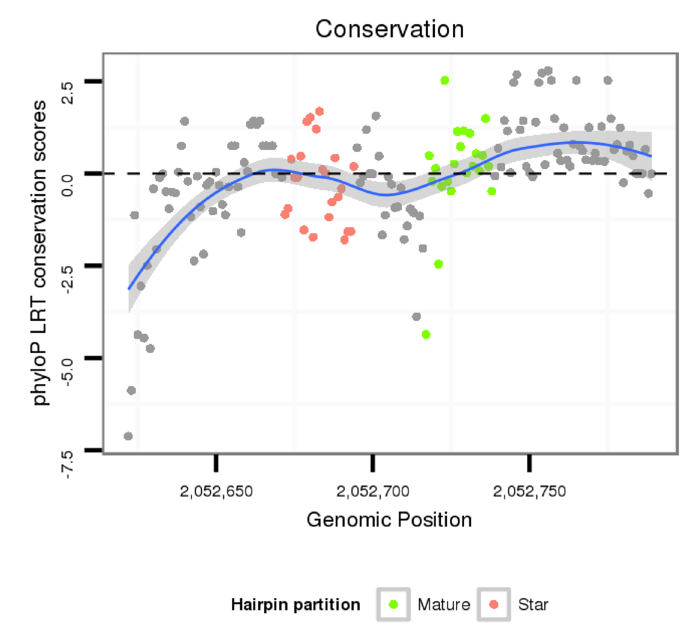
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
(CA)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAAATCGCTTTCCCCTTGTAAATTGCGATGGGAGCGTGAGTGTGTGTCCTTATATGTGTGTGCGTGTTTGAAGACGTTTGCAAAACTGTTTTGTCTACAGACGTACACACACTGAGGCACACGCACACAAACACACACACATACACGCACACGCACACGCACACACCT ************************************(((.(((((((.(((((..(((((((((((..(((.(((((...(((....)))..))))).))))))))))))))).)))))))))))).)))....************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V041 embryo	M046 female body	V110 male body	V056 head	V049 head
TACAGACGTACACACACTGAGG	22	0	1	293.00	293	181	63	30	10	9	0
TACAGACGTACACACACTGAGGT	23	1	1	23.00	23	13	7	0	3	0	0
TATATGTGTGTGCGTGTTTGAAG	23	0	1	21.00	21	5	15	0	0	1	0
TATATGTGTGTGCGTGTTTGAAGA	24	0	1	18.00	18	6	10	0	2	0	0
TATGTGTGTGCGTGTTTGAAGAC	23	0	1	16.00	16	9	1	1	4	0	1
TATGTGTGTGCGTGTTTGAAG	21	0	1	15.00	15	5	5	0	2	2	1
TACAGACGTACACACACTGAG	21	0	1	14.00	14	7	2	2	2	0	1
TATGTGTGTGCGTGTTTGAAGA	22	0	1	14.00	14	4	8	1	0	1	0
TCTACAGACGTACACACACTGA	22	0	1	13.00	13	9	3	1	0	0	0
TATATGTGTGTGCGTGTTTGA	21	0	1	12.00	12	1	5	1	1	2	2
TACAGACGTACACACACTGAGT	22	1	1	11.00	11	7	1	2	1	0	0
TATGTGTGTGCGTGTTTGAAGACG	24	0	1	11.00	11	1	7	0	3	0	0
TACAGACGTACACACACTGAGGA	23	1	1	10.00	10	5	3	1	1	0	0
TACAGACGTACACACACTGAGGC	23	0	1	10.00	10	8	0	1	0	1	0
TACAGACGTACACACACTGAGC	22	1	1	5.00	5	5	0	0	0	0	0
TATATGTGTGTGCGTGTTTGAA	22	0	1	4.00	4	1	3	0	0	0	0
TCTACAGACGTACACACACTGT	22	1	1	4.00	4	4	0	0	0	0	0
TACAGACGTACACACACTGAGA	22	1	1	4.00	4	3	1	0	0	0	0
TCTACAGACGTACACACACTG	21	0	1	3.00	3	1	1	0	1	0	0
TATATGTGTGTGCGTGTTTG	20	0	1	3.00	3	2	0	0	0	1	0
CTACAGACGTACACACACTGAA	22	1	1	2.00	2	1	1	0	0	0	0
TCTACAGACGTACACACAC	19	0	1	2.00	2	2	0	0	0	0	0
TCTACAGACGTACACACACTGC	22	1	1	2.00	2	2	0	0	0	0	0
TTATATGTGTGTGCGTGTTTGAAGA	25	0	1	2.00	2	1	1	0	0	0	0
TATATGTGTGTGCGTGTTT	19	0	4	1.25	5	0	0	1	4	0	0
TACAGACGTACACACACTGA	20	0	1	1.00	1	0	0	0	0	1	0
TACAGACGTACACACACTGG	20	1	1	1.00	1	1	0	0	0	0	0
TTATATGTGTGTGCGTGTTTGAAG	24	0	1	1.00	1	0	1	0	0	0	0
ACAGACGTACACACACTGAGGT	22	1	1	1.00	1	1	0	0	0	0	0
TATGTGTGTGCGTGTTTGAAGACT	24	1	1	1.00	1	0	0	1	0	0	0
TATATGTGTGTGCGTGTTTGAAGAA	25	1	1	1.00	1	1	0	0	0	0	0
ACAGACGTACACACACTGAGG	21	0	1	1.00	1	1	0	0	0	0	0
GTGTGTGCGTGTTTGAAGA	19	0	1	1.00	1	1	0	0	0	0	0
GGAGCGTGAGTGTGTGTCC	19	0	1	1.00	1	0	1	0	0	0	0
TCTACAGACGTACACACACTGAGG	24	0	1	1.00	1	1	0	0	0	0	0
ACAGACGTACACACACTGAGGA	22	1	1	1.00	1	0	0	0	1	0	0
TATATGTGTGTGCGTGTTTGAAT	23	1	1	1.00	1	1	0	0	0	0	0
ATGTGTGTGCGTGTTTGAAGAC	22	0	1	1.00	1	0	0	0	1	0	0
TGGGAGCGTGAGTGTGTGTCC	21	0	1	1.00	1	1	0	0	0	0	0
CTACAGACGTACACACACTGAGG	23	0	1	1.00	1	1	0	0	0	0	0
TCTACAGACGTACACACACTGTT	23	2	1	1.00	1	0	0	1	0	0	0
CTACAGACGTACACACACTG	20	0	1	1.00	1	0	0	1	0	0	0
TGGGAGCGTGAGTGTGTGTC	20	0	1	1.00	1	0	1	0	0	0	0
TACAGACGTACACACACTGAA	21	1	1	1.00	1	0	1	0	0	0	0
TACAGACGTACACACACTGAGGTT	24	2	1	1.00	1	1	0	0	0	0	0
CTACAGACGTACACACACTGA	21	0	1	1.00	1	1	0	0	0	0	0
ATATGTGTGTGCGTGTTTGAAG	22	0	1	1.00	1	1	0	0	0	0	0
TATATGTGTGTGCGTGTTTGAAA	23	1	2	0.50	1	1	0	0	0	0	0
TATGTGTGTGCGTGTTTGAA	20	0	2	0.50	1	0	1	0	0	0	0
ATATGTGTGTGCGTGTTTG	19	0	2	0.50	1	0	0	0	0	1	0
TATGTGTGTGCGTGTTTG	18	0	9	0.11	1	0	1	0	0	0	0

Anti-sense strand reads

TTTTAGCGAAAGGGGAACATTTAACGCTACCCTCGCACTCACACACAGGAATATACACACACGCACAAACTTCTGCAAACGTTTTGACAAAACAGATGTCTGCATGTGTGTGACTCCGTGTGCGTGTGTTTGTGTGTGTATGTGCGTGTGCGTGTGCGTGTGTGGA ************************************(((.(((((((.(((((..(((((((((((..(((.(((((...(((....)))..))))).))))))))))))))).)))))))))))).)))....************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V041 embryo	M046 female body	V110 male body
ATACACACACGCACAAACTTCT	22	0	1	1.00	1	1	0	0	0
TACACACACGCACAAACTTCT	21	0	1	1.00	1	1	0	0	0
ACAGATGTCTGCATGTGTGTGA	22	0	1	1.00	1	0	1	0	0
GTATGTGCGTGTGCGTGTGC	20	0	8	0.13	1	0	0	1	0
TATGTGCGTGTGCGTGTGC	19	0	9	0.11	1	0	0	0	1
TGCGTGTGCGTGTGCGTG	18	0	20	0.05	1	0	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6359:2052622-2052789 +	dmo_80	AAA-ATCGC-TTTC------------------CCC--------------------------------TTG------------------------------TAAATTG---CGATG-GGAGCGTGAGTGTGTGTCCTTATAT-----------------GT---------------GTG----------------------------TGCG-----TGT----------TT------------G----------AAGACGTTTGC---AAAACT---GTT------------TTGTCTACAGA--CGTACACACACT--G--AGGCACACGC--ACACAAACACACACACATA----CACGCACACGCACAC--------GCA--CACACCT-
droVir3	scaffold_12726:946492-946664 -		CAA-ATCAT-TTTC------------------AGT--------------------------------TT-------------------------------GTACAATTTTATG-TC----A-----------ACTGTGTGTGTGT----TTTTTT--------------------TTTCATTTTGCCCCAGCTCGTTGTTGGCTGTGCC-----A--------------------------------------CTTTTGT---TTAG-------------C--------TGATTCA--CATGCACACACA--G--ATACAGAGAC--ACACAGGCACACAGACACA----CTCACTTACACACAC--------GCG--CA--CAC-
droGri2	scaffold_15245:5469077-5469228 -		ACA-TTTTACACCT-TTTGAGTTGGGCACTCT--GGCAG----------------CGTGTTG--GCT-----------GC----A-----------ACATGTCTGTGTAT----TTTCAT----------------ATCCA--G---GC---------------AACA--------------CACATT--CACACACGCACA--C--ACACACACAC--ACACGCACACACACACGCA----CACACACGCACAC--------ACA--CA--CAC-
droWil2	scf2_1100000004521:5857136-5857306 +		CTT-TCCAT------------------------C--------------------------------TGTATCCCTGTTATAGTC----TGAGTGT-----------GGTTG---TGGTG-T---GCATATGT---------GTTG-----------------------------GCG-----CATACA-----TAA-----------ACA--------ACA-------------A-TG---GCAACAACAAGAGTACC-AGCAGTCA----------GCCAGC--CACACATACCCA--C--ACACACACAC--ACACACACACACACACACA----CACACACACACAC--------GCA--GG--CAT-
dp5	XL_group1a:6290827-6290947 -		CGT-GCATGC--AATTCCTTA-TTT-G--CTGTGCG-----ACA--------AT------------G---------TTGAAAT-------------ATG-------------CACTCCATACA--CACACACACACA--C--ACTCACACTC--ACAGGCACACACACACACA----CACACACTCACAGGC--------ACA--CA--CAC-
droPer2	scaffold_47:63342-63478 -		TGG-ACATT---G------------------C--GGGGGATC---GAGGA-G---GTAAATGCCTTCA------------------------------------CACATATTTGCATGCTATAA-------------------ATG-CGACAACATA--CACATACACACA--CAGACACCGACAC--AGAACGACAAACACGTACA----CGAACACGCACACGC--------ACA--CG--CCT-
droAna3	scaffold_12916:12848921-12849007 +		GCA-GGA---CA-GGCTCCC--------TCACACA--CACACACACACA--C--ACACACACAC--ACACACACACACACACACA----CACACACACACAC--------ACA--CA--CAC-
droBip1	scf7180000395970:132167-132231 +		--CAAACACACACA--C--ACAGACACAC--ACACACACACACAGACACA----CATACACACACACAT--------ACA--CT--CAC-
droKik1	scf7180000302258:209254-209376 +		GAG-TGT-------------------GTGTGTGTG--TGCG-CGTGTGCG---TACACTCAAC------------------ACC-AGCAAACATCTGTTGTG--------C-----------A--A--ACACATACAC--ACACACACACACACACACA----CACACACACACACAGAGACACCAGCAGG--TGCA
droFic1	scf7180000454077:391782-391944 +		TTA-TCCTT-T---TGGCTGG---CACTT-TGCGCTGTGTGTGTGT--ACGTTGT--------------------GTGT--------------------GTGTT----TAAGTGTGTGTGT--------------------GC---CAGGTT---GCT-AGCGTTAA----TATGCCACAAG--CTTGCACACACA--C--ACATACACAC--ACAAAACACACACACACA----CACAAGGACGCATGC--------AAA--CA--CTC-
droEle1	scf7180000491006:2706074-2706207 -		CAA-ATCGA-TTTG------------------C--CATTGACTGAAAA-CTCTATAGCCTACTAAAAA-------------------------AT----CG-GTGT-----------AAAAC---GGCTG-A---AAA--A----AAC-AG----------CAAACAAACA--CACGCACGCACA--C--ATGGA------------TACACGCAAC----CACACA-GCACACAC--------ACA--CA--TGC-
droRho1	scf7180000764255:14102-14267 -		GCT-TTGTC-T------------------------------------GTG-----------------------------TTGGTTG--------------------------CAGCC-G---CCAAAAGTATGCAACAGTGTTT------------------GCGTT----TGAA-----TTT---------GGA--------G-CGTCAGC---AGAATG---AGTCAGC-TGAA----TATATCAAGCGTACGCACACACTGG--C--ACTCGCACTC--ACACACACAGACACACAAG----CACACACGTACACAC--------GCA--CA--CACC
droBia1	scf7180000301760:1516021-1516163 +		ATG-GCGAT---G--GCGAGAATG-TGG-ATC----C-----------AGAGGA---------GT---------------GTG------------------------TGCC-----A-------------CTCGGCACATAATTGTTTGAAA--------------------------------CAAATGTAGTG----CA--CACACACT--CGCTC--ACAG-CACACACACACACACACACACACACA----CACACACACACAC--------ACA--CA--CGCT
droTak1	scf7180000415381:115339-115412 +		GC---CACACA--CACACACACACA--C--ACACACACAC--ACACACACACACACACACA----CACACACACACAC--------ACA--CA--CAC-
droEug1	scf7180000409524:744607-744756 +		GCAAATGGC-GGCG------------------C--ATGTGTGTG--TGTGTCTGTGTGCTAGC----------------------------AAGGCTG----CAAGTGT-----------GCGAG---TGCAG-T---GAG---AGT---GTC------------CTGACAACACA--CACACACACACA--C--ACACACACAC--ACACACACACACACACACA----CACACACACACAC--------ACA--CA--CAC-
dm3	chrX:12013610-12013729 -		TGT-TTGTTT---GCCTGTTTG-TTT-GCC----T-----------GTTTGAGTTGCTGT---T---AGAATT---ATT------------TTTTC----CA--CTAACGCAAAGC--C--GCGC-CGCTC--ACACACACACACACACGCA----CACGCACACACACAC--------GCA--CA--CAC-
droSim2	2L:13218031-13218122 -		CCT-TAT---TCGGTTGTACATGTTTGAA-------------------------------AG--CCACGCACTCA--C--ACACACACAC--ACACACACACACACACACA----CACACACACACAC--------ACA--CA--CAC-
droSec2	scaffold_4:2321241-2321325 +		AAT-ACT--GCCATAT-----TCGCCTA--CACACACACACA--C--ACACACACAC--ACACACACACACACACACA----CACACACACACAC--------ACA--CA--CAC-
droYak3	3R:19603982-19604171 +		AAA-AAAGA-TCTGGC----------------C--AAATGACTGTAAT-TTGCATTGGCAAC------TC-ACACAAAGAGACGGCGCGCAGTTTAACACCTGCATGAGTG-TTG-GTC----G-----------GCTTGTGTTTGTGT----TGG---GCC---TTT------------CAATTTAAATA--CAAACACC--CACTC--ACA--CACAC--GCGCACACACTCTCGCACATACACTCGCACACTCAC--------ACA--CA--CATT
droEre2	scaffold_4770:6260001-6260155 -		TGA-ATCGC-GATG------------------T--TTGTGTGTG--TGCG-TGCATGCGTGCTTGTGT--GTTT-----------------GTGTGTGACATGCA-----TAA------------------------------GC---CAAATT---AAT-TGGAGCTT----CATTC----CA--CACACACACACA--C--ACGCACACAC--ACACACACACACACACACA----CACACACACACAC--------ACA--CA--CAC-

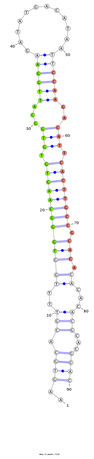
Generated: 09/08/2015 at 07:35 PM

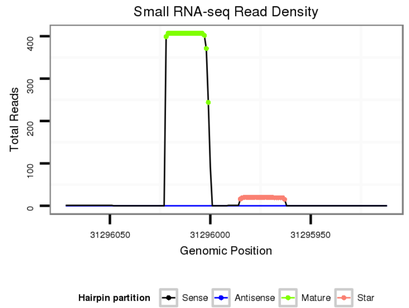
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

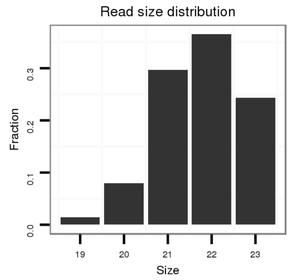
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_72	**scaffold_6540:31295962-31296022 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

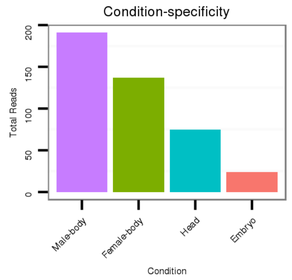
Legend: mature star mismatch in alignment mismatch in read

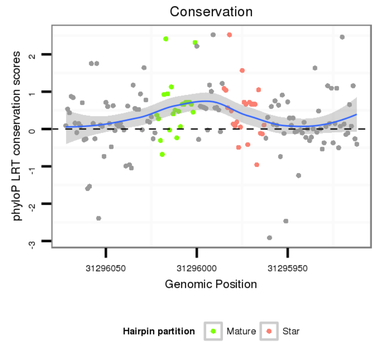
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
(CGTGn	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AACAACAACAAATGCGGCCGACACAGCCACAGCCAAAGTGCACGTTTTGGTGGGCAAGTGTGTGGCATTGGAAGATATGACATAATTCCAAGACATTCACTTGCCGCACACACACGCACGCACGCACACGTATGTACATGTGAAGAAGCAACCAAAAGA	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head	V049 head	M060 embryo	V041 embryo
********************************..((((.(((..(((((((((((((((.(((...(((((((.............)))))))..)))).)))))))).)))).))...))))...))))********************************												
..........TGGGCAAGTGTGTGGCATTGGA..	22	0	1	149.00	149	77	45	13	11	3	0
..........TGGGCAAGTGTGTGGCATTGG..	21	0	1	123.00	123	58	39	18	6	0	2
..........TGGGCAAGTGTGTGGCATTGGAA..	23	0	1	92.00	92	35	29	15	8	4	1
..........TGGGCAAGTGTGTGGCATTG..	20	0	1	30.00	30	18	9	1	2	0	0
..........CCAAGACATTCACTTGCCGCACA..	23	0	1	11.00	11	0	3	0	0	8	0
..........TGGGCAAGTGTGTGGCATTGGAN..	23	1	1	8.00	8	3	3	0	2	0	0
..........TGGGCAAGTGTGTGGCATTGGAAN..	24	1	1	8.00	8	3	4	0	1	0	0
..........TGGGCAAGTGTGTGGCATTGGAAT..	24	1	1	6.00	6	2	2	1	1	0	0
..........TGGGCAAGTGTGTGGCATT..	19	0	1	5.00	5	3	1	0	1	0	0
..........TGGGCAAGTGTGTGGCATTGT..	21	1	1	4.00	4	3	0	0	1	0	0
..........GGGCAAGTGTGTGGCATTGG..	20	0	1	4.00	4	0	4	0	0	0	0
..........CCAAGACATTCACTTGCCGCAC..	22	0	1	4.00	4	0	0	0	0	4	0
..........GGGCAAGTGTGTGGCATTGGA..	21	0	1	3.00	3	0	3	0	0	0	0
..........CAAGACATTCACTTGCCGCACA..	22	0	1	3.00	3	0	1	0	0	2	0
..........TGGGCAAGTGTGTGGCATTGA..	21	1	1	2.00	2	2	0	0	0	0	0
..........TGGGCAAGTGTGTGGCATTGCTT..	23	2	1	1.00	1	0	0	0	1	0	0
..........AAGACATTCACTTGCCGCACA..	21	0	1	1.00	1	0	1	0	0	0	0
..........TGGGCAAGTGTGTGGCATTGGT..	22	1	1	1.00	1	0	1	0	0	0	0
..........GGGCAAGTGTGTGGCATTG..	19	0	1	1.00	1	0	1	0	0	0	0
..........TGGGCAAGTGTGTGGCATTGCCC..	23	2	1	1.00	1	1	0	0	0	0	0
..........TGGGCAAGTGTGTGGCATTGCG..	22	1	1	1.00	1	0	0	0	1	0	0
..........GGGCAAGTGTGTGGCATTGGAT..	22	1	1	1.00	1	0	1	0	0	0	0
..........TGGGCAAGTGTGTGGCATTGGAG..	23	1	1	1.00	1	0	0	0	1	0	0
..........ATAATTCCAAGACATTCACTTGC..	23	0	1	1.00	1	0	1	0	0	0	0
AACAACAACAAATGCGGCCGACAC..	24	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

TTGTTGTTGTTTACGCCGGCTGTGTCGGTGTCGGTTTCACGTGCAAAACCACCGTTCACACACCGTAACCTCTATACTGTATTAAGGTTCTGTAAGTGAACGGCGTGTGTGTGCGTGCGTGTGCATACATGTACACTTCTTCGTTGGTTTTCT	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body
************************************..((((.(((..(((((((((((((.(((...(((((((.............)))))))..)))).)))))))).)))).))...))))...))))********************************							
..........ACGGCGTGTGTGTGTGCGTG..	20	0	2	0.50	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:31295912-31296072 -	dmo_72	AACAACAACAAATGCGGCCGACACAGCCACAGCCAA-AGTGCACGT-TTTG-G----------TG-GGCAAGTGTGTG----------GCATTGGAAGATATGACATAATTCCAAGACATTCACTTGCCG----------CAC--------ACACACACGCACGCACGCACACGTATGTACATG-TGAAGAAG---CAACCAAAA--GA----------
droVir3	scaffold_13047:9345409-9345581 +		AACAACAGAGCATGCACAGCAAAGTGCAC-----GGGGT-TTGCG----------TG-GGCAAGTGTGTG----------GCATTGGAAGATATGACATAATTCCAAGACATTCAGATGGGACACAAA----------AAAAATTCATCTATATTTGT--------ATATATATATATATATATATATTTA-TAAAGAAGCAGGCAGCAAA--GA----------
droGri2	scaffold_14906:3909249-3909445 -		AAGTACAACACGCGGCAGCAGCAGCACAGCAGC-TGCACGT-TTG-GCTGGGCATATTTCT----------A-----------TA----------GTGTATGTGTGTGTGCGTGTGTTTGCATTGGAAGATATGACATAATTCCAAGACATCACTTGGCTTAAAAAAA----------AAA--------GAA----------AGAAAGAAAGAA----------AACAAAA-----GGGGGGGGGGGGGGGGGAAAAGAAAAGS-AAAGCAG---GGACGCAAA--GA----------
droWil2	scf2_1100000004768:303334-303478 -		AACAACAACAAAAACACTACACACAAGCGTT-----TTAAATTG-A----------TTGCCAAGGTGTCTCGCTGCGTAGAAGAAAAAC-CCCC----------C--TAACACACACCCCAAACACA-AC--------ATACA----------CAC--------ACACACACACACACATATGTACAT-T--------T--------T--T----------
dp5	XL_group3b:76531-76683 +		AACAACA----------CAGC-----------CAACACAAATAAC----------A----------GCCCTACCAGCACCATTACAAAAGCAACTTCGGTAAGGAAGCGAAATCAAGAGAGGTATCATTGGTAAA--TACATACAAACATGTATGTACACCT--------ATGTACATACATACATACATACATACAT-T--------T--------T--T----------
droPer2	scaffold_0:3792958-3793000 +		CGT----------T--------T----T----------T----------CCGTAGCAC----------ACACACACACGCACATACATACAC----------T--------T----T-----------
droAna3	scaffold_13266:9293111-9321264 -		AGCAACATCAAGCATAAGCATACGCAACACACAAGCAC-T-------T-C-AATTTGCAGATACTTCACA----------A-----AAACAAAACAAC----GCAGC----------AGGCACTACAACTGTCC----------A-----AAAGCC--TACACGTCCAAGCTG----------TCC----------AATGC----------TCACATACAGTACACACAGTA--CA-T-------T--------T--ACACACA---T--
droBip1	scf7180000396541:604565-604695 -		AGCAATGCAAAATGGCAATTGCAACAGCAACAGCAAGCAAC-T-------T----T----------T----------T----------AAGACACAA----GCTGACACGAAAAGTCACTTCC----------T----------TTATGCAAGCATACAGAGAACA----------GGCCA----------CGCATACA----------TATGCACATTTAACCCA-T-------T--------T--TGTTTA---A---A----------
droKik1	scf7180000302475:408419-408460 +		A----------T--------T----T----------T----------AGATATGACATAATTCCAAGACA----------ATC----------CGCTCACA----------T--------T--------T--GCACCGA---T---T----------
droFic1	scf7180000454072:5117195-5117876 +		AGCAACATACATCTACAATTGTACAACAACAGGCGCTT-----TTAT----T----GGAAAACAGGAGCATAGCTTAGCTTTGGGCTGCTGTTGGCAACTTAAAGTTCAT----------A-----AAAAAGTGAATTAATTAATTGAAATTG----------CAG----------CGCACACA----------CACCACACACACATGCAGAT-T--------T--------T--GCAATG---T---T----------
droEle1	scf7180000491104:2038014-2038112 -		CAG----------T--------T----T----------T----------AACGCAGTGTGTGT----------A-----AAGATATGACATAATTCCAAGACATCTC----------CGCTC----------CGCTCGC----------AGTGCATTGGCACTC-T--------T--------T--GCACCGA---AAAGAAGGAACC----------
droRho1	scf7180000777921:17722-17806 +		CAG----------T--------T----T----------T----------AACGCAGTGTGTGT----------A-----AAGATATGACATAATTCCAAGACATCTC----------CGCTCCCA----------CTC--------T--------T--GCACCGA---AAGCAAAGGA----------
droBia1	scf7180000302098:155004-155111 +		CAG----------T--------T----T----------T----------AACGCAGTGTGTGT----------A-----AAAGATATGACATAATTCCAAGACA----------ATC----------CGCTCGCC----------T--GCGC-TTTGCAGTGCAACTC--------T--------T--GCACCGA---GAAGGTGGATGCGCTCCCTC----------
droTak1	scf7180000415291:10737-10792 +		----------T--------T----T----------T----------AACGCAGTGTGTGT----------A-----AAGATATGACATAATTCCAAGACA----------ATC----------CGCTCGCA----------CTC--------T--------T--GCACCGA---T---T----------
droEug1	scf7180000409759:221225-221274 -		----------T--------T----T----------T----------AACGCAGTGTGTGT----------A-----AAGATATGACATAATTCCAAGACA----------ATC----------CGCTC----------T--------T--------T--GCACCGA---T---T----------
dm3	chr3R:278316-278385 -		CAG----------T--------T----T----------T----------AACGCAGTGTGTGT----------A-----AAGATATGACATAATTCCGGAGACG----------ATC----------CGCTCGCA----------CTC--------T--------T--GCACCGA---T---T----------
droSim2	3r:246190-246259 -		CAG----------T--------T----T----------T----------AACGCAGTGTGTGT----------A-----AAGATATGACATAATTCCGGAGACG----------ATC----------CGCTCGCA----------CTC--------T--------T--GCACCGA---T---T----------
droSec2	scaffold_6:383997-384066 -		CAG----------T--------T----T----------T----------AACGCAGTGTGTGT----------A-----AAGATATGACATAATTCCGGAGACG----------ATC----------CGCTCGCA----------CTC--------T--------T--GCACCGA---T---T----------
droYak3	3L:17013072-17013215 +		AACAACAGCAGCAACAGCAGCAGCAGCAACAGGCAGCAG--------T----T----------T----------GAGCAACAATG----------CA----------ACAGCAACTTTAGCAA----------CAAATGACAGAC----------ACACACACACTCACACACAGACACACACACAGACACACTGCAAGCTG---CA---A---GA----------
droEre2	scaffold_4770:3926007-3926044 -		AAAAGCAACAACAGCAGCCGCACAGCAACAGCAAA-T--------T----T----------T----------A----------T----------AAG----------ACA----------AAG---

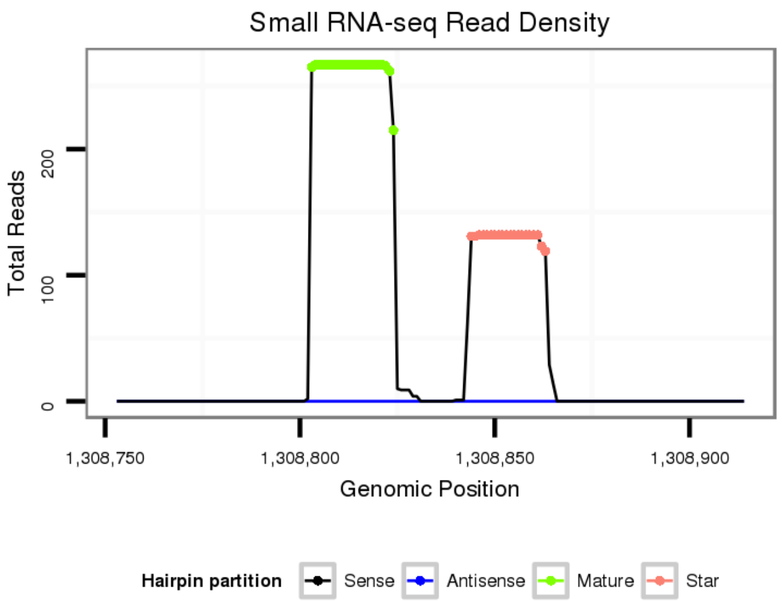
Generated: 09/08/2015 at 07:35 PM

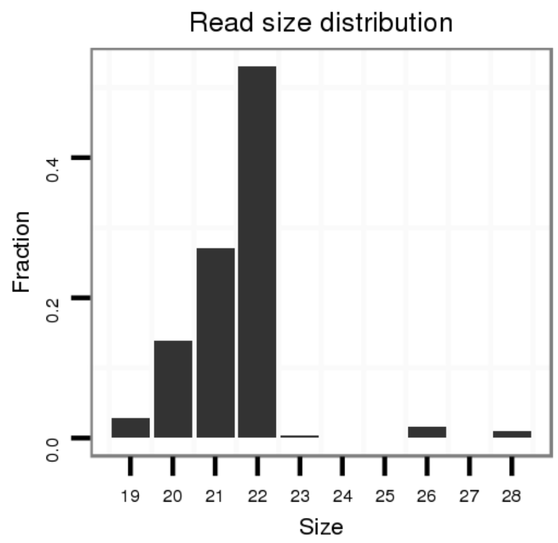
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

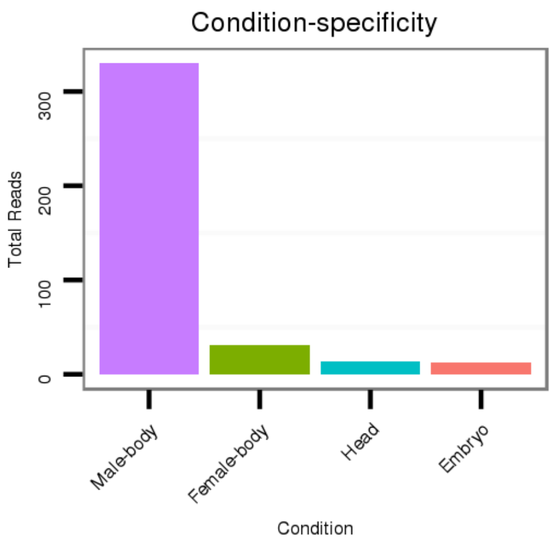
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_61	**scaffold_6308:1308803-1308864 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

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

Predicted structure







No conservation details.

Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dmo_61 scaffold_6308:1308803-1308824 + 2. dmo_38 scaffold_6308:1309091-1309112 +	

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATCTAAGTTAAATCATGTATATAGCAAAAATCTAAGTTAAATCATTTGTTTGCGAGCTATAACCTAGTGGAATACGTTTATTTATCGGTTTTAAGTAGGTTATAGACCGCTGACAAAATGCTTTACTTTGCAACAGGAAAATCGGAAAAACTATCAACTATG **********..((((.(((((((((.(((..((((((((((...(((..((.........))..))).))).))))))))))..))))..))))..))))..)))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V049 head	V056 head	V041 embryo
..........TGCGAGCTATAACCTAGTGGAA..........	22	0	2	202.50	405	362	19	8	3	5	8
..........TGCGAGCTATAACCTAGTGGA..........	21	0	4	46.25	185	155	16	6	3	5	0
..........TAAGTAGGTTATAGACCGCT..........	20	0	1	46.00	46	38	4	2	0	2	0
..........TTAAGTAGGTTATAGACCGCT..........	21	0	1	44.00	44	36	6	0	1	1	0
..........TGCGAGCTATAACCTAGTGGAAA..........	23	1	2	13.50	27	22	3	1	0	1	0
..........TAAGTAGGTTATAGACCGCTG..........	21	0	1	13.00	13	9	2	0	2	0	0
..........TAAGTAGGTTATAGACCGCTGA..........	22	0	1	9.00	9	6	0	0	1	1	1
..........TTAAGTAGGTTATAGACCG..........	19	0	1	8.00	8	6	1	0	0	1	0
..........TGCGAGCTATAACCTAGTGGAC..........	22	1	4	7.25	29	27	0	2	0	0	0
..........TGCGAGCTATAACCTAGTGGAATACG..........	26	0	2	5.50	11	10	0	0	1	0	0
..........TGCGAGCTATAACCTAGTGGAAC..........	23	1	2	5.00	10	9	1	0	0	0	0
..........TGCGAGCTATAACCTAGTGG..........	20	0	4	4.50	18	15	3	0	0	0	0
..........TGCGAGCTATAACCTAGTGGACC..........	23	2	4	4.25	17	15	1	0	0	1	0
..........TTAAGTAGGTTATAGACCGCTGA..........	23	0	1	4.00	4	3	0	1	0	0	0
..........TGCGAGCTATAACCTAGTGGAATACGTT..........	28	0	2	4.00	8	8	0	0	0	0	0
..........TTAAGTAGGTTATAGACCGCTT..........	22	1	1	3.00	3	3	0	0	0	0	0
..........TTAAGTAGGTTATAGACCGC..........	20	0	1	3.00	3	3	0	0	0	0	0
..........TTAAGTAGGTTATAGACCGCTG..........	22	0	1	2.00	2	2	0	0	0	0	0
..........GCGAGCTATAACCTAGTGGAA..........	21	0	2	2.00	4	1	3	0	0	0	0
..........TGCGAGCTATAACCTAGTG..........	19	0	5	1.80	9	7	1	0	1	0	0
..........TTGCGAGCTATAACCTAGTGGAA..........	23	0	2	1.50	3	3	0	0	0	0	0
..........TGCGAGCTATAACCTAGTGGAACC..........	24	2	2	1.50	3	3	0	0	0	0	0
..........TGCGAGCTATAACCTAGTGGAT..........	22	1	4	1.50	6	6	0	0	0	0	0
..........TTGCGAGCTATAACCTAGTGGA..........	22	0	4	1.25	5	4	0	0	0	1	0
..........TAAGTAGGTTATAGACCGCTTT..........	22	2	1	1.00	1	1	0	0	0	0	0
..........TAAGTAGGTTATAGACCGTA..........	20	2	1	1.00	1	1	0	0	0	0	0
..........TTAAGTAGGTTATAGACCGCTA..........	22	1	1	1.00	1	1	0	0	0	0	0
..........TTAAGTAGGTTATAGACCGCC..........	21	1	1	1.00	1	0	0	1	0	0	0
..........AGTAGGTTATAGACCGCTGA..........	20	0	1	1.00	1	1	0	0	0	0	0
..........TAAGTAGGTTATAGACCGCTGATG..........	24	2	1	1.00	1	1	0	0	0	0	0
..........GTTTTAAGTAGGTTATAGACCG..........	22	0	1	1.00	1	0	0	0	0	0	1
..........TAAGTAGGTTATAGACCGCTT..........	21	1	1	1.00	1	1	0	0	0	0	0
..........TAAGTAGGTTATAGACCGC..........	19	0	1	1.00	1	0	1	0	0	0	0
..........TAAGTAGGTTATAGACCGCTGATC..........	24	2	1	1.00	1	1	0	0	0	0	0
..........TAAGTAGGTTATAGACCGCTGAA..........	23	1	1	1.00	1	1	0	0	0	0	0
..........TGCGAGCTATAACCTAGTGGAATACGTC..........	28	1	2	1.00	2	2	0	0	0	0	0
..........TGCGAGCTATAACCTAGTGGAAT..........	23	0	2	1.00	2	1	1	0	0	0	0
..........TGCGAGCTATAACCTAGTGGAAG..........	23	1	2	1.00	2	2	0	0	0	0	0
..........TGCGAGCTATAACCTAGTGGAATAG..........	25	1	2	1.00	2	2	0	0	0	0	0
..........TGTTTGCGAGCTATAACCTAG..........	21	0	5	0.80	4	4	0	0	0	0	0
..........TTATAGACCGCTGACAAAATGC..........	22	0	3	0.67	2	0	0	2	0	0	0
..........TGTTTGCGAGCTATAACCTAGTG..........	23	0	5	0.60	3	2	0	0	0	0	1
..........GCGAGCTATAACCTAGTGGAAG..........	22	1	2	0.50	1	0	1	0	0	0	0
..........TACGTTTATTTATCGGTTTTAAG..........	23	0	2	0.50	1	0	1	0	0	0	0
..........TGCGAGCTATAACCTAGTGGAATAT..........	25	1	2	0.50	1	1	0	0	0	0	0
..........CGAGCTATAACCTAGTGGAA..........	20	0	2	0.50	1	1	0	0	0	0	0
..........TACGTTTATTTATCGGTTTTAAGTCC..........	26	2	2	0.50	1	1	0	0	0	0	0
..........TACGTTTATTTATCGGTTTTAAGTAG..........	26	0	2	0.50	1	1	0	0	0	0	0
..........TGCGAGCTATAACCTAGTGGAATA..........	24	0	2	0.50	1	0	0	0	0	0	1
..........TGCGAGCTATAACCTAGTGGAAGT..........	24	2	2	0.50	1	0	0	0	0	1	0
..........TGCGAGCTATAACCTAGTGGAATA..........	24	0	2	0.50	1	0	0	0	0	0	1
..........TGCGAGCTATAACCTAGTGGAAGT..........	24	2	2	0.50	1	0	0	0	1	0	0
..........TGTTTGCGAGCTATAACCTAGTC..........	23	1	5	0.40	2	2	0	0	0	0	0
..........TACGTTTATTTATCGGTTTC..........	20	1	3	0.33	1	1	0	0	0	0	0
..........TGCGAGCTATAACCTAGTGGC..........	21	1	4	0.25	1	1	0	0	0	0	0
..........TGCGAGCTATAACCTAGTGGTC..........	22	2	4	0.25	1	1	0	0	0	0	0
..........TGCGAGCTATAACCTAGTGGT..........	21	1	4	0.25	1	1	0	0	0	0	0
..........TTGCGAGCTATAACCTAGTGG..........	21	0	4	0.25	1	1	0	0	0	0	0
..........TGCGAGCTATAACCTAGTGGACA..........	23	2	4	0.25	1	1	0	0	0	0	0
..........TGTTTGCGAGCTATAACCTAGT..........	22	0	5	0.20	1	0	0	1	0	0	0
..........TTGCGAGCTATAACCTAGTG..........	20	0	5	0.20	1	0	1	0	0	0	0

Anti-sense strand reads

TAGATTCAATTTAGTACATATATCGTTTTTAGATTCAATTTAGTAAACAAACGCTCGATATTGGATCACCTTATGCAAATAAATAGCCAAAATTCATCCAATATCTGGCGACTGTTTTACGAAATGAAACGTTGTCCTTTTAGCCTTTTTGATAGTTGATAC **********..((((.(((((((((.(((..((((((((((...(((..((.........))..))).))).))))))))))..))))..))))..))))..)))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head	M046 female body	V110 male body
Show Alignment With Reads								

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1308753-1308914 +	dmo_61	ATCTAAGTTAAATCATGTATATAGCAAAAATCTAAGTTAAATCATTTGTTTGCGAGCTATAACCTAGTGGAATACGTTTATTTATCGGTTTTAAGTAGGTTATAGACCGCTGACAAAATGCTTTACTTTGCAACAGGAAAATCGGAAAAACTATCAACTATG

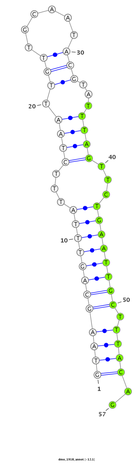
Generated: 09/08/2015 at 08:06 PM

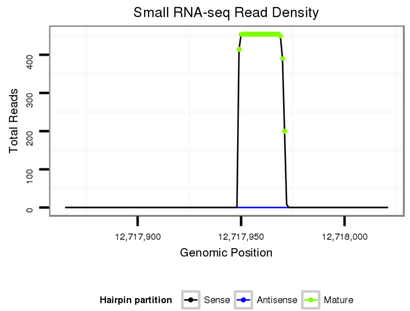
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

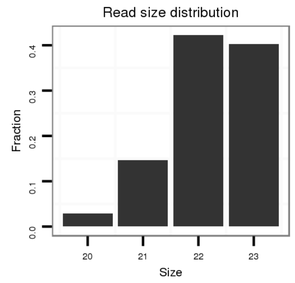
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1918	**scaffold_6540:12717915-12717971 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

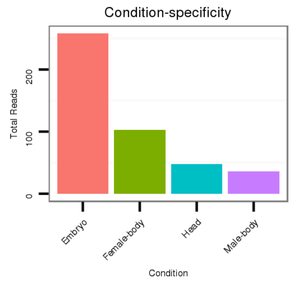
Legend: mature star mismatch in alignment mismatch in read

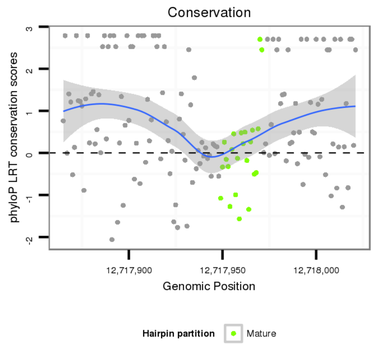
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI24474-in]; CDS [DmojGI24474-cds]; CDS [DmojGI24474-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTTTCCTTGTCTGACATGGAGGATGTCACCTGGCATGGCCTCATTGATTTGTAAGCAGTTTATTTCTAATTGTTGCAATACGTATTTAGTTCTGAATTGCTTTACAGCCTGTTGCACTATCGTCGCGTACTGGCCAGGCAGCCTTTGCTTGCCTACC	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V041 embryo	V056 head	V110 male body	V049 head
**********(((((((((((..((((.(((.(.....))))...))))...)))))))))..))))..**********											
.....TTTAGTTCTGAATTGCTTTACAG.....	23	0	1	179.00	179	83	27	41	13	10	5
.....TTTAGTTCTGAATTGCTTTACA.....	22	0	1	176.00	176	86	44	12	11	17	6
.....TTTAGTTCTGAATTGCTTTAC.....	21	0	1	52.00	52	25	11	1	5	7	3
.....TTAGTTCTGAATTGCTTTACAGT.....	23	1	2	25.50	51	46	1	4	0	0	0
.....TTAGTTCTGAATTGCTTTACA.....	21	0	1	13.00	13	0	9	0	3	0	1
.....TTAGTTCTGAATTGCTTTACAG.....	22	0	1	12.00	12	8	4	0	0	0	0
.....TTTAGTTCTGAATTGCTTTACAGT.....	24	1	2	8.00	16	16	0	0	0	0	0
.....TTAGTTCTGAATTGCTTTACAG.....	23	1	1	3.00	3	0	0	0	3	0	0
.....TTTAGTTCTGAATTGCTTTACAAA.....	24	2	1	3.00	3	0	3	0	0	0	0
.....TTAGTTCTGAATTGCTTTACAGA.....	23	1	1	3.00	3	2	0	1	0	0	0
.....TTTAGTTCTGAATTGCTTTACAAA.....	25	3	1	2.00	2	0	2	0	0	0	0
.....TTTAGTTCTGAATTGCTTTACAGC.....	24	0	1	2.00	2	2	0	0	0	0	0
.....TTTAGTTCTGAATTGCTTTACAG.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TAGTTCTGAATTGCTTTACA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TTTAGTTCTGAATTGCTTTAG.....	21	1	1	1.00	1	0	0	0	1	0	0
.....TTTAGTTCTGAATTGCTTTACAA.....	23	1	1	1.00	1	0	1	0	0	0	0
.....TTTAGTTCTGAATTGCTTTACGC.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TTAGTTCTGAATTGCTTTACAGTT.....	24	2	2	0.50	1	0	0	1	0	0	0
.....TTTAGTTCTGAATTGCTTTA.....	19	1	2	0.50	1	1	0	0	0	0	0
.....TTTAGTTCTGAATTGCTTTACAGTT.....	25	2	2	0.50	1	1	0	0	0	0	0

Anti-sense strand reads

GAAAGGAACAGACTGTACCTCCTACAGTGGACCGTACCGGAGTAACTAAACATTCGTCAAATAAAGATTAACAACGTTATGCATAAATCAAGACTTAACGAAATGTCGGACAACGTGATAGCAGCGCATGACCGGTCCGTCGGAAACGAACGGATGG	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_6540:12717865-12718021 +	dmo_1918	CTTTCCTTGTCTGACATGGAGGATGTCACCTGGCATGGCCTCATTGATTTGTAAGCAGTTTATTTCTA----------ATTGTTGCAATACGTATTT----AGTTCTGAAT----------TG-------C--TTTACAGCCTGTTGCACTATCGTCGCGTACTGGCCAGGCAGCCTTTGCTTGCCTACC
droVir3	scaffold_13047:16399719-16399879 +	TTATCCTGTCGACATGGAGGATGTCACCTGGCAGGCTTATAGATTTGTAGGATTCAATTTGGAAT----------------------CATT-----T---GTT--------TCCCACTT----------TTTAA----------AACTC----------T--ATTTGGT--TTCGTAGTTGCTGCACTATCGTCGCGTCCTGGCAGGCAACAGCAGTCTTCCTATC
droGri2	scaffold_15116:1319419-1319581 +	TTATCCTGTCTGACATGAGGATGTCACCTGGCATGGCCTCATGGATTGTTGGATTTATTTGCAA----------------------TTGCTTGTGCT-TCTCTA----TACTC-----CCCCCAGTTTGTTGCACTACTGTCGCGTCCTGTAGCAGCCAGTCTTCCTATC
droWil2	scf2_1100000004943:4014814-4014976 -	TTGGAATTGCGCGATCTAATGGATGTACCCTAAATGGCTCATTGATTTGTAAGTTATTATTTCCAC----------------------GTTGCTTTATCTTTCATA----------TTTTTTGTCGTT----------ATTCTTTATCC----------T--------C--ATTTAGCCTCGCACTATCGTCGCTCTATTGGTAGCAATTGCCTTTCTTTGCTATC
dp5	2:29687929-29688091 -	CTTATCCTTGTGGGCATGATTCTATGATCTCAGACTGCATGGCATTGATTGATTTGTAAGCCAGCTA------------------------ATGGCTATGT-----GAA----------TCCCTGCCTCTGCTACAT----------ATTCTCCT-CA----------C--------T--TTTACAGTTGTTTGCATGCATCGTCGCATCTGTGCAGCAATTGCCTTTCTTTGCTATC
droPer2	scaffold_6:5060528-5060690 -	CTTATCCTTGTGGGCATGATTCTATGATCTCAGACTGCATGGCATTGATTTGTAAGCCAGCTA------------------------ATGGCTATGA-----GAA----------TCCCTGCCTCTGCTACAT----------ATTCTCCT-CA----------C--------T--TTTACAGTTGTTTGCATGCATCGTCGCATCTGTGCAGCAATTGCCTTTCTTTGCTATC
droAna3	scaffold_13340:15159115-15159273 +	TTATCAGTGGATGGACATGGTGGATGTCAGCTCTAATGGCTTCATTACTTTGTTAGGATTTTGATGAA----------------------ATTGT-----AT-----C--------C--TCCCTCTAAC----------TTTCTGCCACT----------T--------G--ATTCCAGCCTCTTTACATATCGCGTGTCCTTGCAGCAATTGCCTTTCTTTGCTACC
droBip1	scf1800000396708:4869799-4869960 -	TTATCAGTGGATGGACATGGTGGATGTCAGCTCAATGGCTCATTACTTTGTTAGGATTTTG--GACAAT----------------------AC--AT-----CGATTTCT--------TGCTATTT----------TTTGTCTT-AA----------T--------TCGATTCCAGCCTCTTTACATATCGCGTTATTGCTTTCTTTGCTACC
droKik1	scf1800000302707:456825-456987 -	TTATCAGTGGCGATATGGTGGATGTACCCTCAAGGCTCATTGCTTTGTTAGGATTATACGT---TAT-----TCTCAT--TTAAACAGGAATGCAATT----------ACA----------CTTTAATATAAA--TTCCCAGCCTCTTTACATATCGCAGCTATTGCTTTCTTTGCTATC
droFic1	scf1800000454126:216834-216998 +	TTATCAGTGGAGATATGGTGGATGTAGCATCATGGCTCATTGATTGTTAGGATTACCG---TACCGC----------------------ATTTTA-------TG----------------------------------AAGTAGTTGCATCTTAATTTAAATAACT----------C--------C--TTCCAGCTCTTTGCATATCGCAGCTGTCCTGCAGCAATTGCCTTTCTTTGCTACC
droEle1	scf1800000490994:1017368-1017623 -	TTATCAGTGGGGATATGGTGGATGTAGCACTCATGGCTTCATTGATTTGTAGGATTCTTG----GTTTATT---TTCCAACTAAAATCTTCGTTTTGCTGAAATTATAAATG----------------------ATGTGTTTAGTACTTTTCTTACATGGTGTTCGTTCTGTCAGCCTTTGATTTATTAAACTTATTTACTAAGGAAACAAATAACCT----------T--ATTTTTC-TTCCACAGTTTTTGCATATCGTATGGAGAATTGCAGTAGCTTGCCTACC
droRho1	scf1800000771335:25457-25669 +	TTATCAGTGGAGATATGGTGGATGTAGCACTCATGGCATTGATTGCTTTGTAAGATTTTGG----AAT----------------------A----------------------------------CCAAATATGTGTTCGGTATTTTTGTTACACGACGTTCGTTTTGACTGCCGTGAGGTTTTGACACATTT----------ATTAATGAAAAA----------CCC----------T--TCTCC-TCCACAGTTTTTGCATATCGTATGGAGAATTGCAGTAGCTTGCCTACC
droBia1	scf1800000302402:993307-993461 -	TTATCAGTGGGGATATGGTGGATGTACGCTCATGGCATTATGATTTGTAGGATTTTG--GTAAT-C----------------------T----------------------------------TAATTCAACAATTTAAAT----------CCC----------TTCT----------T--TCCACAGTTTTTGCATATCGTATGGAGAATTGCAGTAGCTTGCCTACC
droTak1	scf1800000410451:258532-258694 -	TTATCAGTGGGGATATGGTGGATGTAGCTCATGGCTCATTGATTTGTAGGATTAATT---ATTTATGTAAAA----------TTCATAAATTAAGTTAATTTAA--T----------T--TCCACAGTTTTTGCATATCAAAPAGTTGTGGAGAATTGCAGTAGCTTGCCTACC
droEug1	scf1800000409804:1501095-1501288 +	TTATCAGTGGGGATATGGTTGGATGTAGCTCTAATGGCATTATTGATTTGTAGGATTGTATC--TCCAAT----------------------AAA-----G-C----------TACTTATT-----CCATAAAAGTGTTTCTCT----------TG----------TAATCTAATTATACAATAATTAAATT----------CCC----------TTC----------T--TCCCAGTTTTTGCATATCAAAPAGTTGTGGAGAATTGCAGTAGCTTGCCTACC
dm3	chr3R:15225547-15225776 -	TTATCAGTGGGGATATGGTAGATGTAGCTTAATGGCATTGATTTGTAGGATTGCCT---ATCCCTTTACCTGTAAGTAACATGTTTATAATAGCAAAATTCGCAAATGTCGTGCTCCTTTGTTTGATAATAACATGCGTATAATACTTACAA----TACTTACGTT----------GT--T----------T--TCTACAGTTTTTGCATATCGAAPAGTTGTGGAGAATTGCAGTAGCTTGCCTACC
droSim2	3r:6033600-6033775 +	TTATCAGTGGGGATATGGTAGATGTAGCTTAATGGCATTGATTTGTAGGATTTT---ATACCCCTTATTGT----------------------ATTAACAATGCGTATAATACTTACAA----TACTTACGTT----------GT--T----------T--TCCACAGTTTTTGCATATCGAAPAGTTGTGGAGAATTGCAGTAGCTTGCCTACC
droSec2	scaffold_25:542775-542950 +	TTATCAGTGGGGAATATGGTAGATGTAGCTTAATGGCATTGATTTGTAGGATTATTT---ATACCCTCTACTTGT----------------------ATTAACAATGCGTATAATACTTACAA----TACTTACGTT----------GC--T----------T--TCCACAGTTTTTGCATATCGAAPAGTTGTGGAGAATTGCAGTAGCTTGCCTACC
droYak3	3R:3955888-3955950 -	TTATCAGTGGGGATATGGTAGATGTAACCTCAATGGCATTGATTGATTTGTAGGATTATAT---
droEre2	scaffold_4770:6407099-6407158 +	TTATCCGTGGGGATATGGTAGATGTAACCTCAATGGCATTGATTGATTTGTAGGATTGTT--

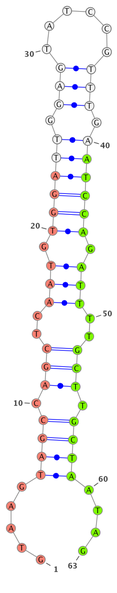
Generated: 09/08/2015 at 10:36 PM

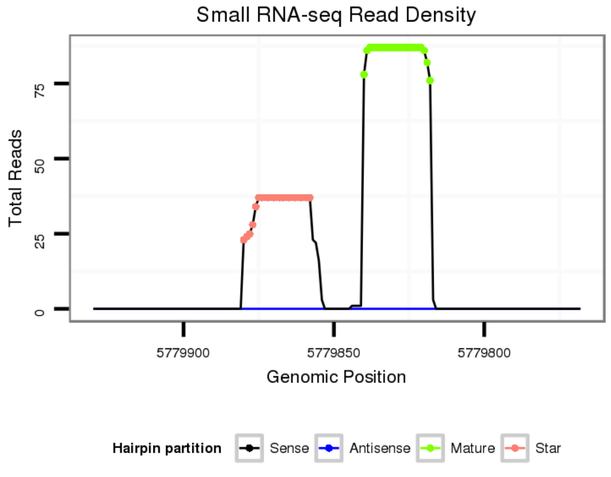
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

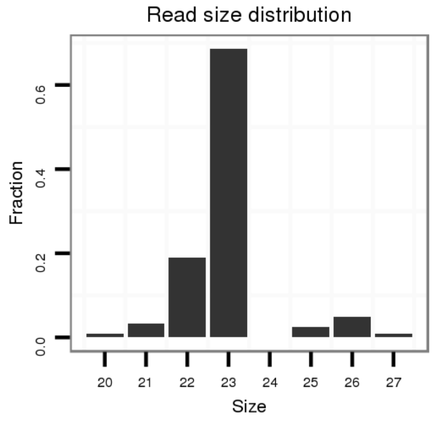
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2366	**scaffold_6680:5779818-5779880 -**	**confident**	**Mirtron**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

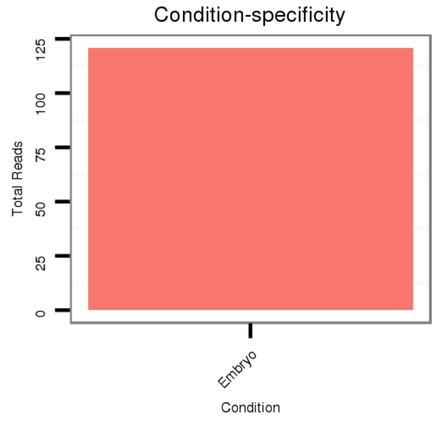
Legend: mature star mismatch in alignment mismatch in read

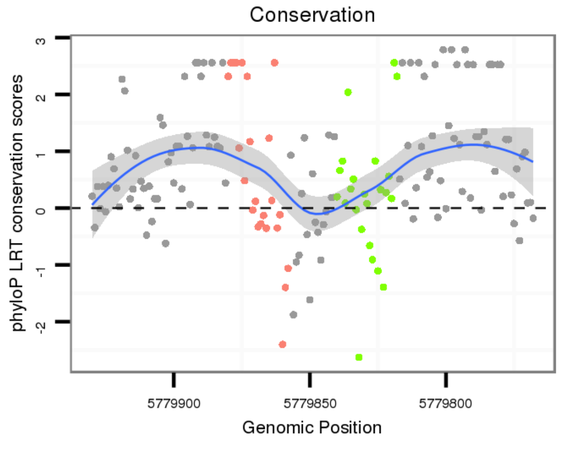
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dmoj\GI12992-in]; intron [Dmoj\GI12348-in]; CDS [Dmoj\GI12348-cds]; CDS [Dmoj\GI12348-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CATCACAACTGACGTCCAAAGACTGCACCAGCAACGCAATGTACAAGCTGGTAAGTAGCCAGCTCAATGTGGATTGGAGTATCCGTTTGAATCCAGATTTTGCTTGCTAATAGCTCCTCCTCGCCGCACTATTGGCCTGCGCCGCCGCCGCTCCCCGTCCAGG	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V041 embryo	V110 male body	V049 head
**********.....((((.(((..(((.(((((((.(((.....))).)))))).))).))..))).))))....**********									
.....ATCCAGATTTTGCTTGCTAATAG.....	23	0	1	66.00	66	49	17	0	0
.....TCCAGATTTTGCTTGCTAATAGT.....	23	1	1	16.00	16	7	9	0	0
.....GTAAGTAGCCAGCTCAATGTGGA.....	23	0	1	14.00	14	11	3	0	0
.....ATCCAGATTTTGCTTGCTAATA.....	22	0	1	6.00	6	5	1	0	0
.....TCCAGATTTTGCTTGCTAATAG.....	22	0	1	6.00	6	5	1	0	0
.....GTAGCCAGCTCAATGTGGATTG.....	22	0	1	6.00	6	2	4	0	0
.....GTAAGTAGCCAGCTCAATGTGGATTG.....	26	0	1	6.00	6	0	6	0	0
.....ATCCAGATTTTGCTTGCTAAT.....	21	0	1	4.00	4	3	1	0	0
.....CCAGATTTTGCTTGCTAATAGT.....	22	1	1	4.00	4	4	0	0	0
.....TCCAGATTTTGCTTGCTAATAGA.....	23	1	1	3.00	3	3	0	0	0
.....GTAAGTAGCCAGCTCAATGTGGATT.....	25	0	1	3.00	3	3	0	0	0
.....TAGCCAGCTCAATGTGGATTGG.....	22	0	1	3.00	3	1	2	0	0
.....AGTAGCCAGCTCAATGTGGATT.....	22	0	1	2.00	2	2	0	0	0
.....TCCAGATTTTGCTTGCTAATAGC.....	23	0	1	2.00	2	2	0	0	0
.....ATCCAGATTTTGCTTGCTAATAC.....	23	1	1	1.00	1	1	0	0	0
.....ATCCAGATTTTGCTTGCTAA.....	20	0	1	1.00	1	1	0	0	0
.....ATCCAGATTTTGCTTGCTAATAGT.....	24	1	1	1.00	1	0	1	0	0
.....TTGAATCCAGATTTTGCTTGCTAATAG.....	27	0	1	1.00	1	1	0	0	0
.....AGTAGCCAGCTCAATGTGGATTG.....	23	0	1	1.00	1	1	0	0	0
.....AAGTAGCCAGCTCAATGTGGATT.....	23	0	1	1.00	1	1	0	0	0
.....CAGATTTTGCTTGCTAATAGA.....	21	1	1	1.00	1	1	0	0	0
.....CCAGATTTTGCTTGCTAATAGC.....	22	0	1	1.00	1	1	0	0	0
.....TAAGTAGCCAGCTCAATGTGGAT.....	23	0	1	1.00	1	1	0	0	0
.....GTAAGTAGCCAGCTCAATGTGGATC.....	25	1	1	1.00	1	1	0	0	0

Anti-sense strand reads

GTAGTGTTGACTGCAGGTTTCTGACGTGGTCGTTGCGTTACATGTTCGACCATTCATCGGTCGAGTTACACCTAACCTCATAGGCAAACTTAGGTCTAAAACGAACGATTATCGAGGAGGAGCGGCGTGATAACCGGACGCGGCGGCGGCGAGGGGCAGGTCC	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_6680:5779768-5779930 -	dmo_2366	CAT---------CACAACTGACGTCCAAAGACTG-CACCAGCAACGCAATGTACAAGCTGGTAAGTAGCCAG--------CT-CAATGTGGATTG---------GA----------------G------TATC----CGTTT--GAATCCA---------GAT-----TT-TGCTTG----------CTAATAGCTCCTCCTCGCCGCACTATTGGCCTGCGCC---GCCGCCGCTCCCCGTCCAGG
droVir3	scaffold_13049:7527839-7528006 -		CAT---------TAAGACCTACATCG-AAAAGCTAACACCAGCAACACCATGTATAGGCTTGTAAGTAGCCCG--------AT-GAATGTCTCTGA---------AA----------A-----T--AGTCTTTG----GCATT--TACT---------CCTGAT-----GTATTTATT----------CCAACAGTTCCTGCTCGGTGCACTTTGGCTTGCGTT---GCCGCCGCTCCACGGCCAGG
droGri2	scaffold_15110:5351780-5351938 +		TAT---------TAAAACTTACAGATAA-----T---AGCTAGCATCATGTACAAAATTGTAATTTGCCTT--------GC-TATTTCATTT--T---------AAT----------AATCCT-------GATT----TATAT--TGAT---------T-GATA-----CATATTTTA----------TTGACAGTTTCTGCTCGGTGCACTCTTGGCTTGTGCC---GCCGCCGCTCCCAGGACAGA
droWil2	scf2_1100000004822:2849747-2849786 -		G--CGGTGTTTTGGCCTGCGCC---ATCGCTGGCAATGCCAATGA
dp5	XR_group6:2360667-2360830 +		G--CGGCACAGCTGCTCCTTGCCGCACTTTGGGATGCGCC---CTGGCCGGCCCCATCAA-CG
droPer2	scaffold_9:654189-654352 +		G--CGGCACAGCTGCTCCTTGCCGCACTTTGGGATGCGCC---CTGGCCGGCCCCATCAA-CG
droAna3	scaffold_13337:1606579-1606741 -		C---CGCACAGCTCCTCATCGCCGCTCCTGGGATGCGCC---CTGGCCGGCCCCTCAA---
droBip1	scf7180000396544:485649-485811 +		C---CGCACAGCTCCTCGTCGCCGCACTCCTGGGATGCGCC---CTGGCCGGCCCCTCAA---
droKik1	scf7180000302391:169794-169946 +		C---CGCCACGCTTTTGGGATGTGCC---CTGGCCGGCCCCTT------
droFic1	scf7180000453839:1053283-1053472 -		CAT---TAGCCCCTCACGTCAACAAACCAGCACCAGCAGCAGCAGCAACATGTTCAAGCTCGTAAGTGGATAACCG---AGCA-GAGTCCTTCTGC---------CT---------------------------GAATCGATTCTCCGAATTCCTAATTGACATCCTT-GGACC-----ATTTCCG--------------AAACAGCTCCTTGTCGTCGGCCTCTTTCGGATGTGCCGCCTTGGCCGGCCCCCTGAA---
droEle1	scf7180000491255:366041-366177 +		G--CGAACAGCTCCTCGTCGTCGGCCTCTTTCGGATGTGCC---CTGGCCGGCCCCCTC-----
droRho1	scf7180000780081:10188-10350 -		C---CGAACAGCTCCTCGTCGTCGGCCTCTTTCGGATGTGCC---CTGGCTGGCCCCTT------
droBia1	scf7180000302193:5979888-5980058 -		C---CGAACAGCTCCTCGTCGTCGGCCTCTTTCGGATGTGCC---CTGGCCGGCCCCCTGAA---
droTak1	scf7180000415773:628618-628782 +		CAGCATTAGTTTCTCAGTCAACAAACCG------T-----GCAGCAACATGTACAAGCTCGTAAGTGGACAA--------CA-GAGTTCGTATCC---------GT---------------------------GGATGGAG----CGAAT--TAATTGACATCCTT-GGACC-----TA----TC----------CCAACAGCTCCTCGTCGCCGGCTCTCTTTCGGATGTGCC---CTGGCCGGCCCCCTGAA---
droEug1	scf7180000409466:5233276-5233435 -		C---CGAACAGCTCCTCGTCGTCGGCCTCTTTCGGATGTGCC---CTGGCCGGCACCCTT------
dm3	chr3L:7079544-7079707 -		CAGCATTAGCCACTCGGTCAACAAACCAG-----T---AGCAGCAACATGTACAAGCTCGTAAGTGGACGG--------CA-GATTCCTTTTGC---------AT---------------------------GGATCCAG----TGATT--TAAT---------T-GGAC-----AATTCTATA----------CCAATAGCTTCTCGTCGTCGGCCTCTTTCGGATGCGCC---CTGGCCGGCCAGTGAA---
droSim2	3L:6945741-6945904 -		CAGCATTAGCCACTCGGTCAACAAACCAG-----T---AGCAGCAACATGTACAAGCTCGTAAGTGGATGG--------CA-GATTCCTTTTGC---------AT---------------------------GGATCCAG----TGATT--TAAT---------T-GGAC-----AATTCTATA----------CCAATAGCTCTCGTCGTCGGCCTCTTTCGGATGCGCC---CTGGCCGGCCAGTGAA---
droSec2	scaffold_2:7005924-7006087 -		CAGCATTAGCCACTCGGTCAACAAACCAG-----T---AGCAGCAACATGTACAAGCTCGTAAGTGGATGG--------CA-GATTCCTTTTGC---------AT---------------------------GGATCCAG----TGATT--TAAT---------T-GGAC-----AATTCTATA----------CCAATAGCTCTCGTCGTCGGCCTCTTTCGGATGCGCC---CTGGCCGGCCAGTGAA---
droYak3	3L:7668853-7669002 -		A---------T---------AACCAG-----T---AGCAGCAACATGTACAAGCTCGTAAGTGGATAAGTGGATAACA-GATTCCTTCTGC---------AT---------------------------GGATCTAC----TGATT--TAAC---------T-GGAC-----TATTCTATA----------CCATTAGCTCCTCGTCGTCGGCCTCTTTCGGATGCGCC---TTGGCCGGCCAGTGAA---
droEre2	scaffold_4784:4268819-4268986 +		A---TTAGCCCCGCGGTCAACAAACCAG-----T---AGCAGCAACATGTACAAGCTCGTAAGTGGATAA--------CA-GATTCCGTCTGC---------AT---------------------------GGATCCAG----TGATT--TAAT---------T-GGAC-----TATTCCATACCAATCCT---ATACCAGCTCCTCGTCGTCGGCCTCTTTCGGATGCGCC---CTGGCCGGCCAGTGAA---

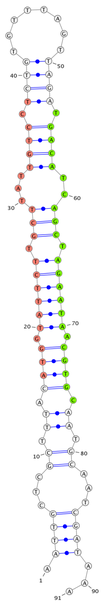
Generated: 09/08/2015 at 10:36 PM

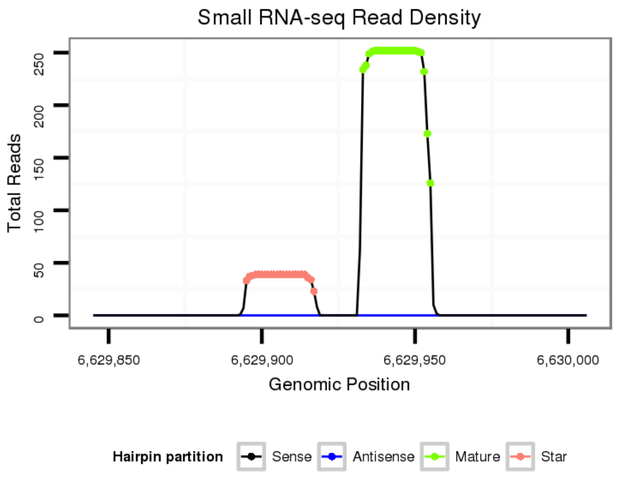
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

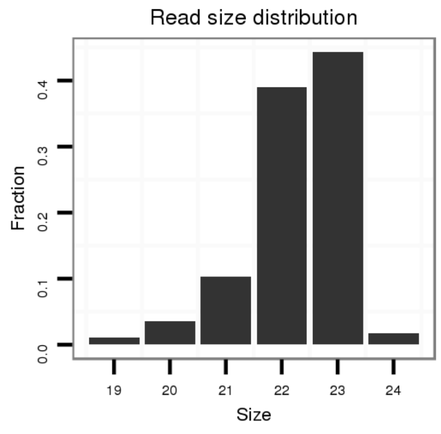
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_74	**scaffold_6540:6629895-6629956 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

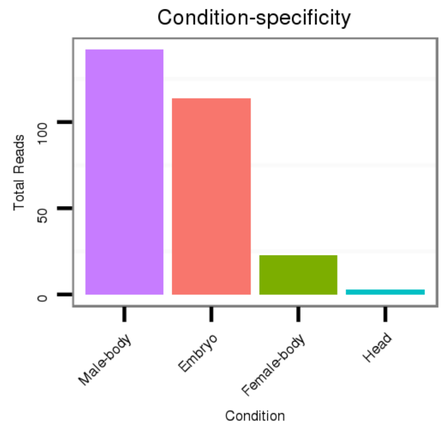
Legend: mature star mismatch in alignment mismatch in read

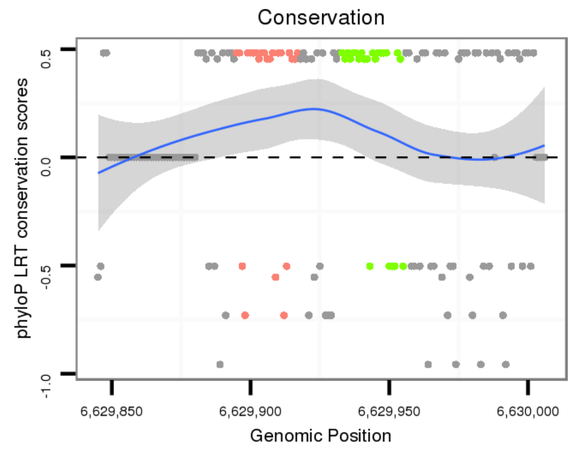
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TCATAGATTGTAATTATATATACCTATATACCATAAATTGCTCGCTTTACATGGTATTCTTGCTTATTGTCCTCTGTGTTTAGTTAGATGACATCAGCTAGAATAACGTGCAATGCAATCGATAAATATCGTTAACTACATCACAGTGAATTCGATTTTTTA **********.((((...((.((.(((((.(((((((.(((...((((.((((........))))).))))..))).))))))).))))).)).))...))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M060 embryo	M046 female body	V041 embryo	V049 head	V056 head
.....TGACATCAGCTAGAATAACGTGC.....	23	0	1	109.00	109	31	62	7	8	1	0
.....TGACATCAGCTAGAATAACGTGT.....	23	1	1	87.00	87	86	0	0	1	0	0
.....ATGACATCAGCTAGAATAACGT.....	22	0	1	48.00	48	43	4	1	0	0	0
.....TGACATCAGCTAGAATAACGTG.....	22	0	1	46.00	46	35	0	4	6	0	1
.....ATGGTATTCTTGCTTATTGTCCT.....	23	0	1	13.00	13	4	8	0	1	0	0
.....ATGACATCAGCTAGAATAACG.....	21	0	1	12.00	12	9	0	2	1	0	0
.....TGACATCAGCTAGAATAACGT.....	21	0	1	11.00	11	9	1	0	1	0	0
.....ATGACATCAGCTAGAATAACGTC.....	23	1	1	11.00	11	11	0	0	0	0	0
.....ACATCAGCTAGAATAACGTGCA.....	22	0	1	8.00	8	3	3	2	0	0	0
.....CATGGTATTCTTGCTTATTGTCC.....	23	0	1	6.00	6	4	2	0	0	0	0
.....TGACATCAGCTAGAATAACG.....	20	0	1	6.00	6	2	2	2	0	0	0
.....ATGGTATTCTTGCTTATTGTCCTC.....	24	0	1	5.00	5	0	4	1	0	0	0
.....ATGACATCAGCTAGAATAACGTT.....	23	1	1	4.00	4	3	1	0	0	0	0
.....ATGGTATTCTTGCTTATTGTCC.....	22	0	1	4.00	4	2	1	0	1	0	0
.....GACATCAGCTAGAATAACGTGC.....	22	0	1	3.00	3	0	2	0	1	0	0
.....ATGGTATTCTTGCTTATTGTCCC.....	23	1	1	3.00	3	0	3	0	0	0	0
.....TGGTATTCTTGCTTATTGTCCTC.....	23	0	1	3.00	3	0	1	2	0	0	0
.....ATGACATCAGCTAGAATAACGTCT.....	24	2	1	3.00	3	3	0	0	0	0	0
.....ACATCAGCTAGAATAACGTGC.....	21	0	1	3.00	3	0	3	0	0	0	0
.....ATGGTATTCTTGCTTATTGT.....	20	0	1	3.00	3	1	1	1	0	0	0
.....TGACATCAGCTAGAATAACGTC.....	22	1	1	2.00	2	1	0	1	0	0	0
.....CATCAGCTAGAATAACGTGCAA.....	22	0	1	2.00	2	1	0	1	0	0	0
.....ACATCAGCTAGAATAACGTGT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TGACATCAGCTAGAATAACTCT.....	22	3	1	1.00	1	0	0	0	1	0	0
.....ATGACATCAGCTAGAATAAC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....ATGGTATTCTTGCTTATTGTC.....	21	0	1	1.00	1	0	0	0	0	1	0
.....TGACATCAGCTAGAATAACGTT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....ATGACATCAGCTAGAATAA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....ACATGGTATTCTTGCTTATTGTC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....GGTATTCTTGCTTATTGTCCT.....	21	0	1	1.00	1	0	1	0	0	0	0
.....ACATCAGCTAGAATAACGTGCC.....	22	1	1	1.00	1	0	1	0	0	0	0
.....ACATCAGCTAGAATAACGTGCAT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....ATCAGCTAGAATAACGTGC.....	19	0	1	1.00	1	0	1	0	0	0	0
.....ATGGTATTCTTGCTTATTGTCCTCC.....	25	1	1	1.00	1	0	1	0	0	0	0
.....TGGTATTCTTGCTTATTGTCCT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TGACATCAGCTAGAATAACGTGA.....	23	1	1	1.00	1	1	0	0	0	0	0
.....CATGGTATTCTTGCTTATTGTCCC.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TGACATCAGCTAGAATAACGTGTC.....	24	2	1	1.00	1	1	0	0	0	0	0
.....GACATCAGCTAGAATAACGTGT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....GTATTCTTGCTTATTGTCCC.....	20	1	1	1.00	1	0	1	0	0	0	0
.....GACATCAGCTAGAATAACGTG.....	21	0	1	1.00	1	0	0	1	0	0	0
.....ACATCAGCTAGAATAACGTGCT.....	22	1	1	1.00	1	0	1	0	0	0	0
.....GTATTCTTGCTTATTGTCC.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TGACATCAGCTAGAATAACTGC.....	22	3	4	0.25	1	0	1	0	0	0	0

Anti-sense strand reads

AGTATCTAACATTAATATATATGGATATATGGTATTTAACGAGCGAAATGTACCATAAGAACGAATAACAGGAGACACAAATCAATCTACTGTAGTCGATCTTATTGCACGTTACGTTAGCTATTTATAGCAATTGATGTAGTGTCACTTAAGCTAAAAAAT **********.((((...((.((.(((((.(((((((.(((...((((.((((........))))).))))..))).))))))).))))).)).))...))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head
.....ATGACATCAGCTAGAATAACGTGC.....	23	0	1	109.00	109	0
.....ATGACATCAGCTAGAATAACGTGT.....	23	1	1	87.00	87	0
.....TGACATCAGCTAGAATAACGT.....	22	0	1	48.00	48	0
.....ATGACATCAGCTAGAATAACGTG.....	22	0	1	46.00	46	1
.....TCATAGATTGTAATTATATATACCTATATACCATAAATTGCTCGCTTTACATGGTATTCTTGCTTATTGTCCTCTGTGTTTAGTTAGATGACATCAGCTAGAATAACGTGCAATGCAATCGATAAATATCGTTAACTACATCACAGTGAATTCGATTTTTTA.....	23	0	1	13.00	13	0
.....ATGACATCAGCTAGAATAACG.....	21	0	1	12.00	12	0
.....TGACATCAGCTAGAATAACGT.....	21	0	1	11.00	11	0
.....ATGACATCAGCTAGAATAACGTC.....	23	1	1	11.00	11	0
.....ACATCAGCTAGAATAACGTGCA.....	22	0	1	8.00	8	0
.....CATGGTATTCTTGCTTATTGTCC.....	23	0	1	6.00	6	0
.....TGACATCAGCTAGAATAACG.....	20	0	1	6.00	6	0
.....ATGGTATTCTTGCTTATTGTCCTC.....	24	0	1	5.00	5	0
.....ATGACATCAGCTAGAATAACGTT.....	23	1	1	4.00	4	0
.....ATGGTATTCTTGCTTATTGTCC.....	22	0	1	4.00	4	0
.....GACATCAGCTAGAATAACGTGC.....	22	0	1	3.00	3	0
.....ATGGTATTCTTGCTTATTGTCCC.....	23	1	1	3.00	3	0
.....TGGTATTCTTGCTTATTGTCCTC.....	23	0	1	3.00	3	0
.....ATGACATCAGCTAGAATAACGTCT.....	24	2	1	3.00	3	0
.....ACATCAGCTAGAATAACGTGC.....	21	0	1	3.00	3	0
.....ATGGTATTCTTGCTTATTGT.....	20	0	1	3.00	3	0
.....TGACATCAGCTAGAATAACGTC.....	22	1	1	2.00	2	0
.....CATCAGCTAGAATAACGTGCAA.....	22	0	1	2.00	2	0
.....ACATCAGCTAGAATAACGTGT.....	21	1	1	1.00	1	0
.....TGACATCAGCTAGAATAACTCT.....	22	3	1	1.00	1	0
.....ATGACATCAGCTAGAATAAC.....	20	0	1	1.00	1	0
.....ATGGTATTCTTGCTTATTGTC.....	21	0	1	1.00	1	0
.....TGACATCAGCTAGAATAACGTT.....	22	1	1	1.00	1	0
.....ATGACATCAGCTAGAATAA.....	19	0	1	1.00	1	0
.....ACATGGTATTCTTGCTTATTGTC.....	23	0	1	1.00	1	0
.....GGTATTCTTGCTTATTGTCCT.....	21	0	1	1.00	1	0
.....ACATCAGCTAGAATAACGTGCC.....	22	1	1	1.00	1	0
.....ACATCAGCTAGAATAACGTGCAT.....	23	1	1	1.00	1	0
.....ATCAGCTAGAATAACGTGC.....	19	0	1	1.00	1	0
.....ATGGTATTCTTGCTTATTGTCCTCC.....	25	1	1	1.00	1	0
.....TGGTATTCTTGCTTATTGTCCT.....	22	0	1	1.00	1	0
.....TGACATCAGCTAGAATAACGTGA.....	23	1	1	1.00	1	0
.....CATGGTATTCTTGCTTATTGTCCC.....	24	1	1	1.00	1	0
.....TGACATCAGCTAGAATAACGTGTC.....	24	2	1	1.00	1	0
.....GACATCAGCTAGAATAACGTGT.....	22	1	1	1.00	1	0
.....GTATTCTTGCTTATTGTCCC.....	20	1	1	1.00	1	0
.....GACATCAGCTAGAATAACGTG.....	21	0	1	1.00	1	0
.....ACATCAGCTAGAATAACGTGCT.....	22	1	1	1.00	1	0
.....GTATTCTTGCTTATTGTCC.....	19	0	1	1.00	1	0
.....TGACATCAGCTAGAATAACTGC.....	22	3	4	0.25	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:6629845-6630006 +	dmo_74	TCATAGATTGTAATTATATATACCTATATACCATAAATTGCTCGCTTTACATGGTATTCTTGCTTATTGTCCTCTGTGTTT--AGTTAGATGACATCAGCTAGAATAACGTGCAATGCAATCGATAA-ATATCGTTAACTACATCACAGTGAATTCGATTTTTTA
droVir3	scaffold_12855:6282497-6282624 +	dvi_24637	ATAT----------ATTGTTTGGTGTACATATTATTCTTGCTAATGATCCTCTGGGATCGCATGGAGATGACATCAGCCAGAATAGTATGTAACACGATGAGTATTAGGCGGTTATATAGGTTA-AGGCAGTTCAATCT----

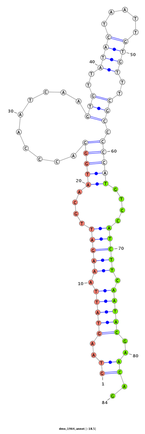
Generated: 09/08/2015 at 08:05 PM

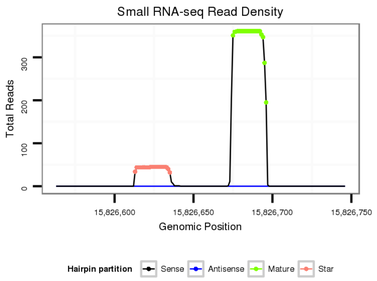
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

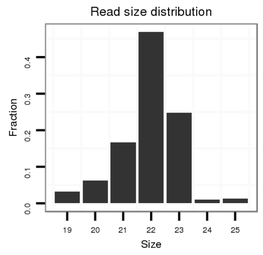
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1964	scaffold_6540:15826613-15826696 +	confident	Mirtron	intron	[View on UCSC Genome Browser (Comell Mirror)]

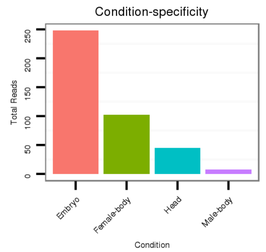
Legend: mature star mismatch in alignment mismatch in read

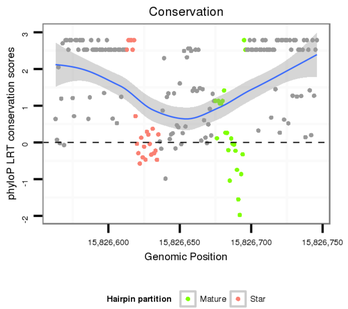
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI24695-in]; CDS [DmojGI24695-cds]; CDS [DmojGI24695-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GCAACACAACAACAATGTATCCCGCACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=TTAAAGATTGCAATGGGACCCAATCAAGTGTTATACTAATTGTGTTTCGCCCCCATGTCCATCTTCAATACGAACAGGGACCACCCACCTCAGGGCCCAATCAAATTTACCATTGCCGATACATTGGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V041 embryo	M046 female body	V056 head	V049 head	V110 male body
((..(((((.(((((.....(((((..........(((..(((((.....)))))..)))).))))))....)))))..))))..												
.....TGTCCATCTTCAATACGAACAGT.....	23	1	1	1632.00	1632	1285	115	60	88	45	39
.....TGTCCATCTTCAATACGAACAGT.....	23	1	1	256.00	256	255	0	0	1	0	0
.....TGTCCATCTTCAATACGAACAG.....	22	0	1	100.00	100	49	13	30	6	2	0
.....ATGTCCATCTTCAATACGAACAG.....	23	0	1	84.00	84	67	3	11	2	1	0
.....ATGTCCATCTTCAATACGAACAGT.....	24	1	1	78.00	78	73	2	2	1	0	0
.....ATGTCCATCTTCAATACGAACA.....	22	0	1	65.00	65	43	9	8	2	3	0
.....TGTCCATCTTCAATACGAACAGTT....	24	2	1	43.00	43	38	2	0	3	0	0
.....ATGTCCATCTTCAATACGAAC.....	21	0	1	33.00	33	15	2	11	3	1	1
.....TGTCCATCTTCAATACGAACAT.....	23	1	1	25.00	25	16	6	2	0	1	0
.....TGTCCATCTTCAATACGAACA.....	21	0	1	25.00	25	5	0	12	5	3	0
.....TGTCCATCTTCAATACGAAC.....	20	0	1	17.00	17	0	0	7	6	3	1
.....GTCCATCTTCAATACGAACAGT.....	22	1	1	14.00	14	10	0	4	0	0	0
...GTAAGTATTAAAGATTGCAATGG.....	23	0	1	13.00	13	3	7	2	0	0	1
.....ATGTCCATCTTCAATACGAACAGT.....	24	1	1	10.00	10	10	0	0	0	0	0
..TAAGTATTAAAGATTGCAATGG.....	22	0	1	9.00	9	2	5	1	0	0	1
...GTAAGTATTAAAGATTGCAATG.....	22	0	1	8.00	8	5	3	0	0	0	0
.....CATCTTCAATACGAACAGT.....	19	1	1	8.00	8	8	0	0	0	0	0
.....ATGTCCATCTTCAATACGA.....	19	0	1	7.00	7	0	0	5	2	0	0
.....CATGTCCATCTTCAATACGAAC.....	22	0	1	7.00	7	7	0	0	0	0	0
...GTAAGTATTAAAGATTGCAATGGGA.....	25	0	1	5.00	5	0	1	0	0	0	4
.....GTCCATCTTCAATACGAACAG.....	21	0	1	5.00	5	0	0	5	0	0	0
.....ATCTTCAATACGAACAGT.....	18	1	1	5.00	5	5	0	0	0	0	0
.....ATGTCCATCTTCAATACGAA.....	20	0	1	4.00	4	0	0	1	2	1	0
.....ATGTCCATCTTCAATACGAACAA.....	23	1	1	4.00	4	4	0	0	0	0	0
.....CCATCTTCAATACGAACAGT.....	20	1	1	4.00	4	3	0	1	0	0	0
...GTAAGTATTAAAGATTGCAAT.....	21	0	1	4.00	4	0	2	1	1	0	0
.....ATGTCCATCTTCAATACGAACAGT.....	24	1	1	3.00	3	3	0	0	0	0	0
.....CATCTTCAATACGAACAGT.....	19	1	1	3.00	3	3	0	0	0	0	0
.....TGTCCATCTTCAATACGAACAGG.....	23	0	1	3.00	3	2	0	0	1	0	0
.....TGTCCATCTTCAATACGAACAGTG.....	24	2	1	3.00	3	1	0	2	0	0	0
...GTAAGTATTAAAGATTGCAATGGG.....	24	0	1	3.00	3	1	1	1	0	0	0
.....TGTCCATCTTCAATACGAA.....	19	0	1	2.00	2	0	0	0	0	2	0
.....TCCATCTTCAATACGAACAG.....	21	1	1	2.00	2	2	0	0	0	0	0
.....GTCCATCTTCAATACGAAC.....	19	0	1	2.00	2	0	0	2	0	0	0
.....GTCCATCTTCAATACGAACAGT.....	22	1	1	2.00	2	2	0	0	0	0	0
.....ATGTCCATCTTCAATACGAACAGTT...	25	2	1	2.00	2	1	1	0	0	0	0
.....TGTCCATCTTCAATACGAACAGTTT...	25	3	1	1.00	1	0	0	1	0	0	0
.....CATGTCCATCTTCAATACGAACAG.....	25	1	1	1.00	1	1	0	0	0	0	0
.....ATGTCCATCTTCAATACGAACT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....CCATGTCCATCTTCAATACGAAC.....	23	0	1	1.00	1	0	0	1	0	0	0
.....ATGTCCATCTTCAATACGAAA.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TGTCCATCTTCAATACGAACATT....	23	2	1	1.00	1	0	0	0	0	1	0
.....GTCCATCTTCAATACGAACAGA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....CATGTCCATCTTCAATACGAACAG.....	25	1	1	1.00	1	1	0	0	0	0	0
.....TCCATCTTCAATACGAACAG.....	20	0	1	1.00	1	0	0	1	0	0	0
.....TGTCCATCTTCAATACGAACAT.....	23	2	1	1.00	1	1	0	0	0	0	0
.....AAGATTGCAATGGGACCCA.....	19	0	1	1.00	1	1	0	0	0	0	0
...GTAAGTATTAAAGATTGCAA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....CATGTCCATCTTCAATACGAACA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....CATGTCCATCTTCAATACGA.....	20	0	1	1.00	1	0	0	1	0	0	0
.....TGTCCATCTTCAATACGAACATT....	23	2	1	1.00	1	0	1	0	0	0	0
.....CATGTCCATCTTCAATACGAACAG.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TCCATCTTCAATACGAACAA.....	20	1	1	1.00	1	1	0	0	0	0	0
.....CCATCTTCAATACGAACAG.....	19	0	1	1.00	1	0	0	1	0	0	0
..TAAGTATTAAAGATTGCAATGGG.....	23	0	1	1.00	1	0	1	0	0	0	0
.....GTCCATCTTCAATACGAACA.....	20	0	1	1.00	1	0	0	1	0	0	0
.....CATCTTCAATACGAACAGTA.....	20	2	1	1.00	1	1	0	0	0	0	0
.....ATGTCCATCTTCAATACGT.....	19	1	1	1.00	1	0	0	0	0	1	0
.....TCCATCTTCAATACGAACAG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....ATCTTCAATACGAACAG.....	18	1	2	1.00	2	2	0	0	0	0	0

Anti-sense strand reads

CGTTGTGTTGTTGTTACATAGGGCGTGGCCACGCAGTGGGGCGGCCGCCATTCATAATTTCTAACGTTACCCTGGGTTAGTTCACAATATGATTAACACAAAGCGGGGGTACAGGTAGAAGTTATGCTTGTCCCTGGTGGTGGAGTCCCGGGTTAGTTTAAATGGTAACGGCTATGTAACCT	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V056 head	V049 head
((..(((((.(((((.....(((((..........(((..(((((.....)))))..)))).))))))....)))))..))))..								

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:15826563-15826746_+	dmo_1964	GCA----------ACACAACAACAATGTATCCCGCACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=-TTAAAGATTGCAATGGGAC-----CCA----------ATC-A-AGTGT----------TAT---ACTAATT--GTGTTTCG----------C---C----------CCC----------ATGTCCATCTT------CAATACG--AACAGGGACCACCACCTCAGGGCCCAATCAAATTTACCATTGCCGATACATTGGA
droVir3	scaffold_13047:5452795-5452977_+	dvi_24636	GCA----------ACACAACAACAATGTATCCCGCACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=-TAC-AGATTGCAGTGGGAC-----CCA----------ATC-A-AGTGT----------TGT---GTAATT--GTGTTTCG----------C---C----------CCC----------ATGTCCATCTT------CAATACG--TACAGGGACCACCACCTCAGGGTCAATCAAATTTACCATTGCCGATACATGGA
droGri2	scaffold_14906:10827906-10828099_+		GCAAG----ATCAACAC-ACAACAACAATGTATCCCGCACCGGTGCGTCACCCCGCCGCCGGGGTAAGTATT-AAGAGATTGCAATGGGAC-----CCA----------ATC-A-AGTGT----------TGT---GTAATT--GTGTTTCG----------C---C----------CC----------ATGTCCATCT-------T-TCGTT-T--CAAGGGACCACCACCTCAGGGCCCAATCAAATTTACCATTGCCGATACATTGGA
droWil2	scaf2_1100000004943:15498544-15498762_+		GCA----------ACAA-AAACAAATGTATCCCGCACCGGTGCGTCACCCGCCGCCGGGGTAAGTA=ACTGC--------TC-TAGAA-T-A-GTC----------T---TACACCTA-GTGTTTA-TGTGACCCA-ATTCAT----------T---T-----TT--CGTTTATCCTAATTGACGACCCGG---TCTCTCTTTC----------T-----T----------TC----------TG----T---T--------T-TATTC-G-AT-AATTT-GAAGGGACCACCACCTCAGGGCCCAATCAAATTTACCATTGCGAACATTGGA
dp5	2:19171210-19171489_-		ATA----------TAA-AAACAACATGTATCCCGACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=-CGACGAAT----------CCA-CATCCATACAGCCCCGCAGAGCCGAGACCCG-C-G-G-TGTGTCCACACTCTCTCGGG---CCTCTCCTCCCCTCCCCCCCACCC----AATCC----CTAATT--GTGTTTCG----------T---C-CTTTTTCTCACTCC-C----------TCTCGCTCGCCGACTGTTTA----------PCCCCCCCGCACTTGGCACAG----------TC----------T---T--------T-----T-GTAAGGGACCACCACCTCAGGGCCCAATCAAATTTACCATTGCCGATACATTGGA
droPer2	scaffold_3:1916524-1916802_-		ATA----------TAA-AAACAACATGTATCCCGACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=-CGTCGAAT----------CCA-CATCCACAGCAGCCCCGCAGAGCCGAGACCCG-C-G-G-TGTGTCCACACTCTCTCGGC---CCTGCGCTCCCCTCCCCCCCACCC----AATCC----CTAATT--GTGTTTCG----------T---C-CTTTTTCTCACTCC-C----------TCTCGCTCGCCGACTGTTTA----------PC-CCCCCGCACTTGGCACAG----------TC----------T---T--------T-----T-GTAAGGGACCACCACCTCAGGGCCCAATCAAATTTACCATTGCCGATACATTGGA
droAna3	scaffold_13340:11273901-11274077_-		GTA-TA----------ATA-AAACAACATGTATCCCGCACCGGTGCGTCACCCCGCCGCGGGGTAAGTA=-GGT----------CCA----------T---T-CATGGTCACTCGCTGTCGGC---TTCTCT----------T---T-CTA-T--GTGTCAC-A----------C---C----------CTCTATCCC----------T---A----------TC----------T---T--------T-----C-GTCTA--TGTAAGGACCACCACCTCAGGGCCCAATGAAGTTACGATGCCGATACGTTAGA
droBip1	scf7180000396691:183495-183691_-		GTA-TATAACGTTAGAATA-AAACAACATGTATCCCGTCACCGGTGCGTCACCCCGCCGCGGGGTAAGTA=-GACCTAGCTGCAATGG-TC----CCA----------T---T-CTAA-T--GTGTCAC-A----------T---CTTTTTCC----------T---T----------CCC----------ATGTATCCATCT------TGTCAC--TGCAAGGACCACCACCTCAGGGCCCAATGAAGTTACGATGCCGATACGTTAGA
droKik1	scf7180000302261:84617-84828_-		GTA----------TAA-AAACAACATGTATCCCGACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=-CACCGA----CGTA----------T---TACC----------T---T-GCCCCGCTAAT-AATGTGTCAC-A----------T---CTCTCTCTAT--A----------T---CTCTCCCCCACCCCAC--GTGTC----------T---CACCTA-CCC---T---------A--CGGTGTCA-AATGGGACCACCACCTCAGGGCCCAATCAAATTTACCATTGCCGAACATTGGA
droFic1	scf7180000454055:1778669-1778919_+		GTA-T-----------CTA-ACAACAACATGTATCCCTCACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=-TATTTGCTT--AAAAAATC----CAGC----------T---T-CACC----------T---T-CAAGTCCGT--T-CTAATT--GTGTTCTT----------T---TCTCTCCCTCTCTCCTCTCTCCCTCTCTC----------T---CCCG--TC---GCCTCATGTGTGCCGCCCACTTA--CT---------CGAC-TC--CACCCACCG----------T---T--------T-----ATTTGGTGTGCG-CGTAAGGACCACCACCTCAGGGCCAATCAAATTTACCATTGCCGAACATTGGA
droEle1	scf7180000491261:839865-840099_+		GTA-T-----------CTA-ACAACAACATGTATCCCTCACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=-CACCAGACC-G-CAGGG-TC----CATC----------T---T-CGCC----------T---T-CCAAATCTT--T-CTAATT--GTGTTTCT----------T---TCTCTATCTA----------T---CCCG--CCGCCTTGCCATT--GTGCGGCCCACAGT--A----------TTGAC-TC--CCGCCACCC----------T---T--------T-----ATCAAGGTTT-CGTAAGGACCACCACCTCAGGGCCAATCAAATTTACCATTGCCGACACATGGA
droRho1	scf7180000780074:219482-219716_+		GTA-T-----------CTA-ACAACAACATGTATCCCTCACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=-CTCCCGAT--CAATGGTC----CATT----------T---T-CGCC----------T---T-CCAGATCCGT----T-CTAATT--GTGTTCTT----------T---TCTCTCTCTC----------T---TCCG--CCACCGGCCATGTTTCCGGCCCACCCT--T----------TTGAC-TC--CACGCACCA----------T---T--------T-----ATCG-CGTTT-CGTAAGGACCACCACCTCAGGGCCAATCAAATTTACCATTGCCGACACATGGA
droBia1	scf7180000302113:2070749-2070960_+		GTA-T-----------CTA-ACAACAACATGTATCCCTCACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=-GACCGCC----------CCA-CC----------CCC----------T---T-CGGAATCCGT----T-CGAATT--GTGTTTCT----------T---TTTCTCCCTC----------T---TCC--CTC---GC---ACGCCATGTGATCCGCCCGC----------T---CACA----------T---T--------TC---T---------CATGT-CGCCT-GC-CACAGGGACCACCACCTCAGGGCCAATCAAATTTACCATTGCCGACACATGGA
droTak1	scf7180000415851:309964-310186_+		GTA-T-----------CTA-ACAACAACATGTATCCCTCACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=-GACCGAC---AAACCCAC----A-C----------T---T-CACC----------T---T-CGGAATCCGT----T-CGAATT--GTGTTTCT----------T---TCTCTCTCTC----------T---TCC--CTC---GC---ACGCCATGTGCTCCGCCCGC----------T---CCA--CCACCTCGGCCATTCTG----------T---ACCACC----------T---T--------TAATCC---TC-GGTATCCAC--CT-ATGCAGGACCACCACCTCAGGGCCAATCAAATTTACCATTGCCGACACATGGA
droEug1	scf7180000409682:743887-744127_+		GTA-T-----------CTA-ACAACAACATGTATCCCTCACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=-GACCGCC----CGAGGGGAC----A-C----------T---T-CACC----------T---T-TTAAATCCGT----T-CGAATT--GTGTTTCT----------T---TCTCTCTCTC----------T---TCC--CATT--AC---GCGCCATTGTACCACCCACTCA--T----------CATCTATTGAACCA-GCGCCCACTC----------T---T--------TC---T---------ACTTAC-TCGCCG-AAGGGACCACCACCTCAGGGCCAATCAAATTTACCATTGCCGACACATGGA
dm3	chr3R:21869053-21869286_+		GTACG----C---TAACAACATGTATCCCTCACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=-GACCGCA----CACTGGTC----CCA-CC----------T---T-CACC----------T---T-CCGAATCCGT----T-CGAATT--GTGTTTAT----------T---TCTCTTTCCA----------T---CACG--GC---GCGCCATTGTGCGCCCCACGTA--CGGAACACCAACCACC----------T---T--------TC---T---------TATTCAC-TCTA--AAGGACCACCACCTCAGGGCCAATCAAATTTACCATTGCCGATACATTGGA
droSim2	3L:21366841-21366974_+		GTACG----C---TAACAACATGTATCCCTCACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=-GACCGCA----CACGGGTC----CCA-CC----------T---T-CACC----------T---T-CCGAATCCGT----T-CGAATT--GTGTTTAT----------T---TCTCTCTCCC----------T---CACG--GC---GCGCCATTGTGCGCCCCACGCA--CGGTAACACCAACCACC----------T---T--------TC---T---------TATTCAC-TCTA--AAGGACCACCACCTCAGGGCCAATCAAATTTACCATTGCCGACACATGGA
droSec2	scaffold_13:663565-663797_+		GTACG----C---TAACAACATGTATCCCTCACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=-GACCGCA----CACGGGTC----CCA-CC----------T---T-CGAATCCGT----T-CGAATT--GTGTTTAT----------T---TCTCTCTCCC----------T---CACG--GC---GCGCCATTGTGCGCCCCACGCA--CGTAACACCAACCACC----------T---T--------TC---T---------TATTCAC-TCTA--AAGGACCACCACCTCAGGGCCAATCAAATTTACCATTGCCGACACATGGA
droYak3	3R:24605979-24606239_+		GTA-T-----------CTA-ACAACAACATGTATCCCTCACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=-GACCGCA----ACTGGGTC----CCA-CC----------T---T-CACC----------T---T-CCGAATCCGT----T-CGAATT--GTGTTTCT----------T---TCTCTCTCTCTCAACCCTCA----------C---CACAACACT---GC---CGGCCATTGTGCCGCCCACGCA--TGGAACACCAAAAACCTCACCTATTTAC----------T---T--------TC---T---------CATTCAC-TCTA--AAGGACCACCACCTCAGGGCCAATCAAATTTACCATTGCCGACACATGGA
droEre2	scaffold_4820:6176657-6176898_-		GTA-T-----------CTA-ACAACAACATGTATCCCTCACCGGTGCGTCACCCCGCCGCCGGGGTAAGTA=-GACCGCA----CACTGGTC----CCA-CC----------T---T-CACC----------T---T-CCGAATCCGT----T-CGAATT--GTGTTTAT----------T---TCTCTCTCTC----------T---C-CGACCC---GTGCCACATGTGCCGCCCACGCA--TGGAACACCAACCACC----------T---T--------TA---T---------TC-ACTATTCAGC-CGA-AAGGACCACCACCTCAGGGCCAATCAAATTTACCATTGCCGACACATGGA

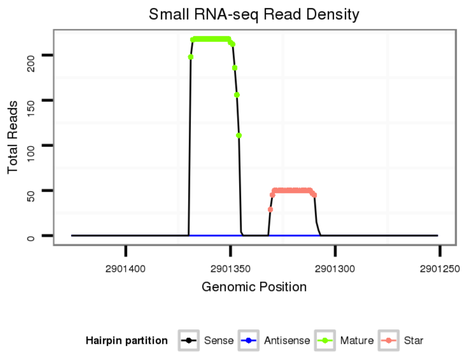
Generated: 09/08/2015 at 07:02 PM

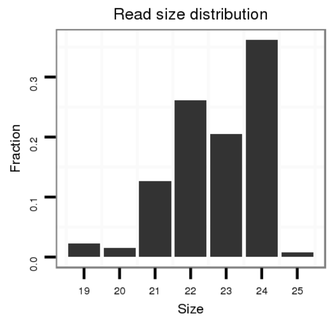
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.len	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

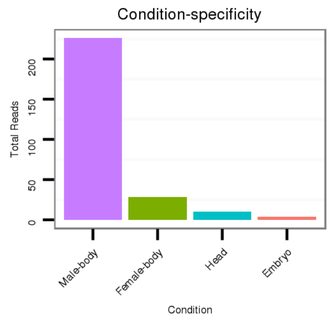
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_204	**scaffold_6328:2901301-2901376 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

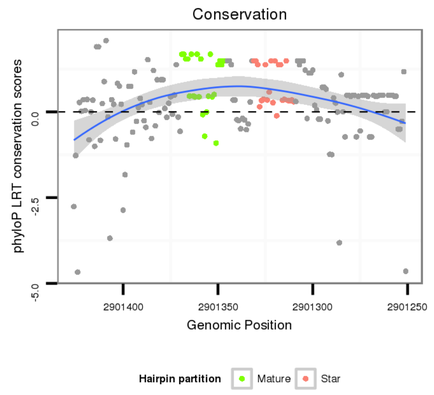
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GAATGGTCGACAATCGATAGATTTATCGATAGCAGTCCGTTCACAATTGCTGTTGATTTGGAATCACGAAACTCATCTGTTATGTAGCGAACGATAACAGTGAGTCTCGCATTCCAACTCAAAGGCAATAATTCAGTAGCAACGTTGTTAGTTTTGGCTCGATAAAAATCGATATT	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head	V049 head	M060 embryo	V041 embryo
**********...(((((((.((((.(((((((..(((.(((((.((((((((((.....)).)))))))))))).)))).)))))))).)))))...**********											
..........TTGGAATCACGAAACTCATCTGTT..	24	0	1	95.00	95	88	7	0	0	0	0
..........TTGGAATCACGAAACTCATCTGTTC..	25	1	1	49.00	49	45	3	0	1	0	0
..........TTGGAATCACGAAACTCATCTGT...	23	0	1	41.00	41	36	3	0	0	2	0
..........TTGGAATCACGAAACTCATCTG....	22	0	1	30.00	30	23	7	0	0	0	0
..........TTGGAATCACGAAACTCATCTGTC..	24	1	1	29.00	29	28	0	1	0	0	0
..........TTGGAATCACGAAACTCATCT.....	21	0	1	25.00	25	20	1	3	1	0	0
..........AACAGTGAGTCTCGCATTCCAA....	22	0	1	23.00	23	21	0	0	2	0	0
..........TGGAATCACGAAACTCATCTGTT...	23	0	1	12.00	12	6	3	2	0	0	1
..........ACAGTGAGTCTCGCATTCCAAC....	22	0	1	8.00	8	6	1	1	0	0	0
..........ACAGTGAGTCTCGCATTCCAA.....	21	0	1	7.00	7	6	0	0	1	0	0
..........CAGTGAGTCTCGCATTCCAACT....	22	0	1	5.00	5	5	0	0	0	0	0
..........TTGGAATCACGAAACTCATCTGTCT..	25	2	1	5.00	5	5	0	0	0	0	0
..........TTGGAATCACGAAACTCAT.......	19	0	1	4.00	4	3	1	0	0	0	0
..........TGGAATCACGAAACTCATCTGT....	22	0	1	4.00	4	2	1	0	0	1	0
..........AACAGTGAGTCTCGCATTCC......	20	0	1	3.00	3	2	1	0	0	0	0
..........TTGGAATCACGAAACTCATCTGTTTC..	26	2	1	3.00	3	3	0	0	0	0	0
..........AACAGTGAGTCTCGCATTCCAAA...	23	1	1	3.00	3	3	0	0	0	0	0
..........ACAGTGAGTCTCGCATTCCAAG....	22	1	1	2.00	2	2	0	0	0	0	0
..........AACAGTGAGTCTCGCATTCCAG....	22	1	1	2.00	2	2	0	0	0	0	0
..........TGGAATCACGAAACTCATCTGTTA...	24	0	1	2.00	2	2	0	0	0	0	0
..........ACAGTGAGTCTCGCATTCCAAT....	22	1	1	2.00	2	2	0	0	0	0	0
..........AACAGTGAGTCTCGCATTCCA.....	21	0	1	2.00	2	1	1	0	0	0	0
..........TTGGAATCACGAAACTCATCTGTTA...	25	0	1	2.00	2	2	0	0	0	0	0
..........TTGGAATCACGAAACTCATCTG.....	22	1	1	1.00	1	1	0	0	0	0	0
..........TTGGAATCACGAAACTCATCTGA....	23	1	1	1.00	1	1	0	0	0	0	0
..........TTGGAATCACGAAACTCATCTGTCTC..	26	3	1	1.00	1	1	0	0	0	0	0
..........TTGGAATCACGAAACTCATCTGTTTCC..	27	3	1	1.00	1	0	1	0	0	0	0
..........GGAATCACGAAACTCATCT.......	19	0	1	1.00	1	0	1	0	0	0	0
..........ACAGTGAGTCTCGCATTCCATT....	22	2	1	1.00	1	0	1	0	0	0	0
..........TGGAATCACGAAACTCATC.......	19	0	1	1.00	1	0	1	0	0	0	0
..........TTGGAATCACGAAACTCATCTGTTCG..	26	2	1	1.00	1	1	0	0	0	0	0
..........AACAGTGAGTCTCGCATTCCAAC....	23	0	1	1.00	1	1	0	0	0	0	0
..........ACAGTGAGTCTCGCATTCCAACT....	23	0	1	1.00	1	1	0	0	0	0	0
..........TGGAATCACGAAACTCATCTGTTT...	24	1	1	1.00	1	1	0	0	0	0	0
..........TTGGAATCACGAAACTCATCTGTTCG..	26	2	1	1.00	1	0	1	0	0	0	0
..........TTGGAATCACGAAACTCATC.......	20	0	1	1.00	1	1	0	0	0	0	0
..........TTGGAATCACGAAACTCATCTGTTAGTC..	28	3	1	1.00	1	1	0	0	0	0	0
..........TGGAATCACGAAACTCATCTGTTCAA..	26	3	1	1.00	1	0	1	0	0	0	0
..........TTGGAATCACGAAACTCATCTGTTT...	25	1	1	1.00	1	1	0	0	0	0	0
..........TTGGAATCACGAAACTCATCTGTTCCC..	27	3	1	1.00	1	0	1	0	0	0	0
..........ACAGTGAGTCTCGCATTCTTG.....	21	3	2	0.50	1	1	0	0	0	0	0
..........ACAGTGAGTCTCGCATTTTG.....	20	3	7	0.14	1	1	0	0	0	0	0

Anti-sense strand reads

CTTACCAGCTGTTAGCTATCTAAATAGCTATCGTCAGGCAAGTGTTAACGACAACTAAACCTTAGTGCTTTGAGTAGACAATACATCGCTTGCTATTGTCACTCAGAGCGTAAGGTTGAGTTTCCGTTATTAAGTCATCGTTGCAACAATCAAAACCGAGCTATTTTTAGCTATAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V049 head	V110 male body
**********...(((((((.((((.(((((((..(((.(((((.((((((((((.....)).)))))))))))).)))).)))))))).)))))...**********							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6328:2901251-2901426 -	dmo_204	GAAT---GGTCGACAATC-GATAGATTTA----TCGA----------TAGCAGTCCGTTCACAATTGCTGTTGATTTGGAATCACGAAACTCATCTGTTATGTAGC----------GAAC----------GATAACAGTGAGTCTCGCATTCCAACTCAAAGGCAAT----------AATTCAGTAGCAACGTTG-------TTAGTTTTGGCTCGATAAAAATCGATATT
droVir3	scaffold_13042:907038-907228 -	dvi_343	GTGGG-CTAT-------G-GATAAACGTATCGATAAGCATAGCGCCCAA----------TGGATTASTTGACAATTGCTGTTGATTTGGAATCACGACACTCGACTGTTATGTAGA----------AAAC----------GATAACAGTGAGTCTCGCGTTCCAACTCAAAGGCAAT----------AATTGTCGAGCAAGTTTGGCGGTCGAATTGGATTTGCGATA--AATCGGCTTT
droGri2	scaffold_15081:2044694-2044817 -	dgr_45	TCGGCT-AA---CAATA----------TGTGTTGGATTGGAATCACGACTCTCGCTGTTATGTAGAAATACATTGTTTAACAA----------T----------AATAACAACGAGTCTCGCGCTTCAAATCAAAAGCAAT----------TGGTTGTTCAGCAAT----------G
droWil2	scaf2_11000000004909:7956611-7956706 +		TTGTA----------TGTTGGATTGGAATCACGACATTCGACTGTTATGTTTACATA---TGTCTAACATTCTGTTATAG----------TATAACAGTGTGTCTTGCGTTCCTACTCAA----------T----------ATTGAT----------G
dp5	XR_group6:6281755-6281782 +		TAT-T-CTATCG---ATGCTATCTATCG----
droPer2	scaffold_0:2844925-2844964 -		CAATCC-AA---CAATC-TATTAATGTA----TCGATCGATC
droAna3	scaffold_13417:2467815-2468020 -	dan_68	ATT--G----------TA-GTGAGTTGGAATCACGACACTCAGCTGTTATGCAAC----------CCTCGCAGGCACCCTTGCAGACGGAACCCCTAAGTAACAGTGAGTCTCGCGTTCTAACTCAAATGCATTCAAGAGCTATTGTCGAAGTTCCGTCGAAGTCGAACGCAGAACGTCGAATGGCAGCGCCTGGCCTAAGGAGATCCCTCCAGCGAACT-------AACGAT----------T
droBip1	scf7180000395874:40214-40381 -		ATT--G----------TA-GTGAGTTGGAATCACGTTACTCAGCTGTTATGCAGC----------CCGCGCAAGCATCCTTGCAGACGGC-CCCCCAAATAACAGTGAGTAATGCGTTGTAGCTCAAATGCATGTTTAGATCGCTTGTCCAGGTCCCA--GATGTTAGACGTGTAATCTCAAGTGAAAGCA----------C
droKik1	scf7180000302639:2182354-2182447 -		AAATATCTAT-------C-TATCTAACTA----ACTTTCTATCTAACTATATTTATTGGTAGCTATCCATCAAAATTTACTATC-TTTGCATGTTTGCATCTTA----------T----------TT----------T
droFic1	scf7180000453316:30248-30278 +		TAT--C-GATC---ATC-TATCTATCTA----T--
droEle1	scf7180000490751:652105-652129 -		TAATTG--AAA---ATG-AATAAATTA----T--
droBia1	scf7180000302126:36937-36989 -		CTTTTT-AT---ATATC-TATCTATCTA----TGAATCTTTT----------TAT----------AA----T----------TT----------TAATT----------ATCAAT----------C
droTak1	scf7180000415254:262240-262264 +		CTATCT-AT---C----TATCTATC-----
droEug1	scf7180000408745:8996-9057 +		TAT--GTGTCG---ATA-TGTCTGTG----TAAACTGTCGATATC----------TGTGT----------T--C----------TA----AATCT----------GTCGAT----------CTG
dm3	chrUextra:27105347-27105392 -		CTATCG-AT---GATC-TATCGATCTA----TCGATCTATC
droSim2	2r:16141848-16141894 -		CCGTCA-AT---CAATC-----ATTTA----GT--
droSec2	scaffold_14049:140-201 -		GATT--CTATCT---ATC-TATCGATCTA----TCTGTCTATCTATCTC----------TGTATC----------C---A----------TC----------TAGCT----------ATCGAT----------CTG
droYak3	X:15893135-15893180 -		TAT--CTATCT---ATC-TATCCATCTA----TTAATGTTCAG----------TG----------CAACT----------GTTCAT----------A
droEre2	scaffold_4845:6459535-6459567 -		CAATCT-AT-----ATC-TATCTATCTA----TTATC----------TG----------T----------ATCAT----------A

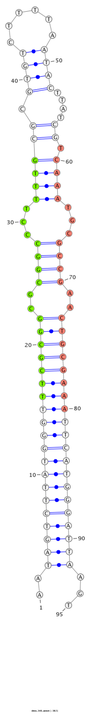
Generated: 09/08/2015 at 08:05 PM

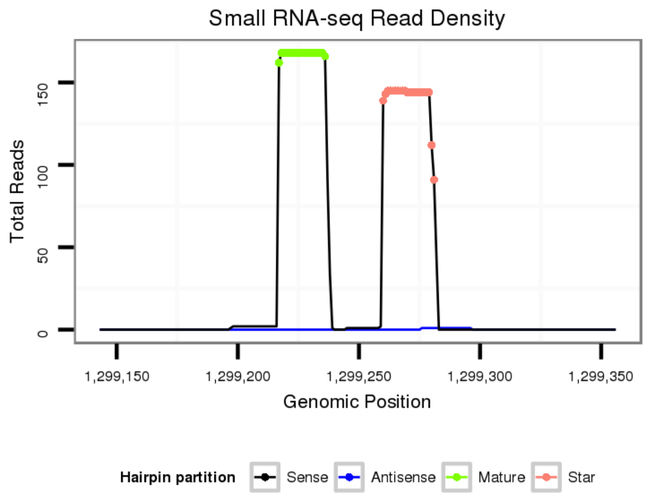
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	4
rescue.candidate	0

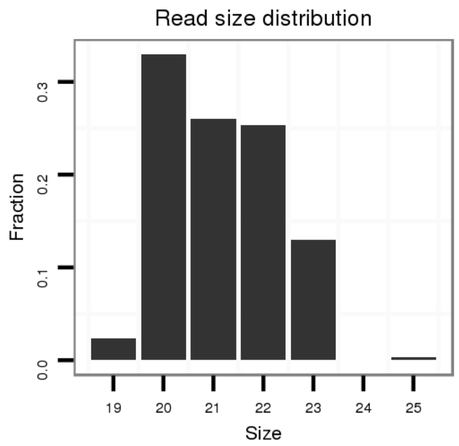
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_340	**scaffold_6308:1299193-1299306 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

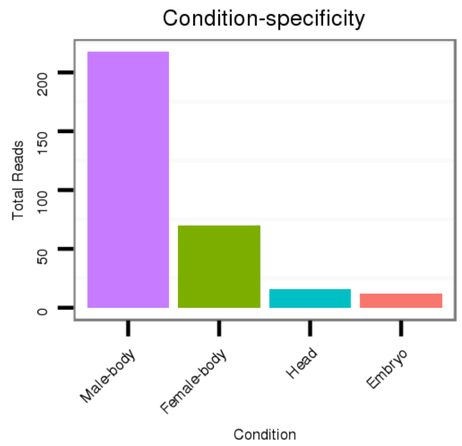
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dmoj\GI10984-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGAAACCCAATTCTTTATACAGCAGGAAAATTTCAATAGACTGATCAATTGAAGTTTGTAATAGTCTTATGGGTTCGCGGCGCGGCCCTTTTGCGCGTGTCTTTTAATACTTATCGTCAAATGCGCCGAACTGCGAAATTCATGGGATTAAGTAAGCAACGTGAATTATCTACATACAAATCTATATAAATATATGAGTTCTGCACGATGGCC	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V049 head	M060 embryo	V056 head	V041 embryo
**********..((((((((((((((((((((..((((...((((((.(((((.....))))).....)))).))))).))))..))))))))))))))))...**********											
.....TTCGCGGCGCGGCCCTTTTG.....	20	0	1	71.00	71	54	15	1	0	1	0
.....TTCGCGGCGCGGCCCTTTTGC.....	21	0	1	56.00	56	39	7	4	2	4	0
.....TCAAATGCGCCGAACTGCGAAA.....	22	0	1	46.00	46	40	5	0	1	0	0
.....TCAAATGCGCCGAACTGCGAAAT.....	23	0	1	40.00	40	31	9	0	0	0	0
.....TTCGCGGCGCGGCCCTTTTGCG.....	22	0	1	32.00	32	7	16	4	2	1	2
.....TCAAATGCGCCGAACTGCGA.....	20	0	1	30.00	30	24	4	0	2	0	0
.....TCAAATGCGCCGAACTGCGAA.....	21	0	1	21.00	21	18	1	0	1	0	1
.....TCAAATGCGCCGAACTGCGAAAA.....	23	1	1	4.00	4	4	0	0	0	0	0
.....TCAAATGCGCCGAACTGCGAAATC.....	24	1	1	4.00	4	2	2	0	0	0	0
.....TCAAATGCGCCGAACTGCGAAAT.....	22	1	1	3.00	3	3	0	0	0	0	0
.....TCGCGGCGCGGCCCTTTTG.....	19	0	1	3.00	3	0	3	0	0	0	0
.....TTCGCGGCGCGGCCCTTTT.....	19	0	1	2.00	2	1	1	0	0	0	0
.....TTCGCGGCGCGGCCCTTTTGCC.....	22	1	1	2.00	2	2	0	0	0	0	0
.....CAAATGCGCCGAACTGCGAAAT.....	22	0	1	2.00	2	0	2	0	0	0	0
.....TCGCGGCGCGGCCCTTTTGC.....	20	0	1	2.00	2	0	2	0	0	0	0
.....TTCGCGGCGCGGCCCTTTTGT.....	21	1	1	2.00	2	2	0	0	0	0	0
.....AAATGCGCCGAACTGCGAAAT.....	21	0	1	2.00	2	0	1	1	0	0	0
.....TCAAATGCGCCGAACTGCGAAAAA.....	24	2	1	2.00	2	2	0	0	0	0	0
.....TCAAATGCGCCGAACTGCGAAAC.....	23	1	1	1.00	1	1	0	0	0	0	0
.....CAAATGCGCCGAACTGCGAAA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TTCGCGGCGCGGCCCTTTTGCGCGC.....	25	1	1	1.00	1	0	0	0	1	0	0
.....TTCGCGGCGCGGCCCTTTTCT.....	21	2	1	1.00	1	1	0	0	0	0	0
.....TTCGCGGCGCGGCCCTTTTGCGT.....	23	1	1	1.00	1	0	0	0	0	1	0
.....TTCGCGGCGCGGCCCTTTTT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....TTTGTAATAGTCTTATGGGT.....	20	0	1	1.00	1	1	0	0	0	0	1
.....TTTTAATACTTATCGTCAAATGCGC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....GTCAAATGCGCCGAACTGCGA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TTCGCGGCGCGGCCCTTTTGCGCC.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TCAAATGCGCCGAACTGCGAAC.....	22	1	1	1.00	1	0	1	0	0	0	0
.....TTCGCGGCGCGGCCCTTTTGTC.....	22	2	1	1.00	1	1	0	0	0	0	0
.....TCAAATGCGCCGAACTGCGAAATA.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TTGTAATAGTCTTATGGGT.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TTCGCGGCGCGGCCCTTTTGCGC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....TCAAATGCGCCGAACTGCGAT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TTCGCGGCGCGGCCCTTTTC.....	20	1	1	1.00	1	0	1	0	0	0	0
.....TTCGCGGCGCGGCCCTTTTGCT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....CAAATGCGCCGAACTGCGA.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TCGCGGCGCGGCCCTTTTGCG.....	21	0	1	1.00	1	0	1	0	0	0	0
.....AAATGCGCCGAACTGCGAA.....	19	0	2	0.50	1	1	0	0	0	0	0

Anti-sense strand reads

TCTTTGGGTTAAGAAATATGTCGTCCTTTTAAAGTTATCTGACTAGTTAACTTCAAACATTATCAGAATACCCAAAGCGCCGCGCCGGGAAAACGCGCACAGAAAATTATGAATAGCAGTTTACGCGGCTTGACGCTTTAAGTACCCTAATTCATTCGTTGCACTTAATAGATGTATGTTTAGATATATTTATATACTCAAGACGTGCTACCGG	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V049 head
**********..((((((((((((((((((((..((((...((((((.(((((.....))))).....)))).))))).))))..))))))))))))))))...**********							
.....CGCTTTAAGTACCCTAATTCA.....	21	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1299141-1299356 +	dmo_340	GCAGAAACCCAATTCTTTATACAGCAGGAAAATTTCAATAGACTGATCAATTGAAGTTTGTAATAGTCTTATGGGTTCGCGGCGCGGCCCTTTTGCGCGTGTCTTTTAATACTTATCGTCAAATGCGCCGAACTGCGAAATTCATGGGATTAAGTAAGCAACGTGAATTATCTACATACAAATCTATATAAATATATGAGTTCTGCACGATGGCC

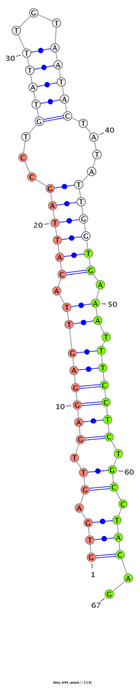
Generated: 09/08/2015 at 08:06 PM

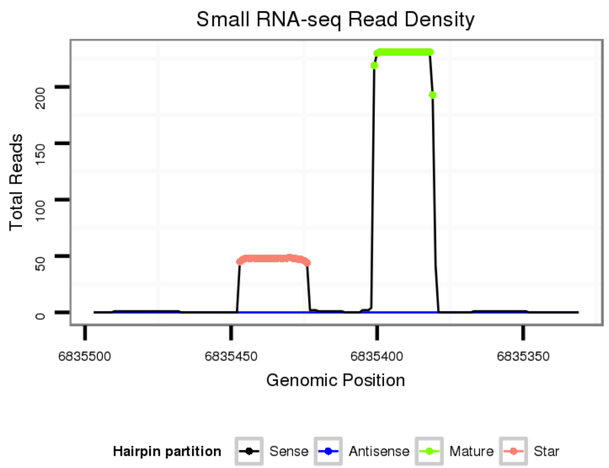
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

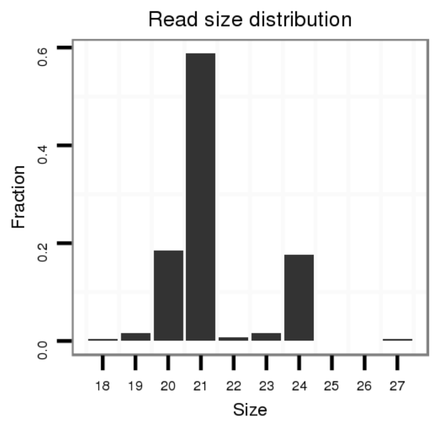
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_694	**scaffold_6473:6835381-6835447 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

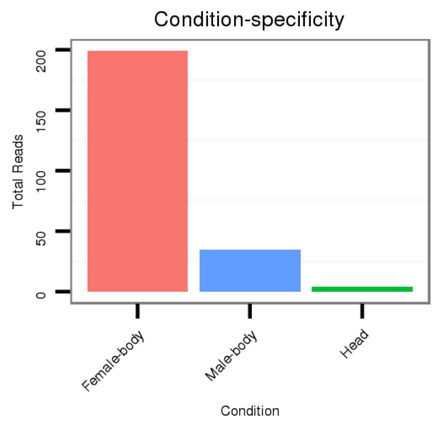
Legend: mature star mismatch in alignment mismatch in read

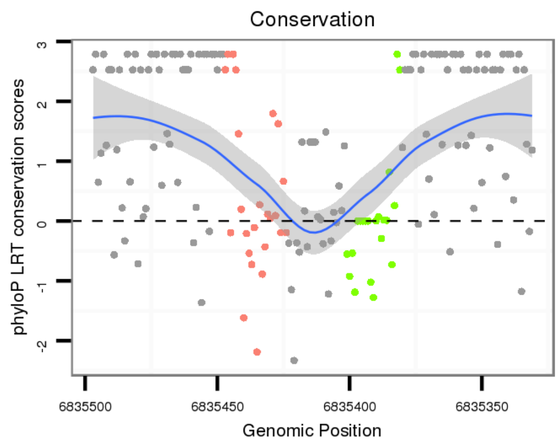
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI14990-in]; CDS [DmojGI14990-cds]; CDS [DmojGI14990-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTGGAGGCGCCAAAGGACGAAGAGACCAGGAAATGGGTCTTGATTTTCAAGTGAGTTGAGGAGTTACATTAGCCTGTATTTGTAATACTATATTGGTGAAATTTCCTCTGCCTACAGCCGCTACGATCTCTACACAAAGAGCGAAGTGGTGCCCGATATTGAAGCTC	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	M060 embryo	V049 head	V056 head
**********(((.((.(((((((.(((((((...(((((...)))))....)))))))..)).)))))).)).))).**********(((.((.(((((((.(((((((...(((((...)))))....)))))))..)).)))))).)).))).**********										
.....TGAAATTTCCTCTGCCTACAGT.....	22	1	1	413.00	413	409	0	4	0	0
.....TGAAATTTCCTCTGCCTACAG.....	21	0	1	140.00	140	140	0	0	0	0
.....TGAAATTTCCTCTGCCTACAGC.....	22	0	1	41.00	41	41	0	0	0	0
.....GTGAGTTGAGGAGTTACATTAGCC.....	24	0	1	40.00	40	4	32	0	3	1
.....TGAAATTTCCTCTGCCTACA.....	20	0	1	34.00	34	34	0	0	0	0
.....GAAATTTCCTCTGCCTACAGT.....	21	1	1	24.00	24	24	0	0	0	0
.....TGAAATTTCCTCTGCCTACAGA.....	22	1	1	22.00	22	22	0	0	0	0
.....GAAATTTCCTCTGCCTACAG.....	20	0	1	8.00	8	8	0	0	0	0
.....TGAAATTTCCTCTGCCTACAGTT.....	23	2	1	7.00	7	7	0	0	0	0
.....GAAATTTCCTCTGCCTACAGA.....	21	1	1	3.00	3	3	0	0	0	0
.....AAATTTCCTCTGCCTACAGT.....	20	1	1	3.00	3	3	0	0	0	0
.....ATTTCCTCTGCCTACAGT.....	18	1	1	2.00	2	2	0	0	0	0
.....GAAATTTCCTCTGCCTACA.....	19	0	1	2.00	2	2	0	0	0	0
.....GTGAAATTTCCTCTGCCTACAG.....	22	0	1	2.00	2	2	0	0	0	0
.....GTGAGTTGAGGAGTTACATTAGC.....	23	0	1	2.00	2	0	2	0	0	0
.....TGAGTTGAGGAGTTACATTAGCC.....	23	0	1	2.00	2	2	0	0	0	0
.....GTGAGTTGAGGAGTTACATC.....	20	1	1	2.00	2	1	1	0	0	0
.....TTGGTGAAATTTCCTCTGCCTACA.....	24	0	1	2.00	2	2	0	0	0	0
.....CGCCAAAGGACGAAGAGACCAGG.....	23	0	1	1.00	1	0	1	0	0	0
.....ATTAGCCTGTATTTGTAAT.....	19	0	1	1.00	1	1	0	0	0	0
.....TGAAATTTCCTCTGCCTACAA.....	21	1	1	1.00	1	1	0	0	0	0
.....GAAATTTCCTCTGCCTACAGC.....	21	0	1	1.00	1	1	0	0	0	0
.....TTGGTGAAATTTCCTCTGCCTACC.....	24	1	1	1.00	1	1	0	0	0	0
.....AAATTTCCTCTGCCTACAG.....	19	0	1	1.00	1	1	0	0	0	0
.....GTGAGTTGAGGAGTTACATTAGCCTGT.....	27	0	1	1.00	1	1	0	0	0	0
.....GTGAGTTGAGGAGTTACA.....	18	0	1	1.00	1	1	0	0	0	0
.....GTGAGTTGAGGAGTTACATT.....	20	0	1	1.00	1	1	0	0	0	0
.....GAAATTTCCTCTGCCTACAGTT.....	22	2	1	1.00	1	1	0	0	0	0
.....GAGTTGAGGAGTTACATTAG.....	20	0	1	1.00	1	0	1	0	0	0
.....TGAAATTTCCTCTGCCTACAGCT.....	23	1	1	1.00	1	1	0	0	0	0
.....TACACAAAGAGCGAAGTGG.....	19	0	1	1.00	1	0	0	0	0	1
.....TGAAATTTCCTCTGCCTACAGTA.....	23	2	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

GACCTCCGCGGTTTCCTGCTTCTCTGGTCCTTTACCCAGAACTAAAAGTTCACTCAACTCCTCAATGTAATCGGACATAAACATTATGATATAACCACTTTAAAGGAGACGGATGTCGGCGATGCTAGAGATGTGTTTCTCGCTTCACCACGGGCTATAACTTCGAG	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body
**********(((.((.(((((((.(((((((...(((((...)))))....)))))))..)).)))))).)).))).**********(((.((.(((((((.(((((((...(((((...)))))....)))))))..)).)))))).)).))).**********						
.....TGAAATTTCCTCTGCCTACAGT.....	22	1	1	413.00	413	409
.....TGAAATTTCCTCTGCCTACAG.....	21	0	1	140.00	140	140
.....TGAAATTTCCTCTGCCTACAGC.....	22	0	1	41.00	41	41
.....GTGAGTTGAGGAGTTACATTAGCC.....	24	0	1	40.00	40	4
.....TGAAATTTCCTCTGCCTACA.....	20	0	1	34.00	34	34
.....GAAATTTCCTCTGCCTACAGT.....	21	1	1	24.00	24	24
.....TGAAATTTCCTCTGCCTACAGA.....	22	1	1	22.00	22	22
.....GAAATTTCCTCTGCCTACAG.....	20	0	1	8.00	8	8
.....TGAAATTTCCTCTGCCTACAGTT.....	23	2	1	7.00	7	7
.....GAAATTTCCTCTGCCTACAGA.....	21	1	1	3.00	3	3
.....AAATTTCCTCTGCCTACAGT.....	20	1	1	3.00	3	3
.....ATTTCCTCTGCCTACAGT.....	18	1	1	2.00	2	2
.....GAAATTTCCTCTGCCTACA.....	19	0	1	2.00	2	2
.....GTGAAATTTCCTCTGCCTACAG.....	22	0	1	2.00	2	2
.....GTGAGTTGAGGAGTTACATTAGC.....	23	0	1	2.00	2	0
.....TGAGTTGAGGAGTTACATTAGCC.....	23	0	1	2.00	2	2
.....GTGAGTTGAGGAGTTACATC.....	20	1	1	2.00	2	1
.....TTGGTGAAATTTCCTCTGCCTACA.....	24	0	1	2.00	2	2
.....CGCCAAAGGACGAAGAGACCAGG.....	23	0	1	1.00	1	0
.....ATTAGCCTGTATTTGTAAT.....	19	0	1	1.00	1	1
.....TGAAATTTCCTCTGCCTACAA.....	21	1	1	1.00	1	1
.....GAAATTTCCTCTGCCTACAGC.....	21	0	1	1.00	1	1
.....TTGGTGAAATTTCCTCTGCCTACC.....	24	1	1	1.00	1	1
.....AAATTTCCTCTGCCTACAG.....	19	0	1	1.00	1	1
.....GTGAGTTGAGGAGTTACATTAGCCTGT.....	27	0	1	1.00	1	1
.....GTGAGTTGAGGAGTTACA.....	18	0	1	1.00	1	1
.....GTGAGTTGAGGAGTTACATT.....	20	0	1	1.00	1	1
.....GAAATTTCCTCTGCCTACAGTT.....	22	2	1	1.00	1	1
.....GAGTTGAGGAGTTACATTAG.....	20	0	1	1.00	1	0
.....TGAAATTTCCTCTGCCTACAGCT.....	23	1	1	1.00	1	1
.....TACACAAAGAGCGAAGTGG.....	19	0	1	1.00	1	0
.....TGAAATTTCCTCTGCCTACAGTA.....	23	2	1	1.00	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:6835331-6835497 -	dmo_694	CTGGAGGCGCCAAAGGACGAAGAGACCAGGAAATGGGTCTTGATTTTCAAGTGAGTTG----------AGGAG----------TT--ACA-TTAGCCTGT-ATTTGT-------AA--------T---ACTA----------TATTGGTGAAATTTCCTCTGCCTACAGCCGCTACGATCTCTACACAAAGAGCGAAGTGGTGCCCGATATTGAAGCTC
droVir3	scaffold_12726:1684491-1684653 +		CTGGAGGCGCCTAAGGATGCTGAGACCAAGAAATGGGTACTCATATTCAAGTGAGTTG----------AAC--------------------------GTTAAGCCCACAT-----CTA--TAAA----------TATATATCTATAACAATAA-----CTCTCCTTACAGCCGCTACGATCTATACACAAAGAGCGAGGTGGTGCCTGATATTGATGCTC
droGri2	scaffold_15203:7984284-7984449 +		CTAGAGGCGCCCCAGGACGAGAACAAGAAATGGGTGCTTATCTTCAAGTGAGTTG----------ATTAT----------TT----TTAACTGC-ACTTTTAG-ATA-AATCT-ATAAC---A----------AATAATTC------TTCTTCTACAGTCGCTACGATCTGTACACAAAGAGTGCTGTGGTGCCCGACATTGAGGCCC
droWil2	scf2_1100000004762:5113615-5113790 +		CTGCAAGCCCCAAGGACGAGGAGACCAAGAAGTGGGTCTTGATATTCAAGTAAGCACAATTCAAATTGATCATTATGCAAATCGGGTGGGAATATTCATGTTCCTTTGGT---------------------------CTT-----CTCTCCTTCTAGTCGCTACGATCTCTACACAAAGAGCGAGGTGGTGCCCGATATTGATGCCC
dp5	XR_group6:2513534-2513699 +		CTGGAGGCCCCAAGGATGAGGAGACCAAGAAATGGGTGCTGATTTTCAAGTGAGTAG----------CTCTG----------CTCTTTCGGTTTA------ACTCTTGTCTTC-AATC--GTAAT---C----------CATAA---T-----GCACCTTTGCAGTCGCTATGATCTGTACACAAAAGCGAGGTAGTGCCAGAGATCGAGGCTC
droPer2	scaffold_9:805821-805986 +		CTGGAGGCCCCAAGGATGAGGAGACCAAGAAATGGGTGCTGATTTTCAAGTGAGTAG----------CTCTG----------CTCTTTCGGTTTA------ACTCTTGACTTC-AATC--GTAAT---C----------CAAA---AT-----TCACCTTTGCAGTCGCTATGATCTGTACACAAAAGCGAGGTAGTGCCAGAGATCGAGGCTC
droAna3	scaffold_13337:1461365-1461527 -		CTGGAGGCGCCCAAGGATGCTGAGACCAAGAAGTGGGTCCTAATTTTCAAGTGAGTAC----------TAATA----------TCCTGCCATTAA------GATTGTAACATA-AA--------A---CCC---------TCCAATAATCGC-----AATTCCCTCTAGTCGCTATGACTTCTACACGAAGAGCGAGGTGGTGCCGGATATTGAGGCTC
droBip1	scf7180000396544:621746-621908 +		CTGGAGGCGCCCAAGGATGCGGAGACTAAGAAGTGGGTCTTGATTTTCAAGTGAGTAT----------TAAAG----------TCGTGCCATTTA------GCTTGTTACATA-AA--------A---CCC---------TCCAATAATCTA-----AATTCCCTCTAGTCGCTATGACTTCTACACGAAGAGCGAGGTGGTGCCCGATATTGAGGCTC
droKik1	scf7180000302391:326172-326333 +		CTGGAGGCCGCCAAGGATGAGGAGACCAAGAAGTGGGTCTGATCTTCAAGTGAGTGT----------TTGTT----------TTTATTTA------G-----A---ATA--TATA-TAATAATAATA----------TATTGATAATAAT-----AATTTCTTGCAGTCGCTACGATCTGTACACGAAGAGCGAGGTAGTTCCGGATATTGATGCCT
droFic1	scf7180000453839:892406-892559 -		CTGGAGGCTCCCGAAGACGAGGAGACCAAGAAGTGGGTCCTAATCTTCAAGTAAGTTA----------ATTACTATA----------TC-----A---A--TGTT----A---TATCCTGTTTATTAATTA------TCCTTTTTTGCAGTCGCTACGATTTGTACACAAGAGCGAAGTGGTTCCGGATATTGAGGCTT
droEle1	scf7180000491255:525467-525624 +		CTGGAGGCTCCCCAAGATGCGGAGACCAAGAAGTGGGTGCTGATCTTCAAGTGAGTTT----------ATTTATTTT----------TTT-----A---AATTT-------A-----A---T---------A---AAACCCCAGTTTAATAACCCA-----TTTTCCCATCAGTCGCTACGATTTGTACACAAGAGCGAGGTGGTTCCGGATATTGAGGCTT
droRho1	scf7180000779507:43408-43564 -		CTGGAGGCACCGCAGGACGCGAGACCAAGAAGTGGGTGCTGATCTTCAAGTGAAGTTT----------ATATTTTAA----------TT-----A---A--T-------A-----GG-A-----A---T-------A---AT-TTTACCTCAGTTTATTAATCAT-----CTTTCCCCCAGTCGCTACGATTTGTACACAAGAGCGAGGTGGTTCCGGATATCGAGGCTT
droBia1	scf7180000302428:4435376-4435533 +		CTGGAGGCTCCACAGGATGCGGAGACCAAGAAGTGGGTGCTCATCTTCAAGTGAAGTTT----------CCTTATATA----------TTC-----A---A--TGAG-----A---T---------A---ATTCTTCCTCAGTTTAATAATGTGT-----GATCCGTTACAGTCGCTACGATTTGTACACGAAGAGCGAGGTGGTTCCGGATATCGATGCTT
droTak1	scf7180000415254:416663-416819 -		CTGGAGGCTCCCCAGGACGCGAGACCAAGAAGTGGGTGCTGATCTTCAAGTGAGTTC----------ATTTGTAAA----------AC-----A---A--TAA-----A---T---------A---ATCCATCTGCGGTTCAATAAAAAT-----GCTTCCTTGCAGTCGCTACGATTTGTACACGAAGAGCGAGGTGGTTCCGGATATTGATGCTT
droEug1	scf7180000409466:4269197-4269353 +		CTGGAGGCACCGCAAGGACGCGAGACCAAGAAGTGGGTGCTAATCTTCAAGTGAGTTT----------ACTTTAAAA----------TC-----A---A--TTA-----A---T---------A---ATTATTTTCAATTTAATAATCAA-----TTTCCTTTGTAGTCGCTATGATTTGTATACTAAGAGCGAGGTGGTTCCTGATATTGAGGCTT
dm3	chr3L:12180162-12180322 +		CTTGAGGCTCCCCAGGATGCGGAGACCAAAAAGTGGGTGCTGATCTTCAAGTAAGTTT----------ATTTTAAGC----------AC-----A---A--TCAT-----A---T---------A---ACA--TATA----A---T---------TTCCCAGTTACATAAGCAA-----TCCTTCTTGCAGTCGCTATGATTTGTACACAAGAGCGAGGTGGTTCCGGATATTGAAGCCT
droSim2	3L:11879024-11879184 +		CTTGAGGCTCCCCAGGATGCGGAGACCAAGAAGTGGGTGCTGATCTTCAAGTGAGTTC----------ATTTTAAAC----------AC-----A---A--TCAT-----A---T---------A---ACA--TATA----A---T---------TACCCAGTTACATAAGCAA-----TCCTTCTTACAGTCGCTACGATTTGTACACAAGAGCGAGGTGGTTCCAGATATTGAAGCCT
droSec2	scaffold_0:4365128-4365288 +		CTTGAGGCTCCCCAGGATGCGGAGACCAAGAAGTGGGTGCTGATCTTCAAGTGAGTTT----------ATTTTAAAC----------AC-----A---A--CCAT-----A---T---------A---ACA--TATA----A---T---------TACCCAGTTACATAAGCAA-----TCCTTCTTGCAGTCGCTATGATTTGTACACAAGAGCGAGGTGGTTCCGGATATTGAAGTCT
droYak3	3L:12228279-12228439 +		CTGGAGGCTCCCCAGGATGCGGAGACCAAGAAGTGGGTGCTCATCTTCAAGTGAGTTC----------ATTTTAAAC----------AG-----A---A--TGAT-----A---T---------A---ATAG--TATA----A---T---------T-CCCGCTTACATAATCAA-----TTCTTCTTGCAGTCGCTATGATTTGTACACAAGAGCGAGGTGGTTCCGGATATTGAGGCCT
droEre2	scaffold_4784:12168745-12168901 +		CTGGAGGCTCCCCAGGATGCGGAGACCAAGAAGTGGGTGCTGATCTTCAAGTGAGTTC----------CGTATAAAC----------AC-----A---A--TAA-----A---T---------A---ATATCTAGCCAGTTACATAAACAT-----TCCGTTTTTGCAGTCGCTATGATTTGTACACAAGAGCGAGGTGGTTCCGGATATTGAAGCTT

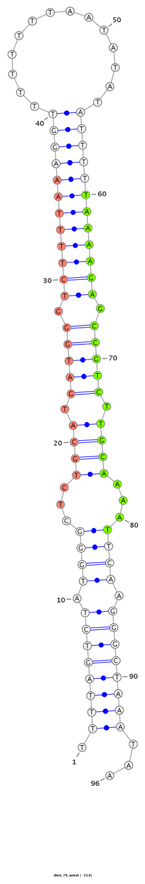
Generated: 09/08/2015 at 07:03 PM

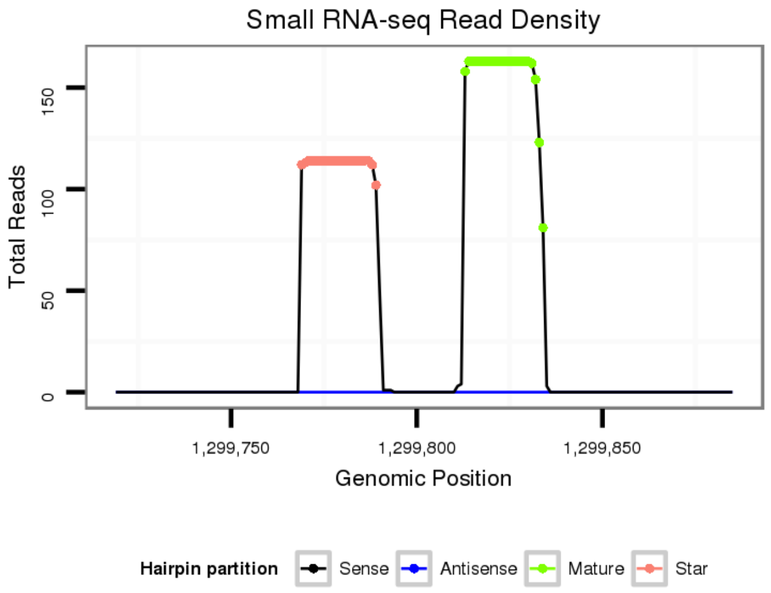
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

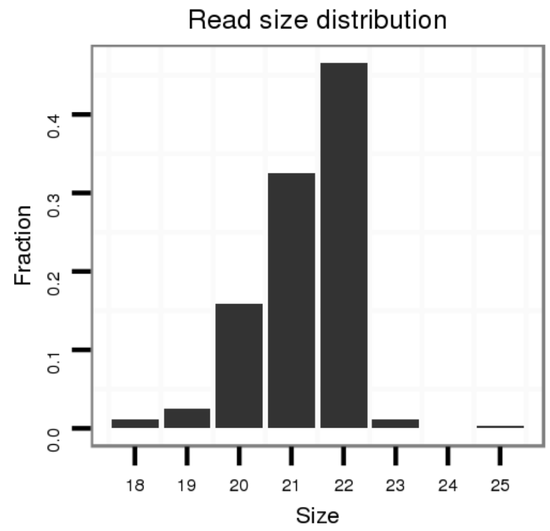
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_76	**scaffold_6308:1299769-1299835 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

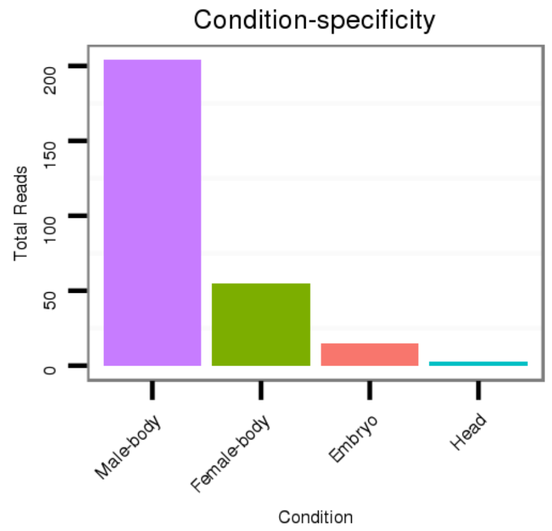
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dmoj\GI10984-in]

Repeatable elements

Name	Class	Family	Strand
AT_rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AGGCAGGAAATTTTTATAGTGCCTGCCAGCAAAATTTTTAGTCTATGGGCTCTGCATGATGGGTCTTTTAAAGGTTTTTTTTAATATATATTTTTAAAAGAGCCGTCTTGCAAAATTCAAGGGCTAAATAAGCAACGAAGCGTGTGGAAAATCAATTCTTTATCTAA	Read size	# Mismatch	Hit Count	Total Norm	Total		V110 male	M046 female body	M060 embryo	V041 embryo	V049 head	V056 head
********************************.(((((((.((((...((((.(((((.((((((((((((.............)))))))))))).)))))...))))).)))))))...********************************.												
.....TAAAAGAGCCGTCTTGCAAAAT.....	22	0	1	78.00	78	66	9	3	0	0	0	0
.....TCTGCATGATGGGTCTTTTAA.....	21	0	1	51.00	51	29	16	0	4	2	0	
.....TCTGCATGATGGGTCTTTTAAA.....	22	0	1	49.00	49	27	15	2	4	0	1	
.....TAAAAGAGCCGTCTTGCAAAA.....	21	0	1	37.00	37	36	1	0	0	0	0	
.....TAAAAGAGCCGTCTTGCAAA.....	20	0	1	30.00	30	29	0	1	0	0	0	
.....TAAAAGAGCCGTCTTGCAAAATC.....	23	1	1	14.00	14	14	0	0	0	0	0	
.....TAAAAGAGCCGTCTTGCAAAAA.....	22	1	1	10.00	10	10	0	0	0	0	0	
.....TCTGCATGATGGGTCTTTTA.....	20	0	1	9.00	9	1	8	0	0	0	0	
.....TAAAAGAGCCGTCTTGCAAAATA.....	23	1	1	6.00	6	5	0	1	0	0	0	
.....TAAAAGAGCCGTCTTGCAA.....	19	0	1	5.00	5	5	0	0	0	0	0	
.....TAAAAGAGCCGTCTTGCAAAT.....	21	1	1	4.00	4	4	0	0	0	0	0	
.....AAAAGAGCCGTCTTGCAAAA.....	20	0	1	4.00	4	1	3	0	0	0	0	
.....TAAAAGAGCCGTCTTGCAAAATT.....	23	0	1	3.00	3	3	0	0	0	0	0	
.....TTTAAAAGAGCCGTCTTGCAA.....	21	0	1	2.00	2	2	0	0	0	0	0	
.....TCTGCATGATGGGTCTTTTAAAA.....	23	1	1	2.00	2	2	0	0	0	0	0	
.....TCTGCATGATGGGTCTTTT.....	19	0	1	2.00	2	0	1	1	0	0	0	
.....TCTGCATGATGGGTCTTTTT.....	20	1	1	2.00	2	1	1	0	0	0	0	
.....TAAAAGAGCCGTCTTGCAAAAC.....	22	1	1	2.00	2	2	0	0	0	0	0	
.....CTGCATGATGGGTCTTTTAAAA.....	22	1	1	1.00	1	0	1	0	0	0	0	
.....TCTGCATGATGGGTCTTTTAC.....	21	1	1	1.00	1	0	1	0	0	0	0	
.....TAAAAGAGCCGTCTTGCAAAAG.....	22	1	1	1.00	1	1	0	0	0	0	0	
.....TAAAAGAGCCGTCTTGCAAAG.....	21	1	1	1.00	1	1	0	0	0	0	0	
.....TAAAAGAGCCGTCTTGCAAAAAAA.....	24	3	1	1.00	1	1	0	0	0	0	0	
.....TAAAAGAGCCGTCTTGCAAC.....	20	1	1	1.00	1	1	0	0	0	0	0	
.....TCTGCATGATGGGTCTTTTAAAGGT.....	25	0	1	1.00	1	1	0	0	0	0	0	
.....TCTGCATGATGGGTCTTTTAAAAA.....	24	2	1	1.00	1	0	1	0	0	0	0	
.....TTTAAAAGAGCCGTCTTGCAAA.....	22	0	1	1.00	1	1	0	0	0	0	0	
.....TCTGCATGATGGGTCTTTTAAAAAA.....	25	3	1	1.00	1	0	1	0	0	0	0	
.....TAAAAGAGCCGTCTTGCAAATC.....	22	2	1	1.00	1	1	0	0	0	0	0	
.....TAAAAGAGCCGTCTTGCAATC.....	21	2	1	1.00	1	1	0	0	0	0	0	
.....CTGCATGATGGGTCTTTTAA.....	20	0	1	1.00	1	1	0	0	0	0	0	
.....TGCATGATGGGTCTTTTA.....	18	0	1	1.00	1	0	1	0	0	0	0	
.....TTTAAAAGAGCCGTCTTGCAAC.....	22	1	1	1.00	1	1	0	0	0	0	0	
.....TTAAAAGAGCCGTCTTGCAAAA.....	22	0	1	1.00	1	1	0	0	0	0	0	
.....TAAAAGAGCCGTCTTGCAATG.....	21	2	1	1.00	1	1	0	0	0	0	0	
.....AAAAGAGCCGTCTTGCAA.....	18	0	1	1.00	1	0	1	0	0	0	0	
.....TAAAAGAGCCGTCTTGCAATT.....	21	2	1	1.00	1	1	0	0	0	0	0	
.....TAAAAGAGCCGTCTTGCAAAATG.....	23	1	1	1.00	1	1	0	0	0	0	0	
.....TCTGCATGATGGGTCTTTTAAT.....	22	1	1	1.00	1	1	0	0	0	0	0	
.....TCTGCATGATGGGTCTTTTCT.....	21	2	1	1.00	1	1	0	0	0	0	0	
.....TAAAAGAGCCGTCTTGCA.....	18	0	1	1.00	1	1	0	0	0	0	0	

Anti-sense strand reads

TCCGTCCTTTAAAAATATCACGGACGGTCGTTTTAAAAATCAGATACCCGAGACGTACTACCCAGAAAATTTCCAAAAAAAATTATATATAAAAATTTTCTCGGCAGAACGTTTTAAGTTCCCGATTTATTCGTTGCTTCGCACACCTTTTAGTTAAGAAATAGATT	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_6308:1299719-1299885 +	dmo_76	AGGCAGGAAATTTTTATAGTGCCTGCCAGCAAAATTTTTAGTCTATGGGCTCTGCATGATGGGTCTTTTAAAGGTTTTTTTTAATATATATTTTTAAAAGAGCCGTCTTGCAAAATTCAAGGGCTAAATAAGCAACGAAGCGTGTGGAAAATCAATTCTTTATCTAA

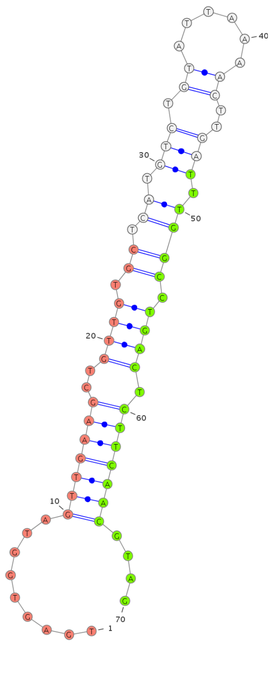
Generated: 09/08/2015 at 08:04 PM

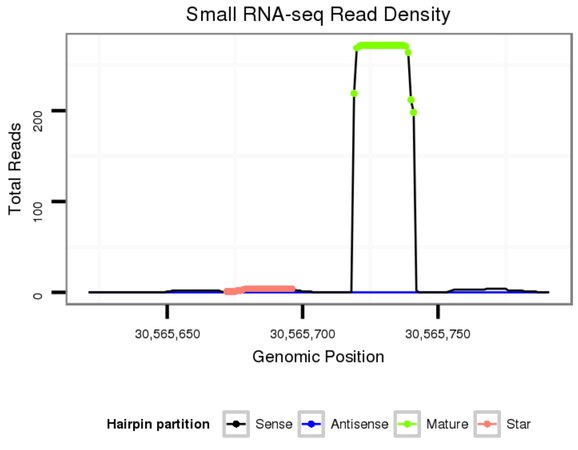
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

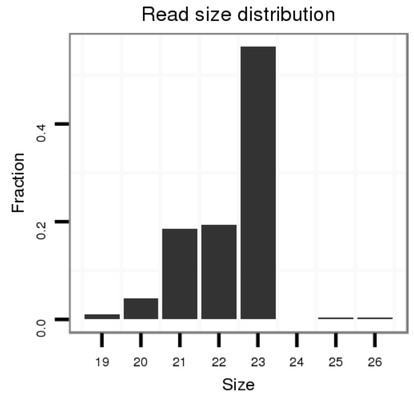
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_95	**scaffold_6540:30565671-30565741 +**	**confident**	**5p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

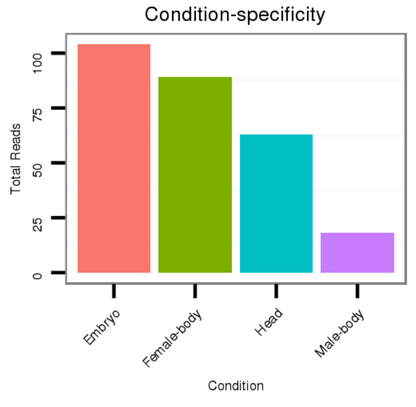
Legend: mature star mismatch in alignment mismatch in read

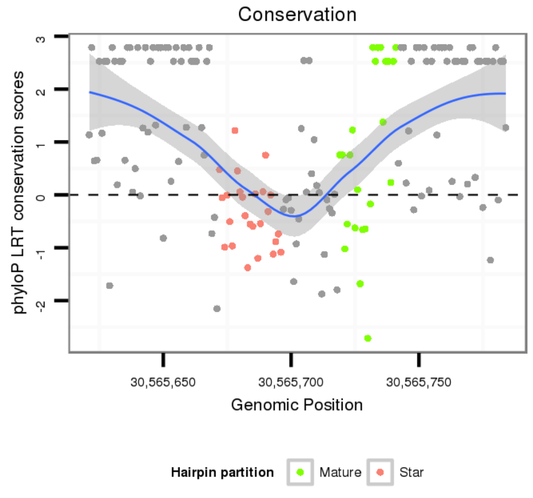
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI10642-in]; CDS [Dmoj\GI10642-cds]; CDS [Dmoj\GI10642-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TCGACAACTTGCGCGCCTCGCCCTTCTTGCTGCAGTACATCCAGGAGAGCGTGAGTGGTAGTTGAAGCTGTTGTGCTCATGTCTGTATTAAAACTTGATTTGGCCTGACTCTTCAACGTAGATACCCGACTACCGCAACTCGGTGATTGTGGCACGTAATCCGGGCGTCGC	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V056 head	V041 embryo	V049 head	V110 male body
**********.....(((((((..((((.((.((.(((.((.....)).)))).)))).)))).)))))....**********											
.....TTTGGCCTGACTCTTCAACGTAG.....	23	0	1	153.00	153	52	50	14	26	4	7
.....TTTGGCCTGACTCTTCAACGT.....	21	0	1	46.00	46	1	3	23	0	10	9
.....TTGGCCTGACTCTTCAACGTAG.....	22	0	1	40.00	40	11	24	0	3	2	0
.....TTTGGCCTGACTCTTCAACGTA.....	22	0	1	12.00	12	3	4	1	2	2	0
.....TTGGCCTGACTCTTCAACGT.....	20	0	1	6.00	6	0	2	2	0	1	1
.....TTGGCCTGACTCTTCAACGTAGT.....	23	1	1	5.00	5	4	1	0	0	0	0
.....TTTGGCCTGACTCTTCAACG.....	20	0	1	5.00	5	2	2	1	0	0	0
.....TTGGCCTGACTCTTCAACGTA.....	21	0	1	2.00	2	0	0	0	0	2	0
.....TTTGGCCTGACTCTTCAACGTAGA.....	24	0	1	2.00	2	1	1	0	0	0	0
.....TTGGCCTGACTCTTCAACG.....	19	0	1	2.00	2	1	0	0	0	1	0
.....TGGCCTGACTCTTCAACGTAG.....	21	0	1	2.00	2	0	2	0	0	0	0
.....TTTGGCCTGACTCTTCAACGTAGT.....	24	1	1	1.00	1	0	0	1	0	0	0
.....TGTGGCACGTAATCCGGGC.....	19	0	1	1.00	1	0	1	0	0	0	0
.....CTGCAGTACATCCAGGAGAG.....	20	0	1	1.00	1	0	0	0	0	0	1
.....TTTGGCCTGACTCTTCAAC.....	19	0	1	1.00	1	0	1	0	0	0	0
.....CAACTCGGTGATTGTGGCAC.....	20	0	1	1.00	1	0	1	0	0	0	0
.....GCAGTACATCCAGGAGAGC.....	19	0	1	1.00	1	0	0	0	0	0	1
.....TTTGGCCTGACTCTTCAACGTAT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TTTGGCCTGACTCTTCAACGTT.....	22	1	1	1.00	1	0	1	0	0	0	0
.....TTTGGCCTGACTCTTCAACGTAC.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TTGGCCTGACTCTTCAACGTT.....	21	1	1	1.00	1	0	0	0	0	1	0
.....TGAGTGGTAGTTGAAGCTGTTGTGC.....	25	0	1	1.00	1	0	1	0	0	0	0
.....GGCCTGACTCTTCAACGTAG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TGGTAGTTGAAGCTGTTGTGCT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....GTAGTTGAAGCTGTTGTGCTCATGTC.....	26	0	1	1.00	1	1	0	0	0	0	0
.....CGCAACTCGGTGATTGTGGCACGTAATC.....	28	0	1	1.00	1	0	0	0	0	0	1
.....GCAACTCGGTGATTGTGGCAC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TAGTTGAAGCTGTTGTGCTCA.....	21	0	1	1.00	1	0	0	0	0	0	1

Anti-sense strand reads

AGCTGTTGAACGCGCGGAGCGGGAAGAACGACGTCATGTAGGTCCTCTCGCACTCACCATCAACTTCGACAACACGAGTACAGACATAATTTTGAACTAAACCGGACTGAGAAGTTGCATCTATGGGCTGATGGCGTTGAGCCACTAACACCGTGCATTAGGCCCGCAGCG	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V049 head
**********.....(((((((..((((.((.((.(((.((.....)).)))).)))).)))).)))))....**********								
.....TTTGGCCTGACTCTTCAACGTAG.....	23	0	1	153.00	153	52	50	14
.....TTTGGCCTGACTCTTCAACGT.....	21	0	1	46.00	46	1	3	23
.....TTGGCCTGACTCTTCAACGTAG.....	22	0	1	40.00	40	11	24	0
.....TTTGGCCTGACTCTTCAACGTA.....	22	0	1	12.00	12	3	4	1
.....TTGGCCTGACTCTTCAACGT.....	20	0	1	6.00	6	0	2	2
.....TTGGCCTGACTCTTCAACGTAGT.....	23	1	1	5.00	5	4	1	0
.....TTTGGCCTGACTCTTCAACG.....	20	0	1	5.00	5	2	2	1
.....TTGGCCTGACTCTTCAACGTA.....	21	0	1	2.00	2	0	0	0
.....TTTGGCCTGACTCTTCAACGTAGA.....	24	0	1	2.00	2	1	1	0
.....TTGGCCTGACTCTTCAACG.....	19	0	1	2.00	2	1	0	0
.....TGGCCTGACTCTTCAACGTAG.....	21	0	1	2.00	2	0	2	0
.....TTTGGCCTGACTCTTCAACGTAGT.....	24	1	1	1.00	1	0	0	1
.....TGTGGCACGTAATCCGGGC.....	19	0	1	1.00	1	0	1	0
.....CTGCAGTACATCCAGGAGAG.....	20	0	1	1.00	1	0	0	0
.....TTTGGCCTGACTCTTCAAC.....	19	0	1	1.00	1	0	1	0
.....CAACTCGGTGATTGTGGCAC.....	20	0	1	1.00	1	0	1	0
.....GCAGTACATCCAGGAGAGC.....	19	0	1	1.00	1	0	0	0
.....TTTGGCCTGACTCTTCAACGTAT.....	23	1	1	1.00	1	1	0	0
.....TTTGGCCTGACTCTTCAACGTT.....	22	1	1	1.00	1	0	1	0
.....TTTGGCCTGACTCTTCAACGTAC.....	23	1	1	1.00	1	1	0	0
.....TTGGCCTGACTCTTCAACGTT.....	21	1	1	1.00	1	0	0	0
.....TGAGTGGTAGTTGAAGCTGTTGTGC.....	25	0	1	1.00	1	0	1	0
.....GGCCTGACTCTTCAACGTAG.....	20	0	1	1.00	1	1	0	0
.....TGGTAGTTGAAGCTGTTGTGCT.....	22	0	1	1.00	1	1	0	0
.....GTAGTTGAAGCTGTTGTGCTCATGTC.....	26	0	1	1.00	1	1	0	0
.....CGCAACTCGGTGATTGTGGCACGTAATC.....	28	0	1	1.00	1	0	0	0
.....GCAACTCGGTGATTGTGGCAC.....	21	0	1	1.00	1	0	1	0
.....TAGTTGAAGCTGTTGTGCTCA.....	21	0	1	1.00	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:30565629-30565792 +	dmo_95	TTGCGCGCCTCGCCCTTCTTGCTGCAGTACATCCAGGAGAGCGTGAGTGGTAGTTGAA------GC-TG--TTGT--GCTC-----ATGTC-TGTATT-----AAAACTTG--------ATT-TGGCCT-----GACTC----------------T-------TCAACGTAGATACCCGACTACCGCAACTCGGTGATTGTGGCACGTAATCCGGGCGTCGCC
droVir3	scaffold_13047:11190045-11190203 -		TTGCGCGCCTCGCCCTTTTGCTGCAGTATATACAGGAGAGCGTGAGTGGGAGGCA--------T--ATAGA--CTCTTTA-TAT----A-CACTA-----------------TC-T---AA-----------CTGATTGGTTTTGACTAGACTTTAGATACCCGACTACCGCAACTCGGTGATTGTGGCACGCAATCCGGGCGGTTGCC
droGri2	scaffold_14624:1098658-1098817 -		TTACGCGCCTCACCCTTCTGCTGCAGTACATCCAGGAGAGCGTGAGTCGAAGTTGGA------TT-TA--ATTT--CTAT-----AGTCC-------------TCAACTAACGTTTTGTATG-TGTTGT-----AT-----------------------CTTTTAGATACCCGACTATCGTAATTCGGTGATTGTGGCTCGCAATCCGGGAGTTGCC
droWil2	scf2_1100000004943:9927772-9927930 -		TTGAGCGCATCTCCCTTCTGTGCAGTACATTCAGGAGAGCGTGAGTGAAATCCTCATGATACC-AA---CTGCGAAAATT-C--------A-----TTAACTAA--------TTT-C---TC-----T-----CTTTG-----------TCAATAGATACCCGATATATAGAAATTGCGTCATTGTGGCCGTAATCCAGGTGTGCCC
dp5	2:819050-819209 +		CTGCGGCCTCGCCCTTCCTTCTGCAGTACATCCAGGAGAGCGTGAGTGCCAGCCATAGAATAGT-CC---G--GAAAATG-CAC----A-GAGAAC-----TAAACTAA--------ATG-C---AT-----CC---------C---------------TTGCAGATACCCGAATATCGCAATTCGGTGATTGTGGCCGCAATCCAGGCGTGCCC
droPer2	scaffold_7:3601102-3601261 +		CTGCGGCCTCGCCCTTCCTTCTGCAGTACATCCAGGAGAGCGTGAGTGCCAGCCATAGAATAGT-CC---G--GAAAATG-CAC----A-GAGAAC-----TAAACTAA--------ATG-C---AT-----CC---------C---------------TTGCAGATACCCGAATATCGCAATTCGGTGATTGTGGCCGCAATCCAGGCGTAGCCC
droAna3	scaffold_12911:4561969-4562118 +		CTAAGCGGCGTCACCCTTTTACTCCAATACATTCAAGAGAGCGTGAGTAAGGAACA--------T---T---TTA-T---ATCCCCTGAATCATATATTTCATTTGTGGAA---------TCCCATAGATTCCCGACTATCGCAATTCGGTGATTGTGGCCGCAACCCGGGCGTGGCT
droBip1	scf7180000396640:1404838-1404990 +		CTAAGCGGCGTCGCCCTTTTGCTCCAATATTATTCAGGAGAGCGTGAGTGCCA------------CA--ACAC--ATAT-----GTCTC-------------CTAAATCATATATTTTATTTGGAAAC-----T---TT-----------------CCACTAGATTCCCGACTATCGTAATTCGGTGATTGTGGCCGCAATCCGGGCGTGGCT
droKik1	scf7180000302390:389690-389842 -		CTGAGCGGCATCGCCTTTTCTGCTCCAATACATTCAGGAGAGCGTAAGTAC--------T-TAA--AT--TTAAAT-----TTAATAAAAATTT-----AATAAT---------TATTAAAATATAT-----CT-----------------TCTTTAGATTCCCGACTATCGCAACTCGGTGATTGTGGCCGCAATCGTGGAGTGGCC
droFic1	scf7180000454106:51109-51256 +		CTGAGCGGCCTCGCCCTTCCTACTCCAATATATTCAGGAAAGCGTGAGTTC--------T-CT---G--GCCCCTTTAGC----T-GATCCT-----TAAA-TAA--------TAG-CAATAC-----CC---------------------GTTCCAGATTCCCGACTATCGCAACTCGGTGATTGTGGCCGCAATCCGGGCGTGCCC
droEle1	scf7180000491280:2749069-2749220 -		CTGAGCGGCATCGCCTTTTCTGCTCCAATACATTCAGGAGAGCGTGAGTAC--------T-CTTTGGG--TACTCTT-CAC----T-TCGAAT-----GAAATTAA--------ACT-TAAGAC-----TC---------------------GTTCAAGATTCCCGACTATCGCAACTCGGTGATTGTGGCCGCAATCCGGGCGTGCCC
droRho1	scf7180000778339:10509-10658 +		CTGAGCGGCATCGCCCTTTCTGCTCCAATATTATTCAGGAGAGCGTGAGTAC--------T-TTA--AG--TTCTCTA-ACC----T-AAGGAAAGAATTCAAACT---------------TAAAAC-----AC---------------------ATTGTAGATTCCTGACTATCGCAACTCGGTGATTGTCGGCCGCAATCCGGGCGTGCCC
droBia1	scf7180000302113:940003-940154 +		CTGAGCGGCGTCGCCCTTTCTGCTCCAATACATTCAGGAGAGCGTGGGTTT--------T-CTGAAGG--CTATCTA-AGT----T-AAGAAG-----GGAACTAA--------TTT-CGTTAC-----TC---------------------CCCGCAGATTCCCGACTATCGCAACTCGGTGATTGTGGCCGCAATCGTGGAGTGGCC
droTak1	scf7180000415367:377023-377177 +		CTGAGCGGCCTCGCCCTTCCTGCTCCAATATTATTCAGGAGAGCGTGGGTTT--------T-TTCTGTAGA--CTATCTT-AAT----T-AAGAAA-----------------TG-C---AT-----TTGAT--GTTATCATAAGCCCTAGATTCCCGACTATCGCAACTCGGTGATTGTGGCCGCAATCCGGGTGTCGCC
droEug1	scf7180000409555:927431-927579 -		CTGAGCGGCATCGCCCTTTCTACTCCAATATTATTCAGGAGAGCGTGAGTTT--------T-TTT---G--CACTGTA-AAC----T-TGGAAT-----GGAACTAA--------ACG-TGTTGA-----TT---------------------TCTCCAGATTCCTGACTACCGCAACTCGGTGATTGTGGCCGCAATCCGGGCGTGCCC
dm3	chr3R:26420656-26420803 -		CTGAGCGGCGTCGCCCTTCTGCTCCAATATTATTCAAGAGAGCGTGGGTAG--------T-GT---G--CAAACTA-AGC----G-AAGATT-----GAAACTAA--------ATG-TGATAA-----TG---------------------CTTCTAGATTCCCGACTATCGAAATTCGGTGATTGTAGGTCGCAATCCGGGCGTGCCC
droSim2	3r:25740732-25740879 -		CTGAGCGGCGTCGCCCTTCTGCTCCAATATTATTCAGGAGAGCGTGGGTAG--------T-CT---G--CACTCTA-AGC----G-AAGATT-----GAAACTAA--------ATG-CGATAT-----TG---------------------CTTCTAGATTCCCGACTATCGAAACTCGGTGATTGTGGCCGCAACCCGGGCGTGCCC
droSec2	scaffold_4:5247538-5247685 -		CTGAGCGGCGTCGCCCTTCTGCTCCAATATTATTCAGGAGAGCGTGGGTAG--------T-CT---G--CACTCTA-AGC----G-AAGATT-----GAAACTAA--------ATG-TGATAT-----TG---------------------CTTCTAGATTCCCGACTATCGAAACTCGGTGATTGTGGCCGCAACCCGGGTGTGCCC
droYak3	3R:27340873-27341020 -		CTGAGCGGCGTCGCCCTTCCTGCTCCAATACATTCAGGAGAGCGTGGGTAG--------T-CT---G--CCATCCA-AGC----G-AGGATT-----GAAACTAA--------ATG-TGATAT-----TA---------------------CTTCTAGATTCCTGACTATCGCAACTCGGTGATTGTAGGTCGCAACCCAGGCGTGCCC
droEre2	scaffold_4820:1581262-1581409 +		CTGAGCGGCATCGCCCTTCCTGCTCCAATACATTCAGGAGAGCGTGGGTAG--------T-CT---G--CAATCTA-AGC----A-AAGATG-----GAAACTAA--------ATG-TGATAT-----TG---------------------CTTCTAGATTCCTGACTACCGAAACTCGGTGATTGTAGGTCGCAACCCGGGCGTGGCC

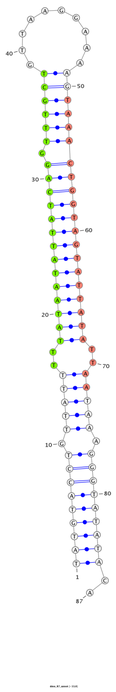
Generated: 09/08/2015 at 07:03 PM

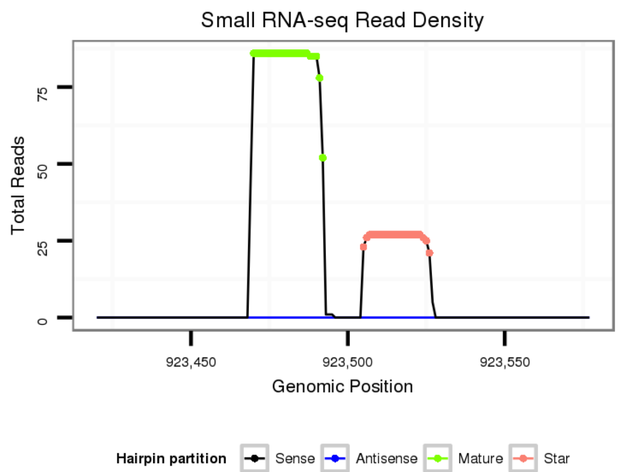
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

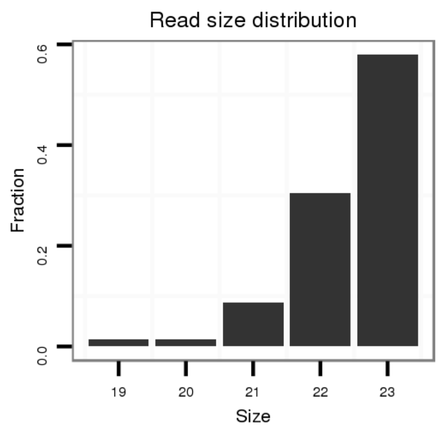
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_87	**scaffold_6359:923470-923527 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

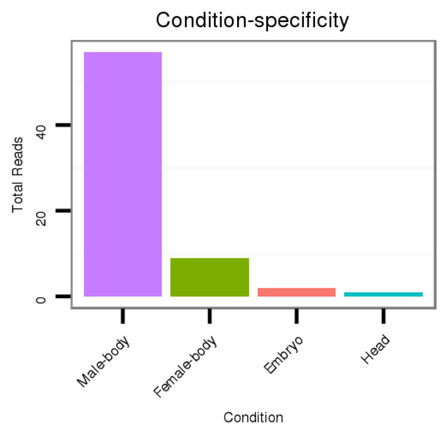
Legend: mature star mismatch in alignment mismatch in read

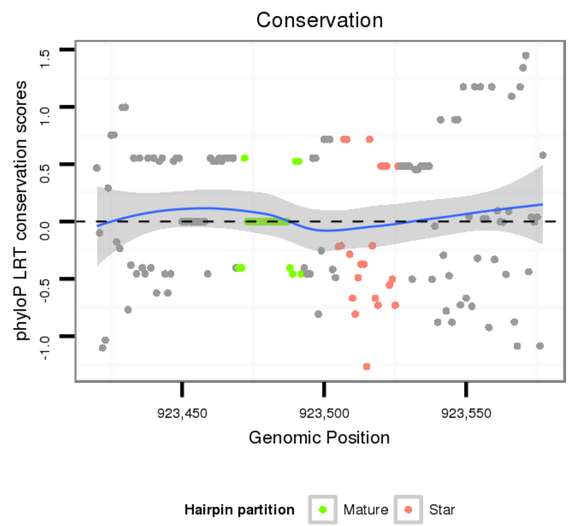
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTTCAGATTTAGTTATATAGATCATATCATCTTTTTATGTACCTGTTATTTTTATAATATTATCAGGTTTGCTGTTAAGGAAAAGTAAACTGGTAGTATTATATTAATAAAGGGTATATACAGTTCAACATAAATAAATACTCATGGCTAGAGAGAGA **********(((((((((.(((((..(((((((((((((((.(((((((.........)))))))))))))))))))..)))))..)))))))))..********** **Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V110 male body**	**M046 female body**	**M060 embryo**	**V049 head**	**V041 embryo**
.....TTTATAATATTATCAGGTTTGCTCC.....	25	2	1	57.00	57	56	1	0	0	0
.....TTTATAATATTATCAGGTTTGCTC.....	24	1	1	54.00	54	54	0	0	0	0
.....TTTATAATATTATCAGGTTTGCT.....	23	0	1	39.00	39	36	2	1	0	0
.....TTTTATAATATTATCAGGTTTGC.....	23	0	1	24.00	24	15	6	2	1	0
.....TAAACTGGTAGTATTATATTAA.....	22	0	1	16.00	16	14	1	0	1	0
.....TTTTATAATATTATCAGGTTTGCC.....	24	1	1	14.00	14	10	3	1	0	0
.....TTTTATAATATTATCAGGTTTGCT.....	24	0	1	12.00	12	12	0	0	0	0
.....TTTTATAATATTATCAGGTTTG.....	22	0	1	6.00	6	2	3	0	1	0
.....TTTTATAATATTATCAGGTTTGCTC.....	25	1	1	5.00	5	5	0	0	0	0
.....TTTATAATATTATCAGGTTTGCTCCC.....	26	3	1	5.00	5	5	0	0	0	0
.....TAAACTGGTAGTATTATATTA.....	21	0	1	4.00	4	1	3	0	0	0
.....AAACTGGTAGTATTATATTAAT.....	22	0	1	3.00	3	3	0	0	0	0
.....TTTATAATATTATCAGGTTTGC.....	22	0	1	2.00	2	0	2	0	0	0
.....AAACTGGTAGTATTATATTAATC.....	23	1	1	2.00	2	2	0	0	0	0
.....TAAACTGGTAGTATTATATTAAA.....	23	1	1	2.00	2	2	0	0	0	0
.....TTTATAATATTATCAGGTTTGCTTC.....	25	2	1	2.00	2	2	0	0	0	0
.....TAAACTGGTAGTATTATATTAAT.....	23	0	1	1.00	1	1	0	0	0	0
.....TTTATAATATTATCAGGTTTGT.....	22	1	1	1.00	1	1	0	0	0	0
.....TTTTATAATATTATCAGGT.....	19	0	1	1.00	1	1	0	0	0	0
.....TTTATAATATTATCAGGTTTGCTCCA.....	26	3	1	1.00	1	1	0	0	0	0
.....TTTTATAATATTATCAGGTTTGT.....	23	1	1	1.00	1	1	0	0	0	0
.....TAAACTGGTAGTATTATATTC.....	21	1	1	1.00	1	1	0	0	0	0
.....TTTATAATATTATCAGGTTTGCCC.....	24	2	1	1.00	1	1	0	0	0	0
.....TTTTATAATATTATCAGGTTTG.....	21	0	1	1.00	1	1	0	0	0	0
.....TTTTATAATATTATCAGGTTTGCTGTT.....	27	0	1	1.00	1	1	0	0	0	0
.....TAAACTGGTAGTATTATAT.....	19	0	1	1.00	1	0	0	0	0	1
.....TTTATAATATTATCAGGTTTGCC.....	23	1	1	1.00	1	1	0	0	0	0
.....TTTTATAATATTATCAGGTTTC.....	22	1	1	1.00	1	0	1	0	0	0
.....AACTGGTAGTATTATATTAAT.....	21	0	1	1.00	1	0	1	0	0	0
.....TAAACTGGTAGTATTATATT.....	20	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

AAAGTCTAAATCAATATATCTAGTATAGTAGAAAAATACATGGACAATAAAAATATTATAATAGTCCAAACGACAATTCCTTTTCATTTGACCATCATAATATAATTATTTCCCATATATGTCAAGTTGTATTTATTTATGAGTACCGATCTCTCTCT **********(((((((((.(((((..(((((((((((((((.(((((((.........)))))))))))))))))))..)))))..)))))))))..********** **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_6359:923420-923577 +	dmo_87	TTTCAGATTTAGTTATATAGATCATATCATCTTTTTATGTACCTGTTATTTTTATAATATTATCAGGTTTGCTGTT---------AAGGAAAAGTAAACTGGTAGTATTATATTAATAAAGGGTATATACAGTTCAACATAAATAAATACTCATGGCTAGAGAGAGA
droVir3	scaffold_12822:3599883-3599967 -		TTGAA----------CAAATTTAAATGCTCGCTAGGATAACCATAAAAGGTATACAGAAAAGAATAGAGATAGGCACAGCTAGAGAGAGAGACA
droGri2	scaffold_15203:8968454-8968539 -		AAATT----TACATTTGAAAAGCAACACAT---------AACCTGTTATCCCT----------CAGCAAAAAAAAAAAGAAGAAAAAGAGAACTGGTAATGT----------TTTTTT
droWil2	scf2_1100000004540:1435807-1435841 -		TTCAA----------CAACAAAAAATAACACAGAGAGAGAGAGA
droPer2	scaffold_0:3787800-3787841 -		TAT----------GCAAGTCAAAAGATACAAAGATACAGAGCAGAGAGAGA
droFic1	scf7180000453926:400318-400336 -		TTTTAGACATAGT----------TTTGTA
droEle1	scf7180000491008:688104-688111 -		----------GACAGATA

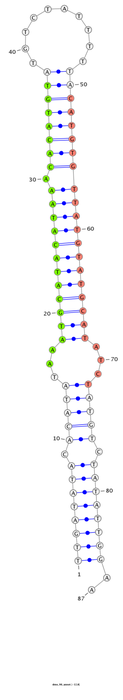
Generated: 09/08/2015 at 07:34 PM

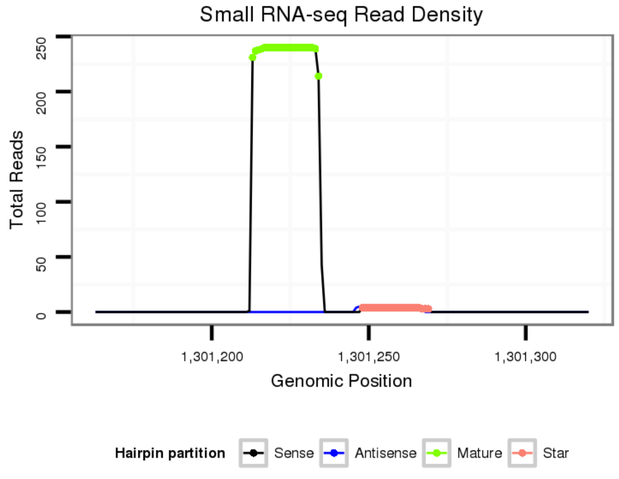
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

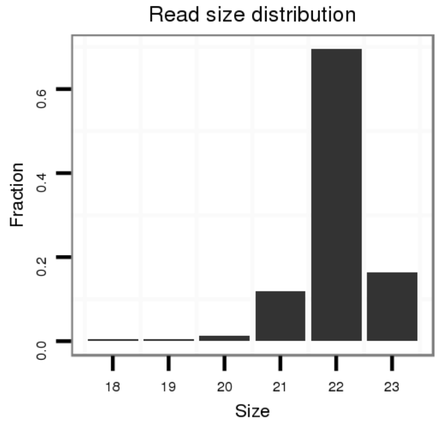
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_90	**scaffold_6308:1301213-1301270 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

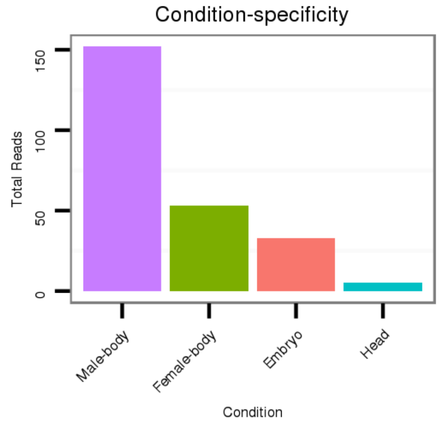
Legend: mature star mismatch in alignment mismatch in read

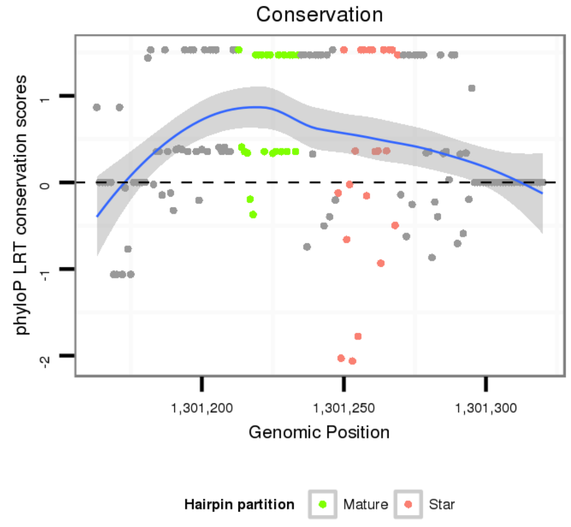
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dmoj\GI10984-in]

Repeatable elements

Name	Class	Family	Strand
(TATATG)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TACCATCGAGAGCTCGCGATATACATGGCTCTATATTGATATACACATATAAATGCATACATAAACACATGTATGTCTATTTTTACATGTGTTATGTATGCATATCTATGTCTATATTGGAATGCATAGGTGCCTAAAGGCTTTCTTTTCCCTTAGGG **********(((((((.(((((...(((((((((((.(((((((((.....)))))))))))))))))))...)))))).)))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V056 head	V041 embryo	V049 head
..........AAATGCATACATAAACACATGT..........	22	0	1	164.00	164	135	16	10	2	1	0
..........AAATGCATACATAAACACATGTA..........	23	0	1	40.00	40	6	15	18	1	0	0
..........AAATGCATACATAAACACATG..........	21	0	1	25.00	25	7	15	1	1	0	1
..........AAATGCATACATAAACACATGTC..........	23	1	1	5.00	5	3	2	0	0	0	0
..........AATGCATACATAAACACATGT..........	21	0	1	4.00	4	2	2	0	0	0	0
..........AAATGCATACATAAACACATGC..........	22	1	1	3.00	3	0	0	3	0	0	0
..........CATGTGTTATGTATGCATATCT..........	22	0	1	3.00	3	0	1	1	0	1	0
..........AATGCATACATAAACACATGTA..........	22	0	1	2.00	2	0	2	0	0	0	0
..........AAATGCATACATAAACACATGTT..........	23	1	1	1.00	1	1	0	0	0	0	0
..........AAATGCATACATAAACACATGTAAA..........	25	2	1	1.00	1	0	0	1	0	0	0
..........CATGTGTTATGTATGCATA..........	19	0	1	1.00	1	1	0	0	0	0	0
..........GCATACATAAACACATGT..........	18	0	1	1.00	1	0	0	1	0	0	0
..........TGCATACATAAACACATGTA..........	20	0	1	1.00	1	0	1	0	0	0	0
..........TAAATGCATACATAAACACATGT..........	23	0	1	1.00	1	0	1	0	0	0	0
..........AAATGCATACATAAACACATGTAA..........	24	1	1	1.00	1	0	1	0	0	0	0
..........ATGCATACATAAACACATGT..........	20	0	1	1.00	1	1	0	0	0	0	0
..........AAATGCATACATAAACACAT..........	20	0	1	1.00	1	0	1	0	0	0	0
..........AAATGCATACATAAACACATGTAC..........	24	1	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

ATGGTAGCTCTCGAGCGCTATATGTACCGAGATATAACTATATGTGTATATTTACGTATGTATTTGTGTACATACAGATAAAAATGTACACAATACATACGTATAGATACAGATATAACCTTACGTATCCACGGATTTCCGAAAGAAAAGGGAATCCC **********(((((((.(((((...(((((((((((.(((((((((.....)))))))))))))))))))...)))))).)))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V110 male body
..........ATGTACACAATACATACGTATA..........	22	0	1	4.00	4	2	2	0
..........TGTACACAATACATACGTATA..........	21	0	1	1.00	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1301163-1301320 +	dmo_90	TACCATCGAGAGCTCGCGATATACATGGCTCTATATTGATATACACATATAAATGCATACATAAACACATGTATGTCTATTTTTACATGTGTTATGTATGCATATCTATGTCTATATTGG-AATGCATAGGTGCCTAAAGGCTTTCTTTTCCCTTAGGG
droVir3	scaffold_13047:3570108-3570221 -		----------ATATATATATATATATATATATATATATATATAAAATATATATATATATATTATATCTATATATATGTTATATATGTATATATCTATATATACA-TACACATCTAAA----------
droGri2	scaffold_15126:6700918-6701032 +		----------ATATACATAGACATATATGTATATATATATATATATATATATATATATATATGTATGTGTATGATATATGTATATCTGTGTATATAAATGACATATATGTCTA----------
droWil2	scf2_1100000012590:868-981 +		----------ATATATATGTATATATATATATATATATATATATATATGTATATATATACATATATATGCACATATGTATGTATATACA-TATATATATATGC----------
dm3	chrUextra:7277937-7278051 +		----------ATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATATA-TATATATATATAC----------
droSim2	2L:11683535-11683655 +		T-----CGAGTGC------TTTATATATATATATATATATATATATATATATATATATATATATATATATATATATATATTTCTGCCTGATATATATATATATATATATATATATA-TATATATATATA----------
droEre2	scaffold_4690:9443753-9443816 +		T------ATATTAA------TTCGTACATATATGTACATACATATGTGCATATG----------TGTGTGCGACATGTACAGATAT----------|----------

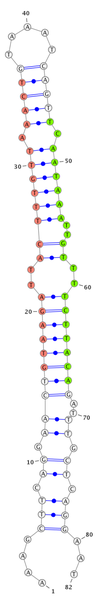
Generated: 09/08/2015 at 08:05 PM

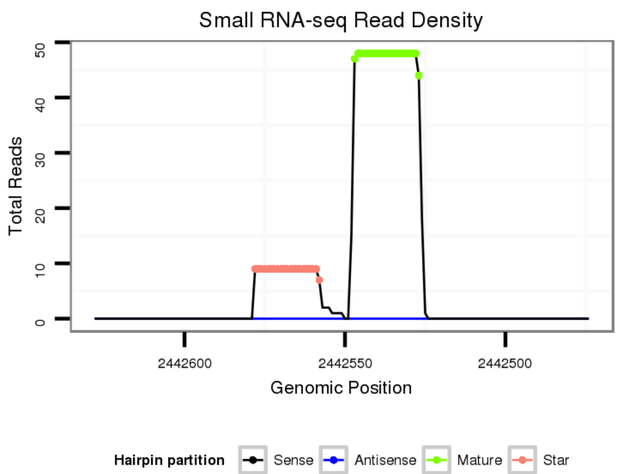
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

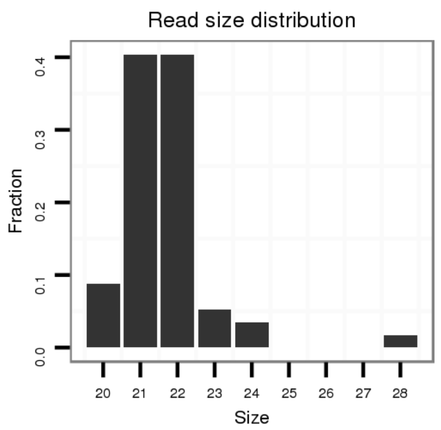
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_110	**scaffold_6540:2442524-2442578 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

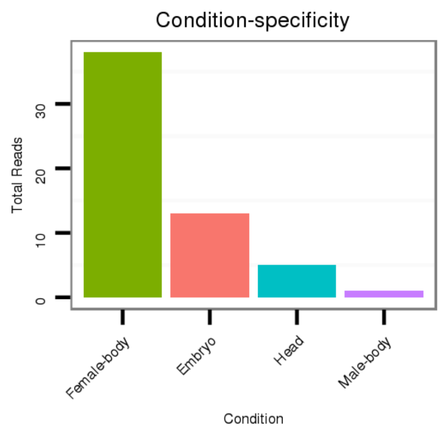
Legend: mature star mismatch in alignment mismatch in read

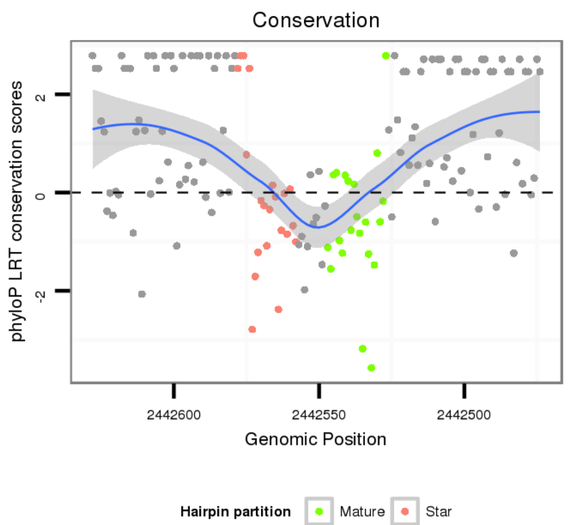
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI23724-in]; CDS [Dmoj\GI23724-cds]; CDS [Dmoj\GI23724-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGCACCGTATTGCCCGACCACTGCAATACCCTGCAAAAGCTTCAGGAACTGTAAGATTACTTTGTTAAACTGTAAATCAGTTCAATAAATTGTTTTCTTACAGATTTGCTCAGGAATTAAAAACCTATGGACGATTTGCTCTTGGCCTTGCCATG											
***********************************....(((.((.((((((((((..(((((((((.(((((.....))))).)))))))..))..)))))))..))).)))...***********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V056 head	V049 head	V110 male body	V041 embryo
.....TCAATAAATTGTTTTCTTACAGT.....	23	1	1	96.00	96	49	7	20	14	4	2
.....TTCAATAAATTGTTTTCTTACAGT.....	24	1	1	53.00	53	42	5	3	0	3	0
.....TCAATAAATTGTTTTCTTACA.....	21	0	1	16.00	16	0	13	1	1	1	0
.....TCAATAAATTGTTTTCTTACAGC.....	23	1	1	15.00	15	15	0	0	0	0	0
.....TCAATAAATTGTTTTCTTACAG.....	22	0	1	13.00	13	2	11	0	0	0	0
.....TCAATAAATTGTTTTCTTACAGTC.....	24	2	1	11.00	11	10	1	0	0	0	0
.....TTCAATAAATTGTTTTCTTACAGC.....	24	1	1	11.00	11	11	0	0	0	0	0
.....TTCAATAAATTGTTTTCTTACA.....	22	0	1	10.00	10	1	6	1	2	0	0
.....GTAAGATTACTTTGTTAAACT.....	21	0	1	5.00	5	4	0	0	0	0	1
.....CAATAAATTGTTTTCTTACAGT.....	22	1	1	4.00	4	3	1	0	0	0	0
.....TCAATAAATTGTTTTCTTAC.....	20	0	1	3.00	3	0	3	0	0	0	0
.....TTCAATAAATTGTTTTCTTACAG.....	23	0	1	3.00	3	1	2	0	0	0	0
.....AATAAATTGTTTTCTTACAGT.....	21	1	1	2.00	2	2	0	0	0	0	0
.....GTAAGATTACTTTGTTAAAC.....	20	0	1	2.00	2	2	0	0	0	0	0
.....TTCAATAAATTGTTTTCTTAC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....GTAAGATTACTTTGTTAAACTGTAAATC.....	28	0	1	1.00	1	1	0	0	0	0	0
.....GTAAGATTACTTTGTTAAACTGTA.....	24	0	1	1.00	1	0	1	0	0	0	0
.....TCAATAAATTGTTTTCTTACAGG.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TTCAATAAATTGTTTTCTTACAGA.....	24	0	1	1.00	1	1	0	0	0	0	0
.....GTAAGATTACTTTGTTAAACC.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TCAATAAATTGTTTTCTTACATT.....	23	2	1	1.00	1	0	0	0	1	0	0
.....CAATAAATTGTTTTCTTACAG.....	21	0	1	1.00	1	0	1	0	0	0	0
.....AAATTGTTTTCTTACAGT.....	18	1	4	0.25	1	1	0	0	0	0	0

Anti-sense strand reads

ACGTGGCATAACGGGCTGGTGACGTTATGGGACGTTTTCGAAGTCCTTGACATTCTAATGAAACAATTTGACATTTAGTCAAGTTATTTAACAAAAGAATGTCTAAACGAGTCCTTAATTTTTGGATACCTGCTAAACGAGAACCGGAACGGTAC						
************************************....(((.((.((((((((((..(((((((((.(((((.....))))).)))))))..))..)))))))..))).)))...***********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body
.....TCAATAAATTGTTTTCTTACAGG.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TTCAATAAATTGTTTTCTTACAGA.....	24	0	1	1.00	1	1	0	0	0	0	0
.....GTAAGATTACTTTGTTAAACC.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TCAATAAATTGTTTTCTTACATT.....	23	2	1	1.00	1	0	0	0	1	0	0
.....CAATAAATTGTTTTCTTACAG.....	21	0	1	1.00	1	0	1	0	0	0	0
.....AAATTGTTTTCTTACAGT.....	18	1	4	0.25	1	1	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:2442474-2442628 -	dmo_110	TGCACCGTATTGCCCGACCACTGCAATACCCTGCAAAAGCTTCAGGAACTGTAAGATTACTTTGT---TAAA----------CTGTAAATCAGTTCA----------AT------AA----------ATTG---------TTTTCTTACAGATTTGCTCAGGAATTAAAAACCTATGGACGATTTGCTCTTGGCCTTGCCATG
droVir3	scaffold_13047:6607615-6607772 -		TGCAACGTTTTGCCAGAGCAATGCAATACACTGCAAAAGTTCAGGAACTGTAGGCGTGAATTG----TG--------A---GCTAATAGCGG----------C----T----AAA--TTA--------A---TTATA---TCACTTTTACAGCTTTGCTCAGGAACTGAAAACCTATGGACGATTTGCCCTTGGACTGGCTATG
droGri2	scaffold_14830:1360155-1360321 -		TGCACCATTCTGCCGGAGCAATGCAATACACTGCAAAAATTTCAAGAACTGTAAGTGAATTTTAA----GTCATGTTAGAA-CTGTGGAATAATCAA----------T-------AA----------TTGA-----ATTTATTTCGTATAGCTTTGCTCAGGAACTGAAAACCTATGGAAGATTTGCTCTCGGTCTGGCCATG
droWil2	scf2_1100000004902:4682807-4682971 -		TGGTCCAATTTGCCGGATTATTGCAATAGGGTGGAAAAGATTCAGGATCTGTAAGTACTT-----------------------TTAAGTAACTCATGTAGTCTCTCCTTTTAAACCCA-TA--------T-----AT-ATTAAATTTACAGCTTTGCCGCAGAGTTAAAAAGTTACGGGCGTTTGCGCTTTGGGCCTGGCTTTG
dp5	2:29137768-29137929 +		TGCACTGAACTGCCAGAACACTGCAATACCCTGGAGAAGCTCCAAAACTGTAAGATAAGGAATGCGTTTTA----------AA----------TT----AAA--ATAAATTTATCCATCTTAAT-----TTTCGCTCAAGCTTTGCCAGGAGCTGAAAGCCTATGGACGCTTTGCCCTGGGTCTTGCCATG
droPer2	scaffold_6:4461788-4461949 +		TGCACTGAACTGCCAGAACACTGCAATACCCTGGAAAAGCTCCAAAACTGTAAGATAAGGAATGCGTTTTA----------AA----------TT----AAA--ATAAATTTATCCATCTTAAT-----TTTCGCTCAAGCTTTGCCAGGAGCTGAAAGCCTATGGACGCTTTGCCCTGGGTCTTGCCATG
droAna3	scaffold_13340:15811132-15811293 +		TGCACGGCTCTGCCCGAGCAATGGCAGCAGCTAGAGAAGCTACAGGATCTGTAAGCAGAAGCTG----GT--------TCTC----------TTTTTTTTTCATTTTTAATTA-TA--------A-----T-----CTCTTTATCTTATAAGCTTTGCTGAGGAACTTAAATCCTATGGACGATTTGGCCTTGGATTGGCGTTG
droBip1	scf7180000396708:4222313-4222469 -		TGCACGACTCTGCCCGAGCAATGTGAGCAGATTAGAGAAGCTCCAAGATCTGTAAGTGGATAACTA----AT--------TCTT----------AATTTTTATC-----------AATATTTAA-----T-----GGTTTAATTTTTAAGCTTTGCTCACGAACTTAAATCCTATGGCGCGATTTGCCCTTGGATTGGCCTTG
droKik1	scf7180000302809:241004-241165 -		TGCACACTCTGCCGGACCACTGTGACAGACTGCAAAAGTTGCAGGATCTGTATGGCAATCTGTTCAAA---------------GAAAATCATCA----------T-------TAGTAATGCTCTTTTTCC-----CCACTGTCTAGCTTTGCCAGGAGGCTGAAGACCTACGGCCGTTTCGCTCTTGGCCTGGCCATG
droFic1	scf7180000453800:521385-521542 +		TGCACGACTTTGCCGGTTCACTGTGACAGCGTTGCAGAAGCTGCAGGATCTGTAAGCAAATTATTA----AT--------ACATTTGAAATAACTAT----------TA-------GA----------T----AAACACCCGTTTTTTTAGTTTCGCCGCAGGAGCTGAAGACTTACGGACGCTTTGCTCTTGGTCTGGCCATG
droEle1	scf7180000491008:2215621-2215784 -		TGCACGACATTGCCGAAACACTGCGACAGATTGCAGAAACTCCAGGACCTGTAAGCATGTGATAT----GA--------ATAATGTCATCAACTAA----------TA-------GA----------TGTTGAATTCGTTTACTGCTCTAGTTTTGCCGCAGGAGCTGAAGACTTACGGACGCTTTGCCCTTGGCCTGGCCATG
droRho1	scf7180000773440:9846-10005 +		TGCACGACTTTGCCGAATCACTGCGATACATTGCAGAAACTCCAGGATCTGTAAGGATTTGTTTT----AT--------ATAGAGTGATCAGTTCA----------TT-------AA----------TAGTTTACA----CACCGCTTTAGTTTTGCCGCAGGAGCTAAAGACTTACGGACGCTTTGCTCTTGGCCTGGCGATG
droBia1	scf7180000299102:1923386-1923542 -		TGCACAACCTTGCCCGACCACTGCGACAGATTAGAGAAGCTCCAGGATCTGTAAGGATATGATAA----GG--------ATAGAGAGATCAGTTCA----------TT-------GA----------TGTAAT------CCTTCTTTCAGATTTTGCCGCAGGAGCTGAAGACTTACGGACGCTTTGCTCTGGGCCTGGCCATG
droTak1	scf7180000414450:178318-178428 +		TGCACAAACCTGCCGGATCACTGCGACAGATTGCAGAAGCTCCAGGATCTGTAAGAGAATTATTG----TG--------ATTA-TTAGAGATTGGA----------T----------TTTA----A--GTGAACT-----CGTTTTTTTAAATAT----------
droEug1	scf7180000409246:393524-393687 +		TGCACAAATTTGCCAGATCACTGCGACAGTTGCAGAAGCTCCAAGATCTGTAAGCATGTGATTC----TG--------ACTGAGAGCATCCGTACA----------TA-------AA----------AGTTATTTACACTTCCCGTTTAGTTTTGCCGCAGGAACTAAAAAGTTACGGACGCTTTGCTCTTGGTCTAGCCATG
dm3	chr3R:14043265-14043425 +		TGCACAAATTTGCCGGACCACTGCGACAGCGTTACAGAAGCTCCAGGATCTGTAAGCAAATGATTTTTTAAG----------AGTTAAAATAGTTAA----------TT-------GA----------TGTTTTAT-----ATGTCCATAGTTTTGCCGCAGGAGCTGAAGACATACGGACGCCTTTGCATTGGTTTGGCATTG
droSim2	3r:7235633-7235793 -		TGCACCAATTTGCCGGACCACTGCGACAGATTACAGAAGCTACAGGATCTGTAAGCGAATGATTTTTAAAG----------AGGGAAAATAGTTAA----------TT-------GA----------TGTTTTAT-----ATCTCTATAGCTTTGCCGCAGGAGCTGAAGACATACGGACGCTTTGCTCTTGGCTTGGCATTG
droSec2	scaffold_12:106826-106986 -		TGCACCAATTTGCCGGACCACTGCGACAGATTACAGAAGCTACAGGATCTGTAAGCGAAAGATTTTTAAAG----------AGGGAAAATAGTTAA----------TT-------TA----------TGTTCTAT-----ATCACCATAGCTTTGCCGCAGGAGCTGAAGACATACGGACGCTTTGCTCTTGGCTTGGCATTG
droYak3	3R:2651111-2651273 +		TGCACAACTTTGCCGGACCACTGCGACAGATTACAGAAGCTTCAGGACCTGTAAGCAAATGATTT----TA--------GCAG-GGAAAATAGTCAA----------TT-------AA----------TGTATTATATGCCTTTTGTCATAGTTTCGCCGCAGGAGCTAAAGACATACGGCCGCTTTGCTCTTGGCCTGGCATTG
droEre2	scaffold_4770:7591766-7591936 -		TGCACAACTTTGCCGGACCACTGCGACAGATTACAGAAGCTACAGGACCTGTAAGCAAATGATTTT--ACGGAATTT-----TCTGGGAATATAATCAA----------TC-------GA----------TTTATTAAACGCCTTTCGCCATAGTTTTGCCGCAGGAGCTGAAGACATACGGACGCTTTGCTCTTGGCCTGGCATTG

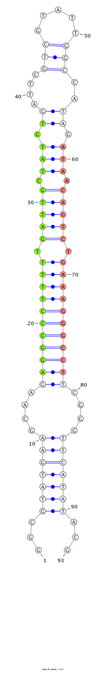
Generated: 09/08/2015 at 09:53 PM

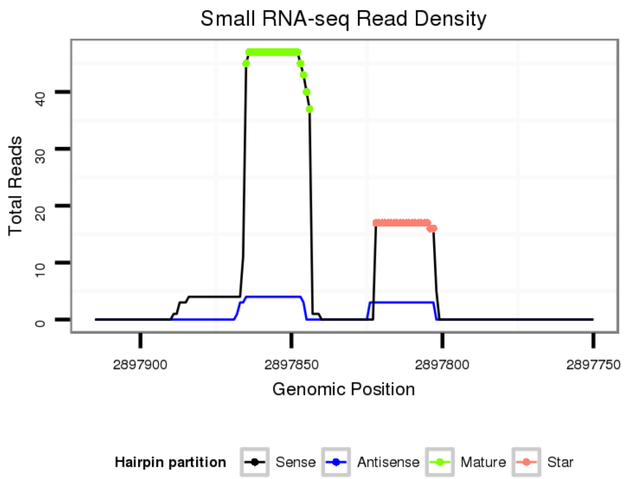
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

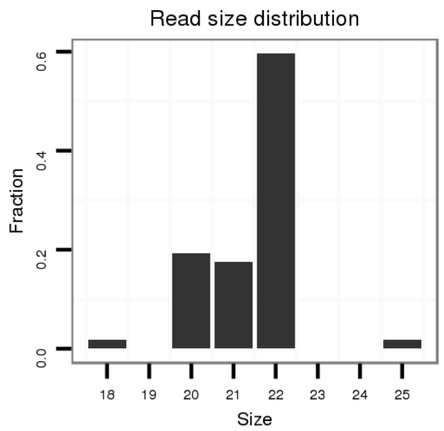
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_91	**scaffold_6328:2897800-2897865 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

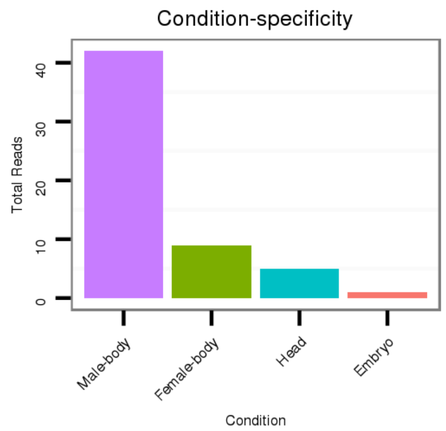
Legend: mature star mismatch in alignment mismatch in read

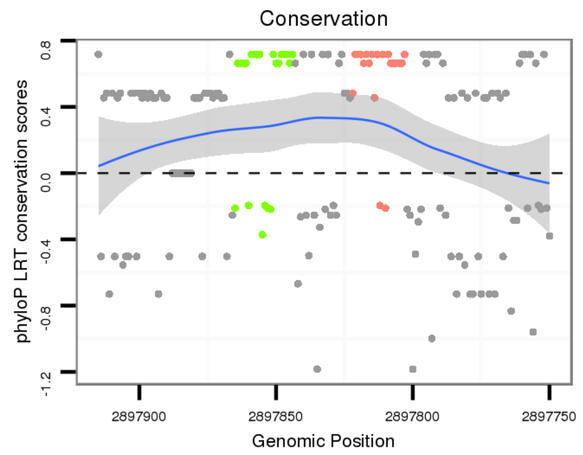
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATCTCAGCTAGGAAGTGAGTGCAACGCCGTGGATAGGCGTATGAAGCAAGAGGCCCTTTTTGATTGCTATGTGATTCGTCGTATTGGCCATAGATAACAGTCTGAAAGGGCCTTCGGGTTCATATACGGTGCCATCTCTGCCGCTCACAATCGGCAATATCGATTT **********...(((((((....((((((((((.(((((.(((.((....(((.....)))..))).)))).)))))).)))))))))).....))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head	M060 embryo	V049 head	V041 embryo
.....ATAACAGTCTGAAAGGGCCTTT.....	22	1	1	70.00	70	69	1	0	0	0	0
.....ATAACAGTCTGAAAGGGCCTTTT.....	23	2	1	36.00	36	33	2	1	0	0	0
.....AGGCCCTTTTTGATTGCTATGT.....	22	0	1	34.00	34	28	1	5	0	0	0
.....AGGCCCTTTTTGATTGCTATGTC.....	23	1	1	21.00	21	19	2	0	0	0	0
.....ATAACAGTCTGAAAGGGCCTTTTC.....	24	3	1	12.00	12	12	0	0	0	0	0
.....ATAACAGTCTGAAAGGGCCT.....	20	0	1	11.00	11	9	1	0	1	0	0
.....ATAACAGTCTGAAAGGGCCTT.....	21	0	1	5.00	5	3	2	0	0	0	0
.....ATAACAGTCTGAAAGGGCCTTTTT.....	24	3	1	4.00	4	4	0	0	0	0	0
.....ATAACAGTCTGAAAGGGCCTTTCT.....	24	3	1	4.00	4	4	0	0	0	0	0
.....AGGCCCTTTTTGATTGCTATG.....	21	0	1	3.00	3	1	2	0	0	0	0
.....GAGGCCCTTTTTGATTGCTAT.....	21	0	1	3.00	3	2	0	0	1	0	0
.....GAGGCCCTTTTTGATTGCT.....	19	0	1	2.00	2	1	0	0	0	1	0
.....ATAACAGTCTGAAAGGGCCTTTC.....	23	2	1	2.00	2	2	0	0	0	0	0
.....GAGGCCCTTTTTGATTGCTA.....	20	0	1	2.00	2	2	0	0	0	0	0
.....GTGGATAGGCGTATGAAGCAAG.....	22	0	1	2.00	2	2	0	0	0	0	0
.....GGCCCTTTTTGATTGCTATGT.....	21	0	1	2.00	2	0	2	0	0	0	0
.....AACAGTCTGAAAGGGCCTTTTT.....	22	3	3	1.33	4	1	2	0	0	0	1
.....AGGCCCTTTTTGATTGCTATGTCT.....	24	2	1	1.00	1	1	0	0	0	0	0
.....ATAACAGTCTGAAAGGGCCTTTCC.....	24	3	1	1.00	1	1	0	0	0	0	0
.....GAGGCCCTTTTTGATTGCTATGTC.....	24	1	1	1.00	1	1	0	0	0	0	0
.....GATAGGCGTATGAAGCAAG.....	19	0	1	1.00	1	1	0	0	0	0	0
.....AGGCCCTTTTTGATTGCTATGTGAT.....	25	0	1	1.00	1	0	1	0	0	0	0
.....GAGGCCCTTTTTGATTGCC.....	19	1	1	1.00	1	0	0	0	1	0	0
.....AACAGTCTGAAAGGGCCTTTCC.....	22	3	1	1.00	1	1	0	0	0	0	0
.....GAGGCCCTTTTTGATTGCTCC.....	21	2	1	1.00	1	0	0	0	0	1	0
.....CCGTGGATAGGCGTATGAAGCAAG.....	24	0	1	1.00	1	1	0	0	0	0	0
.....ATAACAGTCTGAAAGGGCCTTTTA.....	24	3	1	1.00	1	1	0	0	0	0	0
.....ATAACAGTCTGAAAGGGC.....	18	0	1	1.00	1	1	0	0	0	0	0
.....AGGCCCTTTTTGATTGCTATGTCC.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TAACAGTCTGAAAGGGCCTTTT.....	22	2	1	1.00	1	1	0	0	0	0	0
.....AACAGTCTGAAAGGGCCTTTTA.....	22	3	2	0.50	1	1	0	0	0	0	0
.....ATAACAGTCTGAAAGGGCCTTTCA.....	24	3	2	0.50	1	1	0	0	0	0	0

Anti-sense strand reads

TAGAGTCGATCCTTCACTCACGTTGCGGCACCTATCCGCATACTTCGTTCTCCGGGAAAAACTAACGATACACTAAGCAGCATAACCGGTATCTATTGTCAGACTTTCCCGGAAGCCCAAGTATATGCCACGGTAGAGACGGCGAGTGTTAGCCGTTATAGCTAAA **********...(((((((....((((((((((.(((((.(((.((....(((.....)))..))).)))).)))))).)))))))))).....))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V056 head	V049 head	V110 male body
.....TCTATTGTCAGACTTTCCCGGA.....	22	0	1	3.00	3	1	2	0	0	0
.....TCTCCGGGAAAAACTAACGATA.....	22	0	1	2.00	2	2	0	0	0	0
.....TCCGGGAAAAACTAACGATA.....	20	0	1	1.00	1	0	0	1	0	0
.....TTCTCCGGGAAAAACTAACGAT.....	22	0	1	1.00	1	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6328:2897750-2897915 -	dmo_91	ATCTCAGCTAGGAAGT---GAGTGCAACGCCGTGGATAGGCGTATGAAGCAAGAGGCCCTTTTTGATTGCTATGTGATTCGTCGTATTGGCCATAGATAACAGTCTGAAAGGGCCTTCGGGTTCATAT------ACGGTGCCATCTCTGCCGCTCACAATCGGCAATATCGAT---TT
droVir3	scaffold_13042:903140-903308 -	dvi_187	ACCTAAACTTAAAATTTAGAGTGCCACGT--------GGCATATGAAGCGAAAGGCCCTTTTCGACTGCTATGTGCATTTTTGACTACTCATAGATAACAGTCTGAAAGGGCCTTTTGGCTCACGATGCAAACACAGCGATAACGATAACGATAACGAT-AACAATAACGATAACTT
droGri2	scaffold_15081:2041269-2041363 -	dgr_24	A----------------------------------AAGGGCCTTTTTTAGCTGCTATGTGAATTTTTCGACTAATCA----TAACAGT-TTAAGAGGGCCTATCCTCTCAAATG---ACGCA----------CGGGCAACACGCATT---CG

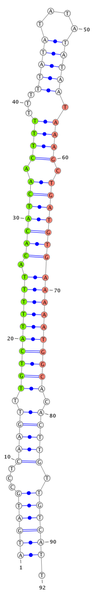
Generated: 09/08/2015 at 08:05 PM

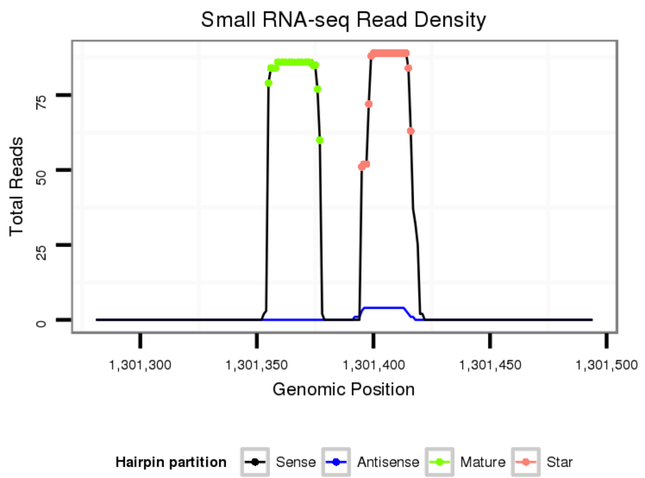
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	3
rescue.candidate	2

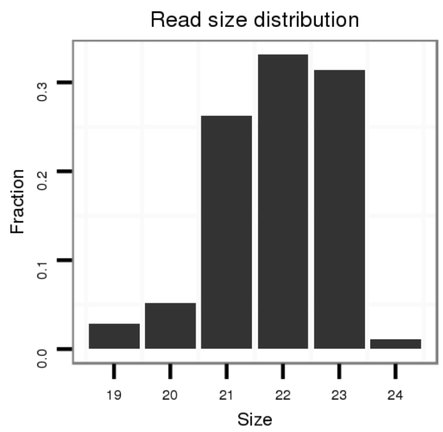
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_341	**scaffold_6308:1301331-1301444 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

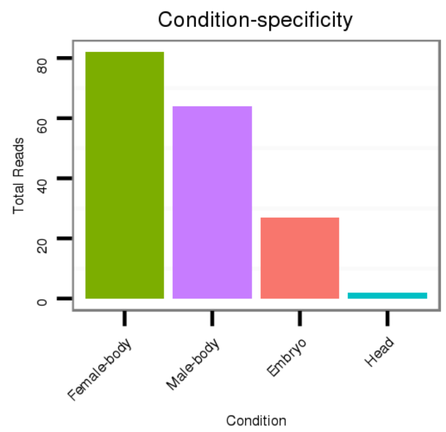
Legend: mature star mismatch in alignment mismatch in read

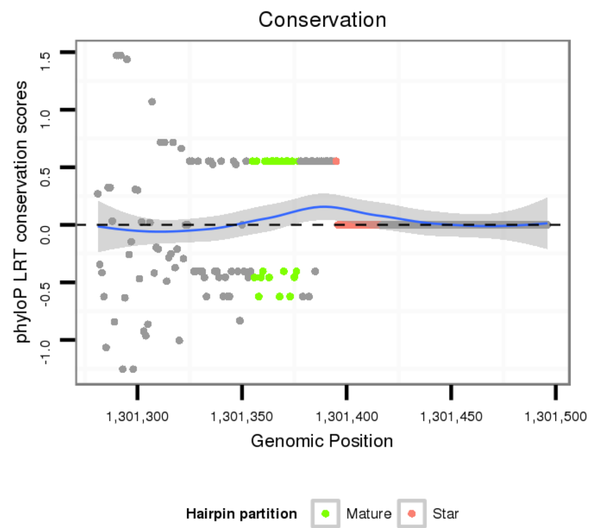
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dmoj\GI10984-in]

Repeatable elements

Name	Class	Family	Strand
AT_rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GGAATGCATAGGTGCCTAAAGGCTTTCTTTTCCCTTAGGGATTACGTACTCATCCGATAATGATGCCTCAAGTTTGTCATTTTTACACATCAACTTTTTTTTATATATATATAATAAAGCTGATGTGAAAAATGGCACACTTGTTGTCATTAGCAAAACTTCGGAGCAATTAGCAATGCGTCCATTAAGTGTTGAAGTAAGTGAAATTTATTAA **********(((((((...(((((.(((((((((((.(((((((.((((...(((((....)))))).)))).)))))))))))))))))).)))))).)))))))**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	M060 embryo	V041 embryo	V049 head	V056 head
..........TGTCATTTTTACACATCAACTTT..........	23	0	1	52.00	52	40	4	6	1	1	0
..........TAAAGCTGATGTGAAAAATGGC..........	22	0	1	25.00	25	0	19	4	1	0	1
..........TAAAGCTGATGTGAAAAATGG..........	21	0	1	21.00	21	0	21	0	0	0	0
..........TGTCATTTTTACACATCAACTT..........	22	0	1	16.00	16	12	2	2	0	0	0
..........GCTGATGTGAAAAATGGCACA..........	21	0	1	12.00	12	6	5	1	0	0	0
..........AGCTGATGTGAAAAATGGCACA..........	22	0	1	11.00	11	2	3	5	1	0	0
..........TGTCATTTTTACACATCAACTTTC..........	24	1	1	9.00	9	4	5	0	0	0	0
..........AGCTGATGTGAAAAATGGCAC..........	21	0	1	6.00	6	5	0	1	0	0	0
..........TAAAGCTGATGTGAAAAATG..........	20	0	1	5.00	5	0	5	0	0	0	0
..........TAAAGCTGATGTGAAAAATGGTC..........	23	2	1	5.00	5	0	5	0	0	0	0
..........TGTCATTTTTACACATCAACTTC..........	23	1	1	5.00	5	3	0	2	0	0	0
..........TGTCATTTTTACACATCAACT..........	21	0	1	5.00	5	5	0	0	0	0	0
..........GTCATTTTTACACATCAACTTT..........	22	0	1	4.00	4	4	0	0	0	0	0
..........AGCTGATGTGAAAAATGGCA..........	20	0	1	3.00	3	0	3	0	0	0	0
..........TGTCATTTTTACACATCAACTTTCC..........	25	2	1	3.00	3	3	0	0	0	0	0
..........TGTCATTTTTACACATCAACTTTT..........	24	0	1	2.00	2	2	0	0	0	0	0
..........AGCTGATGTGAAAAATGGCACAA..........	23	1	1	2.00	2	0	2	0	0	0	0
..........TTTGTCATTTTTACACATCAACT..........	23	0	1	2.00	2	2	0	0	0	0	0
..........GTCATTTTTACACATCAACTTTC..........	23	1	1	2.00	2	2	0	0	0	0	0
..........TGTCATTTTTACACATCAACTTTA..........	24	1	1	2.00	2	1	0	1	0	0	0
..........GCTGATGTGAAAAATGGCA..........	19	0	1	2.00	2	0	2	0	0	0	0
..........TGTCATTTTTACACATCAACTTTAA..........	25	2	1	2.00	2	2	0	0	0	0	0
..........TGTCATTTTTACACATCAACTTTCCC..........	26	3	1	2.00	2	2	0	0	0	0	0
..........ATTTTTACACATCAACTTT..........	19	0	1	2.00	2	1	0	1	0	0	0
..........GCTGATGTGAAAAATGGCAC..........	20	0	1	1.00	1	0	0	1	0	0	0
..........GCTGATGTGAAAAATGGCACACT..........	23	0	1	1.00	1	0	0	1	0	0	0
..........TTTGTCATTTTTACACATCAACC..........	23	1	1	1.00	1	0	0	1	0	0	0
..........AAAGCTGATGTGAAAAATGGC..........	21	0	1	1.00	1	0	0	1	0	0	0
..........TTGTCATTTTTACACATCAACT..........	22	0	1	1.00	1	1	0	0	0	0	0
..........TGTCATTTTTACACATCAACTA..........	22	1	1	1.00	1	1	0	0	0	0	0
..........GCTGATGTGAAAAATGGCACT..........	21	1	1	1.00	1	0	1	0	0	0	0
..........AGCTGATGTGAAAAATGGCACT..........	22	1	1	1.00	1	0	1	0	0	0	0
..........TGTCATTTTTACACATCAA..........	19	0	1	1.00	1	1	0	0	0	0	0
..........TGTCATTTTTACACATCAACTTTAAA..........	26	3	1	1.00	1	1	0	0	0	0	0
..........TGTCATTTTTACACATCAACTTTTCC..........	26	2	1	1.00	1	1	0	0	0	0	0
..........GTCATTTTTACACATCAACTT..........	21	0	1	1.00	1	1	0	0	0	0	0
..........CTGATGTGAAAAATGGCACACT..........	22	0	1	1.00	1	0	0	1	0	0	0
..........TGTCATTTTTACACATCAACTAAA..........	24	3	2	0.50	1	1	0	0	0	0	0

Anti-sense strand reads

CCTTACGTATCCACGGATTTCCGAAAGAAAAGGGAATCCCTAATGCATGAGTAGGCTATTACTACGGAGTTCAAACAGTAAAAATGTGTAGTTGAAAAAAATATATATATATTATTTCGACTACACTTTTTACCGTGTGAACAACAGTAATCGTTTTGAAGCCTCGTTAATCGTTACGCAGGTAATTCACAACTTCATTCACTTTAAATAATT **********(((((((...(((((.(((((((((((.(((((((.((((...(((((....)))))).)))).)))))))))))))))))).)))))).)))))))**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body
..........ATTTCGACTACACTTTTTACC..........	21	0	1	1.00	1	0	1
..........ATTTCGACTACACTTTTTAC..........	20	0	1	1.00	1	1	0
..........TTTCGACTACACTTTTTACCGT..........	22	0	1	1.00	1	1	0
..........ATTATTTCGACTACACTTTTTA..........	22	0	1	1.00	1	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1301279-1301494 +	dmo_341	TTGGAATGCATAGGTG-CCTAAAGGCTTTCTTTTCCCTTAGGGATTACGTACTCATCCGAT-----AATGATGCCTCAAGTTTGTCATTTTTACACATCAACTTTTTTTTATATATATATAATAAAGCTGATGTGAAAAATGGCACACTTGTTGTCATTAGCAAAACTTCGGAGCAATTAGCAATGCGTCCATTAAGTGTTGAAGTAAGTGAAATTTATTAA
droVir3	scaffold_12875:15865082-15865123 -		TAGCTCGGTATAAATG-CTAAAACTATACTTTTGTTTCATGG----------[-----]----------
droGri2	scaffold_15203:5567941-5568058 +		TAAGGATATATACTTATGTGGTTGATTTTCTTTGCTTTGAGT--TATATGTAAATCTATTCAGATCTGTGTGTG-TATATATTATATATTTAAATATAATTTTGTTGTTGTATATATATA----------
droWil2	scf2_1100000004768:2265616-2265642 -		TCTACATATATATTA-TATATAGATTT----------[-----]----------
dm3	chrUextra:28410578-28410597 +		CATATATACATATTG-CATA----------[-----]----------
droSim2	2r:11683644-11683655 +		TATATATATATA----[-----]----------

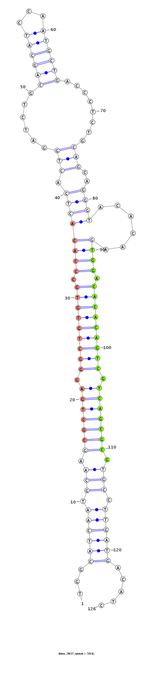
Generated: 09/08/2015 at 08:06 PM

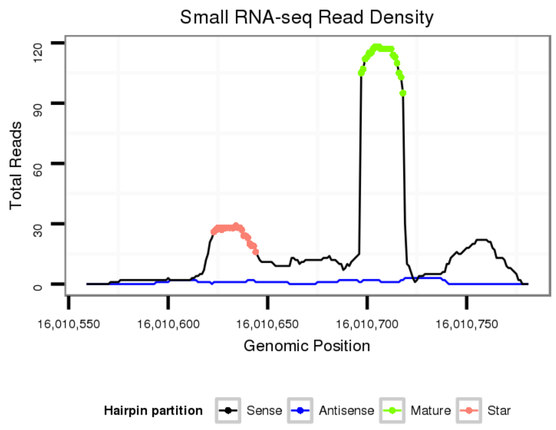
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

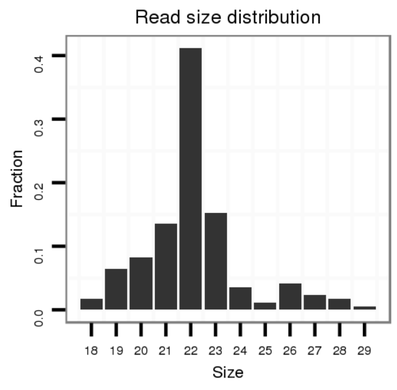
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2837	**scaffold_6496:16010609-16010731 +**	**confident**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

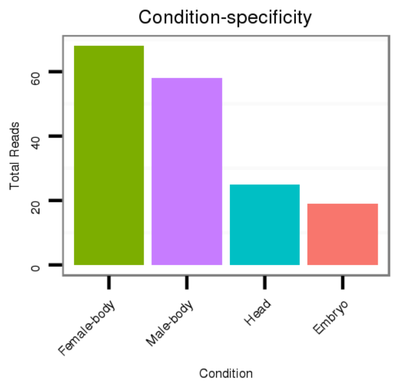
Legend: mature star mismatch in alignment mismatch in read

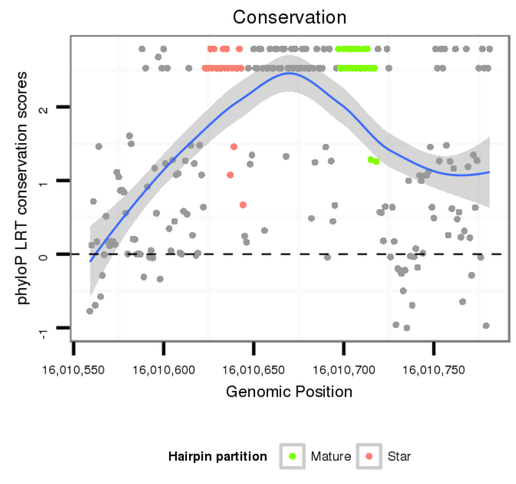
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dmoj\GI20807-cds]; utr5 [utr5_plus_5398]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CCAAAAATTATAATAACAACAACAACAACAGCAGCCACAGCAACATAGCTGGCATCAATGCAAGCGCTGAGGGCTGTGTGCCCACACTCACTGGATCTGCAGCATCCAATGCTGACCCTCTGCAGCAGGGTACACAAGTGGACACAGTCGTCAGCGCGTGCCTTGATGACATCACGAATGTTGCAACAGCAGCTGAAGCAGAGCAACACAACGGCCTCACT **********...(((((((.(((.(((((((.(((((((((.(((((((.(((.....(((((((...)))))))).....)))..))))).....))))..))))))))).))))))).)))..))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	V056 head	V049 head	M060 embryo	V041 embryo
.....TGGACACACAGTCGTCAGCGCG.....	22	0	1	60.00	60	14	24	7	10	0	5
.....TGGACACACAGTCGTCAGCGCGT.....	23	0	1	18.00	18	6	6	2	1	2	1
.....TGGACACACAGTCGTCAGCGTT.....	22	2	1	10.00	10	2	4	3	1	0	0
.....TGGACACACAGTCGTCAGCGC.....	21	0	1	8.00	8	3	4	0	1	0	0
.....CGCTGAGGGCTGTGTGCCCACA.....	22	0	1	3.00	3	1	0	0	0	0	2
.....TGGACACACAGTCGTCAGCGT.....	21	1	1	3.00	3	0	3	0	0	0	0
.....ATCCAATGCTGACCCTCTGCAGCAGG.....	26	0	1	3.00	3	3	0	0	0	0	0
.....TGGACACACAGTCGTCAGCGCT.....	22	1	1	3.00	3	1	1	0	0	1	0
.....CAAGCGCTGAGGGCTGTGT.....	19	0	1	3.00	3	3	0	0	0	0	0
.....CACAGTCGTCAGCGCGTGCCT.....	21	0	1	2.00	2	2	0	0	0	0	0
.....GGACACACAGTCGTCAGCGCG.....	21	0	1	2.00	2	0	1	1	0	0	0
.....GTACACAAGTGGACACACAGTCGTCAG.....	27	0	1	2.00	2	1	1	0	0	0	0
.....GCAAGCGCTGAGGGCTGTGT.....	20	0	1	2.00	2	1	1	0	0	0	0
.....CACACAGTCGTCAGCGCGTGCC.....	22	0	1	2.00	2	1	0	1	0	0	0
.....GTTGCAACAGCAGCTGAAGCAGAGC.....	25	0	1	2.00	2	0	2	0	0	0	0
.....TGGACACACAGTCGTCAGCG.....	20	0	1	2.00	2	0	1	1	0	0	0
.....AGCTGAAGCAGAGCAACACAACGGCCT....	27	0	1	2.00	2	2	0	0	0	0	0
.....AGCGCTGAGGGCTGTGTGCCCAC.....	23	0	1	2.00	2	0	0	1	0	1	0
.....CACTCACTGGATCTGCAGC.....	19	0	1	2.00	2	1	1	0	0	0	0
.....TGCAACAGCAGCTGAAGCAGA.....	21	0	1	2.00	2	0	2	0	0	0	0
.....ACACACAGTCGTCAGCGCGTGC.....	22	0	1	2.00	2	0	1	0	0	0	1
.....ATGACATCACGAATGTTGCAACAGC.....	25	0	1	2.00	2	2	0	0	0	0	0
.....AAGCGCTGAGGGCTGTGT.....	18	0	1	2.00	2	2	0	0	0	0	0
.....GACACACAGTCGTCAGCGCG.....	20	0	1	2.00	2	1	1	0	0	0	0
.....TGGACACACAGTCGTCAGC.....	19	0	1	2.00	2	1	1	0	0	0	0
.....AAGCGCTGAGGGCTGTGTGCCT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....AGCAGCTGAAGCAGAGCAACA.....	21	0	1	1.00	1	0	0	0	1	0	0
.....AGTGGACACACAGTCGTCAGCGCGTGCC.....	28	0	1	1.00	1	0	1	0	0	0	0
.....CAAGTGGACACACAGTCGTC.....	20	0	1	1.00	1	0	1	0	0	0	0
.....GTACACAAGTGGACACACA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....AGCGCTGAGGGCTGTGTGCCCA.....	22	0	1	1.00	1	0	0	0	0	0	1
.....TGATGACATCACGAATGTTGCA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....AGCGCTGAGGGCTGTGTGCCCACAC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....GTGTGCCCACACTCACTGGA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TGGACACACAGTCGTCAGCGCGC.....	23	1	1	1.00	1	0	1	0	0	0	0
.....GCAGCTGAAGCAGAGCAACACAACGGC.....	27	0	1	1.00	1	1	0	0	0	0	0
.....ACACACAGTCGTCAGCGA.....	18	1	1	1.00	1	0	0	0	0	1	0
.....TACACAAGTGGACACACAGTCGTCAGC.....	27	0	1	1.00	1	0	1	0	0	0	0
.....GCTGACCCTCTGCAGCAGG.....	19	0	1	1.00	1	1	0	0	0	0	0
.....GCAACAGCAGCTGAAGCAGAGC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....AGCGCTGAGGGCTGTGTGCCCACACT.....	26	0	1	1.00	1	1	0	0	0	0	0
.....CAAGCGCTGAGGGCTGTGTGCCT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....AGCTGAAGCAGAGCAACACA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....CATCCAATGCTGACCCTCTGCAGCAGG.....	27	0	1	1.00	1	1	0	0	0	0	0
.....TGGACACACAGTCGTCAGCGCGA.....	23	1	1	1.00	1	1	0	0	0	0	0
.....ACACAAGTGGACACACAGTCGTC.....	23	0	1	1.00	1	1	0	0	0	0	0
.....ATCCAATGCTGACCCTCTGCAGCAGGGTA.....	29	0	1	1.00	1	1	0	0	0	0	0
.....AGCTGAAGCAGAGCAACACAAC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....CTGAAGCAGAGCAACACAACGGC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....AGCGCTGAGGGCTGTGTGCC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GAAGCAGAGCAACACAACG.....	19	0	1	1.00	1	0	1	0	0	0	0
.....ACACTCACTGGATCTGCAGC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GCCCACACTCACTGGATCTGC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GACACACAGTCGTCAGCGCGC.....	21	1	1	1.00	1	1	0	0	0	0	0
..........ATAACAACAACAACAACAGCAGCCACAGC.....	29	0	1	1.00	1	1	0	0	0	0	0
.....GTGGACACACAGTCGTCAGCGCG.....	23	0	1	1.00	1	1	0	0	0	0	0
.....CAATGCAAGCGCTGAGGGCTG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CAGCAGGGTACACAAGTGG.....	19	0	1	1.00	1	0	1	0	0	0	0
.....AGGGCTGTGTGCCCACACTCACTGG.....	25	0	1	1.00	1	1	0	0	0	0	0
.....AACATAGCTGGCATCAATGCAAGCGCT.....	27	0	1	1.00	1	0	1	0	0	0	0
..............AACAACAACAACAGCAGCCACAGCA.....	25	0	1	1.00	1	1	0	0	0	0	0
.....AGTGGACACACAGTCGTCAGCT.....	22	1	1	1.00	1	0	1	0	0	0	0
.....CTCACTGGATCTGCAGCATCC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....GTTGCAACAGCAGCTGAAGCAGA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....CGCTGAGGGCTGTGTGCCCATT.....	22	2	1	1.00	1	1	0	0	0	0	0
.....CAGCTGAAGCAGAGCAACAC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GCGCTGAGGGCTGTGTGCC.....	19	0	1	1.00	1	0	0	0	0	1	0
.....GCCCACACTCACTGGATCTGCAG.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GCATCAATGCAAGCGCTGAGGGCTGTGC.....	28	1	1	1.00	1	0	0	0	0	1	0
.....GCTGAGGGCTGTGTGCCC.....	18	0	1	1.00	1	0	0	0	0	1	0
.....ATCCAATGCTGACCCTCTGCAGCAGGGT.....	28	0	1	1.00	1	1	0	0	0	0	0
.....ACATCACGAATGTTGCAACAGC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....GGACACACAGTCGTCAGCGCGT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....AAGCGCTGAGGGCTGTGTGCC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....CTGGCATCAATGCAAGCGCTGATC.....	24	2	1	1.00	1	0	0	1	0	0	0
.....GCCCACACTCACTGGATCTGCAGCAT.....	26	0	1	1.00	1	1	0	0	0	0	0
.....CAAGCGCTGAGGGCTGTGTGC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....GTTGCAACAGCAGCTGAAGCA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GATGACATCACGAATGTTGCAACAGC.....	26	0	1	1.00	1	1	0	0	0	0	0
.....AAGTGGACACACAGTCGTCAG.....	21	0	1	1.00	1	0	1	0	0	0	0
.....ACACAAGTGGACACACAGTCGTCAGC.....	26	0	1	1.00	1	0	1	0	0	0	0
.....AACAGCAGCTGAAGCAGAGCAACAC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TGGACACACAGTCGTCAGCGCGTTT.....	25	2	1	1.00	1	0	1	0	0	0	0
.....GCCCACACTCACTGGATCTGCAGC.....	24	0	1	1.00	1	1	0	0	0	0	0
.....CAACAGCAGCTGAAGCAGAGCAACAC.....	26	0	1	1.00	1	1	0	0	0	0	0
.....ACAAGTGGACACACAGTCGTC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....AACATAGCTGGCATCAATGC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....CTGCAGCAGGGTACACAAGT.....	20	0	1	1.00	1	0	1	0	0	0	0
.....ATCCAATGCTGACCCTCTGC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....CAAGCGCTGAGGGCTGTGTGCCCA.....	24	0	1	1.00	1	0	1	0	0	0	0
.....CTGAGGGCTGTGTGCCCACAC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....ATGTTGCAACAGCAGCTGAAGCAGAG.....	26	0	1	1.00	1	1	0	0	0	0	0
.....ATCCAATGCTGACCCTCTGCAGC.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GCTGAAGCAGAGCAACACAACGG.....	23	0	1	1.00	1	1	0	0	0	0	0
.....ACACAAGTGGACACACAGTCGTCA.....	24	0	1	1.00	1	0	1	0	0	0	0
.....ATGCAAGCGCTGAGGGCTGTG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GCGCTGAGGGCTGTGTGCCC.....	20	0	1	1.00	1	0	0	0	0	1	0
.....TGCAAGCGCTGAGGGCTGTGTGA.....	23	1	1	1.00	1	0	1	0	0	0	0
.....GACACACAGTCGTCAGCGCGTG.....	22	0	1	1.00	1	0	0	0	0	1	0
.....ATCCAATGCTGACCCTCTGCAGCA.....	24	0	1	1.00	1	1	0	0	0	0	0
.....GCCCACACTCACTGGATCTGCAGCATCC.....	28	0	1	1.00	1	1	0	0	0	0	0
.....AGCATCCAATGCTGACCCTCTGC.....	23	0	1	1.00	1	0	0	0	0	1	0
.....ATGCTGACCCTCTGCAGCAGG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GACACACAGTCGTCAGCGCGTGC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....GACACACAGTCGTCAGCGCGT.....	21	0	1	1.00	1	0	1	0	0	0	0
.....CGCTGAGGGCTGTGTGCCCACC.....	22	1	1	1.00	1	0	0	0	1	0	0
.....ACAAGTGGACACACAGTCGTCAGC.....	24	0	1	1.00	1	0	1	0	0	0	0
.....TGCAACAGCAGCTGAAGCAGAGC.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GAAGCAGAGCAACACAACGGC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....AAGCGCTGAGGGCTGTGTGCCCAC.....	24	0	1	1.00	1	0	0	0	0	1	0
.....ACAGTCGTCAGCGCGTGCCT.....	20	0	1	1.00	1	1	0	0	0	0	0
.....ATCAATGCAAGCGCTGAGGGCTGTGT.....	26	0	1	1.00	1	0	1	0	0	0	0
.....CAACAGCAGCTGAAGCAGA.....	19	0	3	0.67	2	2	0	0	0	0	0
.....GCAACAGCAGCTGAAGCAGAG.....	21	0	2	0.50	1	1	0	0	0	0	0
.....ACAACAACAACAACAGCAGCCACAGC.....	26	0	2	0.50	1	1	0	0	0	0	0
.....CAACAACAACAGCAGCCACAGC.....	22	0	2	0.50	1	1	0	0	0	0	0
.....AACAACAACAACAACAGCAGCCACAGC.....	27	0	2	0.50	1	1	0	0	0	0	0
.....GCAACAGCAGCTGAAGCAGA.....	20	0	3	0.33	1	1	0	0	0	0	0
.....AACAACAACAACAGCAGCCAC.....	21	0	13	0.15	2	1	1	0	0	0	0
.....CAACAACAACAACAGCAGCCA.....	21	0	20	0.05	1	1	0	0	0	0	0
.....AATAACAACAACAACAACAGCAGC.....	24	0	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

GGTTTTTAATATTATTGTTGTTGTTGTTGTCGTCGGTGTCGTTGTATCGACCGTAGTTACGTTCGCGACTCCCGACACACGGGTGTGAGTGACCTAGACGTCGTAGGTTACGACTGGGAGACGTCGTCCCATGTGTTCACCTGTGTGTCAGCAGTCGCGCACGGAACTACTGTAGTGCTTACAACGTTGTCGTCGACTTCGTCTCGTTGTGTTGCCGGAGTGA **********...(((((((.(((.(((((((.(((((((((.(((((((.(((.....(((((((...)))))))).....)))..))))).....))))..))))))))).))))))).)))..))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	V049 head	V041 embryo	M060 embryo
.....CCCATGTGTTCACCTGTGTGT.....	21	0	1	1.00	1	1	0	0	0	0
.....ACGGAACTACTGTAGTGCTTA.....	21	0	1	1.00	1	1	0	0	0	0
.....GCGACTCCCGACACACGGGTG.....	21	0	1	1.00	1	1	0	0	0	0
.....CGGAACTACTGTAGTGCTTAC.....	21	0	1	1.00	1	1	0	0	0	0
.....GCACGGAACTACTGTAGTGCT.....	21	0	1	1.00	1	1	0	0	0	0
.....GGAGACGTCGTCCCATGTGTT.....	21	0	1	1.00	1	1	0	0	0	0
.....TGTATCGACCGTAGTTACGTT.....	21	0	1	1.00	1	1	0	0	0	0
.....GTGTCGTTGTATCGACCGTAG.....	21	0	1	1.00	1	1	0	0	0	0
.....CCTGTGTGTCAGCAGTCGCGCA.....	22	0	1	1.00	1	0	0	1	0	0
.....GGTGTGAGTGACCTAGACGTC.....	21	0	1	1.00	1	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6496:16010559-16010781 +	dmo_2837	CCAAAAT----------T----A----------TAATAACAAC-------AACAACAACAGCAGCCACAGCAACATAG---CTGGCATCAATGCAAGCGCTGAGGGCTGTGTGCCCACACTCACTGGATCTGCAGCATCCA------ATGCTGACCCTCTGCAGCAGGGTAC---AC---AAGTGGACACACAGTCGTCAGCGCGTGCCTTGATGACATCACGAATGTTGCAACAGCAGCTGAAGCAGAGCAACACAACGGCCTCACT
droVir3	scaffold_12875:10928661-10928859 -		CCAAAAAG----------C----AG----A----------GC----------------------AA-----------CAG------CAACAGAG---CTAGCGTCAATGCAAACGCTGAGGGCTGTGTGTGCCACACTCACTGGATCTGCAGCATCCA------ATGCTGACCCTCTGCAGCAGGGTAC---AC---AAGTGGACACACAGTCGTCAGCGCATGCCTTGACCTGGAAGAG---GTTGCAACAGCAGCTGAAGCAGAGCAACACAACGGCCTCGCT
droGri2	scaffold_15245:4030250-4030466 -	dgr_446	CCAAGAAA----------A----A----------------------GAGTC-----TCAGCAACAAG---AAC---AGTAGCAACGGCT---CTGGCGTCAATGCAGAGCGCTGAGGGCTGTGCGTCCACATACACTGGATCTGCAGCATCCA------ATGCTGACCCTCTGCGCAGGGTAT---AT---TAGTGGACACACAGTCGTCAGCGCGTGCATTGGCGCTGAAGCGATTGCTGCAACAGCAGCTGAAGCAGACACACACGACAGCATCGCT
droWil2	scf2_1100000004512:1834883-1835103 +	dwi_4564	CAACAAGC----------C----AAAGTCAAC-GC--------------------TAAC------AGCAACGGTATCAGCTGA----CCAGTCAGCTTAGGCGCTGAGGGCTGTGCGTCCACAAACTTGGATCTGCAGCATCCATATTATAATGCTGACCCTCTGCGCAGGGTTTAACAGAACTGGTGGACACACAGTCGTCAGCGCGTTCGCTGATA------GGGGAACTGAAACTGGAGTTGAAACGCACACGAACTATGGCCTCACT
dp5	3:17670180-17670377 +		ACACAAGCAGCA---GCA----C--------GCCAAAAACATC----------------------ACC---TGCAACAGC---T---CCAATGCCAACACAGGCGCTGAGGGCTGTGCGTCCACAATGCTTGGATCGCAGCATCCA------ATGCTGACCCTCTGCGCAGGGTAC---AC---TAGTGGACACACAGTCGTCAGCGCGTCTGTTGGCG----------GAACAGCTGAAAAGCAGCAAGCACATAGCCTCGCT
droPer2	scaffold_31:119667-119864 -		ACACAAGCAGCA---GCA----C--------GCCAAAAACATC----------------------ACC---TGCAACAGC---T---CCAATGCCAACACAGGCGCTGAGGGCTGTGCGTCCACAATGCTTGGATCGCAGCATCCA------ATGCTGACCCTCTGCGCAGGGTAC---AC---TAGTGGACACACAGTCGTCAGCGCGTCTGTTGGCG----------GAACAGCTGAAAAGCAGCAAGCACATAGCCTCGCT
droAna3	scaffold_13266:6927954-6928162 -		TCCAAATC----------C----A----------CCGCCACAAGCATCATCAC---AAC---AGCAACAGCAATC---CAACGCCAGCATAAGGCGCTGAGGGCTGTGCGTCCACAAACTTGGATCGCAGCATCCA------ATGCTGACCCTCTGCAGCAGGGTAC---ACATCAAGTGGACACACAGTCGTCAGCGCGTCTGCTGACG----------GAGCAGCTGAAGAGCAGCCGGAGCCTGGCTTCTCT
droBip1	scf7180000396423:466013-466221 -		TCCAAAAA----------C----G----------CCGCCACAAGCATCATCCCCAAT---AAC---AGCAACAGCAATC---CAACGCCAGCATAAGGCGCTGAGGGCTGTGCGTCCACAAACTTGGATCGCAGCATCCA------ATGCTGACCCTCTGCAGCAGGGTAC---AGATCAAGTGGACACACAGTCGTCAGCGCGTCTGCTGACG----------GAGCAGCTGAAGAGCAGCCAGACGCCTGGCTTCTCT
droKik1	scf7180000302476:2162659-2162875 +		AGC--AGCA-----GTA----C----A-CGGCCAAGAGCATCGCCGCCAC---------AAACA-----ACCAG-AGCACCAGCAATC---CAACGCCAGCGTAGGCGCTGAGGGCTGTGCGTCCACATTGCTTGGATCTGCAGCATCCA------ATGCTGACCCTCTGCGCAGGGTAC---ACAACAAGTGGACACACAGTCGTCAGCGCGTCTGCTGGCG----------GAGCAGCTGAAAAGCAGCCGGAGCCTGAGATCACT
droFic1	scf7180000454044:485770-485963 +		C-AGCAATA----------C----A----------AC----------------------ACCAGAAGCATCAGGCAAAGCAACCCGCTCAGCGGCGGCGCTGAGGGCTGTGCGTCCACAAACTTGGATCTGCAGCATCCA------ATGCTGACCCTCTGCGCAGGGTAC---AGAACAAGTGGACACACAGTCGTCAGCGCGTCTGCTGGCC----------GAGCAGCTGAAGAGCAGCCGGAGCATGGCCTCGCT
droEle1	scf7180000491232:360019-360219 -		GCAGCAGCAGCAGCAATG----C----A----------AC----------------------ACCCAAAGCATCAGGCAATC---CAACGCCAGCGCGAGGCGCTGAGGGCTGTGCGTCCACAACTTGGATCTGCAGCATCCA------AGCTGACCCTCTGCGCAGGGTAT---AGAACAAGTGGACACACAGTCGTCAGCGCGTCTGCTGGCG----------GATCAGCTGAAGAGCAGGCGGAGCATGGCCTCGCT
droRho1	scf7180000777447:11709-11900 -		CCAAAGAGCA----------C----A----T----------AC----------------------ACCAGCAGCATCAGGCAATC---CAACGCCAGCGGCAGGCGCTGAGGGCTGTGCGTCCACAAACTTGGATCTGCAGCATCCA------AGCTGACCCTCTGCGCAGGGTAT---AGAACAAGTGGACACACAGTCGTCAGCGCGTCTGCTGGCG----------GAGCAGCTGAAGAGCAGCCGGAGCATGGCCTCGCT
droBia1	scf7180000301754:456600-456791 -		ACAGCAGCA----------C----A----------AC----------------------ACCAGAAGCATCAGGCAATC---CATCGCCAACAGCAGGCGCTGAGGGCTGTGCGTCCACACACTTGGATCTGCAGCATCCA------AGCTGACCCTCTGCGCAGGGTAT---AGAACAAGTGGACACACAGTCGTCAGCGCGTCTGCGCTGGCG----------GAGCAGCTGAAGAGCAGCAAGAGCCTGGCCTCGCT
droTak1	scf7180000415376:44709-44911 +		CAAAACAC----------CCGGA----------------------TATCAACAGCAGGCAATC---AGCACCAGCAATC---CAACGCCTGCGCAGGCGCTGAGGGCTGTGCGTCCACAGACTTGGATCTGCAGCATCCA------AGCTGACCCTCTGCGCAGGGTAC---AGAACAAGTGGACACACAGTCGTCAGCGCGTCGCGCTGGCG----------GAGCAGCTGAGGAGCAGCAAGAGCCTGGCCTCGCT
droEug1	scf7180000409474:913360-913551 -		ACAGCAACA----------C----G----A----------AC----------------------ACCAGAACGATCAGGCAATC---CAACGCCAGCGGCAGGCGCTGAGGGCTGTGCGTCCACAACTTGGATCTGCAGCATCCA------AAGCTGACCCTCTGCGAAGGGTAT---AGAACAAGTGGACACACAGTCGTCAGCGCGTCTGCTGACG----------GAGGAGCTGAAGAACAGCAGGAGCATGGCATCACT
dm3	chr2R:17031928-17032119 +		ACAGCAGCA----------C----C----A----------AC----------------------ACCAGATGCATCAGGCAATC---CAACGCCAGCGGCAGGCGCTGAGGGCTGTGCGTCCACAACTTGGATCTGCAGCATCCA------AGCTGACCCTCTGCGCAGGGTAT---AGAACAAGTGGACACACAGTCGTCAGCGCGTCTGCTGGCG----------GAGCAGCTGAAGAGCAGCAAGAGCCTGGCCTCACT
droSim2	2r:17589291-17589482 +	dsi_32103	ACAGCAGCA----------C----C----A----------AC----------------------ACCAGATGCATCAGGCAATC---CAACGCCAGCGGCAGGCGCTGAGGGCTGTGCGTCCACAACTTGGATCTGCAGCATCCA------AGCTGACCCTCTGCGCAGGGTAT---AGAACAAGTGGACACACAGTCGTCAGCGCGTCTGCTGGCG----------GAGCAGCTGAAGAGCAGCAAGAGCCTGGCCTCACT
droSec2	scaffold_9:360604-360795 +		ACAGCAGCA----------C----C----A----------AC----------------------ACCAGATGCATCAGGCAATC---CAACGCCAGCGGCAGGCGCTGAGGGCTGTGCGTCCACAACTTGGATCTGCAGCATCCA------AAGCTGACCCTCTGCGCAGGGTAT---AGAACAAGTGGACACACAGTCGTCAGTGCGTCTACTGGCG----------GAGCAGCTGAAGAGCAGCAAGAGCCTGGCCTCACT
droYak3	2R:12162172-12162363 -	dya_1613	ACAGCAGCA----------C----C----A----------AC----------------------ACCAGATGCATCAGGCAATC---CAACGCCAGCGGCAGGCGCTGAGGGCTGTGCGTCCACAACTTGGATCTGCAGCATCCA------AAGCTGACCCTCTGCGCAGGGTAT---AGAACAAGTGGACACACAGTCGTCAGCGCGTCTGCTGGCG----------GAGCAGCTGAAGAGCAGCAAGAGCCTGGCCTCACT
droEre2	scaffold_4845:11176483-11176674 +	der_1491	ACAAGAGCA----------C----C----A----------AC----------------------ACCAGATGCATCAGGCAATC---CAACGCCAGCGCAAAGAGGCGCTGAGGGCTGTGCGTCCACAACTTGGATCTGCAGCATCCA------AAGCTGACCCTCTGCGCAGGGTAT---AGAACAAGTGGACACACAGTCGTCAGCGCGTCTGCTGGCG----------GAGCAGCTGAAGAGCAGCAAGAGCTTGGCCTCACT

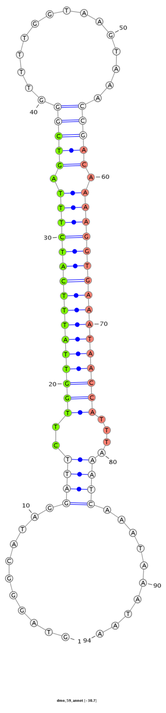
Generated: 09/08/2015 at 07:36 PM

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

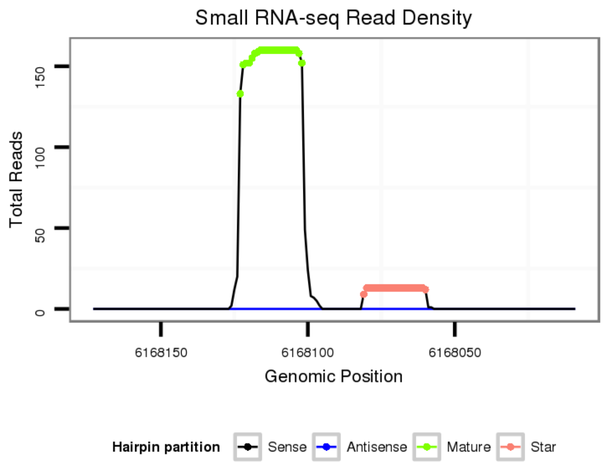
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_59	**scaffold_6473:6168059-6168123 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

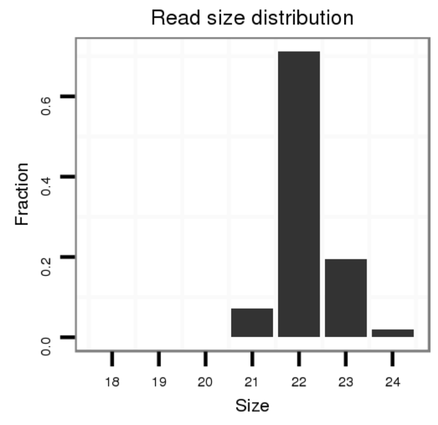
Legend: mature star **mismatch in alignment** mismatch in read

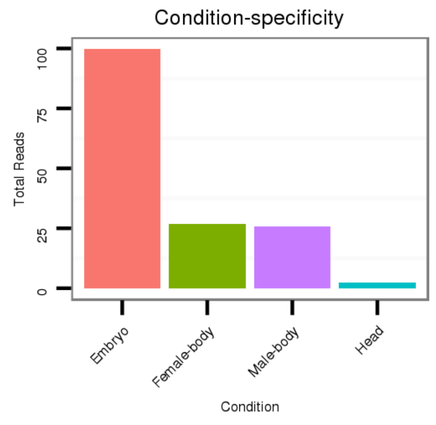
Predicted structure

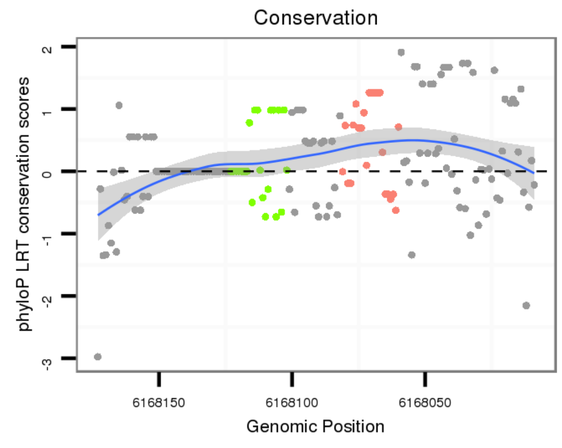


Show Alternate Folds









Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATTTAGAAAAAATAATAAATTAATCAACATTTCCAGTAGGGCATAGGATTCTTGGTTATTTCATCTTTAGTCGGGTTTTGGTAAGTAAACCGACAAAAGGTGAAATAACCATTTAAATCAAATAAATAATAAACTAGTGAGAGAGAGAGAGTGTGCTCTAGGCGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
**********.....((((..((((((((((((((((.(((((.............)))))).))))))))))))))))....))))).....**********											
.....CTTGGTTATTTCATCTTTAGTC.....	22	0	1	90.00	90	62	11	14	1	1	1
.....CTTGGTTATTTCATCTTTAGTCG.....	23	0	1	17.00	17	6	6	5	0	0	0
.....TTGGTTATTTCATCTTTAGTCGG.....	23	0	19	13.16	250	97	37	103	10	2	1
.....ACAAAAGGTGAAATAACCATTT.....	22	0	1	8.00	8	8	0	0	0	0	0
.....TTCTTGGTTATTTCATCTTTAGTC.....	24	0	1	7.00	7	6	0	0	1	0	0
.....TTGGTTATTTCATCTTTAGTCG.....	22	0	19	5.47	104	8	65	26	3	1	1
.....TCTTGGTTATTTCATCTTTAGTC.....	23	0	1	5.00	5	4	1	0	0	0	0
.....CTTGGTTATTTCATCTTTAGT.....	21	0	1	3.00	3	2	1	0	0	0	0
.....CAAAAGGTGAAATAACCATTT.....	21	0	1	3.00	3	2	0	0	1	0	0
.....TTATTTCATCTTTAGTCGGGTT.....	22	0	1	3.00	3	2	0	0	1	0	0
.....CTTGGTTATTTCATCTTTAGTCGG.....	24	0	1	3.00	3	2	1	0	0	0	0
.....GTTATTTCATCTTTAGTCGGGT.....	22	0	1	2.00	2	2	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTCG.....	21	0	20	1.50	30	0	24	0	6	0	0
.....TTGGTTATTTCATCTTTAGTCGGT.....	24	1	19	1.05	20	13	2	4	0	1	0
.....ATTCTTGGTTATTTCATCTTTAGT.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TCTTGGTTATTTCATCTTTAGT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGGTA.....	23	1	1	1.00	1	0	1	0	0	0	0
.....ACAAAAGGTGAAATAACCATTC.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TTCTTGGTTATTTCATCTTTAG.....	22	0	1	1.00	1	1	0	0	0	0	0
.....ATTCTTGGTTATTTCATCTTTAGTC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....ACAAAAGGTGAAATAACCATT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TCTTGGTTATTTCATCTTTAGTCG.....	24	0	1	1.00	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CAAAAGGTGAAATAACCATTTAA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....CAAAAGGTGAAATAACCATTC.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TCTTGGTTATTTCATCTTTAGTCGA.....	25	1	1	1.00	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGGTC.....	23	1	1	1.00	1	1	0	0	0	0	0
.....CTTGGTTATTTCATCTTTAGTCC.....	23	1	1	1.00	1	0	0	1	0	0	0
.....ATTTCATCTTTAGTCGGGTTT.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TATTTCATCTTTAGTCGGGTTT.....	22	0	1	1.00	1	0	0	0	1	0	0
.....TTCTTGGTTATTTCATCTTTAGT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TCTTGGTTATTTCATCTTTAG.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TTCTTGGTTATTTCATCTTTAGTCG.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGC.....	24	1	19	0.84	16	2	4	10	0	0	0
.....TGGTTATTTCATCTTTAGTCGG.....	22	0	20	0.70	14	14	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTC.....	21	0	19	0.47	9	6	2	1	0	0	0
.....GTTATTTCATCTTTAGTCG.....	19	0	20	0.15	3	2	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGA.....	23	1	19	0.11	2	2	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGT.....	20	0	19	0.11	2	0	1	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGTC.....	25	2	19	0.11	2	1	0	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCAA.....	23	2	19	0.05	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGTAA.....	26	3	19	0.05	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCA.....	22	1	19	0.05	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGC.....	23	1	19	0.05	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGT.....	23	1	19	0.05	1	0	0	0	1	0	0
.....GGTTATTTCATCTTTAGTCG.....	20	0	20	0.05	1	0	1	0	0	0	0
.....TTATTTCATCTTTAGTCG.....	18	0	20	0.05	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGC.....	20	1	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCGG.....	21	0	20	0.05	1	0	0	0	0	0	1
.....TGGTTATTTCATCTTTAGTC.....	20	0	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

TAAATCTTTTTTATTATTTAATTAGTTGTAAAGGTCATCCCGTATCCTAAGAACCAATAAAGTAGAAATCAGCCCAAAACCATTCATTTGGCTGTTTTCCACTTTATTGGTAAATTTAGTTTATTTATTATTTGATCACTCTCTCTCTCACACGAGATCCGCT	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_6473:6168009-6168173 -	dmo_59	ATTTAGAAAAAATAATAAATTAATCAACATTTCCAGTAGGGCATAGGATTCTTGGTTATTTCATCTTTAGTCGGGTTTTGGTAAGTAAAC---CGACAAAAGGTGAAATAACCATTTAAATC---------AAATAAATAATAAACT--------------------AGTGAGAGA---------GAGAGAGTGTGCTCTAGGCGA
droVir3	scaffold_12928:824671-824794 -		TTCTTGACAA----------ATTGGGTTTGATTCAGATTTTGGTTCGTCTATTTTTGA----------CCACAACTAAAATACATAAA---------ATATTGGAACTCCGTCTTCTTTAAGTAATAACAAC---------AAGTGAAAGTGCTCTAGTAGC
droGri2	scaffold_15245:8690683-8690770 -		TTTGGGCGAGTCTACTCGACTA----------TGAAATATTCTTATAAAATC---------AAATAAATATTATAATT--------------------GGTAAA--CGAGTGCTGAACTAGAGTGTCCTCT------
droWil2	scf2_1100000004762:1608722-1608772 -		GAAAAA----------AGGTTAAATAATTATTTAAATT---------AATAAAAG---------AACTTAA------AAACTAG
dp5	XL_group1e:68149-68182 +		AAATA----------ATAAATTAAAAA---------AAATAAATAATAAATT--------------------A----------------------
droPer2	scaffold_27:1191709-1191728 +		TTTTACACAA----------A-A---------AAATAAAT--
droKik1	scf7180000302698:60420-60484 +		TAAA----------C---AGGGGGAA---GAAATAAGTAAATAAATA---------AAATTAATAATAAAAC--------------------TGTGAAA-CA---------AGTAAAATG----------
droEle1	scf7180000491011:476440-476482 -		AAATAT----------TTAAAAC---------AATTCGATTATAAAAT--------------------GTTGAGAGA---------GAGA----G----------
dm3	chrUextra:1926738-1926774 +		TTGGTC----------ATTTTATCTTTATTTGGTTTT----------TAT-----------------------TAAGCGA
droSim2	31:22297700-22297751 -		AAGTAA----------ATACGCA---------AA------ATAAAATT--------------------ATTCAAAGC---------AAGAGAGAATGCTCTAGTCGA

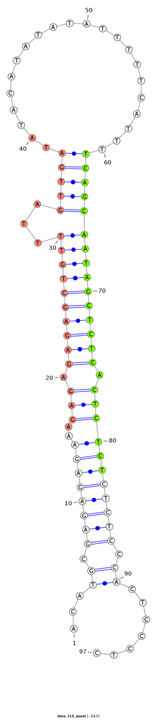
Generated: 09/08/2015 at 07:36 PM

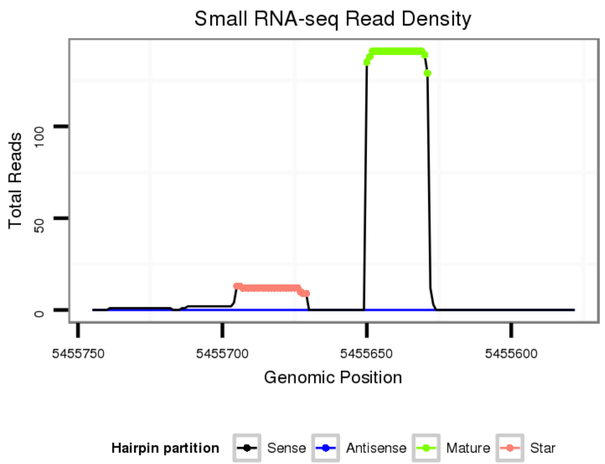
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

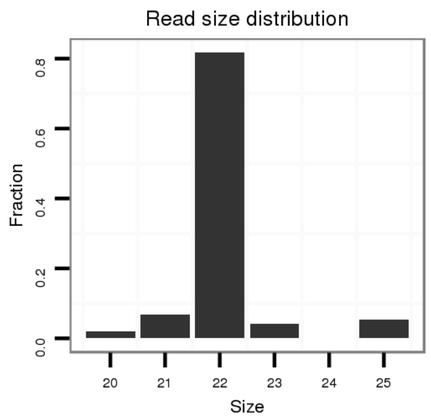
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_319	**scaffold_6540:5455628-5455695 -**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

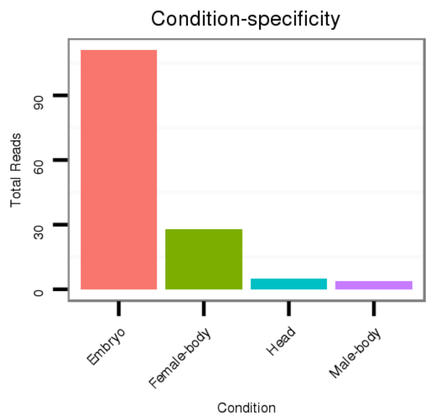
Legend: mature star **mismatch in alignment** mismatch in read

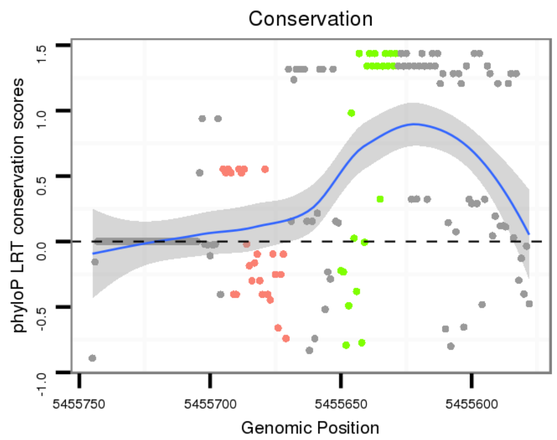
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI23559-in]

Repeatable elements

Name	Class	Family	Strand
G-rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATAGAAAGATCGATGCAGCTGATGGATCAATGGATACATGCGAGAGAGAAAGAGAGAGAGCTGTTTTAGTTGATATACATATATATTTTTCATTTTCAGCAATAGCTCTCACTCTCTCTCTCCCACTCCCTCTCTTCTTGTCACCCTCTTCCTCTCCTTCTATGGACA **********...((.(((((((((..(((.((((((((((...(((((.....)))))))))))))))))).)))))))))).))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V041 embryo	V056 head	V110 male body	V049 head
TCAGCAATAGCTCTCACTCTCT	22	0	1	117.00	117	89	20	5	2	0	1
TCAGCAATAGCTCTCACTCTCC	22	1	1	29.00	29	28	1	0	0	0	0
TCAGCAATAGCTCTCACTCTC	21	0	1	9.00	9	5	2	1	0	0	1
AGAGAGAGAGCTGTTTTAGTTGATA	25	0	1	8.00	8	4	0	0	0	4	0
TCAGCAATAGCTCTCACTCTCTC	23	0	1	6.00	6	2	4	0	0	0	0
CAGCAATAGCTCTCACTCTCTC	22	0	1	2.00	2	2	0	0	0	0	0
AGCAATAGCTCTCACTCTCTCC	22	1	1	2.00	2	2	0	0	0	0	0
AGCAATAGCTCTCACTCTCTCT	22	0	1	2.00	2	2	0	0	0	0	0
AGAGAGAGAGCTGTTTTAGTTG	22	0	1	2.00	2	1	0	0	1	0	0
TCAGCAATAGCTCTCACTCT	20	0	1	2.00	2	0	2	0	0	0	0
AAGAGAGAGAGCTGTTTTAGTTGATA	26	0	1	1.00	1	1	0	0	0	0	0
AGATCGATGCAGCTGATGGATC	22	0	1	1.00	1	0	1	0	0	0	0
GGATACATGCGAGAGAGAA	19	0	1	1.00	1	0	0	0	1	0	0
ATACATGCGAGAGAGAAAG	19	0	1	1.00	1	0	0	0	0	1	0
TCAGCAATAGCTCTCACTCTCTCT	24	0	1	1.00	1	0	0	1	0	0	0
AAGAGAGAGAGCTGTTTTAGTTGA	24	0	1	1.00	1	0	0	1	0	0	0
CAGCAATAGCTCTCACTCTC	20	0	1	1.00	1	1	0	0	0	0	0
AGCAATAGCTCTCACTCTCTC	21	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

TATCTTTCTAGCTACGTCGACTACCTAGTTACCTATGTACGCTCTCTCTTTCTCTCTCTCGACAAAATCAACTATATGTATATATAAAAAGTAAAAGTCGTTATCGAGAGTGAGAGAGAGGGTGAGGGAGAGAAGAACAGTGGGAGAAGGAGAGGAAGATACCTGT **********...((.(((((((((..(((.((((((((((...(((((.....)))))))))))))))))).)))))))))).))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	V049 head
TCAGCAATAGCTCTCACTCTCTCT	24	0	1	1.00	1	0	0	1	0	0
AAGAGAGAGAGCTGTTTTAGTTGA	24	0	1	1.00	1	0	0	1	0	0	0
CAGCAATAGCTCTCACTCTC	20	0	1	1.00	1	1	0	0	0	0	0
AGCAATAGCTCTCACTCTCTC	21	0	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_6540:5455578-5455745 -	dmo_319	ATAGAAAGATCGATGCAGCTGATGGATCAATGGATACATGCGAGAGAGAAAGAGAGAGAGCTGTTTTAGTTGATACATATATATTTTTCATTTTCAGCAATAGCTCTCACTCTCTCTCTCCCACTCCCTCTCTTCTT-GTCACCCTCTTCCTCT-CCTTCTATGGACA
droVir3	scaffold_13324:2915498-2915563 -		----------TGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAT-GTCGCATTTTTTTCTGT-GTTTCTGTAGGCT
droGri2	scaffold_15110:10362271-10362372 -		C----------GAGAGAGACAGAGGAAGAGTGACGCTGTCAATCTTACATATACAATTTATTTCTCTCACTCGCTCTCTCTCTCTCTCTCTCTCTCT------CTCTCTGTC---C----------
droWil2	scf2_1100000004909:4729681-4729791 +		GA----------AAGTGAA---------ATGGCG---GCATTCCTTCATATTGTGTTTCTCTCTCTC----TCTCTCTCTCTCTCTCTCTCTCTCTCTCT-CTCTCTCTCTCTCTCTCT-CTCTCTATATATA
droYak3	2L:3897171-3897264 -		AT----------ATACATATATATTTCTTTGTCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCATGGTCGCTCTTTTCTCCGCTTGCTATG----

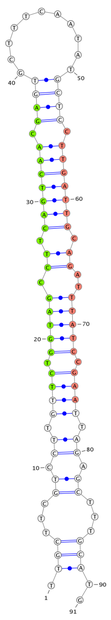
Generated: 09/08/2015 at 07:35 PM

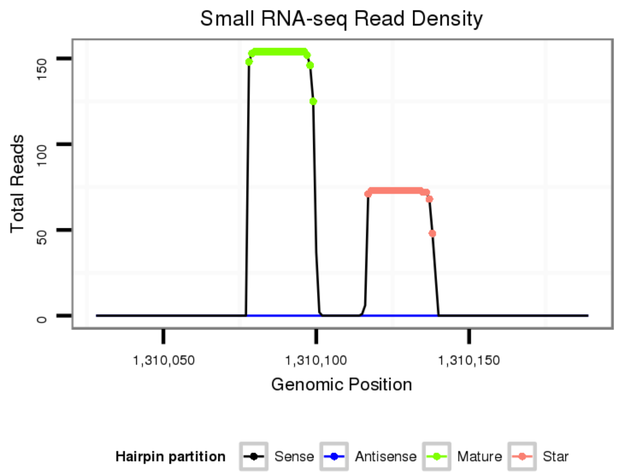
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

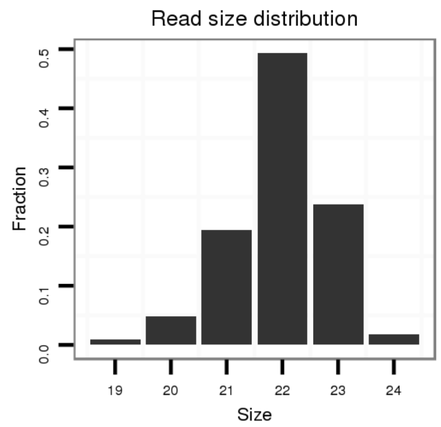
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_113	**scaffold_6308:1310078-1310139 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

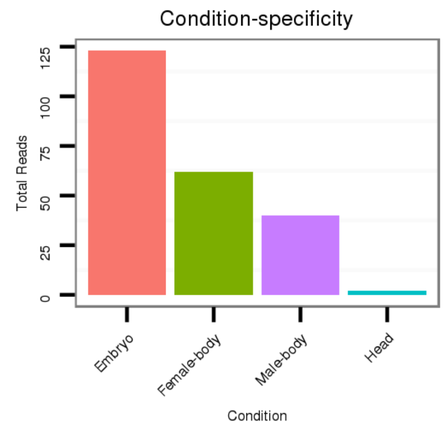
Legend: mature star mismatch in alignment mismatch in read

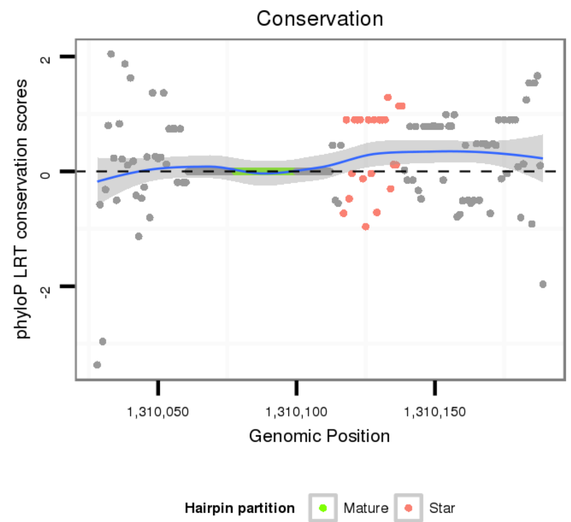
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CGTGTATATATATATTCGTCTTCTTAATTCAATTATTGCTTCGTCCTTGTTCTGGTAGCCTTCAGTCAACGAGTGCTTTCAATATGCTCCTTGATTGCAGATTTATCCGAATTAGAGCTTTGCATGTGCAACAGATGATATGAACACAGATAGTCAAAATAA **********.(((...((.((.(((((.(((((.((.(((((((.((((..........)))).)))))))..))..)))))..)))).)).))...)))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V049 head	V056 head
..........TCTGGTAGCCTTCAGTCAACGA..........	22	0	1	86.00	86	63	22	1	0	0	0
..........TCTGGTAGCCTTCAGTCAACGAG..........	23	0	1	32.00	32	25	5	2	0	0	0
..........CTTGATTGCAGATTTATCCGAA..........	22	0	1	22.00	22	0	3	17	1	0	1
..........CTTGATTGCAGATTTATCCGAAT..........	23	0	1	21.00	21	10	10	0	1	0	0
..........TCTGGTAGCCTTCAGTCAACG..........	21	0	1	20.00	20	10	9	1	0	0	0
..........CTTGATTGCAGATTTATCCGA..........	21	0	1	19.00	19	0	3	15	0	1	0
..........CTTGATTGCAGATTTATCCGAAA..........	23	1	1	9.00	9	0	0	9	0	0	0
..........TCTGGTAGCCTTCAGTCAAC..........	20	0	1	6.00	6	4	2	0	0	0	0
..........CTTGATTGCAGATTTATCCG..........	20	0	1	3.00	3	0	1	2	0	0	0
..........TCTGGTAGCCTTCAGTCAACGAGT..........	24	0	1	2.00	2	1	1	0	0	0	0
..........TCTGGTAGCCTTCAGTCAACGAGA..........	24	1	1	2.00	2	1	1	0	0	0	0
..........CCTTGATTGCAGATTTATCCGAAT..........	24	0	1	2.00	2	2	0	0	0	0	0
..........CTGGTAGCCTTCAGTCAACGA..........	21	0	1	2.00	2	1	1	0	0	0	0
..........TCTGGTAGCCTTCAGTCAA..........	19	0	1	2.00	2	2	0	0	0	0	0
..........CTGGTAGCCTTCAGTCAACGAG..........	22	0	1	2.00	2	0	2	0	0	0	0
..........TCTGGTAGCCTTCAGTCAACA..........	21	1	1	1.00	1	0	1	0	0	0	0
..........CCTTGATTGCAGATTTATCCGA..........	22	0	1	1.00	1	0	1	0	0	0	0
..........CTTGATTGCAGATTTATCCGAAAA..........	24	2	1	1.00	1	0	0	1	0	0	0
..........CCTTGATTGCAGATTTATCCG..........	21	0	1	1.00	1	0	0	1	0	0	0
..........CCTTGATTGCAGATTTATCCGAAA..........	24	1	1	1.00	1	0	0	1	0	0	0
..........CCTTGATTGCAGATTTATCCGAA..........	23	0	1	1.00	1	0	0	0	1	0	0
..........CTGGTAGCCTTCAGTCAACG..........	20	0	1	1.00	1	0	1	0	0	0	0
..........TTGATTGCAGATTTATCCGAAT..........	22	0	1	1.00	1	1	0	0	0	0	0
..........TTGATTGCAGATTTATCCGAA..........	21	0	1	1.00	1	1	0	0	0	0	0
..........TCCTTGATTGCAGATTTATC..........	20	0	1	1.00	1	0	0	1	0	0	0
..........CTTGATTGCAGATTTATCCGAAC..........	23	1	1	1.00	1	1	0	0	0	0	0
..........TGGTAGCCTTCAGTCAACGAG..........	21	0	1	1.00	1	0	1	0	0	0	0
..........CTTGATTGCAGATTTATCCGAC..........	22	1	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

Show Alignment With Reads

GCACATATATATATAAGCAGAAGAATTAAGTTAATAACGAAGCAGGAACAAGACCATCGGAAGTCAGTTGCTCACGAAAGTTATACGAGGAACTAACGTCTAAATAGGCTTAATCTCGAAACGTACACGTTGTCTACTATACTTGTGTCTATCAGTTTTATT **********.(((...((.((.((((.((((((.((.(((((((.((((..........)))).)))))))..))..)))))..)))).)).))...)))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body
..........CTGGTAGCCTTCAGTCAACG..........	20	0	1	1.00	1	0	1	0	0	0	0
..........TTGATTGCAGATTTATCCGAAT..........	22	0	1	1.00	1	1	0	0	0	0	0
..........TTGATTGCAGATTTATCCGAA..........	21	0	1	1.00	1	1	0	0	0	0	0
..........TCCTTGATTGCAGATTTATC..........	20	0	1	1.00	1	0	0	1	0	0	0
..........CTTGATTGCAGATTTATCCGAAC..........	23	1	1	1.00	1	1	0	0	0	0	0
..........TGGTAGCCTTCAGTCAACGAG..........	21	0	1	1.00	1	0	1	0	0	0	0
..........CTTGATTGCAGATTTATCCGAC..........	22	1	1	1.00	1	0	0	1	0	0	0

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1310028-1310189 +	dmo_113	CGTGTATATATATATTCGTCTTCTTAATTCAATTATTGCTTCGTCCTTGTTCTGGTAGCCTTCAGTCAACGAGTGCTTTCAATATGCTCCTTGATTGCA--G---ATTTATCCGAATTAGAGCTTTGCATGTGCAACA----------GATGATATGAACACAGA-------TAGTCAAAAT---AA
droVir3	scaffold_12970:1531936-1532061 +		TACATATATATATATACACCTACGT----------GTACATAGATTGAA--GTGAAGTTATTTA----------T--ACATTCGCATATATATATGTATCTATGTATGTGTGTCGAAACATGCACACAGAAACTATTATATACAAAAT---AT
droGri2	scaffold_15245:229983-230010 +		TATATATATATATATATATTCTTA--AT
droWil2	scf2_1100000004513:5944704-5944764 +		CAG-TATGTTTT----------TTAATTGAATA---ATTTATCTGAAT----------AATAGG----------AAAAA-------TATCTAAAATAACAG
droAna3	scaffold_13266:9158655-9158665 -		AATAGAAAT----------AG
droBip1	scf7180000396423:643856-643870 +		TGTGTATGTGTAT----------GT
droKik1	scf7180000302577:1308261-1308295 -		GAGATATGTATATCGTAATGTTTTAATTTAGC----------TA
droRho1	scf7180000777063:132337-132349 +		ATA----------TA
droTak1	scf7180000415378:295789-295804 +		CACATACATA----------AT
droEug1	scf7180000409466:845087-845141 -		TTA----------TTTGAAACAAATGTTTGCATATGCATTTTCGCATGTATGTATATAT----------AATAT---AT
dm3	chr3L:3122114-3122119 -		AAA----------T--GT
droSim2	3l:2980103-2980107 -		AAC----------AA
droSec2	scaffold_2:3115847-3115851 -		AAC----------AA
droYak3	2L:15567814-15567841 -		TGTATATACATATAAATGTCTTTTTT----------AT
droEre2	scaffold_4929:20280242-20280260 -		CATGTATGTATGTATTT----------AT

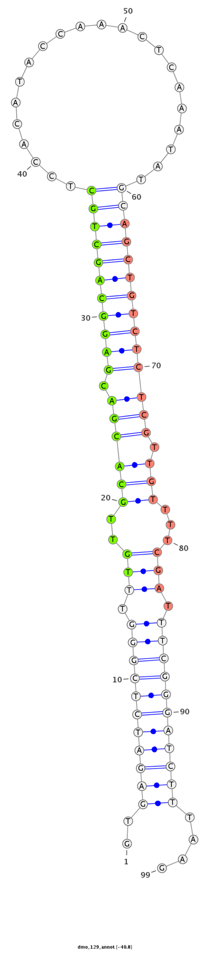
Generated: 09/08/2015 at 08:05 PM

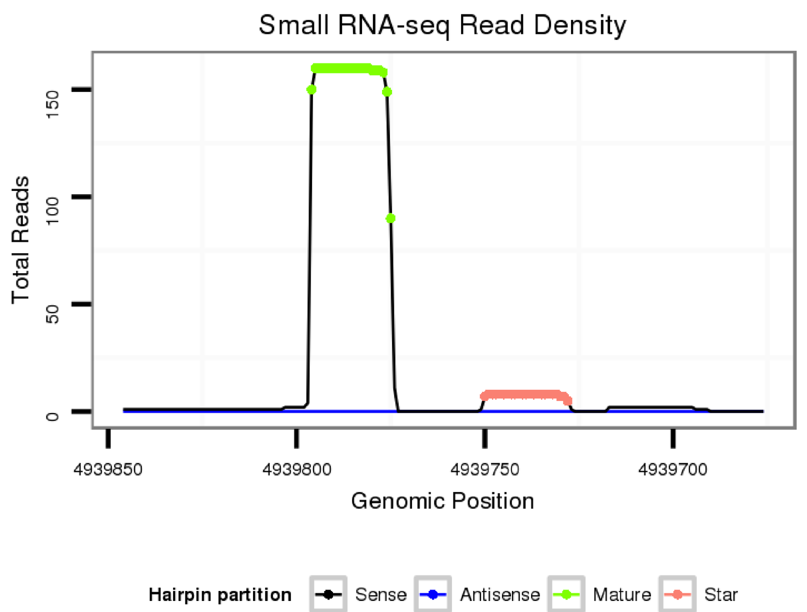
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

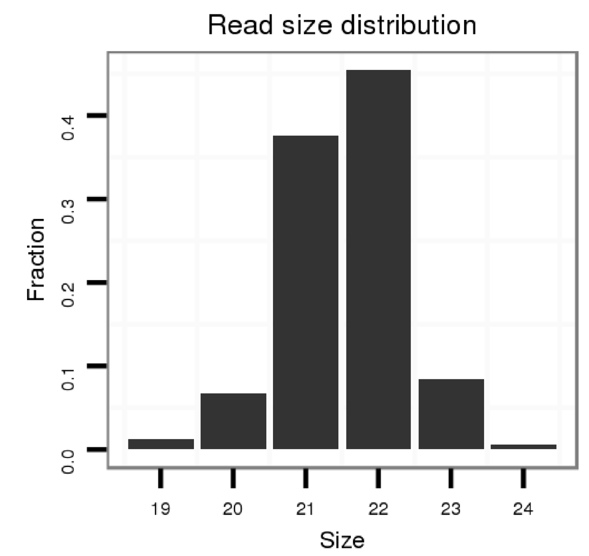
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_129	**scaffold_6540:4939726-4939796 -**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

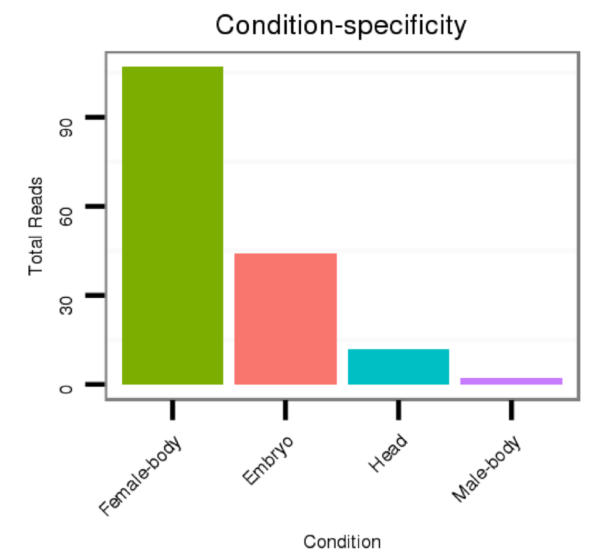
Legend: mature star mismatch in alignment mismatch in read

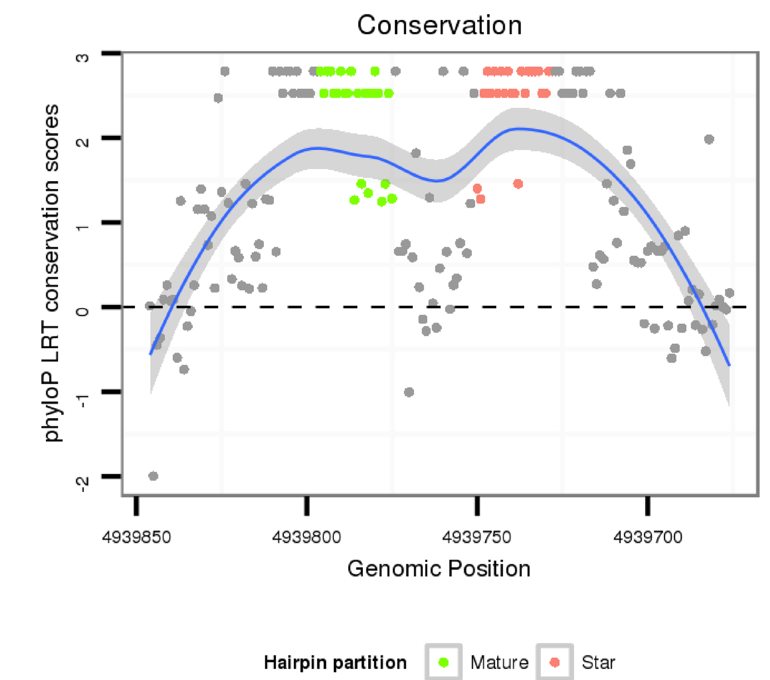
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dmoj\GI23585-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTCCTGAACAAGGAGTGTGGGTTGTGCAAAAATATGTGAGATCTCGGGTTTGTTGCACGACGAGGCAGCTGCTCCACATACCAAACTCAAATATGCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTTAAGACGACGTGACCCCAGCCACTCCCAGTGATAAGCAACA **********************************..((((((((((.(((..((((((.((((((((((((......................)))))))))))))).))))...))).)))))))))))....************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V041 embryo	V056 head	V049 head	V110 male body
....TGTTGCACGACGAGGCAGCTGC....	22	0	1	73.00	73	36	27	6	1	3	0
....TGTTGCACGACGAGGCAGCTG....	21	0	1	56.00	56	48	1	2	3	1	1
....TGTTGCACGACGAGGCAGCTGCT....	23	0	1	9.00	9	6	3	0	0	0	0
....TGTTGCACGACGAGGCAGCT....	20	0	1	8.00	8	4	0	0	2	1	1
....GTTGCACGACGAGGCAGCTGC....	21	0	1	5.00	5	5	0	0	0	0	0
....AGCTGTCTCTCGTTGTTTTCGAT....	23	0	1	4.00	4	1	3	0	0	0	0
....TGTTGCACGACGAGGCAGCTGCC....	23	1	1	2.00	2	0	2	0	0	0	0
....GTTGCACGACGAGGCAGCTGCT....	22	0	1	2.00	2	2	0	0	0	0	0
....GTTGCACGACGAGGCAGCTG....	20	0	1	2.00	2	2	0	0	0	0	0
....TCGGGTTTGTTGCACGACGAGGC....	23	0	1	1.00	1	1	0	0	0	0	0
....TGTTGCACGACGAGGCAGCTA....	21	1	1	1.00	1	1	0	0	0	0	0
....AGCTGTCTCTCGTTGTTTTCGATT....	24	0	1	1.00	1	0	0	1	0	0	0
....GTTGCACGACGAGGCAGCT....	19	0	1	1.00	1	1	0	0	0	0	0
....AGCTGTCTCTCGTTGTTTTC....	20	0	1	1.00	1	0	1	0	0	0	0
....GCTGTCTCTCGTTGTTTTCGA....	21	0	1	1.00	1	1	0	0	0	0	0
....TGTGCAAAAATATGTGAGATCTCGGGTT....	28	0	1	1.00	1	1	0	0	0	0	0
....TTAAGACGACGTGACCCCAGCCA....	23	0	1	1.00	1	0	0	0	0	0	1
....TTAAGACGACGTGACCCCAGCCACTCC....	27	0	1	1.00	1	1	0	0	0	0	0
....TTGTTGCACGACGAGGCAGCTGC....	23	0	1	1.00	1	1	0	0	0	0	0
....TTGTTGCACGACGAGGCAGCTG....	22	0	1	1.00	1	1	0	0	0	0	0
....CAGCTGTCTCTCGTTGTTTTCGA....	23	0	1	1.00	1	1	0	0	0	0	0
TTCCTGAACAAGGAGTGTGGGT....	22	0	1	1.00	1	0	0	0	1	0	0
....TGTTGCACGACGAGGCAGC....	19	0	1	1.00	1	0	0	0	1	0	0

Anti-sense strand reads

AAGGACTTGTTCCTCACACCCAACACGTTTTTATACACTCTAGAGCCCAAACAACGTGCTGCTCCGTCGACGAGGTGTATGGTTTGAGTTTATACGTCGACAGAGAGCAACAAAAGCTAAAGCCCTAGAAATTCTGCTGCACTGGGGTCGGTGAGGGTCACTATTCGTTGT **********************************..((((((((((.(((..((((((.((((((((((((......................)))))))))))))).))))...))).)))))))))))....************************************	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_6540:4939676-4939846 -	dmo_129	TTC-CTGAACAAGGAGTG----------T----------------------GG----------GTTGTGC-AAA----------------------AATA-TGTGAGATCTCGGGTTTGTTGCACGACGAGGCAGCTGCTCCACA---------TA----------CC---------A------------------------------AA-CT-CAAATATGCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTTAAGACGACG--------------------------TGACCCCAGCCA---------CTCCC-AGTGATAAGC--AAC-A
droVir3	scaffold_13047:936843-937018 -	dvi_125	AT-------CAAGGAGTG----------C----------------------T-G----------GTTGAGA-GAC----------------------AATG-TGTGAGATCTCGGGTTTGTTGCACGACGAGGCAGCTGCTCCAAA---------TG----------CC---------AAATA------------------------------------TTCAAATACGCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTTGCGACAACGT--GATC--------------------------CCAACCATCCCGGCCGTGACCCAGTGATAAGC--A---A
droGri2	scaffold_14906:5355404-5355604 +	dgr_461	TTA-G--------GAGTG----------TG--------------------CATGTAATTGGCTGGTTGAGA-TATATATATATATATATATGTATATAAT-TGTGAGATCTCGGGTTTGTTGCACGACGTGGCAGCTGCTCCAAA---------TG----------CA---------A------------------------------AAACT-CGAAAACGCAGCTGTCTCTCGATGTTTTCGATTTCGGGATCTTGTCATCGGCG--------------------------TGACCTCAACCAACCAAAC-------------TAATCAACTAATC-A
droWil2	scf2_1100000004902:91563-91744 -	dwi_5414	----------------TTCT----------TT--------------------GTGT----------GTTGC-C-AAG----------------------CGTCCTATAAGATCTCGGGTTTGTTGCACGATGAGACAGCCGCTAAACCCCC-CCT--TGCCACACCCTCT----------TTG----C----A-ATGGTAAATACCTCCCTT--TCGAA-AT-------------TGTT------------------------------A-T-TATTTATGCCGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTATTTACGACC---CAGTGA--
dp5	2:7251727-7252004 -	dps_3825	-------------TGTGCGAGAGAGTGTACGAGAGTATATCTAATCTATAGA----------GTTTT-CCATG----------------------CGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTCCAGACCCACCTCTTT----------------------------CCC-AGCAGACGCCATTGTGATGATGTTGTTGATGATGATGATGAGGAGGAGGAGAGAAGGAGGAGGAGGGCTTATCCACT-TGCAAACGCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGTCAACGACGC--CATTAAC-------------CATTG-------------GAACCACTACG-AATACA--AATATA--T
droPer2	scaffold_0:1112328-1112589 -	dpe_2479	-------------GTG----------TACGAGAGTATATCTAATCTATAGA----------GTTTT-CCATG----------------------CGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTCCAGACCCACCTCTTT----------------------------CCC-AGCAGACGCCATTGTGAT------GTTGATGATGATGATGAGGAGGAGGAGAGAAGGAGGAGGAGGGCTTATCCACT-TGCAAACGCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGTCAACGACGC--CATTAAC-------------CATTG-------------GAACCACTACG-AATACG--AATATAT-A
droAna3	scaffold_13340:938714-938905 +	dan_4037	TAC-AGA----TACAGTG----------CC--------------------T---------GGTGT-C-CAG----------------------CGCC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAACCCTC--CT---GGGGGAGCCCGTA--A------AAA----C----AAAAGACAAACAGCCCACTC--CCAGA-AA------------------------------TA-CT-ATAATACGCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGTCAACGGCGCATCATCGA--TA-----TA--
droBip1	scf7180000394085:58806-58995 -		CC-----------CGTG----------TC--------------------CAGC----------G-TGT-C-AAG----------------------CGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAGCCTCC--C---------GGGGGAGGGGAAAACAAAC----AGC----------CCACTC--CCAGA-AA------------------------------AG-CT-TCCATACGCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGTCAACGGCGC---ATCCACCAT-----T-ACGA----------------------------GGGATTA-----C-CA
droKik1	scf7180000302475:1404674-1404875 +		TGT-GTATCCAGCAAGTG----------TC--------------------CAGA----------GTTGT-C-AAG----------------------CGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAGCCCCT-CCACATG----------GAAAACAAAATAATAAAATATAA----------TACTCCC-CCCA-AC------------------------------CCCAT-TTAATACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGTCAACGACGC--CTACAGA---CGATCTAAA--
droFic1	scf7180000453800:2293382-2293554 +		---------------AGTG----------TC--------------------CAGA----------GTTGT-C-AAG----------------------CGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAACCCTC-CC-------------ACAAGA------AAA----C----AGAA----------TACACCCACA-A-AC------------------------------CCCAT-TTAATACTCAACTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC--AATCGA--TT-----TGAAGAC--
droEle1	scf7180000490995:524612-524789 -		---------------AGTG----------TC--------------------CAGA----------GTTGT-C-AAG----------------------CGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAATCCCC--------------ACGAGA-----AAA----C----AAAA----------TACACC--CACA-AC------------------------------CCCAT-TTAATACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC--AGTCGA--TC-----TGAAGACCATG------------------------A-----C-CC
droRho1	scf7180000777158:35527-35696 -		---------------AGTG----------TC--------------------CAGA----------GTTGT-C-AAG----------------------CGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAATCCCC--------------ACGAGA-----AAA----C----AAAA----------TACACC--CACA-AC------------------------------CCCAT-TTAATACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC--CATCGA--TC-----TGAAGAC--
droBia1	scf7180000302402:8304642-8304838 +		---------------AGTG----------TC--------------------CAGA----------GTTGT-C-AAG----------------------CGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAAGCCCC-CCTCC-G-AGG-----AC--AGAAAAAAAA----C----AAAA----------GACCCACCCACA-AC------------------------------CCCAT-TTAATACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC--CTTCGA--TTCGATCCGAAGACCCTG------------------------A--C-CC
droTak1	scf7180000415380:1425653-1425834 -		----------------------------TC--------------------CAGA----------GTTGT-C-AAG----------------------CGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAAGCCCC--C---------ACAAGA------AAA----C----AAAA------A--CTACACC--CACA-AC------------------------------CCCAT-TTAATACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC--CATCGA--TTTGATGTGAAGACCCTG------------------------A--C-CC
droEug1	scf7180000409692:687983-688177 +		---------------AGTG----------TC--------------------CAGA----------GTTGT-C-AAG----------------------CGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAATCCCC-CTT--TG---T-----ATAAAA------AAACAA--------AC------AATCTACACC--CACA-AC------------------------------CCCAT-TTAATACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGA--TATCAAACTTTGATCTGAAGACCCTG------------------------A--C-CC
dm3	chr3R:6216951-6217131 +	dme_373	---------------AGTG----------TC--------------------CAGA----------GTTGT-C-AAG----------------------CGTC-AGTAAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAACCCC--------------GCA---------AAATAATC----AAAA----------TACACCCCCACA-AT------------------------------CGCAT-TTACTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC--CATCGA--AT-----TGAAGACATTG------------------------A--C-CC
droSim2	3r:14862283-14862463 -	dsi_32455	---------------AGTG----------TC--------------------CAGA----------GTTGT-C-AAG----------------------CGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAACCCC--------------GCA---------AAATAATC----AAAA----------TACACCCCCACA-AC------------------------------CCCAT-TTACTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC--CATCGA--AT-----TGAAGACATTG------------------------A--C-CC
droSec2	scaffold_0:15728327-15728507 -	dse_1842	---------------AGTG----------TC--------------------CAGA----------GTTGT-C-AAG----------------------CGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGATAAACCCC--------------GCA---------AAATAATC----AAAA----------TACACCCCCACA-AC------------------------------CCCAT-TTAGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC--CATCGA--AT-----TGAAGACATTG------------------------A--C-CC
droYak3	3R:10242705-10242897 +	dya_1794	TGT--ATCTATAAAGTG----------TC--------------------CAGA----------GTTGT-C-AAG----------------------CGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAACCCC--A----------GCA---------AAACAATC----AAAA----------TACACCCCCACA-AC------------------------------CCCAT-TTAGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC--CATCGA--AT-----TGAAGACATTG------------------------A--C-CC
droEre2	scaffold_4770:15403319-15403516 -	der_1519	TCTTGTATCTATAAAGTG----------TC--------------------CAGA----------GTTGT-C-AAG----------------------CGTC-AGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAACGCCC-CC----------GCA---------AAACAATT----AAAA------A--ATACACCC-CGCA-AC------------------------------CCCAT-TTAGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC--CATCGA--AT-----TGAAGACATTG------------------------A--C-CC

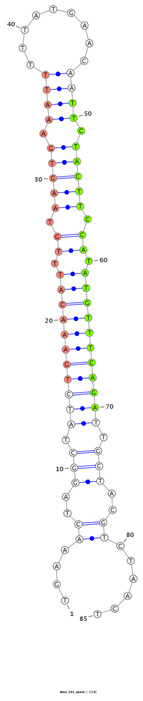
Generated: 09/08/2015 at 07:36 PM

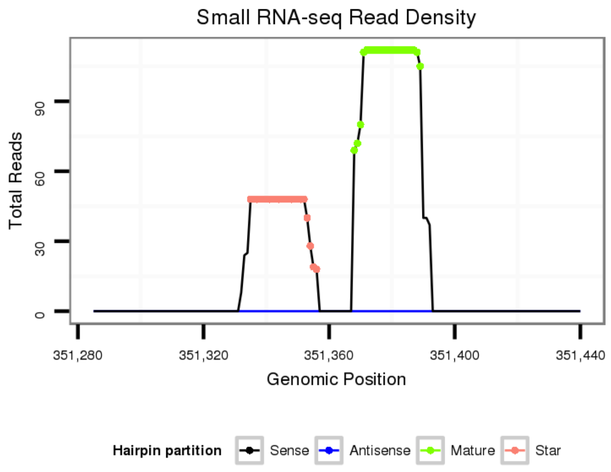
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	3
rescue.candidate	9

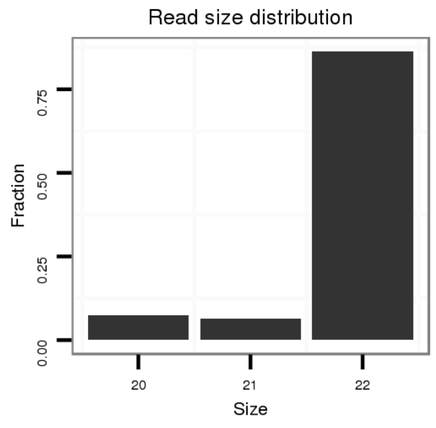
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_101	**scaffold_6328:351335-351390 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

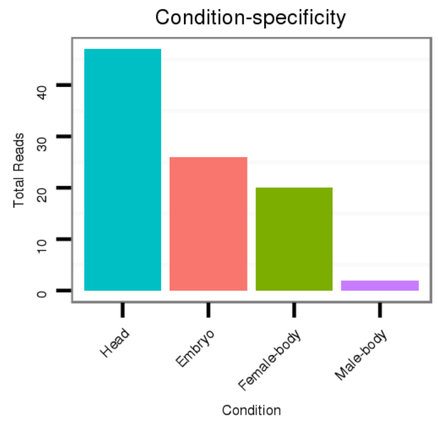
Legend: mature star mismatch in alignment mismatch in read

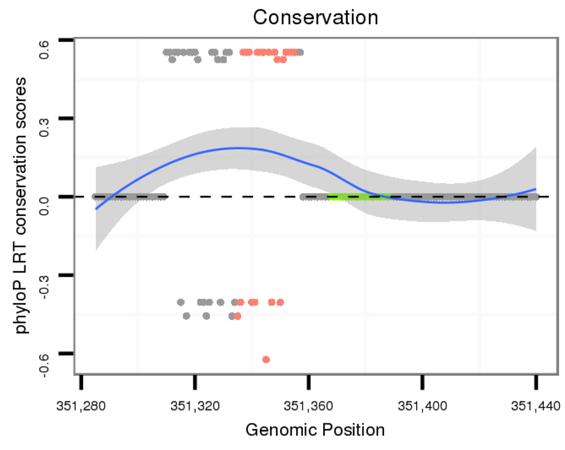
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTCCAGATAGCTCAAATGGCAAAAGAACAACTATTTGAAACTAGGCTATCTGAAACATTTGTAAGTGAAATTTTTATGAACAATTCTACTTCCATATGTTTCAGATTGCTACGTCTAACTACTACAATCCCGATGTTCCTGCCAACTGTTTGAGCA **********....((..(((.(((((((((((.((.(((((.((((.........)))).)))))).)).)))))))))))).)))..))......**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head	M046 female body	M060 embryo	V049 head	V041 embryo	V110 male body
....TTCTACTTCCATATGTTTCAGA....	22	0	1	64.00	64	14	15	17	11	6	1
....TACTTCCATATGTTTCAGATTG....	22	0	1	28.00	28	6	12	3	5	2	0
....TGAAACATTTGTAAGTGAAATT....	22	0	1	18.00	18	10	4	2	1	0	1
....CTACTTCCATATGTTTCAGATTG....	23	0	1	8.00	8	1	3	2	0	2	0
....TCTGAAACATTTGTAAGTGA....	20	0	1	6.00	6	4	1	0	1	0	0
....ATCTGAAACATTTGTAAGTGAA....	22	0	1	6.00	6	1	1	3	1	0	0
....TCTGAAACATTTGTAAGTGAAA....	22	0	1	5.00	5	0	0	3	2	0	0
....TCTGAAACATTTGTAAGTGAA....	21	0	1	5.00	5	1	1	0	3	0	0
....TTCTACTTCCATATGTTTCAG....	21	0	1	4.00	4	2	0	0	2	0	0
....TGAAACATTTGTAAGTGAAA....	20	0	1	4.00	4	2	0	1	1	0	0
....TACTTCCATATGTTTCAGATTGT....	23	1	1	4.00	4	2	0	0	1	1	0
....TACTTCCATATGTTTCAGATT....	21	0	1	3.00	3	1	1	1	0	0	0
....ATCTGAAACATTTGTAAGTGA....	21	0	1	2.00	2	2	0	0	0	0	0
....TCTACTTCCATATGTTTCAG....	20	0	1	2.00	2	2	0	0	0	0	0
....CTGAAACATTTGTAAGTGAA....	20	0	1	1.00	1	0	1	0	0	0	0
....TGAAACATTTGTAAGTGAAAT....	21	0	1	1.00	1	1	0	0	0	0	0
....CTACTTCCATATGTTTCAGAC....	21	1	1	1.00	1	0	0	1	0	0	0
....TCTGAAACATTTGTAAGTGAAT....	22	1	1	1.00	1	0	0	0	0	0	1
....TTCTACTTCCATATGTTTCA....	20	0	1	1.00	1	0	1	0	0	0	0
....ACTTCCATATGTTTCAGATTG....	21	0	1	1.00	1	0	1	0	0	0	0
....TTCTACTTCCATATGTTTCAGAA....	23	1	1	1.00	1	0	0	0	1	0	0
....CTACTTCCATATGTTTCAGATTT....	23	1	1	1.00	1	0	0	0	1	0	0
....TCTACTTCCATATGTTTCAGA....	21	0	1	1.00	1	0	0	0	1	0	0

Anti-sense strand reads

AAGGTCTATCGAGTTTACCGTTTTCTTGTTGATAAACTTTGATCCGATAGACTTTGTAAACATTCACTTTAAAAATACTTGTTAAGATGAAGGTATACAAAGTCTAACGATGCAGATTGATGATGTTAGGGCTACAAGGACGGTTGACAAACTCGT **********....((..(((.(((((((((((.((.(((((.((((.........)))).)))))).)).)))))))))))).)))..))......**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V049 head	M046 female body	V110 male body
....ACTTCCATATGTTTCAGATTG....	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_6328:351285-351440 +	dmo_101	TTCCAGATAGCTCAAATGGCAAAAGAACAACTATTTGAAACTAGGCTATCTGAAACATTTGTAAGTGAAATTTTTATGAACAATTCTACTTCCATATGTTTCAGATTGCTACGTCTAACTACTACAATCCCGATGTTCCTGCCAACTGTTTGAGCA
droGri2	scaffold_15110:14614387-14614434 +		----------AACAATTTTTTGGTTTAGACTAATAAAAATGTTTTTGAGCGAAATTT----------

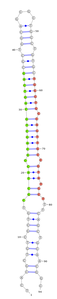
Generated: 09/08/2015 at 05:36:12 PM

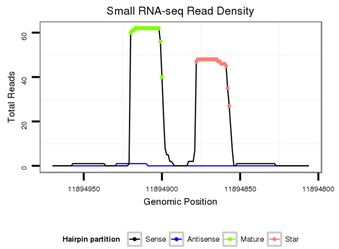
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

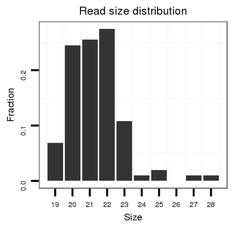
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_261	**scaffold_6540:11894856-11894920 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

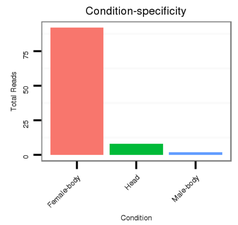
Legend: mature star **mismatch in alignment** mismatch in read

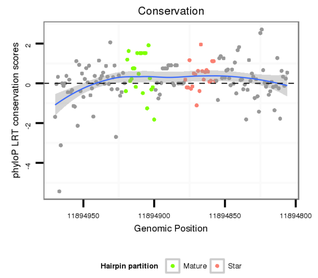
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GCACGACGCAGAAGAACAACAAAACGGCATTGCAGTCACGCTGTCGCTGTCGCTACCGCAGCTGCAGTCACGCTGTCGCTGTGCTGGCTGCCAGTTGCCGTATGCTTTCAGCTGCAACGGCCAACGTCGGCAGTCGTCAGTTTTAATTTCCACATCG						M046 female body	V056 head	V049 head	V110 male body	V041 embryo
********************************...((.(((.((((..(((((.(((((((((((((((((((.(((.....))))).)))))))))))))))))))).)))..)))).)))..))..********************************	Read size	# Mismatch	Hit Count	Total Norm	Total					
.....CGCTACCGCAGCTGCAGTCAG.....	21	0	1	17.00	17	17	0	0	0	0
.....CGCTACCGCAGCTGCAGTCA.....	20	0	1	16.00	16	13	1	1	1	0
.....CGCTACCGCAGCTGCAGTCAGC.....	22	0	1	14.00	14	14	0	0	0	0
.....TGGCTGCCAGTTGCCGTATGCT.....	22	0	1	10.00	10	10	0	0	0	0
.....TGGCTGCCAGTTGCCGTATG.....	20	0	1	9.00	9	6	2	0	1	0
.....TGGCTGCCAGTTGCCGTATGCTT.....	23	0	1	8.00	8	8	0	0	0	0
.....TGGCTGCCAGTTGCCGTATGC.....	21	0	1	6.00	6	5	0	1	0	0
.....TGGCTGCCAGTTGCCGTATGCTTT.....	24	0	1	6.00	6	6	0	0	0	0
.....CGCTACCGCAGCTGCAGTC.....	19	0	1	5.00	5	4	1	0	0	0
.....CGCTACCGCAGCTGCAGTCAGCG.....	23	0	1	3.00	3	3	0	0	0	0
.....CGCTACCGCAGCTGCAGTCAGCGCT.....	25	0	1	2.00	2	2	0	0	0	0
.....CTGGCTGCCAGTTGCCGTATGC.....	22	0	1	2.00	2	2	0	0	0	0
.....TGGCTGCCAGTTGCCGTATGCTTA.....	24	1	1	2.00	2	1	1	0	0	0
.....CTGGCTGCCAGTTGCCGTATGCTT.....	25	2	1	1.00	1	1	0	0	0	0
.....CGCTACCGCAGCTGCAGTCACC.....	21	0	1	1.00	1	1	0	0	0	0
.....GCTGCAACGGCCAACGTCGGCAGTC.....	25	0	1	1.00	1	1	0	0	0	0
.....TGGCTGCCAGTTGCCGTAT.....	19	0	1	1.00	1	1	0	0	0	0
.....GGCTGCCAGTTGCCGTATGCTT.....	23	1	1	1.00	1	1	0	0	0	0
.....GAACAACAAAACGGCATTGCA.....	21	0	1	1.00	1	1	0	0	0	0
.....CGCTACCGCAGCTGCAGTCAGGCGCTGG.....	27	0	1	1.00	1	1	0	0	0	0
.....TGTGCTGGCTGCCAGTTGCCG.....	21	0	1	1.00	1	0	1	0	0	0
.....CGCTACCGCAGCTGCAGTCAGCGCTGGC.....	28	0	1	1.00	1	1	0	0	0	0
.....CGCTACCGCAGCTGCAGTCAG.....	22	1	1	1.00	1	1	0	0	0	0
.....TCGCTACCGCAGCTGCAGTC.....	20	0	1	1.00	1	0	1	0	0	0
.....CTGGCTGCCAGTTGCCGTATG.....	21	0	1	1.00	1	0	1	0	0	0
.....GGCTGCCAGTTGCCGTATGCTT.....	22	0	1	1.00	1	1	0	0	0	0
.....TGTGCTGGCTGCCAGTTGC.....	19	0	1	1.00	1	0	1	0	0	0
.....TACCGCAGCTGCAGTCAGGCGCT.....	22	0	1	1.00	1	1	0	0	0	0
.....CTGGCTGCCAGTTGCCGTATGCTTT.....	25	0	1	1.00	1	1	0	0	0	0
.....CTGGCTGCCAGTTGCCGTATGCTT.....	24	0	1	1.00	1	1	0	0	0	0
.....CGCTACCGCAGCTGCAGTCT.....	20	1	2	0.50	1	1	0	0	0	0

Anti-sense strand reads

CGTGCTGCGTCTTCTTGTTGTTTGCGTAACGTCAGTGCGACAGCGACACGACGTGGCGTCGACGTCAGTGCGACCGTCGCGACGGACACGACCGACGGTCAACGGCATACGAAAGTCGACGTTGCCGGTTGCAGCCGTCAGCAGTCAAAATTAAAGGTGTAGC						V056 head	V110 male body
********************************...(((.(((.((((..(((((.(((((((((((((((((((.(((.....))))).)))))))))))))))))))).)))..)))).)))..))..********************************	Read size	# Mismatch	Hit Count	Total Norm	Total		
.....ACAGCGACAGCGATGGCGTC.....	20	0	1	1.00	1	1	0

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:11894806-11894970 -	dmo_261	GCACGACGCAG---A-AGAACA-ACA-A---AAC----------GGCATTGCAGTCA-CGCTGTCGC----------TGTCGC------TACCGCAGCTGC----------AGT----------CAG-C-GCTGGCAGCGCTGCCTGTG----------TG----------G----------C----------CT----------GCCAGT----------T-GC-CGT----ATGCT----------TCAGCTGCAACGGCCA----------AC-GTCGGCAGT-CGTCAGTTTTAAT-TTCCACA---TC-G
droVir3	scaffold_12855:2693642-2693892 +	dvi_106	-AVCAGCG----AA-A-GAACA-GCATT----------ACATTGCAGTCGCA-CGCTTCGC-T--GTC----AGTCG-----AGCTGCAGTTGACGTCGACAGCC-----GTTCGG----------C-----------CGCTGCC----------CGTTG----------G----------C----------CT----------GCCAGC----------T-GC-CGT----TGGCT----------TCAGCTGCAACGGCCAAGTCGTT--T-A-TGCCAGT-CGTCAGTTTTAAT-TTCCACA---TC-G
droGri2	scaffold_3013:1634-1800 -		GCCGCG-----CAGCAGC-CGT-T-TG-T-----CAGCAG-CGGCAGCAGTAGCAGCAGCAGCGGCAGC----------TGCAGC----------G-----AG-----AGC-----GCAGCAGCAGC----------G-CG----------G----------C----------CT----------GCAGCA----------GCAGCAGCAGCC----------T-GC-CGT----TGGCAGCAG----------TCAGCTGCAACGGCCAG-CGGCGTT--T-A-TGCCAGT-CGTCAGTTTTAAT-TTCCACA---TC-G
droWil2	scf2_1100000004902:11175878-11176092 +	dwi_5427	-AGTAACAG----AA-A-GAACA-AAAAGAAG----------TAAAAAGAAAAACTTAAAAACTGCACAGTTGCAGTC----------ATGCTGCTGCCTCTGCTGCAGTCGACTATT----------C-----------CC-----CTGCTGCT----------C-GT----------G----------C----------CT----------GCTGTC----------GCAGTTGCTGTTGGC----------T-GC-CGT----TTTT-GCAGTTTGGTT-TGGCTCTGCCAGCATCAGTCTTAAT-TTCCACA---TC-G
dp5	scaffold_5843:5026999 -	dpa_117	ACACCTGCG----T-----T-------T-A-GT----------GTGCTGCAGTCGA-CGCTCGC-T--GTTCGGCAGCG-----GCTGCAGCGC----------TGCGCCTTCTCTCCC----------GCTGCAGCGC----------TGGTGCCTC----------G----------C----------CT----------GCAGCG----------CGGCGCAGCCC----------T-GC-CGT----TGGCAGCAG----------TCGGTGCCTC----------GA-GCGGCAG-CGTCAGTTTAT-TTCCACA---TC-G
droPer2	scaffold_19:732305-732461 -	dpa_2527	ACACCTGCG----T-----T-------T-A-GT----------GTGCTGCAGTCGA-CGCTCGC-T--GTTCGGCAGCG-----GCTGCAGCGC----------TGCGCCTTCTCTCCC----------GCTGCAGCGC----------TGAGCGC----------G----------C----------CT----------GCAGCATGTGAGGCCAGCCCG----------T-GC-CGT----TGGCAGCAG----------TCGGTGCCTC----------GA-GCGGCAG-CGTCAGTTTAT-TTCCACA---TC-G
droAna3	scaffold_13340:6482827-6483013 +	dan_4066	AACCCGCGG----T-----T-CAG-T--AAC----AAACT----------CCAGTCTGCTGC----------GTGCTGCAGTCGA-TCGAT-T--TGCCGCCGTCGA-CGCTCGC-T--GTTCGGCAGCG-----GCTGCAGCGC----------ACTGCTGCTGCTGCTGCTGCTGCAGACCTTCTC----------TT-G----------TCGCCGCTGGCAG----------T-GC-CGT----TGGCAGCAG----------TCGGTGCCTC----------G-GTGGGCAG-CGTCAGTTTAT-TTCCACA---TC-G
droBip1	scf7180000396708:2366170-2366342 -		C-TATACCCAG---AAG-A-GAGAA-CGCCAA----AAC----------AAACT----------CCAGTCGGCTGC----------GTGCTGCAGTCGA-TCG-T--T----------ACC----------TGT-CTG----------CTACCGC----T-CTGC----------TGCCGCCTGCAGCGCCTTCTCTG----------T----------G----------C----------CT----------TT-G----------TGCCGCCTGTGGCAG----------ATTC----------C-GTGGGCAG-CGTCAGTTTAT-TTCCACA---TC-G
droKik1	scf7180000302698:592427-592570 +		GCACGC----T-CAG-A-GAACA-ACA-T----A----------AA-GTCGCAGTCGCA-TCGCAGC---AGAAGTC-CAGCCAG-----CAGCAGC----------GCAGCCGCC----------G----------C----------CT----------GCAGCAGCAGC----------T-GC-CGT----TGGCAGCAG----------TCAGCAGCAGCCGCAGCAGCAGCAGC-T-AGCCAGCAACGCCAGCATAGGCAGCC-T-AGCCAGCAGCAGCCAT-TCCACA---TC-A
droPic1	scf7180000454072:3124495-3124653 +		GCGGCGCG---A-CAGCAG-CAT-T-AAA----AAACGGC-CATTGGCAGTGGCAGCGGCAGCGGCAAT----------AT----------C----------AG-----AGC-----CAGCTGC----------ATCAACC-----GCCAGCGGCA-----A-CC----------C----------C----------CT----------GCAGCAGCAACA----------T-GC-CGT----TGGCAGCAG----------TCAGCTGCAACGGCCAGTCGGCGTT--T-A-TGCCAGT-CGTCAGTTTAT-TTCCACA---TC-G
droEle1	scf7180000490751:1099816-1099998 -		GGCGCGAACAG--CAGCAG-CAT-T-AAA----AGCAACAG-CAACAGCAACAGCAGCAGCAGCAACAACAGCAGGA----------ATCCGGCCAGCAACGGCGC-T----------C---CCATCG----------G----------C----------C----------CT----------GCAGCA----------ACCTGGGCG----------T----------G----------C----------CT----------GCTGGCAGCATCGCAGGCCCAGCAGGCAGTCACGCCGCTCAGCAGCAT-T----------C----------C-TCCACAGCAGCAT-TCCACA---TC-G
droRho1	scf7180000779488:520569-520733 +		GCGTCATTGCAGCAGCAG-----T-CT-T----GCAGCAACAC-GTCATCACCAATGTCAC-CGACATTC----------GCGCAGATTAT----------G-CT----------G----------C----------C----------CT----------AGTTG----------C----------C----------C----------CT----------AGCACGGCGTC----------T----------C----------C----------CT----------ACTC----------AGC----------T----------C----------C----------CT----------CCAGCACAACAGCAGCAACGCAGCAACAG----------T----------C----------C----------CT----------AGCAACAGCTCAGCAGCCGCTGCAGCAG-T----------C----------C----------CT----------AGCAACAGCTCAGCAGCCGCTGCAGCAG-AGATC
droTak1	scf7180000298389:380158-380333 +		GCGCGACGCG-----A-G-GCA-T-GCAG-T---GCC----ACCATCGAAAT----------ACCCACGGCCACGCTGCTGCAGGCCACCACCGCCAGCCAGGTGCAATCGCAGCTG----------C----------C----------C----------CT----------CGCGGGCAG----------C----------C----------C----------CT----------CAGCTGCAAGTGCAGCTGCAGCAGCTGCAGCAG-T----------C----------C----------CT----------AGCAGCAGCTGCAGCAGCTGCAGCAG-AGATC
droTak1	scf7180000415245:186297-186462 +		GCGCGACGCG-----A-AGAACA-GCA-T-GAA----AAC----------CAGCTGCAGTCGCA-TCGCAGC-T----------C----------C----------C----------CT----------CCGTCG----GCACTTGGCGAGCGT-GCA----TTTTCAGCTTGGCAA----TTC----------C-GTGGGCAG-CTCAGTTTAT-TTCCACA---TC-G
droRug1	scf7180000409470:253078-253208 +		A-AAAACAG----A-AGAAA-T-GCA-T-GAA-AAGAAC----------CAGCTGCAGTCGA-TCGCGT-T----------C----------C----------C----------CT----------CCAGCTG----GCACTTGGCGACATT-CA----TTTCCAGCTTGGCAA----TTC----------C-GTGGGCAG-CTCAGTTTAT-TTCCACA---TC-G
dm3	chrX:10813996-10814161 +		GCGCGCGCG----T-CAACAGC-GCA-T-GCAGC----A-C----------AA-----TGCTGCAGTCACACTATC----------C----------C----------C----------CT----------TTGGACCGGATGGCGGAATGCGAGGATTCAGCGAGCGCGGAGTGCCGCAAGGAGCGGCCGGCGTATCGCAC----------AA----------T----------TTGGACCGGATGGCGGAATGCGAGGATTCAGCGAGCGCGGAGTGCCGCAAGGAGCGGCCGGCGTATCGCAC----------AA----------C----------CGATTGCAATC----------C-GTGGGCAG-CTCAGTTTAT-TTCCACA---TC-G
droSim2	lr:1528611-15128753 -	das_31066	ATACGCGCG----T-AAACAGC-GCA-T-GCA----A-C----------AA-----TGCTGCAGTCACACTATC----------C----------C----------C----------CT----------AGTGCCACCGCTGCGACTCCGCCGAGGT-GCA----TTTCCAGCTTGGCGC----TTC----------C-GTGGGCAG-CTCAGTTTAT-TTCCACA---TC-G
droSec2	scaffold_0:15993590-15993732 +	dse_332	ATACGCGCG----T-AAACAGC-GCA-T-GCA----A-C----------AA-----TGCTGCAGTCGACACTATC----------C----------C----------C----------CT----------AGTGCCACCGCTGCGACTCCGCCGAGGT-GCA----TTTCCAGCTTGGCGC----TTC----------C-GTGGGCAG-CTCAGTTTAT-TTCCACA---TC-G
droYak3	3R:9967346-9967503 +	dya_1810	ATACGCGCG----T-AAACAGC-GCA-T-GCA----A-C----------AA-----TGCTGCAGTCGACACTATC----------C----------C----------C----------CT----------CTGCTGGTGCCGCTGCGACTCCGCCGAGGT-GCA----TTTCCAGCTTGGCGC----TTC----------C-GTGGGCAG-CTCAGTTTAT-TTCCACA---TC-G
droRer2	scaffold_4929:9419355-9419512 +		C-TATACCCAG---T-AAGAACA-T-GCA----TGC--TA----------AGGCGCCGCCGCA-CGCTCGC-T----------C----------C----------C----------CT----------AGCAGG----CAGCGGCCAGCAGC----------AT----------C----------C----------CT----------CTGATGAGCAGCGC----------T----------C----------C----------CT----------CAGCTGCAAGTGCAGCTGCAGCAGCTGCAGCAG-T----------C----------C----------CT----------AGCAGCAGCTGCAGCAGCTGCAGCAG-AGATC

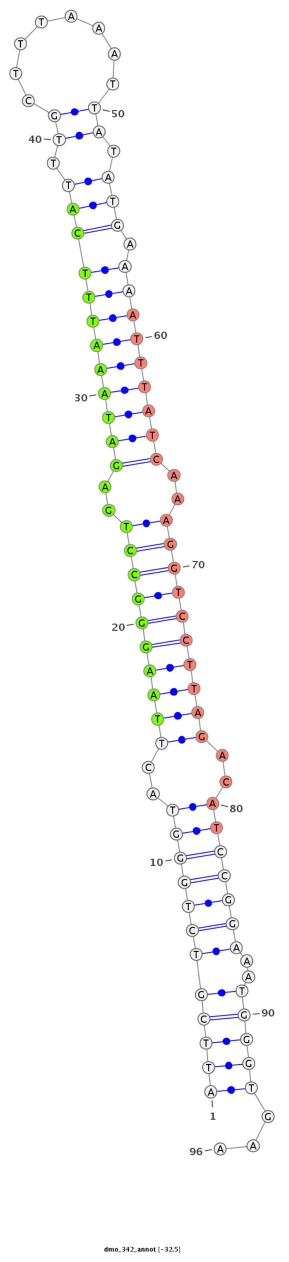
Generated: 09/08/2015 at 07:37 PM

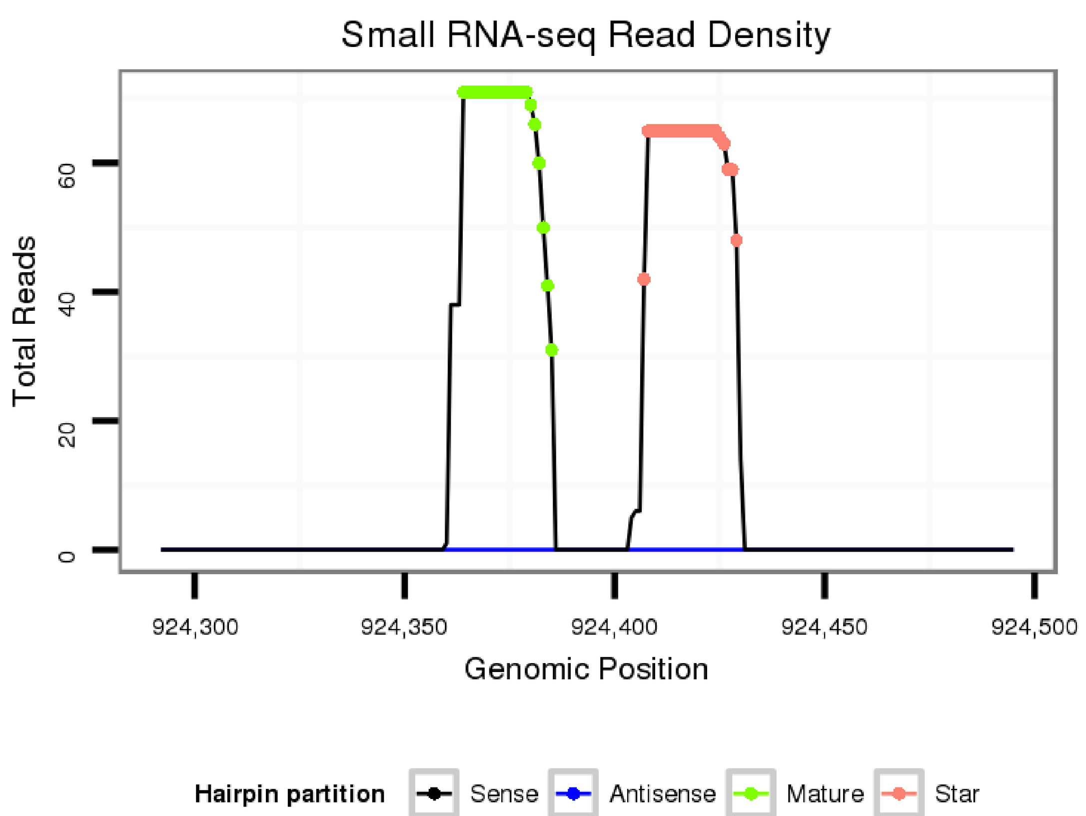
PASS/FAIL	
crit.star	1
crit.loop	0
crit.stem	1
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.offset	0
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.abundant	0
rescue.confident	0
rescue.candidate	1

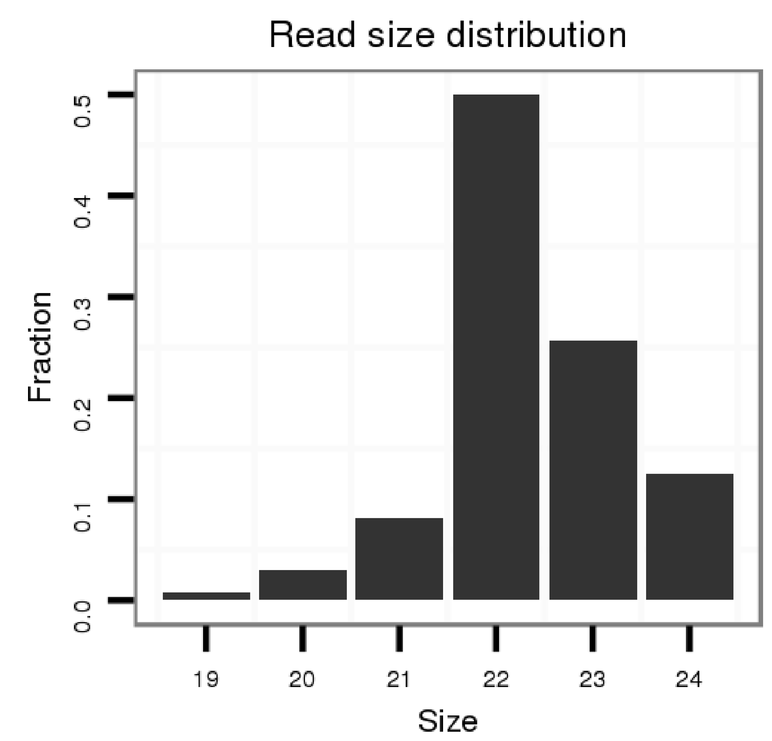
ID: dmo_342	Coordinate: scaffold_6359:924342-924445 +	Confidence: Known Ortholog	Class: Canonical miRNA	Genomic Locale: intergenic	[View on UCSC Genome Browser {Cornell Mirror}]

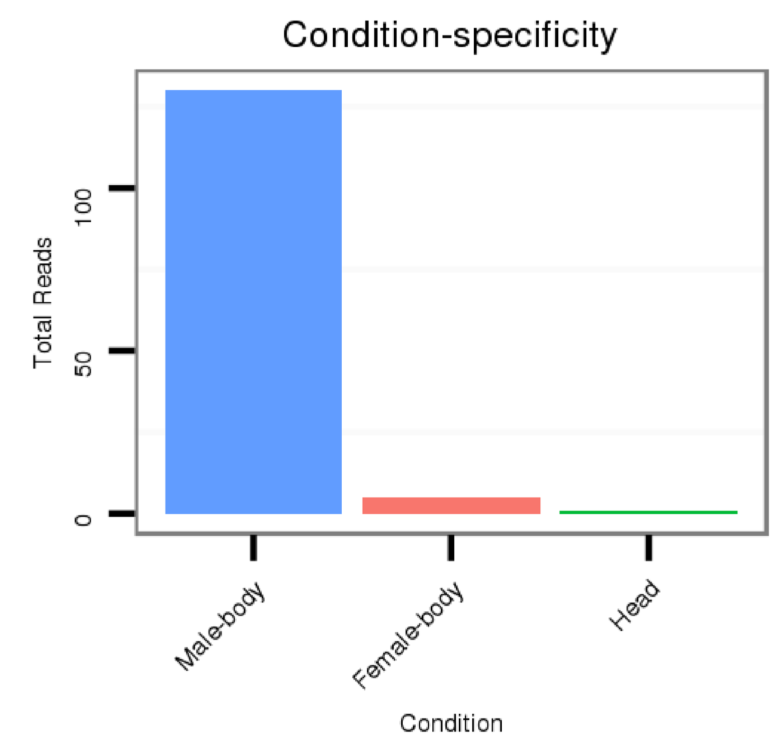
Legend: mature star mismatch in alignment mismatch in read

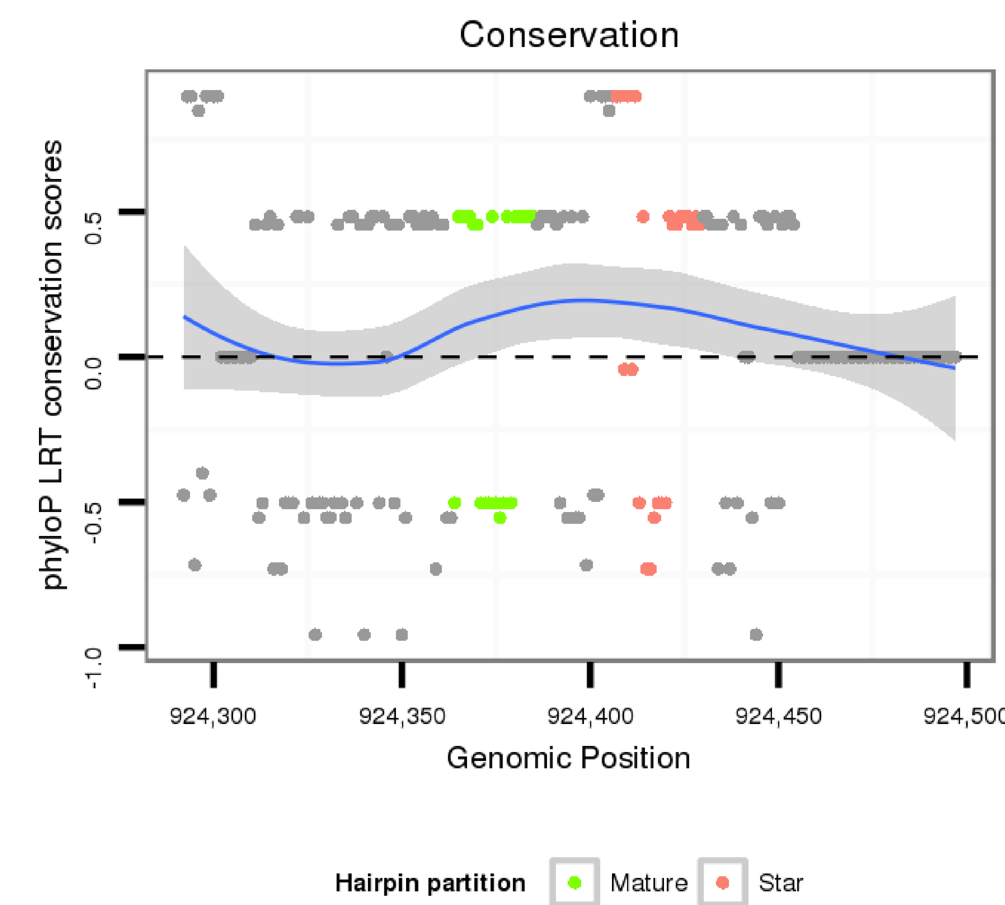
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATGTATATATTCTTTATGTGCATCTATCTTTTCCATATACATATGCGCTATATCGCCATTCGTCTGGGTACTTAAGGGCCTGAGATAAATTTCATTTGCTTTAAATTATATGAAAATTTATCAAAGGTCCTTAGACATCCGGAAATGGGTGAAGCAACAAGCATACGCTGCATGTATAGCCATGGAACTCATCATTATTCTCGA ***((((((((((((..((((((((((..((((((((((((.((........)).))).)))))))))..))))))))))..)))))))..)))))...***	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V049 head	V056 head
....TAAGGGCCTGAGATAAATTTCA..	22	0	1	31.00	31	30	0	0	0	1
....ATTTATCAAAGGTCCTTAGACAT..	23	0	1	18.00	18	15	3	0	0	0
....TTTATCAAAGGTCCTTAGACAT..	22	0	1	16.00	16	16	0	0	0	0
....ACTTAAGGGCCTGAGATAAATT...	22	0	1	10.00	10	10	0	0	0	0
....ACTTAAGGGCCTGAGATAAATTT..	23	0	1	9.00	9	9	0	0	0	0
....ATTTATCAAAGGTCCTTAGACA...	22	0	1	9.00	9	8	1	0	0	0
....ATTTATCAAAGGTCCTTAGACATC...	24	0	1	9.00	9	9	0	0	0	0
....ACTTAAGGGCCTGAGATAAATTTC...	24	0	1	8.00	8	8	0	0	0	0
....ACTTAAGGGCCTGAGATAAAT..	21	0	1	6.00	6	6	0	0	0	0
....TTTATCAAAGGTCCTTAGACATC...	23	0	1	5.00	5	5	0	0	0	0
....ACTTAAGGGCCTGAGATAAA...	20	0	1	3.00	3	3	0	0	0	0
....ATTTATCAAAGGTCCTTAGACATCT..	25	1	1	3.00	3	3	0	0	0	0
....ACTTAAGGGCCTGAGATAAATTTTC..	25	2	1	3.00	3	3	0	0	0	0
....AAAATTTATCAAAGGTCCTTAGA...	23	0	1	3.00	3	3	0	0	0	0
....ACTTAAGGGCCTGAGATAAATTC..	23	1	1	2.00	2	2	0	0	0	0
....TTTATCAAAGGTCCTTAGACA...	21	0	1	2.00	2	2	0	0	0	0
....AAAATTTATCAAAGGTCCTTAGT...	23	1	1	2.00	2	2	0	0	0	0
....TAAGGGCCTGAGATAAATTTC...	21	0	1	2.00	2	2	0	0	0	0
....AAATTTATCAAAGGTCCTTAGA...	22	0	1	1.00	1	1	0	0	0	0
....ACTTAAGGGCCTGAGATAA..	19	0	1	1.00	1	1	0	0	0	0
....ATTTATCAAAGGTCCTTAGACATA...	24	1	1	1.00	1	1	0	0	0	0
....ACTTAAGGGCCTGAGATAAATTTA...	24	1	1	1.00	1	1	0	0	0	0
....ACTTAAGGGCCTGAGATAAATTCT...	24	2	1	1.00	1	1	0	0	0	0
....ACTTAAGGGCCTGAGATAAATTAA...	24	2	1	1.00	1	0	0	1	0	0
....TAAGGGCCTGAGATAAATTTCAA...	23	1	1	1.00	1	1	0	0	0	0
....ATTTATCAAAGGTCCTTAGACT...	22	1	1	1.00	1	1	0	0	0	0
....AAAATTTATCAAAGGTCCTTA...	21	0	1	1.00	1	1	0	0	0	0
....AAAATTTATCAAAGGTCCTTAG..	22	0	1	1.00	1	0	1	0	0	0
....ATTTATCAAAGGTCCTTAGACATCA..	25	1	1	1.00	1	0	0	0	1	0
....TACTTAAGGGCCTGAGATAA..	20	0	1	1.00	1	1	0	0	0	0
....ACTTAAGGGCCTGAGATAAATTA..	23	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

TACATATATAAGAAATACACGTAGATAGAAAAGGTATATGTATACGCGATATAGCGGTAAGCAGACCCATGAATTCCCGGACTCTATTTAAAGTAAACGAAATTTAATATACTTTTAAATAGTTTCCAGGAATCTGTAGGCCTTTACCCACTTCGTTGTTCGTATGCGACGTACATATCGGTACCTTGAGTAGTAATAAGAGCT ***((((((((((((..((((((((((..((((((((((((.((........)).))).)))))))))..))))))))))..)))))))..)))))...***	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_6359:924290-924495 +	dmo_342	ATATGTATATATTCTTTATGTGCATCTATCTTTTCCATATACATATGCGCTATATCGCCATTCGTCTGGGTACTTAAGGGCCTGAGATAAATTTCATTTGCTTTAAATTATATGAAAATTTATCAAAGGTCCTTAGACATCCGGAAATGGGTGAAGCAACAAGCATACGCTGCATGTATAGCCATGGAACTCATCATTATTCTCGA
droVir3	scaffold_13042:4534917-4535067 +	dvi-mir-9546	TTAGGCAAAT---------GAACAGCGGCTTTATTGGCTAGCGAATACCCTACA-CACGTTTCGTCTTGGATTTTAAGGATTTATAACAAATTTCATTTGTTATTTAGTTAATGAAAATTTGTACTGAATCCTTAGACATCCTGGCACG--ACAAGTAGCAAG--
droWil2	scf2_1100000004540:1429500-1429523 -		ATATGTATAT---TTATATGAAATTAT--

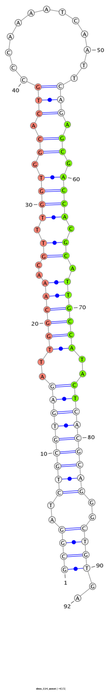
Generated: 09/08/2015 at 07:37 PM

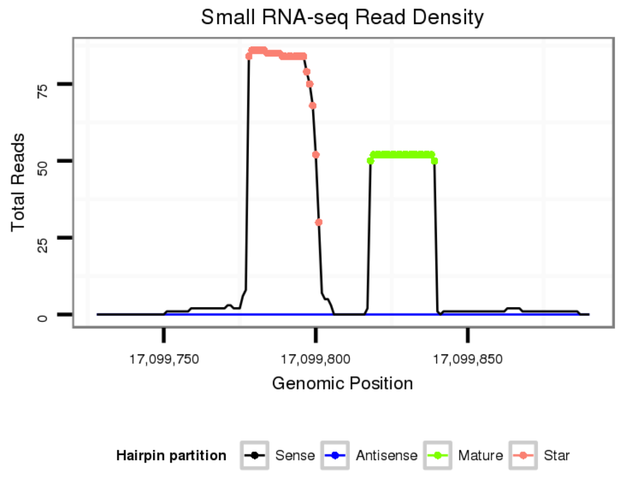
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	1
rescue.confident	1
rescue.candidate	0

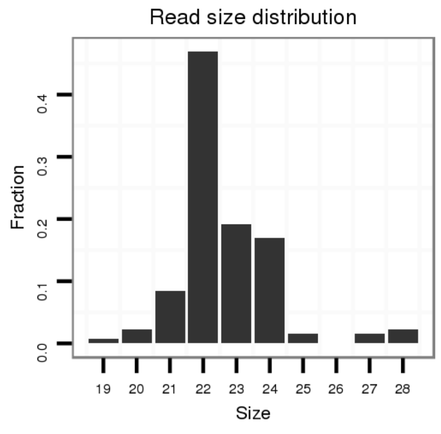
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_114	**scaffold_6680:17099778-17099840 +**	**confident**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

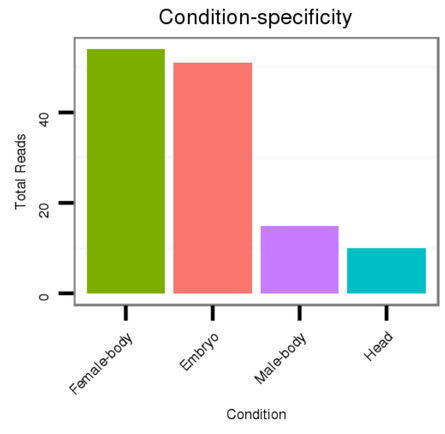
Legend: mature star mismatch in alignment mismatch in read

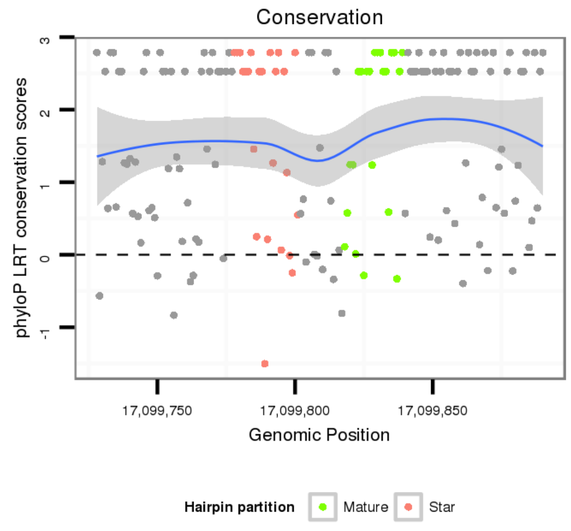
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [DmojGI13634-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATGCCTTTGCCACGGCGCAAGGCTGGCCCGCCGATGCGGATCTGCGTGAGATTGGCAAACGTTTGGTGGCACTGCCCAAAATCAATTCAGAGCGACCACGCATTGCCATACTCACGCAGGGCTGTGACCCCGTGCTGCTCATCCAGCACGACAAGGTCCAGGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V056 head	V041 embryo	V049 head
**********(((((..(((((((((..((((((..((.((((.((.(((.............))))).)).)))).)).)))))).))))))..))))))..**********											
.....AGCGACCACGCATTGCCATACT.....	22	0	1	45.00	45	14	30	0	1	0	0
.....ATTGGCAAACGTTTGGTGGCACTG.....	24	0	1	22.00	22	12	2	5	0	1	2
.....ATTGGCAAACGTTTGGTGGCACT.....	23	0	1	21.00	21	4	7	3	5	2	0
.....ATTGGCAAACGTTTGGTGGCAC.....	22	0	1	15.00	15	9	4	1	1	0	0
.....ATTGGCAAACGTTTGGTGGCA.....	21	0	1	7.00	7	0	2	5	0	0	0
.....AGCGACCACGCATTGCCATACG.....	22	1	1	5.00	5	5	0	0	0	0	0
.....ATTGGCAAACGTTTGGTGGCACC.....	23	1	1	4.00	4	3	0	0	0	1	0
.....ATTGGCAAACGTTTGGTGGCACTGCCCA.....	28	0	1	3.00	3	2	1	0	0	0	0
.....ATTGGCAAACGTTTGGTGGC.....	20	0	1	3.00	3	0	1	0	0	1	1
.....AGATTGGCAAACGTTTGGTGG.....	21	0	1	3.00	3	0	1	1	1	0	0
.....GAGCGACCACGCATTGCCATACG.....	23	1	1	3.00	3	3	0	0	0	0	0
.....GCGACCACGCATTGCCATACT.....	21	0	1	2.00	2	0	2	0	0	0	0
.....ATTGGCAAACGTTTGGTGGCACTGC.....	25	0	1	2.00	2	1	0	0	0	1	0
.....AGCGACCACGCATTGCCATAC.....	21	0	1	2.00	2	0	2	0	0	0	0
.....ATTGGCAAACGTTTGGTGGCACTGT.....	25	1	1	2.00	2	0	0	0	2	0	0
.....ATTGGCAAACGTTTGGTGGCACTGCCC.....	27	0	1	2.00	2	2	0	0	0	0	0
.....GAGCGACCACGCATTGCCATACT.....	23	0	1	2.00	2	1	1	0	0	0	0
.....ATTGGCAAACGTTTGGTGGCACTT.....	24	1	1	1.00	1	0	1	0	0	0	0
.....ATTGGCAAACGTTTGGTGG.....	19	0	1	1.00	1	0	0	1	0	0	0
.....AGATTGGCAAACGTTTGGTGGC.....	22	0	1	1.00	1	0	1	0	0	0	0
.....ATTGGCAAACGTTTGGTGGCAA.....	22	1	1	1.00	1	0	0	0	1	0	0
.....GATTGGCAAACGTTTGGTGG.....	20	0	1	1.00	1	0	1	0	0	0	0
.....GAGCGACCACGCATTGCCATACTTC.....	25	2	1	1.00	1	0	1	0	0	0	0
.....TTGGCAAACGTTTGGTGGCACTG.....	23	0	1	1.00	1	0	1	0	0	0	0
.....AGCGACCACGCATTGCCATACTCC.....	24	1	1	1.00	1	0	1	0	0	0	0
.....AGCGACCACGCATTGCCATACTC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....CGCAGGGCTGTGACCCCGTGCTGCTC.....	26	0	1	1.00	1	0	1	0	0	0	0
.....GCGTGAGATTGGCAAACG.....	18	0	1	1.00	1	0	0	0	0	0	1
.....ATTGGCAAACGTTTGGTGGCT.....	21	1	1	1.00	1	0	1	0	0	0	0
.....AGCGACCACGCATTGCCATACTT.....	23	1	1	1.00	1	0	1	0	0	0	0
.....TGCTCATCCAGCACGACAAGGTCC....	24	0	1	1.00	1	0	1	0	0	0	0
.....CGATGCGGATCTGCGTGAGATTGGC.....	25	0	1	1.00	1	0	1	0	0	0	0
.....TGGCCCGCCGATGCGGATCTGC.....	22	0	1	1.00	1	0	1	0	0	0	0
.....GATTGGCAAACGTTTGGTGGCAC.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TTGGCAAACGTTTGGTGGCACT.....	22	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

TACGGAAACGGTGCCGCGTTCCGACCGGGCGGCTACGCCTAGACGCACTCTAACCGTTTGCAAACCACCGTGACGGGTTTTAGTTAAGTCTCGCTGGTGCGTAACGGTATGAGTGCGTCCCGACACTGGGGCACGACGAGTAGGTCGTGCTGTTCCAGGTCCT	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body
**********(((((..(((((((((..((((((..((.((((.((.(((.............))))).)).)))).)).)))))).))))))..))))))..**********						
.....AGCGGTTCGCCGAGGCCCACGCAGTGGCCCTAGCG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGAGAAGAAAAACCCGACGCGCCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATCAGCAGGA---TTCGGTCCAGGA	22	0	1	15.00	15	9
.....AGGCGTTTGCCGAGGCCCACGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGATTGGTGGCGATGGAGAAGAAAAACCCGACGCGCCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATTCAGCAGGA---TTCGGTCCAGGA	22	0	1	7.00	7	0
.....AGCGTTCGCCGAGGCCCACGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGAGAAGAAAAACCCGACGCGCCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATTCAGCAGGA---TTCGGTCCAGGA	22	0	1	3.00	3	0
.....AGCGCTTCGCCGAGGCCCAGAGCTGGCCCGAGTG---GGGATCTGCGAGAGATTGGCAAGCGGCTGGTGGCGTTCGATAAGCTGAATACCTCAAAGCCTCGAATTGCCATTCTCACGCAGGGTTGCGATCCCGTGCTGCTGTTCCAGCAGGA---CTCGGTCAGGA	23	1	1	3.00	3	3
.....AGCGCTTCGCCGAGGCCCAAAAATGGCCGAGCG---AGGATCTGCGTGAGATTGGCAAACGTCTGGTGGCAATGGACAAACTAAATCCGTCGCGCCACGCATTGCCATCCTCACGCAGGGTTGTGATCCCGTCCTGCTCATCCAGCAGGA---TTCGGTCGCAGGA	25	0	1	2.00	2	1
.....AGCGCTTCGCCGAGAAACAGAATTGGCCCAGCG---GGGATCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGACAAACTGAATCCGCGCGCCGCGCATTGCCATACTCACGCAGGGCTGCGATCCCGTCCTGCTCATCCAGCAGGA---TTCGGTCGCAGGA	21	0	1	2.00	2	0
.....AGCGCTTCGCCGAGGCCCAGAACTGGCCCAGCG---GGGATCTGCGCGAGATTGGCAAGCGCCTGGTGGCGATGGACAAGCTGAATCCGACGCGACCCGCCATTGCCATACTCACGCAGGGCTGCGATCCCGTGCTGCTCATCCAGCAGGA---TTCGGTCCAGGA	23	0	1	2.00	2	1
.....AGCGCTTCGCCGAGGCCCAGAAGTGGCCCAAGCG---GGGATCTGCGCGAGATTGGCAAGCGCCTGGTGGCGCTGGACAAGCTGAATCCGCGCGCCGCGCATTGCCATACTCACGCAGGGCTGCGATCCCGTCCTGCTCATCCAGCAGGA---CTCGGTCAGGA	24	1	1	1.00	1	0
.....AGCGCTTCGCCGAGGCCCAGAGTTGGCCCAGCG---GGGATCTGCGCGAGATTGGCAAGCGCCTGGTGGCGCTGGACAAGCTGAATCCGCGCGCCGCGCATTGCCATCCTCACGCAGGGCTGCGATCCCGTCCTGCTCATCCAGCAGGA---CTCGGTCAGGA	25	2	1	1.00	1	0
.....AAGCGCTTCGCCGAGGCCCAGAATTGGCCCAAGTG---GGGATCTTCGTGAGATTGGCAAGCGTCTGGTGGCGATGGCAAATTAAATACGACGCGGCCGCGCATTGCTATCCTCACGCAGGGCTGTGATCCTGTCCTGCTTATCCAACAGGA---CTCGGTACAGGA	24	1	1	1.00	1	0
.....AGCGCTTCGCCGAGGCCCAGCAGTGGCCCTAGCG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGAGAAGAAAAACCCGACGCGCCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATTCAGCAGGA---TTCGGTCCAGGA	22	0	1	1.00	1	0
.....AGCGCTTCGCCGAGGCCCAGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGATTGGTGGCGATGGAGAAGAAAAACCCGGCGCCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATTCAGCAGGA---TTCGGTCCAGGA	23	0	1	1.00	1	0
.....AGCGCTTCGCCGAGGCCCAGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGAGAAGAAAAACCCGACGCGCCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTGCTGCTTATTCAGCAGGA---TTCGGTCCAGGA	21	0	1	1.00	1	0
.....AGCGCTTCGCCGAGGCCCAGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGAGAAGAAAAACCCGACGCGACGCGCCGCATTGCCATTCCTCACGCAGGGTTGCGATCCTGTGCTGCTCATCCAGCAGGA---TTCGGTCCAGGA	22	0	1	1.00	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6680:17099728-17099890 +	dmo_114	ATGCCTTTGCCACGGCGCAAGGCTGGCCCGCCGATGCGGATCTGCGTGAGATTGGCAAACGTTTGGTGGCACTGCCCAAAATCAATTCAGAGCGACCACGCATTGCCATACTCACGCAGGGCTGTGACCCCGTGCTGCTCATCCAGCACGA---CAAGGTCCAGGA
droVir3	scaffold_13049:22492168-22492330 +	dvi_158	AGGCCTTTGCCACTGCGCAAGGTTGGCCCGCCGACAATGATCTGCGTGAGATTGGCAAGCGCCTGGTCGCGCTGAATAAACTCAATACGGCGCGACCACGCATTGCCATACTCACGCAGGGCTGTGACCCCGTGCTGCTATACAGCACGA---TTCGGTCCAGGA
droGri2	scaffold_15121:203629-203794 +	dgr_465	AGGGTTTGCCACGGCACAAGGCTGGCCGCCGATGAGGATCTGCGTGAGATTGGCAGGCGTCTGGTTGCACTGGACAAATTGAATTCAGCGCGACCACGCATTGCGCATACTCACGCAGGGCTGTGATCCCGTGCTGCTCATCCAGCACGACGCTCCGGTCCAGGA
droWil2	scf2_1100000004511:5276766-5276925 +	dwi_5417	ATGCCTTTGCCACTGGCCAGGGCTGGCCAACGG---ATGATCTGCGCGAGATTGGCAAACGTATAGTCGGTCTGGAGAAACTAAATCCAAGTCCGCCACGCATTGCCATACTAACGCAGGGCTGTGATCCGGTGTTGCTCATTCAAAAAGA---TTCGGTTGAAGA
dp5	XR_group6:4377279-4377438 -	dps_3829	ATGCCTTTGCTACGGCCCAGGGCTGGCCGACCG---AAGATCTGCGCGAGATTGGCAAGCGTCTGGTGGCGCTGGACAAACTGAATCCGGCGCGACCTCGCATTGCCATACTAACGCAGGGCTGTGATCCCGTGCTGCTCATCCAGCGGGA---CTCGGTTGAAGA
droPer2	scaffold_9:2666460-2666619 -	dpe_2483	ATGCCTTTGCTACGGCCCAGGGCTGGCCGACCG---AAGATCTGCGCGAGATTGGCAAGCGTCTGGTGGCGCTGGACAAACTGAATCCGGCGCGACCTCGCATTGCCATACTAACGCAGGGCTGTGATCCCGTGCTGCTCATCCAGCGGGA---CTCGGTTGAAGA
droAna3	scaffold_13337:4137411-4137570 +	dan_4038	AGGCCTTCGCCGAGGCCCAGAGCTGGCCGAGTG---GGGATCTGCGAGAGATTGGCAAGCGGCTGGTGGCGTTCGACAAGCTGAACTCGTCGACGCCGCGCATTGCCATTCTCACGCAGGGCTGTGATCCCGTGCTGCTCTTCCAGCAGGA---CTCGGTCAGGA
droBip1	scf7180000395450:265916-266075 +		AAGCCTTCGCCGAGGCCCAGAGCTGGCCGAGTG---GGGATCTGCGAGAGATTGGCAAGCGCTGGTGGCGTTCGATAAGCTGAATACCTCAAAGCCTCGAATTGCCATTCTCACGCAGGGTTGCGATCCCGTGCTGCTGTTCCAGCAGGA---CTCGGTCAGGA
droKik1	scf7180000302272:666730-666889 -		AGGCCTTTGCCGAGGCCCAAAAATGGCCGAGCG---AGGATCTGCGTGAGATTGGCAAACGTCTGGTGGCAATGGACAAACTAAATCCGTCGCGCCACGCATTGCCATCCTCACGCAGGGTTGTGATCCCGTCCTGCTCATCCAGCAGGA---TTCGGTCGCAGGA
droFic1	scf7180000454048:724250-724409 +		AGGCCTTCGCCGAGAAACAGAATTGGCCCAGCG---GGGATCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGACAAACTGAATCCGCGCGCCGCGCATTGCCATACTCACGCAGGGCTGCGATCCCGTCCTGCTCATCCAGCAGGA---TTCGGTCGCAGGA
droEle1	scf7180000491255:1412102-1412261 -		AGGCCTTCGCCGAGGCCCAGAACTGGCCCAGCG---GGGATCTGCGCGAGATTGGCAAGCGCCTGGTGGCGATGGACAAGCTGAATCCGACGCGACCCGCCATTGCCATACTCACGCAGGGCTGCGATCCCGTGCTGCTCATCCAGCAGGA---TTCGGTCCAGGA
droRho1	scf7180000769477:983-1142 +		AGGCCTTCGCCGAGGCCCAGAACTGGCCCAAGCG---GGGATCTGCGCGAGATTGGCAAGCGACTGGTGGCGCTGGACAAACTGAATCCGCGCGCCGCGCCGCATTGCCATACTCACGCAGGGCTGCGATCCCGTGCTGCTCATCCAGCAGGA---TTCGGTCGCAGGA
droBia1	scf7180000302193:2253869-2254028 -		AGGCCTTCGCCGAGGCCCAGAGTTGGCCCAGCG---GGGATCTGCGCGAGATTGGCAAGCGGCTGGTGGCGTTCGACAAACTGAATCCGCGCGCCGCGCCGCATTGCCATTCTCACGCAGGGCTGCGACCCCGTGCTGCTGTTCCAGCAGGA---TTCGGTCCAGGA
droTak1	scf7180000415706:66160-66319 -		AGGCCTTCGCCGAGGCCCAGAGTTGGCCCAGCG---GGGATCTGCGCGAGATTGGCAAGCGCCTGGTGGCGCTGGACAAGCTGAATCCGCGCGCCGCGCCGCATTGCCATCCTCACGCAGGGCTGCGATCCCGTCCTGCTCATCCAGCAGGA---CTCGGTCAGGA
droEug1	scf7180000409711:6101278-6101437 -		AAGCCTTCGCCGAGGCCCAGAATTGGCCAAGTG---GGGATCTTCGTGAGATTGGCAAGCGTCTGGTGGCGATGGCAAATTAAATACGACGCGGCCGCGCATTGCTATCCTCACGCAGGGCTGTGATCCTGTCCTGCTTATCCAACAGGA---CTCGGTACAGGA
dm3	chr3L:13013589-13013748 -	dme_245	AGGGCGTTCGCCGAGGCCCACGCAGTGGCCCTAGCG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGAGAAGAAAAACCCGACGCGCCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATTCAGCAGGA---TTCGGTCCAGGA
droSim2	3l:12704038-12704197 -	dsi_32458	AGGGCGTTCGCCGAGGCCCACGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGATTGGTGGCGATGGAGAAGAAAAACCCGGCGCCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATTCAGCAGGA---TTCGGTCCAGGA
droSec2	scaffold_0:5185174-5185333 -	dse_1846	AGTGCGTTCGCCGAGGCCCACGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGATTGGTGGCGATGGAGAAGAAAAACCCGGCGCCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATTCAGCAGGA---TTCGGTCCAGGA
droYak3	3L:13092492-13092651 -	dya_1798	AGGCCTTCGCCGAGGCCCAGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGAGAAGAAAAACCCGACGCGCCGCGCATTGCCATCCTCACGCAGGGCTGCGATCCTGTGCTGCTTATTCAGCAGGA---TTCGGTCCAGGA
droEre2	scaffold_4784:13021122-13021281 -	der_1523	AGGCCTTCGCCGAGGCCCAGCAGTGGCCCAGCG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGAGAAGAAAAACCCGACGCGACGCGCCGCATTGCCATCCTCACGCAGGGTTGCGATCCTGTGCTGCTCATCCAGCAGGA---TTCGGTCCAGGA

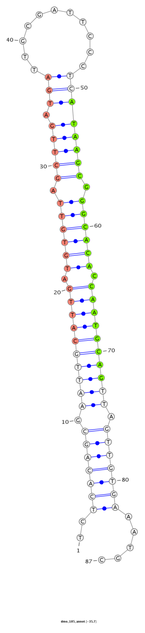
Generated: 09/08/2015 at 07:37 PM

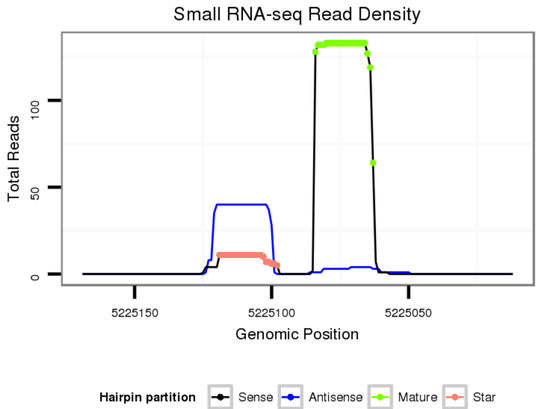
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	10

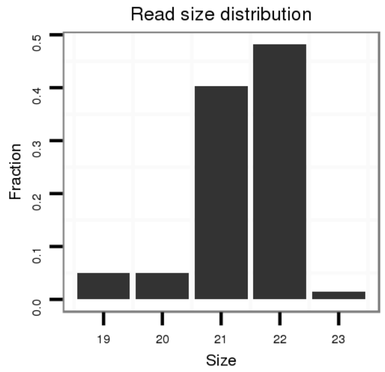
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_105	**scaffold_6540:5225062-5225119 -**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

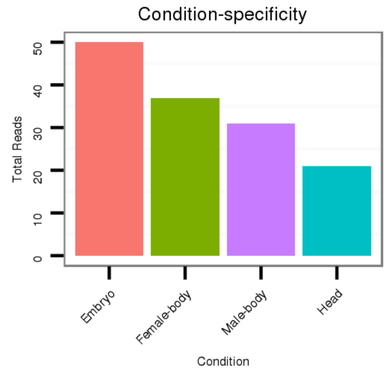
Legend: mature star mismatch in alignment mismatch in read

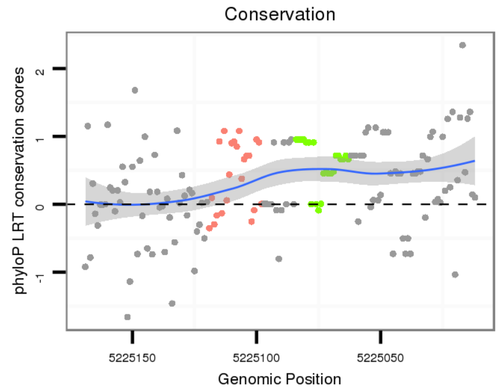
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI23565-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TCAACGTTAGACCTATTGCATCACTCGGATCAATCTCTCACAGCGAATTGCATTGATGTGTTAGCTTGATGATTGCGATTCCCTCATAAGCGGGCACACCAATGCAGTTAGTTGTGAAATGCCGGACCGCAGGCATTGGCAAGACACTAGCACGTAAC **********..(((((((.(((((((((((.(((((((.((((((.(((((.(((.....)))))))).)))))))).))))))))))).)))))))).....**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M060 embryo**	**M046 female body**	**V110 male body**	**V049 head**	**V041 embryo**	**V056 head**
.....ATAAGCGGGCACACCAATGCAG.....	22	0	1	57.00	57	9	11	15	8	9	5
.....ATAAGCGGGCACACCAATGCA.....	21	0	1	54.00	54	22	13	11	2	3	3
.....ATAAGCGGGCACACCAATGC.....	20	0	1	7.00	7	2	5	0	0	0	0
.....ATAAGCGGGCACACCAATG.....	19	0	1	6.00	6	1	2	1	0	0	2
.....CATTGATGTGTTAGCTTGATGA.....	22	0	1	5.00	5	0	3	0	0	1	1
.....TAAGCGGGCACACCAATGCAGT.....	22	0	1	4.00	4	2	0	2	0	0	0
.....AATTGCATTGATGTGTTAGCTT.....	22	0	1	3.00	3	0	1	2	0	0	0
.....ATAAGCGGGCACACCAATGCAA.....	22	1	1	3.00	3	2	1	0	0	0	0
.....ATAAGCGGGCACACCAATGCT.....	21	1	1	2.00	2	1	0	1	0	0	0
.....ATAAGCGGGCACACCAATGCAGT.....	23	0	1	2.00	2	0	0	2	0	0	0
.....GCGGGCACACCAATGCAGTTAGT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....CATTGATGTGTTAGCTTGATGAA.....	23	1	1	1.00	1	0	0	1	0	0	0
.....GAATTGCATTGATGTGTTAGCT.....	22	0	1	1.00	1	0	1	0	0	0	0
.....ATAAGCGGGCACACCAATT.....	19	1	1	1.00	1	0	0	1	0	0	0
.....AATTGCATTGATGTGTTAGCTC.....	22	1	1	1.00	1	1	0	0	0	0	0
.....CATTGATGTGTTAGCTTGATG.....	21	0	1	1.00	1	0	1	0	0	0	0
.....CATAAGCGGGCACACCAATGC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....ATAAGCGGGCACACCAAG.....	18	1	1	1.00	1	0	1	0	0	0	0
.....CATTGATGTGTTAGCTTGA.....	19	0	1	1.00	1	0	1	0	0	0	0
.....CATAAGCGGGCACACCAATGCA.....	22	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

AGTTGCAATCTGGATAACGTAGTGAGCCTAGTTAGAGAGTGTCGCTTAACGTAACTACACAATCGAACTACTAACGCTAAGGGAGTATTCGCCCGTGTGGTTACGTCAATCAACACTTTACGGCCTGGCGTCCGTAACCGTTCTGTGATCGTGCATTG **********..(((((((.(((((((((((.(((((((.((((((.(((((.(((.....)))))))).)))))))).))))))))))).)))))))).....**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M046 female body**	**V110 male body**
.....ACGTAACTACACAATCGAACTA.....	22	0	1	24.00	24	24	0
.....TAACGTAACTACACAATCGAACT.....	23	0	1	4.00	4	4	0
.....TAACGTAACTACACAATCGAAC.....	22	0	1	3.00	3	3	0
.....ACGTAACTACACAATCGAACT.....	21	0	1	3.00	3	3	0
.....CGTAACTACACAATCGAACTA.....	21	0	1	3.00	3	3	0
.....TCGCCCGTGTGGTTACGTCAA.....	21	0	1	2.00	2	2	0
.....GGTTACGTCAATCAACACTTTA.....	22	0	1	1.00	1	1	0
.....TTAACGTAACTACACAATCGAACT.....	24	0	1	1.00	1	1	0
.....CGTAACTACACAATCGAACT.....	20	0	1	1.00	1	1	0
.....AGTATTCGCCCGTGTGGTTACGT.....	23	0	1	1.00	1	1	0
.....CGTAACTACACAATCGAACTAC.....	22	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:5225012-5225169 -	dmo_105	T---CAACG-TTAG----------A-CCTATTGCATC-------ACTCGGATCAA-TCTCTCA------CAGCG----------AATTGCATTGATGTGTTAG------CTTGATGATTGCGATTCCCTCATAAGCGGGCA----------CACCAATGCAGTTAGTTGTGAAATGCCGGACCGCAGGCATTGGCAAGAC----------ACT--------AGCACGTAAC
droVir3	scaffold_13047:1194005-1194161 -	dvi_24638	C---CAACG-TA-G----------A-CATTTTGTATC-------ACTTGTACTTT-TTCTCA------CAGCG----------AATTGTATTGATGTGTTAG------CTTAATGATTGCGACTCCCTCATAAGCGGGCA----------CACCAATGCAGTTATTGTGAAATGCCGTACGAAGTGCATTGGCAAGAC----------ACC--------AGCACGTAAC
droGri2	scaffold_14906:5077573-5077683 +		T---CATCA-TC---GATGCAC----------------------TCGGTTCTT-TTGCTCA------CAGCACAAATAG-------C----------AATTGCATTGATGTGTTGG------CTTA----------ATGCAGTTATTGTGAAATGCC----------TAGCAAGAC----------ACC--------AGCACGTAAC
droWil2	scf2_1100000004902:74499-74554 +		C---CGAAG-AT-G-ATGATGTG------GC-----------------TG-------------A-TTACTTC------GGAAACGAAGCGAAAGGAAACACTTCCTT----GCGGGAA----------AGTTGAATCACTCGCGTT----------GCATTCGT----------TCACTTAAG
dp5	2:7233611-7233738 +		A---CAATT-GT---------------------------------A-TTACTTC------GGAAACGAAGCGAAAGGAAACACTTCCTT----GCGGGAA----------GTTCAGTTCAGTACGATCTTTCGCTACCAAGGAA----------CACAAGTCACCACATCACCGGCACAAATCAAAGACGTATG
droPer2	scaffold_0:1094300-1094427 +		A---CAATT-GT---------------------------------A-TTACTTC------GGAAACGAAGCAAAAGGAAACACTTCCTT----GCGGGAA----------GTTCAGTTCAGTACGATCTTTCGTTACCAAGGAA----------CACACGTCACCACATCACCGGCACAAATCAAAGACGTATG
droAna3	scaffold_13340:867474-867591 +		T---GCTGA-CC-GACCGCGTCGC-TTGTAACTCCGG-AATC-------------------AA-ACTAAAA-------CGGA----------GAT----------CTGGCCATGCAGTGTTTATAAGCAT-AAGGTTCGAT----------GTCCACCGCC----------ACTTCGGTGCC--------AGCGCATCAG
droKik1	scf7180000302475:1425663-1425724 -		T---GCAGA-CT---CCGAGGCAC-TTTTCTTC---T--AGACTGTTCCACCAATCGCGAC----------ACCTTCAAGCCA----------CA--------GCA
droFic1	scf7180000453800:2313424-2313510 -		T--TGGGGT-TT---CCGATTCAA-TGCTGCACA--A-AT-------G--------AGTTCCACTGGGTTCTTCA----AAA----G----------GGGTAAATGTGGATACCAAACGCGAC----------CA--------ACGTACT
droEle1	scf7180000490995:508693-508799 +		T---GCAAG-TT---CCGAGGCCA-TATTTCACA--A-ATGAT-AGATG-GATATATAATATCACTGG-CCTTCAAAGGGG---GT----------AATCAGAACACCGATTTACCAACCGCGAA----------CA--------ACGAACT
droRho1	scf7180000777158:16595-16699 +		G-ATCAAAG-TT---CCGAGGCAG-TGTTGCACA--A-ATTAA-CTGTTGGGA----CTTTTACTGG-CATTCA----AGGGGGGC----------AAGAGGACACCGATTTACCAACCGCGAC----------CA--------ACGAACT
droBia1	scf7180000302402:8322695-8322793 -		G-ATGCAAG-TT---CCGAGGCGG-CATTGCAAA--A-GTCATTTCATT--------ATTTCACTGA-TTGCTCA----AGGGGGGT----------GAGAACACCGATTTACCAACCGCGAC----------CA--------ACGTACT
droTak1	scf7180000415380:1406305-1406406 +		G-ATTCAAG-TT---CCAAAGCACAAATTGCACA--A-ATTATGAAATT--------ATTTCACTGG-CTCTTCAAT--AGGGGGGT----------ATGAGCACCGATTTACCAATCGCGAC----------CA--------ACGTACT
droEug1	scf7180000409692:709967-710062 -		T---CAAAG-TT---CCGAGGCGA-AGTTGCACAATGGATTATTATATT--------ATGCTCACTGA-TATTTCA----AGA---GT----------GATATTTCGATTTACCAACCGCGAC----------CA--------ACGTACT
dm3	chr3R:6233744-6233845 -		CGATTGAAGTTC---CCGAGGCAA-TTGTGGTCAACA-ATTATTGTATG--------ATTTTACTGA-TTCCTCG----GGGTATCG----------AAGTACCTCGATTTACCAACCGCGAC----------CA--------ACGTACT
droSim2	3r:14843003-14843100 +		T---GCAAG-TT---CCGAGGCAA-TTGTGGTCAACA-ATTATTGTATG--------ATTTTACTGA-TTCCTCG----GGGTATCG----------AAGTACATCGATTTACCAACCGCAC----------CA--------ACGTACT
droSec2	scaffold_0:15709572-15709669 +		T---GCAAG-TT---CCGAGGCAA-TTGTGGTCAACA-ATTATTGTATG--------ATTTTACTGA-TTCCTCG----GGGTATCG----------AAGTACATCGATTTACCAACCGCAC----------CA--------ACGTACT
droYak3	3R:10262259-10262357 -		T---GCAAG-TT---CCGAGGCAA-TTGTGGCCATCA-AATTATTTATG--------ATCTTACTGA-TTCTTCG----AGGGATCG----------AAGAACATCGATTTACCAACCGCGAC----------CA--------ACGTACT
droEre2	scaffold_4770:15384157-15384255 +		T---GCAAG-TT---CCGAGGCAA-CTGTGGGCAACA-ATTATTGTATG--------ATTCTAACAGA-TTCGTCG----GGGGATCG----------AAGAACATCGATTTACCAACCGCGAC----------CA--------ACGTACT

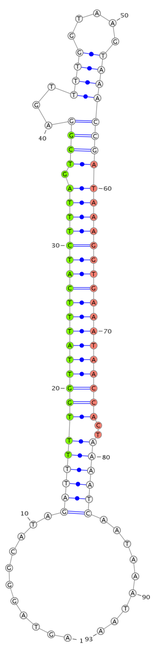
Generated: 09/08/2015 at 07:37 PM

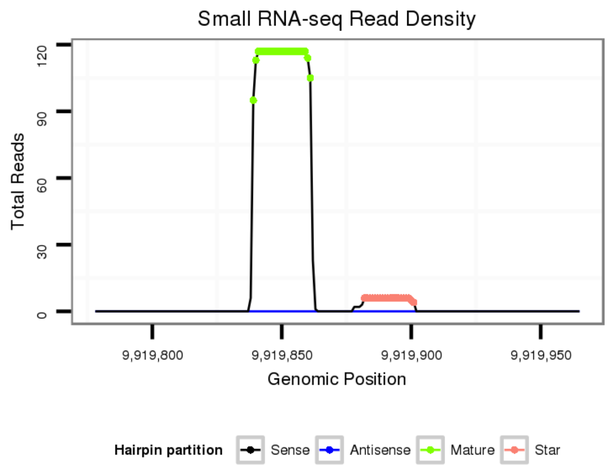
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

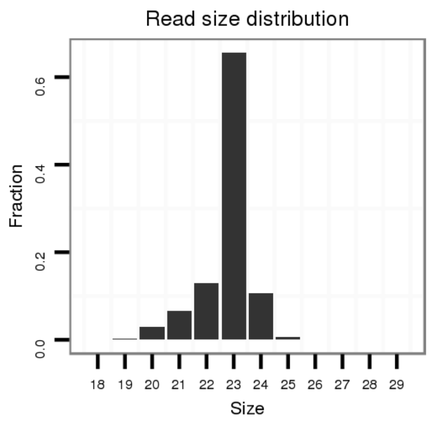
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3152	**scaffold_6473:9919828-9919915 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

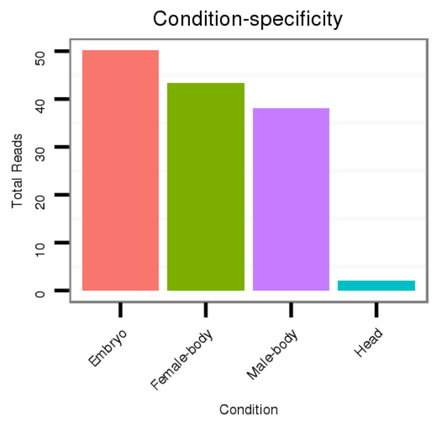
Legend: mature star mismatch in alignment mismatch in read

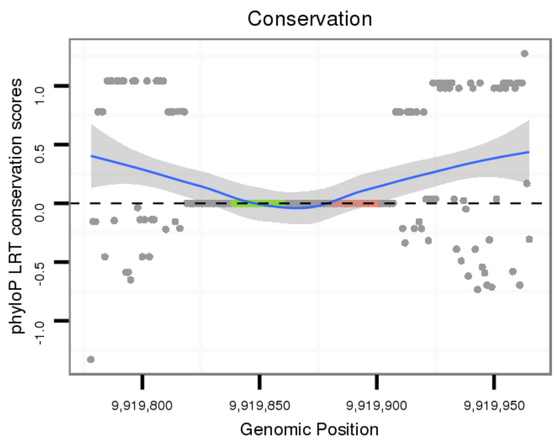
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dmo_3141 scaffold_6473:8642796-8642818 + 2. dmo_3142 scaffold_6473:8643620-8643642 - 3. dmo_3138 scaffold_6473:8659793-8659815 + 4. dmo_3143 scaffold_6473:8660822-8660844 - 5. dmo_3150 scaffold_6473:9914890-9914912 - 6. scaffold_6473:9917724-9917746 + 7. dmo_3152 scaffold_6473:9919839-9919861 + 8. dmo_3148 scaffold_6473:9927476-9927498 + 9. scaffold_6473:9933776-9933798 + 10. scaffold_6473:9934446-9934468 - 11. dmo_3147 scaffold_6473:9937954-9937976 + 12. scaffold_6473:9938818-9938840 - 13. dmo_3146 scaffold_6473:9971832-9971854 - 14. dmo_3132 scaffold_6473:10161098-10161120 + 15. dmo_3133 scaffold_6473:10162165-10162187 - 16. dmo_3134 scaffold_6473:10167212-10167234 + 17. dmo_3136 scaffold_6473:10168425-10168447 - 18. scaffold_6473:10193224-10193246 +	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

TCTTCTTAATGAATTTTTAACAAATAATAAATATATCCACATTTCCAGTAGGGCATAGATTTTTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATAAATAAACTAGTGAGAGAGAGAGTGCTCTAGTAACTCTGCTCGACTAGCACATAC **********.....(((((((((((((((((((((((.((((...((((.....))))))))))))))))))))))))..))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
..........TTTGGTTATTTCATCTTTAGTCG..........	23	0	18	70.28	1265	258	545	378	69	11	4
..........TTGGTTATTTCATCTTTAGTCGG..........	23	0	19	13.16	250	97	37	103	10	2	1
..........TTTGGTTATTTCATCTTTAGTC..........	22	0	18	8.50	153	93	19	33	3	4	1
..........TTTGGTTATTTCATCTTTAGTCGG..........	24	0	18	8.44	152	82	14	48	7	0	1
..........TTGGTTATTTCATCTTTAGTCG..........	22	0	19	5.47	104	8	65	26	3	1	1
..........TTTTGGTTATTTCATCTTTAGTCG..........	24	0	18	5.17	93	17	35	34	4	3	0
..........ATAAAGGTGAAATAACCACT..........	20	0	19	3.42	65	61	2	0	2	0	0
..........TTTGGTTATTTCATCTTTAGT..........	21	0	18	3.11	56	21	14	16	1	4	0
..........TGGTTATTTCATCTTTAGTCG..........	21	0	20	2.70	54	2	24	21	6	1	0
..........ACCGATAAAGGTGAAATAACCAC..........	23	0	15	1.67	25	25	0	0	0	0	0
..........TGGTTATTTCATCTTTAGTCGGA..........	23	0	20	1.35	27	21	1	5	0	0	0
..........TGGTTATTTCATCTTTAGTCGG..........	22	0	20	1.25	25	0	6	16	2	1	0
..........GATAAAGGTGAAATAACCACT..........	21	0	18	1.11	20	17	2	0	1	0	0
..........TTGGTTATTTCATCTTTAGTCGGT..........	24	1	19	1.05	20	13	2	4	0	1	0
..........ACCGATAAAGGTGAAATAACCA..........	22	0	20	1.05	21	17	3	1	0	0	0
..........TTTTGGTTATTTCATCTTTAGTC..........	23	0	18	1.00	18	13	1	4	0	0	0
..........ATAAAGGTGAAATAACCACC..........	20	1	19	0.95	18	18	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGGC..........	25	1	18	0.89	16	2	0	14	0	0	0
..........TTGGTTATTTCATCTTTAGTCGGC..........	24	1	19	0.84	16	2	4	10	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGA..........	24	1	18	0.67	12	7	5	0	0	0	0
..........TTTTTGGTTATTTCATCTTTAGTCG..........	25	0	18	0.61	11	3	3	5	0	0	0
..........TTTGGTTATTTCATCTTTAGTCA..........	23	1	18	0.56	10	3	4	2	1	0	0
..........ACCGATAAAGGTGAAATAACC..........	21	0	20	0.50	10	9	1	0	0	0	0
..........TTGGTTATTTCATCTTTAGTC..........	21	0	19	0.47	9	6	2	1	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGC..........	24	1	18	0.44	8	2	1	5	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGT..........	24	1	18	0.39	7	1	1	5	0	0	0
..........GTTATTTCATCTTTAGTCGGA..........	21	0	20	0.35	7	7	0	0	0	0	0
..........TTATTTCATCTTTAGTCGGAGTTT..........	24	0	18	0.33	6	4	2	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCT..........	23	1	18	0.33	6	1	0	1	3	1	0
..........TTTGGTTATTTCATCTTTAGTCAA..........	24	2	18	0.28	5	0	5	0	0	0	0
..........CGATAAAGGTGAAATAACCACT..........	22	0	18	0.28	5	5	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGC..........	21	1	18	0.28	5	5	0	0	0	0	0
..........GATAAAGGTGAAATAACCACTA..........	22	0	18	0.28	5	4	0	0	0	1	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
..........TTTTGGTTATTTCATCTTTAGT..........	22	0	18	0.22	4	0	1	2	0	1	0
..........TTTTTGGTTATTTCATCTTTAGTC..........	24	0	18	0.22	4	3	1	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
..........TTTGGTTATTTCATCTTTAGTCC..........	23	1	18	0.17	3	2	0	0	0	1	0
..........TTTGGTTATTTCATCTTTAG..........	20	0	18	0.17	3	2	1	0	0	0	0
..........CGATAAAGGTGAAATAACCACC..........	22	1	18	0.17	3	3	0	0	0	0	0
..........TTTTGGTTATTTCATCTTTAG..........	21	0	18	0.17	3	0	3	0	0	0	0
..........GTTATTTCATCTTTAGTCG..........	19	0	20	0.15	3	2	0	1	0	0	0
..........CCGATAAAGGTGAAATAACCA..........	21	0	20	0.15	3	2	1	0	0	0	0
..........TTATTTCATCTTTAGTCG..........	18	0	20	0.15	3	1	2	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCGGAA..........	25	1	18	0.11	2	1	0	1	0	0	0
..........CCGATAAAGGTGAAATAACCAC..........	22	0	18	0.11	2	2	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGGT..........	25	1	18	0.11	2	0	1	1	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCGG..........	25	0	18	0.11	2	2	0	0	0	0	0
..........TTTTTGGTTATTTCATCTTTAGT..........	23	0	18	0.11	2	1	1	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTT..........	22	1	18	0.11	2	2	0	0	0	0	0
..........ATAAAGGTGAAATAACCACTT..........	21	1	19	0.11	2	1	0	0	1	0	0
..........TTGGTTATTTCATCTTTAGTCGGTC..........	25	2	19	0.11	2	1	0	1	0	0	0
..........TTGGTTATTTCATCTTTAGTCGA..........	23	1	19	0.11	2	2	0	0	0	0	0
..........TTGGTTATTTCATCTTTAGT..........	20	0	19	0.11	2	0	1	1	0	0	0
..........AAACCGATAAAGGTGAAATAAC..........	22	0	20	0.10	2	2	0	0	0	0	0
..........TATTTCATCTTTAGTCGGAGTT..........	22	0	20	0.10	2	2	0	0	0	0	0
..........ACCGATAAAGGTGAAATAACCACA..........	24	1	15	0.07	1	0	1	0	0	0	0
..........ACCGATAAAGGTGAAATAACCACT..........	24	0	15	0.07	1	1	0	0	0	0	0
..........ATTTTTGGTTATTTCATCTTTAG..........	23	0	15	0.07	1	0	1	0	0	0	0
..........ATTTTTGGTTATTTCATCTTT..........	21	0	15	0.07	1	0	1	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCGGA..........	24	0	18	0.06	1	0	0	1	0	0	0
..........CGATAAAGGTGAAATAACCACA..........	22	1	18	0.06	1	0	1	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGTC..........	25	2	18	0.06	1	1	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTA..........	22	1	18	0.06	1	1	0	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCGT..........	25	1	18	0.06	1	0	0	1	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGGAG..........	26	0	18	0.06	1	0	0	1	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCA..........	24	1	18	0.06	1	1	0	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCT..........	24	1	18	0.06	1	0	1	0	0	0	0
..........TTTTTGGTTATTTCATCTTTAGTCC..........	25	1	18	0.06	1	0	1	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGC..........	22	1	18	0.06	1	1	0	0	0	0	0
..........TTTTTGGTTATTTCATCTTTA..........	21	0	18	0.06	1	0	1	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCTT..........	24	2	18	0.06	1	1	0	0	0	0	0
..........TTATTTCATCTTTAGTCGGAGTTTTGGTA..........	29	0	18	0.06	1	1	0	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCGC..........	25	1	18	0.06	1	1	0	0	0	0	0
..........ATTTCATCTTTAGTCGGAGTTT..........	22	0	18	0.06	1	1	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGGA..........	25	0	18	0.06	1	1	0	0	0	0	0
..........GAGTTTTGGTAAGTAAACCG..........	20	0	18	0.06	1	1	0	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCGA..........	25	1	18	0.06	1	1	0	0	0	0	0
..........TTTTTGGTTATTTCATCTTTAGTCGA..........	26	1	18	0.06	1	0	0	1	0	0	0
..........GATAAAGGTGAAATAACCAC..........	20	0	18	0.06	1	1	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTG..........	22	1	18	0.06	1	1	0	0	0	0	0
..........GATAAAGGTGAAATAACCACTAAC..........	24	1	18	0.06	1	1	0	0	0	0	0
..........AAAGGTGAAATAACCACT..........	18	0	19	0.05	1	1	0	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCGC..........	23	1	19	0.05	1	1	0	0	0	0	0
..........ATAAAGGTGAAATAACCACTGT..........	22	2	19	0.05	1	0	0	1	0	0	0
..........TTGGTTATTTCATCTTTAGTCA..........	22	1	19	0.05	1	0	1	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCGGTAA..........	26	3	19	0.05	1	0	1	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCAA..........	23	2	19	0.05	1	0	1	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCGT..........	23	1	19	0.05	1	0	0	0	1	0	0
..........ATAAAGGTGAAATAACCACTTT..........	22	2	19	0.05	1	1	0	0	0	0	0
..........GTTATTTCATCTTTAGTCGGAA..........	22	1	20	0.05	1	1	0	0	0	0	0
..........TTATTTCATCTTTAGTCGGA..........	20	0	20	0.05	1	1	0	0	0	0	0
..........TTGGTTATTTCATCTTTAGC..........	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
..........CGATAAAGGTGAAATAACCC..........	20	1	20	0.05	1	1	0	0	0	0	0
..........GGTTATTTCATCTTTAGTCGGC..........	22	1	20	0.05	1	1	0	0	0	0	0
..........TGGTTATTTCATCTTTAGTCGGT..........	23	1	20	0.05	1	1	0	0	0	0	0
..........GTTATTTCATCTTTAGTCGGC..........	21	1	20	0.05	1	1	0	0	0	0	0
..........TTATTTCATCTTTAGTCGGAGTT..........	23	0	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

AGAAGAATTACTTAAAAATTGTTTATTATTTATATAGGTGTAAAGGTCATCCCGTATCTAAAAACCAATAAAGTAGAAATCAGCCTCAAAACCATTCATTTGGCTATTTCCACTTTATTGGTGATTTTAGTTATTTATTTGATCACTCTCTCTCACGAGATCATTGAGACGAGCTGATCGTGTATG **********.....(((((((((((((((((((((((.((((...((((.....))))))))))))))))))))))))..))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V049 head	M046 female body	V110 male body	M060 embryo
..........AGGTCATCCCGTATCTAAAAACCAATA..........	27	0	14	0.07	1	0	1	0	0
..........AAGAAATCAGCCTCAAAACCAT..........	22	1	18	0.06	1	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:9919778-9919965 +	dmo_3152	TCTTCTTAATGAATTTTTAACAAATAATAAATATATCCACATTTCCAGTAGGGCATAGATTTTTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATAAATAAACTAGTGAGAGAGAGAGTGCTCTAG----TAACTCTGCTCGACTAGCACATAC
droGri2	scaffold_15081:4074197-4074246 +		A----------GAGAGAGAGAGAGATCGAGCGACAAACACTCGACTAACAATAC
droKik1	scf7180000302258:83296-83326 -		T-----TAATAAATTGGAAACAAATAATAAATA----------TAT
dm3	chr2R:8701636-8701679 -		TTCTCTCAATGAATTTTCAATGCGTCGCAAATTTATTGTCA----------TTT
droSim2	2r:1865243-1865301 -		C----------AATTCATATATAAAAAAAGAGAGAATGCAATAG----TCAGTTCCCGACTATCATATAC

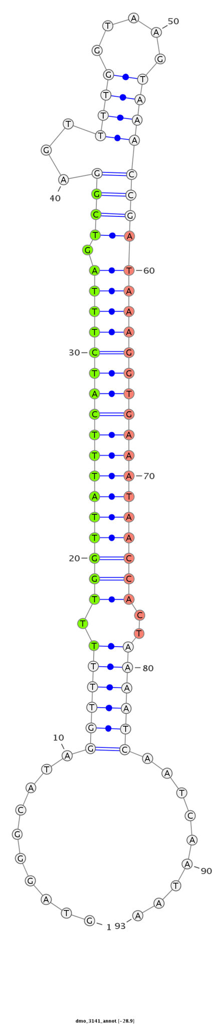
Generated: 09/08/2015 at 07:41 PM

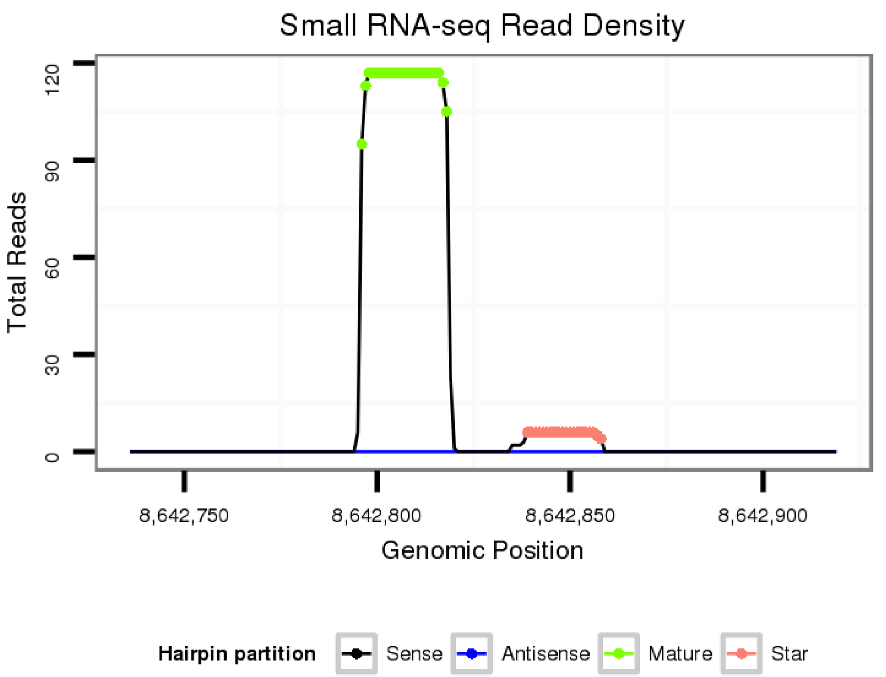
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

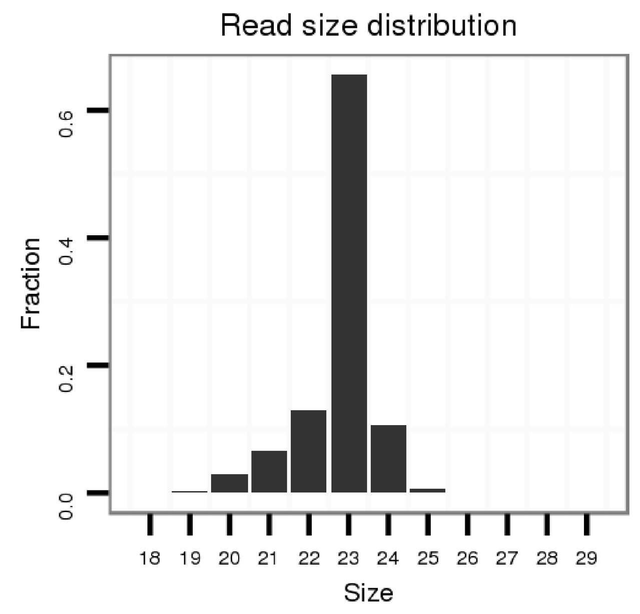
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3141	**scaffold_6473:8642786-8642869 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

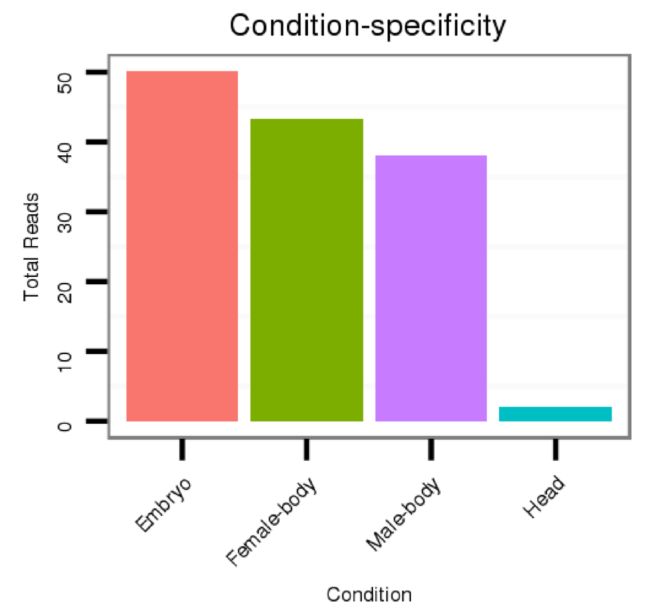
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dmo_3141 scaffold_6473:8642796-8642818 +	1. dmo_3139 scaffold_6308:570088-570107 +
2. dmo_3142 scaffold_6473:8643620-8643642 -	2. dmo_3140 scaffold_6308:570824-570843 -
3. dmo_3138 scaffold_6473:8659793-8659815 +	3. dmo_3141 scaffold_6473:8642839-8642858 +
4. dmo_3143 scaffold_6473:8660822-8660844 -	4. dmo_3142 scaffold_6473:8643580-8643599 -
5. dmo_3150 scaffold_6473:9914890-9914912 -	5. dmo_69 scaffold_6473:8659160-8659179 -
6. scaffold_6473:9917724-9917746 +	6. dmo_3144 scaffold_6473:8660595-8660614 -
7. dmo_3152 scaffold_6473:9919839-9919861 +	7. dmo_3145 scaffold_6473:9912692-9912711 -
8. dmo_3148 scaffold_6473:9927476-9927498 +	8. dmo_3149 scaffold_6473:9914072-9914091 +
9. scaffold_6473:9933776-9933798 +	9. dmo_3150 scaffold_6473:9914850-9914869 -
10. scaffold_6473:9934446-9934468 -	10. dmo_3151 scaffold_6473:9918530-9918549 -
11. dmo_3147 scaffold_6473:9937954-9937976 +	11. dmo_3152 scaffold_6473:9919882-9919901 +
12. scaffold_6473:9938818-9938840 -	12. dmo_3148 scaffold_6473:9927519-9927538 +
13. dmo_3146 scaffold_6473:9971832-9971854 -	13. dmo_3147 scaffold_6473:9937997-9938016 +
14. dmo_3132 scaffold_6473:10161098-10161120 +	14. dmo_3146 scaffold_6473:9971792-9971811 -
15. dmo_3133 scaffold_6473:10162165-10162187 -	15. dmo_68 scaffold_6473:10161327-10161346 +
16. dmo_3134 scaffold_6473:10167212-10167234 +	16. dmo_3133 scaffold_6473:10162125-10162144 -
17. dmo_3136 scaffold_6473:10168425-10168447 -	17. dmo_3135 scaffold_6473:10167441-10167460 +
18. scaffold_6473:10193224-10193246 +	18. dmo_3137 scaffold_6473:10168232-10168251 -
	19. dmo_3153 scaffold_6473:10193453-10193472 +

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTCTTCACTAATTTTAAAAAAATAATAAATACATCCACATTTCCAGTAGGGCATAGGTTTTTTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATCAATAATAAACTAGCGAGAGAGAGTCCTCTAGTAAAGACTGCTCGACTAGCA	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
..........((((((.(((((((((((((((((.((((...((((.....))))))))))))))))))))))))))..))))))........											
...TTTGGTTATTTCATCTTTAGTCG...	23	0	18	70.28	1265	258	545	378	69	11	4
...TTGGTTATTTCATCTTTAGTCGG...	23	0	19	13.16	250	97	37	103	10	2	1
...TTTGGTTATTTCATCTTTAGTC...	22	0	18	8.50	153	93	19	33	3	4	1
...TTTGGTTATTTCATCTTTAGTCGG...	24	0	18	8.44	152	82	14	48	7	0	1
...TTGGTTATTTCATCTTTAGTCG...	22	0	19	5.47	104	8	65	26	3	1	1
...TTTTGGTTATTTCATCTTTAGTCG...	24	0	18	5.17	93	17	35	34	4	3	0
...ATAAAGGTGAAATAACCACT...	20	0	19	3.42	65	61	2	0	2	0	0
...TTTGGTTATTTCATCTTTAGT...	21	0	18	3.11	56	21	14	16	1	4	0
...TGGTTATTTCATCTTTAGTCG...	21	0	20	2.70	54	2	24	21	6	1	0
...ACCGATAAAGGTGAAATAACCAC...	23	0	15	1.67	25	25	0	0	0	0	0
...TGGTTATTTCATCTTTAGTCGGA...	23	0	20	1.35	27	21	1	5	0	0	0
...TGGTTATTTCATCTTTAGTCGG...	22	0	20	1.25	25	0	6	16	2	1	0
...GATAAAGGTGAAATAACCACT...	21	0	18	1.11	20	17	2	0	1	0	0
...TTGGTTATTTCATCTTTAGTCGGT...	24	1	19	1.05	20	13	2	4	0	1	0
...ACCGATAAAGGTGAAATAACCA...	22	0	20	1.05	21	17	3	1	0	0	0
...TTTTGGTTATTTCATCTTTAGTC...	23	0	18	1.00	18	13	1	4	0	0	0
...ATAAAGGTGAAATAACCACC...	20	1	19	0.95	18	18	0	0	0	0	0
...TTTGGTTATTTCATCTTTAGTCGGC...	25	1	18	0.89	16	2	0	14	0	0	0
...TTGGTTATTTCATCTTTAGTCGGC...	24	1	19	0.84	16	2	4	10	0	0	0
...TTTGGTTATTTCATCTTTAGTCGA...	24	1	18	0.67	12	7	5	0	0	0	0
...TTTTTGGTTATTTCATCTTTAGTCG...	25	0	18	0.61	11	3	3	5	0	0	0
...TTTGGTTATTTCATCTTTAGTCA...	23	1	18	0.56	10	3	4	2	1	0	0
...ACCGATAAAGGTGAAATAACC...	21	0	20	0.50	10	9	1	0	0	0	0
...TTGGTTATTTCATCTTTAGTC...	21	0	19	0.47	9	6	2	1	0	0	0
...TTTGGTTATTTCATCTTTAGTCGC...	24	1	18	0.44	8	2	1	5	0	0	0
...TTTGGTTATTTCATCTTTAGTCGT...	24	1	18	0.39	7	1	1	5	0	0	0
...GTTATTTCATCTTTAGTCGGA...	21	0	20	0.35	7	7	0	0	0	0	0
...TTATTTCATCTTTAGTCGGAGTTT...	24	0	18	0.33	6	4	2	0	0	0	0
...TTTGGTTATTTCATCTTTAGTCT...	23	1	18	0.33	6	1	0	1	3	1	0
...TTTGGTTATTTCATCTTTAGC...	21	1	18	0.28	5	5	0	0	0	0	0
...CGATAAAGGTGAAATAACCACT...	22	0	18	0.28	5	5	0	0	0	0	0
...GATAAAGGTGAAATAACCACTA...	22	0	18	0.28	5	4	0	0	0	1	0
...TTTGGTTATTTCATCTTTAGTCAA...	24	2	18	0.28	5	0	5	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
...TTTTGGTTATTTCATCTTTAGT...	22	0	18	0.22	4	0	1	2	0	1	0
...TTTTTGGTTATTTCATCTTTAGTC...	24	0	18	0.22	4	3	1	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
...TTTGGTTATTTCATCTTTAG...	20	0	18	0.17	3	2	1	0	0	0	0
...TTTGGTTATTTCATCTTTAGTCC...	23	1	18	0.17	3	2	0	0	0	1	0
...CGATAAAGGTGAAATAACCACC...	22	1	18	0.17	3	3	0	0	0	0	0
...TTTTGGTTATTTCATCTTTAG...	21	0	18	0.17	3	0	3	0	0	0	0
...TTATTTCATCTTTAGTCG...	18	0	20	0.15	3	1	2	0	0	0	0
...CCGATAAAGGTGAAATAACCA...	21	0	20	0.15	3	2	1	0	0	0	0
...TTTTGGTTATTTCATCTTTAGTCGG...	25	0	18	0.11	2	2	0	0	0	0	0
...TTGGTTATTTCATCTTTAGTCGGAA...	25	1	18	0.11	2	1	0	1	0	0	0
...TTTTTGGTTATTTCATCTTTAGT...	23	0	18	0.11	2	1	1	0	0	0	0
...TTTGGTTATTTCATCTTTAGTCGGT...	25	1	18	0.11	2	0	1	1	0	0	0
...TTTGGTTATTTCATCTTTAGTT...	22	1	18	0.11	2	2	0	0	0	0	0
...CCGATAAAGGTGAAATAACCAC...	22	0	18	0.11	2	2	0	0	0	0	0
...TTGGTTATTTCATCTTTAGTCGGTC...	25	2	19	0.11	2	1	0	1	0	0	0
...TTGGTTATTTCATCTTTAGTCGA...	23	1	19	0.11	2	2	0	0	0	0	0
...TTGGTTATTTCATCTTTAGT...	20	0	19	0.11	2	0	1	1	0	0	0
...ATAAAGGTGAAATAACCACTT...	21	1	19	0.11	2	1	0	0	1	0	0
...AAACCGATAAAGGTGAAATAAC...	22	0	20	0.10	2	2	0	0	0	0	0
...TATTTCATCTTTAGTCGGAGTT...	22	0	20	0.10	2	2	0	0	0	0	0
...ACCGATAAAGGTGAAATAACCACT...	24	0	15	0.07	1	1	0	0	0	0	0
...ACCGATAAAGGTGAAATAACCACA...	24	1	15	0.07	1	0	1	0	0	0	0
...TTTTGGTTATTTCATCTTTAGC...	22	1	18	0.06	1	1	0	0	0	0	0
...TTTTGGTTATTTCATCTTTAGTCA...	24	1	18	0.06	1	1	0	0	0	0	0
...GATAAAGGTGAAATAACCAC...	20	0	18	0.06	1	1	0	0	0	0	0
...TTGGTTATTTCATCTTTAGTCGGA...	24	0	18	0.06	1	0	0	1	0	0	0
...TTTTTGGTTATTTCATCTTTAGTCC...	25	1	18	0.06	1	0	1	0	0	0	0
...TATTTCATCTTTAGTCGGAGTTTTGGTA...	29	0	18	0.06	1	1	0	0	0	0	0
...TTTTTGGTTATTTCATCTTTA...	21	0	18	0.06	1	0	1	0	0	0	0
...TTTTGGTTATTTCATCTTTAGTCGC...	25	1	18	0.06	1	1	0	0	0	0	0
...ATTTCATCTTTAGTCGGAGTTT...	22	0	18	0.06	1	1	0	0	0	0	0
...TTTTGGTTATTTCATCTTTAGTCT...	24	1	18	0.06	1	0	1	0	0	0	0
...GATAAAGGTGAAATAACCACTAAC...	24	1	18	0.06	1	1	0	0	0	0	0
...TTTTGGTTATTTCATCTTTAGTCGA...	25	1	18	0.06	1	1	0	0	0	0	0
...TTTGGTTATTTCATCTTTAGTCGGA...	25	0	18	0.06	1	1	0	0	0	0	0
...TTTTGGTTATTTCATCTTTAGTCGT...	25	1	18	0.06	1	0	0	1	0	0	0
...CGATAAAGGTGAAATAACCACA...	22	1	18	0.06	1	0	1	0	0	0	0
...TTTGGTTATTTCATCTTTAGTG...	22	1	18	0.06	1	1	0	0	0	0	0
...TTTGGTTATTTCATCTTTAGTCTT...	24	2	18	0.06	1	1	0	0	0	0	0
...TTTGGTTATTTCATCTTTAGTA...	22	1	18	0.06	1	1	0	0	0	0	0
...TTTGGTTATTTCATCTTTAGTCGGAG...	26	0	18	0.06	1	0	0	1	0	0	0
...TTTGGTTATTTCATCTTTAGTCGTC...	25	2	18	0.06	1	1	0	0	0	0	0
...TTTTTGGTTATTTCATCTTTAGTCGA...	26	1	18	0.06	1	0	0	1	0	0	0
...GAGTTTTGGTAAGTAAACCG...	20	0	18	0.06	1	1	0	0	0	0	0
...CATCCACATTTCCAGTAGGGC...	21	0	18	0.06	1	0	0	1	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
...TTGGTTATTTCATCTTTAGTCGC...	23	1	19	0.05	1	1	0	0	0	0	0
...TTGGTTATTTCATCTTTAGTCGGTAA...	26	3	19	0.05	1	0	1	0	0	0	0
...TTGGTTATTTCATCTTTAGTCGT...	23	1	19	0.05	1	0	0	0	1	0	0
...TTGGTTATTTCATCTTTAGTCAA...	23	2	19	0.05	1	0	1	0	0	0	0
...TTGGTTATTTCATCTTTAGTCA...	22	1	19	0.05	1	0	1	0	0	0	0
...ATAAAGGTGAAATAACCACTGT...	22	2	19	0.05	1	0	0	1	0	0	0
...TTGGTTATTTCATCTTTAGC...	20	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
...TGGTTATTTCATCTTTAGTCGGT...	23	1	20	0.05	1	1	0	0	0	0	0
...GGTTATTTCATCTTTAGTCGGC...	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
...TTATTTCATCTTTAGTCGGAGTT...	23	0	20	0.05	1	1	0	0	0	0	0
...GTTATTTCATCTTTAGTCGGAA...	22	1	20	0.05	1	1	0	0	0	0	0
...GGTTATTTCATCTTTAGTCG...	20	0	20	0.05	1	0	1	0	0	0	0

Anti-sense strand reads

AAGAAGTGATTAAAATTTTTTTATTATTTATGTAGGTGTAAAGGTCATCCCGTATCCAAAAAACCAATAAAGTAGAAATCAGCCTCAAAACCATTCATTTGGCTATTTCCACTTTATTGGTGATTTTAGTTAGTTATTATTTGATCGCTCTCTCTCAGGAGATCATTTCTGACGAGCTGATCGT	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo
..........((((((.(((((((((((((((((.((((...((((.....))))))))))))))))))))))))))..))))))........								
...AAGAAATCAGCCTCAAAACCAT...	22	1	18	0.06	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:8642736-8642919 +	dmo_3141	TTCTTCACTAATTTTAAAAAAATAATAAATACATCCACATTTCCAGTAGGGCATAGGTTTTTTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATCAATAATAAACTAGCGAGAGAGAGTCCTCTAGTAAAGACTGCTCGACTAGCA

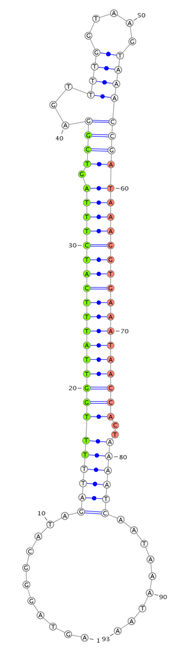
Generated: 09/08/2015 at 07:41 PM

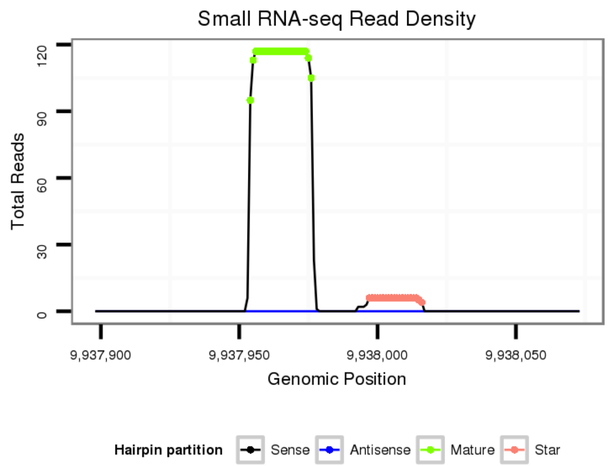
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

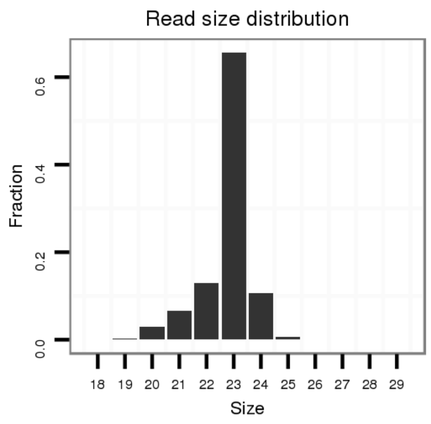
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3147	**scaffold_6473:9937948-9938023 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

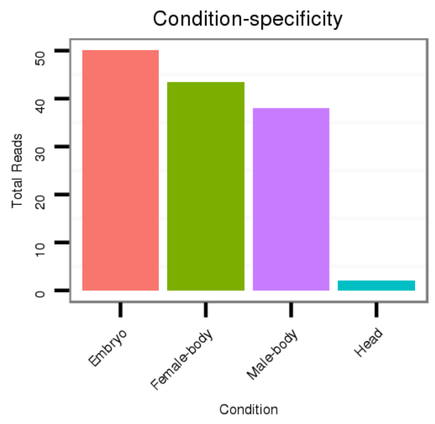
Legend: mature star mismatch in alignment mismatch in read

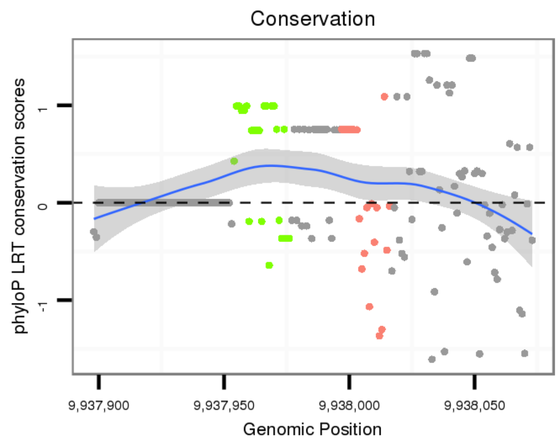
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
Homo6	DNA	hAT-Pegasus	-

mature

1. dmo_3141 scaffold_6473:8642796-8642818 +
2. dmo_3142 scaffold_6473:8643620-8643642 -
3. dmo_3138 scaffold_6473:8659793-8659815 +
4. dmo_3143 scaffold_6473:8660822-8660844 -
5. dmo_3150 scaffold_6473:9914890-9914912 -
6. scaffold_6473:9917724-9917746 +
7. dmo_3152 scaffold_6473:9919839-9919861 +
8. dmo_3148 scaffold_6473:9927476-9927498 +
9. scaffold_6473:9933776-9933798 +
10. scaffold_6473:9934446-9934468 -
11. dmo_3147 scaffold_6473:9937954-9937976 +
12. scaffold_6473:9938818-9938840 -
13. dmo_3146 scaffold_6473:9971832-9971854 -
14. dmo_3132 scaffold_6473:10161098-10161120 +
15. dmo_3133 scaffold_6473:10162165-10162187 -
16. dmo_3134 scaffold_6473:10167212-10167234 +
17. dmo_3136 scaffold_6473:10168425-10168447 -
18. scaffold_6473:10193224-10193246 +

star

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

TTCATTAATTTTGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGATTTTTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATAAATAAAGTAGTGAGAGTGCTCTAGTAGAGACTGCTCGACTAGCAGAT **********.....(((((((((((((((((((((((.((((...((((.....))))))))))))))))))))))))..))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
.....TTTGGTTATTTCATCTTTAGTCG.....	23	0	18	70.28	1265	258	545	378	69	11	4
.....TTGGTTATTTCATCTTTAGTCGG.....	23	0	19	13.16	250	97	37	103	10	2	1
.....TTTGGTTATTTCATCTTTAGTC.....	22	0	18	8.50	153	93	19	33	3	4	1
.....TTTGGTTATTTCATCTTTAGTCGG.....	24	0	18	8.44	152	82	14	48	7	0	1
.....TTGGTTATTTCATCTTTAGTCG.....	22	0	19	5.47	104	8	65	26	3	1	1
.....TTTTGGTTATTTCATCTTTAGTCG.....	24	0	18	5.17	93	17	35	34	4	3	0
.....ATAAAGGTGAAATAACCACT.....	20	0	19	3.42	65	61	2	0	2	0	0
.....TTTGGTTATTTCATCTTTAGT.....	21	0	18	3.11	56	21	14	16	1	4	0
.....TGGTTATTTCATCTTTAGTCG.....	21	0	20	2.70	54	2	24	21	6	1	0
.....ACCGATAAAGGTGAAATAACCAC.....	23	0	15	1.67	25	25	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTCGGA.....	23	0	20	1.35	27	21	1	5	0	0	0
.....TGGTTATTTCATCTTTAGTCGG.....	22	0	20	1.25	25	0	6	16	2	1	0
.....GATAAAGGTGAAATAACCACT.....	21	0	18	1.11	20	17	2	0	1	0	0
.....TTGGTTATTTCATCTTTAGTCGGT.....	24	1	19	1.05	20	13	2	4	0	1	0
.....ACCGATAAAGGTGAAATAACCA.....	22	0	20	1.05	21	17	3	1	0	0	0
.....TTTTGGTTATTTCATCTTTAGTC.....	23	0	18	1.00	18	13	1	4	0	0	0
.....ATAAAGGTGAAATAACCACC.....	20	1	19	0.95	18	18	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGC.....	25	1	18	0.89	16	2	0	14	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGC.....	24	1	19	0.84	16	2	4	10	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGA.....	24	1	18	0.67	12	7	5	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCG.....	25	0	18	0.61	11	3	3	5	0	0	0
.....TTTGGTTATTTCATCTTTAGTCA.....	23	1	18	0.56	10	3	4	2	1	0	0
.....ACCGATAAAGGTGAAATAACC.....	21	0	20	0.50	10	9	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTC.....	21	0	19	0.47	9	6	2	1	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGC.....	24	1	18	0.44	8	2	1	5	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGT.....	24	1	18	0.39	7	1	1	5	0	0	0
.....GTTATTTCATCTTTAGTCGGA.....	21	0	20	0.35	7	7	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCT.....	23	1	18	0.33	6	1	0	1	3	1	0
.....TTATTTCATCTTTAGTCGGAGTTT.....	24	0	18	0.33	6	4	2	0	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
.....TTTGGTTATTTCATCTTTAGC.....	21	1	18	0.28	5	5	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCAA.....	24	2	18	0.28	5	0	5	0	0	0	0
.....ATAAAGGTGAAATAACCAC.....	19	0	19	0.26	5	5	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGT.....	22	0	18	0.22	4	0	1	2	0	1	0
.....GATAAAGGTGAAATAACCACC.....	21	1	18	0.22	4	4	0	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTC.....	24	0	18	0.22	4	3	1	0	0	0	0
.....ATAAAGGTGAAATAACCACTA.....	21	0	19	0.21	4	4	0	0	0	0	0
.....ACCGATAAAGGTGAAATAACC.....	22	1	20	0.20	4	4	0	0	0	0	0
.....CGATAAAGGTGAAATAACCACC.....	22	1	18	0.17	3	3	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCC.....	23	1	18	0.17	3	2	0	0	0	1	0
.....TTTGGTTATTTCATCTTTAG.....	20	0	18	0.17	3	2	1	0	0	0	0
.....TTTTGGTTATTTCATCTTTAG.....	21	0	18	0.17	3	0	3	0	0	0	0
.....TTATTTCATCTTTAGTCG.....	18	0	20	0.15	3	1	2	0	0	0	0
.....GTTATTTCATCTTTAGTCG.....	19	0	20	0.15	3	2	0	1	0	0	0
.....TTTGGTTATTTCATCTTTAGTT.....	22	1	18	0.11	2	2	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGT.....	25	1	18	0.11	2	0	1	1	0	0	0
.....TTTTTGGTTATTTCATCTTTAGT.....	23	0	18	0.11	2	1	1	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGG.....	25	0	18	0.11	2	2	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGAA.....	25	1	18	0.11	2	1	0	1	0	0	0
.....CCGATAAAGGTGAAATAACCAC.....	22	0	18	0.11	2	2	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGT.....	20	0	19	0.11	2	0	1	1	0	0	0
.....ATAAAGGTGAAATAACCACTT.....	21	1	19	0.11	2	1	0	0	1	0	0
.....TTGGTTATTTCATCTTTAGTCGGTC.....	25	2	19	0.11	2	1	0	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCGA.....	23	1	19	0.11	2	2	0	0	0	0	0
.....TATTTCATCTTTAGTCGGAGTTT.....	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
.....ATTTTTGGTTATTTCATCTTT.....	21	0	15	0.07	1	0	1	0	0	0	0
.....ACCGATAAAGGTGAAATAACCACT.....	24	0	15	0.07	1	1	0	0	0	0	0
.....ATTTTTGGTTATTTCATCTTTAG.....	23	0	15	0.07	1	0	1	0	0	0	0
.....ACCGATAAAGGTGAAATAACCACA.....	24	1	15	0.07	1	0	1	0	0	0	0
.....GAGTTTTGGTAAGTAAACCG.....	20	0	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCT.....	24	1	18	0.06	1	0	1	0	0	0	0
.....ATTTCATCTTTAGTCGGAGTTT.....	22	0	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTA.....	22	1	18	0.06	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGA.....	25	0	18	0.06	1	1	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTTTTGGTA.....	29	0	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGG.....	25	1	18	0.06	1	1	0	0	0	0	0
.....GATAAAGGTGAAATAACCACTAAC.....	24	1	18	0.06	1	1	0	0	0	0	0
.....TTTTTGGTTATTTCATCTTTA.....	21	0	18	0.06	1	0	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCTT.....	24	2	18	0.06	1	1	0	0	0	0	0
.....GATAAAGGTGAAATAACCAC.....	20	0	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGT.....	25	1	18	0.06	1	0	0	1	0	0	0
.....CGATAAAGGTGAAATAACCACA.....	22	1	18	0.06	1	0	1	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGA.....	25	1	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCA.....	24	1	18	0.06	1	1	0	0	0	0	0
.....CATCCACATTTCCAGTAGGGC.....	21	0	18	0.06	1	0	0	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGA.....	24	0	18	0.06	1	0	0	1	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCC.....	25	1	18	0.06	1	0	1	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGC.....	22	1	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGAG.....	26	0	18	0.06	1	0	0	1	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCGA.....	26	1	18	0.06	1	0	0	1	0	0	0
.....TTTGGTTATTTCATCTTTAGTG.....	22	1	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGTC.....	25	2	18	0.06	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGT.....	23	1	19	0.05	1	0	0	0	1	0	0
.....AAAGGTGAAATAACCACT.....	18	0	19	0.05	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCA.....	22	1	19	0.05	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCAA.....	23	2	19	0.05	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGC.....	23	1	19	0.05	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGTAA.....	26	3	19	0.05	1	0	1	0	0	0	0
.....ATAAAGGTGAAATAACCACTTT.....	22	2	19	0.05	1	1	0	0	0	0	0
.....ATAAAGGTGAAATAACCACTGT.....	22	2	19	0.05	1	0	0	1	0	0	0
.....TGGTTATTTCATCTTTAGTCGGT.....	23	1	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCGGC.....	22	1	20	0.05	1	1	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTC.....	20	0	20	0.05	1	1	0	0	0	0	0
.....CGATAAAGGTGAAATAACC.....	20	1	20	0.05	1	1	0	0	0	0	0
.....CCGATAAAGGTGAAATAACCA.....	21	0	20	0.05	1	0	1	0	0	0	0
.....TTATTTCATCTTTAGTCGGA.....	20	0	20	0.05	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGAA.....	22	1	20	0.05	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGC.....	20	1	20	0.05	1	1	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTTT.....	23	0	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCGG.....	21	0	20	0.05	1	0	0	0	0	0	1

Anti-sense strand reads

AAGTAATTAAAACTTGTTTATTATTTATGTAGGTGTAAAGGTCATCCCGTATCTAAAAACCAATAAAGTAGAAATCAGCCTCAAAACCATTCATTTGGCTATTTCCACTTTATTGGTGATTTTAGTTATTTATTTCATCACTCTCACGAGATCATCTCTGACGAGCTGATCGTCTA **********.....(((((((((((((((((((((((.((((...((((.....))))))))))))))))))))))))..))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo
.....TCATCTCTGACGAGCTGATCG....	21	0	9	0.11	1	1	0	0
.....AGGTCATCCCGTATCTAAAAACCAATA.....	27	0	14	0.07	1	0	1	0
.....AAGAAATCAGCCTCAAAACCAT.....	22	1	18	0.06	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:9937898-9938073 +	dmo_3147	TTCATTAATTTTGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGATTT----TTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACC----------ACTAAAATCAATAAATAA----------AGTAGTGAGAGTGCTCTAGTAGAGA---CTGCTCGAC----TAGCAGAT
droVir3	scaffold_12723:2377100-2377182 +		TT----------TTAAT-----------A---------TAAATAATAAATAAATAAAAATATATAAAAACAAGCAGAGTGTTCTAGTCGAAA---GTGCCCGAC----TAGGGCAT
droWil2	scf2_1100000004967:219291-219355 +		AA----------GTAAT-----------A---------ACAAATAAGAAGAAATAAGCAA---------TACATTAAATAAA---TATCATAATGATCCAATAGAG
droKik1	scf7180000299115:5970-6006 -		AT----------TT----TTGGTCATTTTATATT----------ATTTCAGAT----TTTTGCTA
droRho1	scf7180000765731:17051-17171 -		TT----------TTAGTTTGGT-----ATTTTGTTATAAATATAGTTAAGTAGCCCGATAAAGGTATTGTCTGCTTTCGGATTGATAAATTAAAAAATGTAGAAAATAAATAA----------A----------GAA---TTGTCTAGC----AAGCAGAA
droTak1	scf7180000414239:47197-47269 +		TA----------A----------AATAATG----------ATCTAAGTAAATAAATAA----------ACAAGAGAGAAGCTATAGTCGGTGGGTGTCCCGAC----TATCTAAT
dm3	chr4:662567-662610 -		AA----------A----------ATTTCAGAT----TTTTGCTA
droYak3	2R:554655-554730 +		AT----------AGAAT-----------TTAATCAAAT----------ATTTAAAATAATAAATAA----------ACGAAAGAAGCTTTAGTCGAG---TTCTCCAAT----TATGTGAT

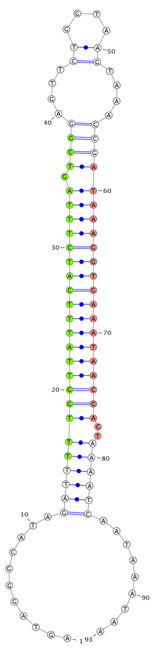
Generated: 09/08/2015 at 07:41 PM

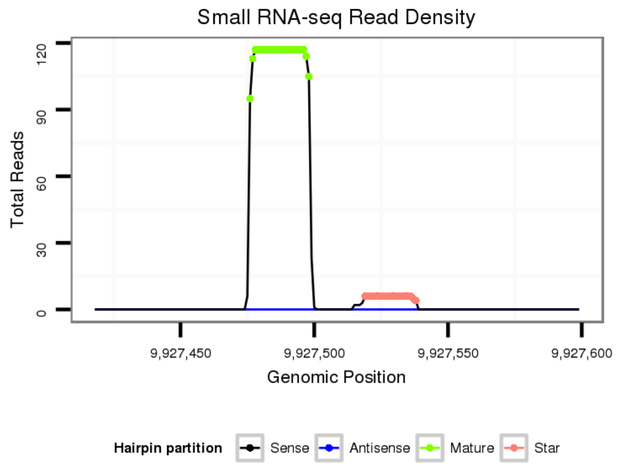
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

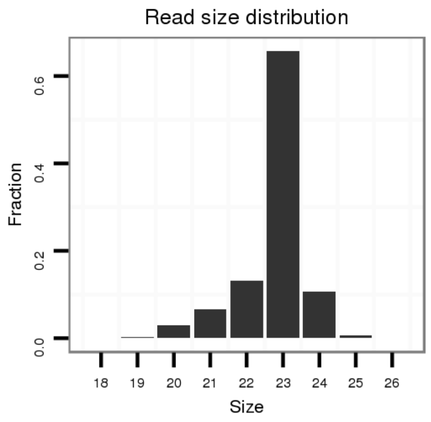
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3148	**scaffold_6473:9927468-9927549 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

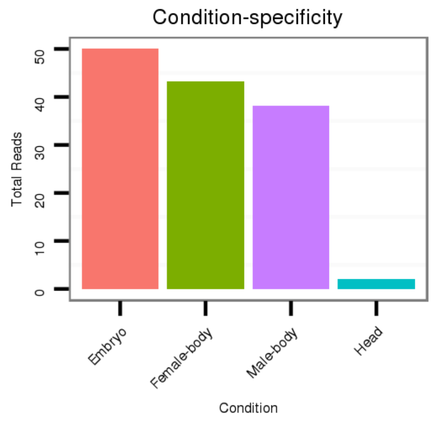
Legend: mature star mismatch in alignment mismatch in read

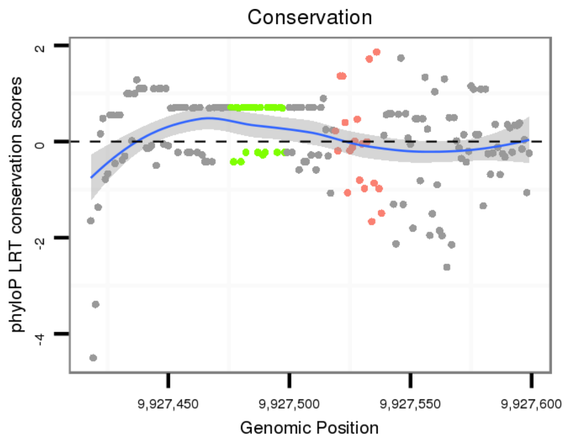
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dmo_3141 scaffold_6473:8642796-8642818 + 2. dmo_3142 scaffold_6473:8643620-8643642 - 3. dmo_3138 scaffold_6473:8659793-8659815 + 4. dmo_3143 scaffold_6473:8660822-8660844 - 5. dmo_3150 scaffold_6473:9914890-9914912 - 6. scaffold_6473:9917724-9917746 + 7. dmo_3152 scaffold_6473:9919839-9919861 + 8. dmo_3148 scaffold_6473:9927476-9927498 + 9. scaffold_6473:9933776-9933798 + 10. scaffold_6473:9934446-9934468 - 11. dmo_3147 scaffold_6473:9937954-9937976 + 12. scaffold_6473:9938818-9938840 - 13. dmo_3146 scaffold_6473:9971832-9971854 - 14. dmo_3132 scaffold_6473:10161098-10161120 + 15. dmo_3133 scaffold_6473:10162165-10162187 - 16. dmo_3134 scaffold_6473:10167212-10167234 + 17. dmo_3136 scaffold_6473:10168425-10168447 - 18. scaffold_6473:10193224-10193246 +	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

TCTTAATGAATTTTTAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGATTTTTGGTTATTTCATCTTTAGTCGGAGTTCTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATAAATAATAAACTAGTGAGAGAGAGTGCTCTAGGCTAGACTGTTCGACTAGCA	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
**********.....(((((((((((((((((((((((.((((....((....))....)))))))))))))))))))))))..)))))).....**********											
.....TTTGGTTATTTCATCTTTAGTCG.....	23	0	18	70.28	1265	258	545	378	69	11	4
.....TTGGTTATTTCATCTTTAGTCGG.....	23	0	19	13.16	250	97	37	103	10	2	1
.....TTTGGTTATTTCATCTTTAGTC.....	22	0	18	8.50	153	93	19	33	3	4	1
.....TTTGGTTATTTCATCTTTAGTCGG.....	24	0	18	8.44	152	82	14	48	7	0	1
.....TTGGTTATTTCATCTTTAGTCG.....	22	0	19	5.47	104	8	65	26	3	1	1
.....TTTTGGTTATTTCATCTTTAGTCG.....	24	0	18	5.17	93	17	35	34	4	3	0
.....ATAAAGGTGAAATAACCACT.....	20	0	19	3.42	65	61	2	0	2	0	0
.....TTTGGTTATTTCATCTTTAGT.....	21	0	18	3.11	56	21	14	16	1	4	0
.....TGGTTATTTCATCTTTAGTCG.....	21	0	20	2.70	54	2	24	21	6	1	0
.....ACCGATAAAGGTGAAATAACCAC.....	23	0	15	1.67	25	25	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTCGGA.....	23	0	20	1.35	27	21	1	5	0	0	0
.....TGGTTATTTCATCTTTAGTCGG.....	22	0	20	1.25	25	0	6	16	2	1	0
.....ACCGATAAAGGTGAAATAACCA.....	22	0	20	1.20	24	17	3	1	3	0	0
.....GATAAAGGTGAAATAACCACT.....	21	0	18	1.11	20	17	2	0	1	0	0
.....TTGGTTATTTCATCTTTAGTCGGTT.....	24	1	19	1.05	20	13	2	4	0	1	0
.....TTTTGGTTATTTCATCTTTAGTC.....	23	0	18	1.00	18	13	1	4	0	0	0
.....ATAAAGGTGAAATAACCACC.....	20	1	19	0.95	18	18	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGC.....	25	1	18	0.89	16	2	0	14	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGC.....	24	1	19	0.84	16	2	4	10	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGA.....	24	1	18	0.67	12	7	5	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCG.....	25	0	18	0.61	11	3	3	5	0	0	0
.....TTTGGTTATTTCATCTTTAGTCA.....	23	1	18	0.56	10	3	4	2	1	0	0
.....ACCGATAAAGGTGAAATAACC.....	21	0	20	0.50	10	9	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTC.....	21	0	19	0.47	9	6	2	1	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGC.....	24	1	18	0.44	8	2	1	5	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGT.....	24	1	18	0.39	7	1	1	5	0	0	0
.....GTTATTTCATCTTTAGTCGGA.....	21	0	20	0.35	7	7	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCT.....	23	1	18	0.33	6	1	0	1	3	1	0
.....GATAAAGGTGAAATAACCACTA.....	22	0	18	0.28	5	4	0	0	0	1	0
.....TTTGGTTATTTCATCTTTAGC.....	21	1	18	0.28	5	5	0	0	0	0	0
.....CGATAAAGGTGAAATAACCACT.....	22	0	18	0.28	5	5	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCAA.....	24	2	18	0.28	5	0	5	0	0	0	0
.....ATAAAGGTGAAATAACCAC.....	19	0	19	0.26	5	5	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGT.....	22	0	18	0.22	4	0	1	2	0	1	0
.....TTTTTGGTTATTTCATCTTTAGTC.....	24	0	18	0.22	4	3	1	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
.....TTATTTCATCTTTAGTCGGAGTTC.....	24	0	10	0.20	2	2	0	0	0	0	0
.....ACCGATAAAGGTGAAATAACCC.....	22	1	20	0.20	4	4	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCC.....	23	1	18	0.17	3	2	0	0	0	1	0
.....TTTGGTTATTTCATCTTTAG.....	20	0	18	0.17	3	2	1	0	0	0	0
.....TTTTGGTTATTTCATCTTTAG.....	21	0	18	0.17	3	0	3	0	0	0	0
.....CGATAAAGGTGAAATAACCACC.....	22	1	18	0.17	3	3	0	0	0	0	0
.....GTTATTTCATCTTTAGTCG.....	19	0	20	0.15	3	2	0	1	0	0	0
.....TTATTTCATCTTTAGTCG.....	18	0	20	0.15	3	1	2	0	0	0	0
.....CCGATAAAGGTGAAATAACCAC.....	22	0	18	0.11	2	2	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTT.....	22	1	18	0.11	2	2	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGAA.....	25	1	18	0.11	2	1	0	1	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGG.....	25	0	18	0.11	2	2	0	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGT.....	23	0	18	0.11	2	1	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGT.....	25	1	18	0.11	2	0	1	1	0	0	0
.....ATAAAGGTGAAATAACCACTT.....	21	1	19	0.11	2	1	0	0	1	0	0
.....TTGGTTATTTCATCTTTAGTCGGTC.....	25	2	19	0.11	2	1	0	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCGA.....	23	1	19	0.11	2	2	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGT.....	20	0	19	0.11	2	0	1	1	0	0	0
.....AAACCGATAAAGGTGAAATAAC.....	22	0	20	0.10	2	2	0	0	0	0	0
.....TATTTCATCTTTAGTCGGAGTT.....	22	0	20	0.10	2	2	0	0	0	0	0
.....ATTTTTGGTTATTTCATCTTTAG.....	23	0	15	0.07	1	0	1	0	0	0	0
.....ACCGATAAAGGTGAAATAACCACT.....	24	0	15	0.07	1	1	0	0	0	0	0
.....ACCGATAAAGGTGAAATAACCACA.....	24	1	15	0.07	1	0	1	0	0	0	0
.....ATTTTTGGTTATTTCATCTTT.....	21	0	15	0.07	1	0	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGA.....	25	0	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCT.....	24	1	18	0.06	1	0	1	0	0	0	0
.....TTTTTGGTTATTTCATCTTTA.....	21	0	18	0.06	1	0	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTA.....	22	1	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCTT.....	24	2	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCA.....	24	1	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGT.....	25	1	18	0.06	1	0	0	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGA.....	24	0	18	0.06	1	0	0	1	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGA.....	25	1	18	0.06	1	1	0	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCC.....	25	1	18	0.06	1	0	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGTC.....	25	2	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGC.....	25	1	18	0.06	1	1	0	0	0	0	0
.....GATAAAGGTGAAATAACCAC.....	20	0	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGAG.....	26	0	18	0.06	1	0	0	1	0	0	0
.....TTTTGGTTATTTCATCTTTAGTC.....	22	1	18	0.06	1	1	0	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCGA.....	26	1	18	0.06	1	0	0	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCAA.....	23	2	19	0.05	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGT.....	23	1	19	0.05	1	0	0	0	1	0	0
.....TTGGTTATTTCATCTTTAGTCGGTAA.....	26	3	19	0.05	1	0	1	0	0	0	0
.....ATAAAGGTGAAATAACCACTGT.....	22	2	19	0.05	1	0	0	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCA.....	22	1	19	0.05	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGC.....	23	1	19	0.05	1	1	0	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
.....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
.....GTTATTTCATCTTTAGTCGGC.....	21	1	20	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
.....GGTTATTTCATCTTTAGTCGGC.....	22	1	20	0.05	1	1	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGA.....	20	0	20	0.05	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGAA.....	22	1	20	0.05	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGC.....	20	1	20	0.05	1	1	0	0	0	0	0
.....CCGATAAAGGTGAAATAACCA.....	21	0	20	0.05	1	0	1	0	0	0	0

Anti-sense strand reads

AGAATTACTTAAAAATTGTTTATTATTTATGTAGGTGTAAAGGTCATCCCGTATCTAAAAACCAATAAAGTAGAAATCAGCCTCAAGACCATTCATTTGGCTATTTCCACTTTATTGGTGATTTTAGTTATTTATTATTTGATCACTCTCTCTCACGAGATCCGATCTGACAAGCTGATCGT	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body
********** .....(((((((((((((((((((((((.((((....((....))....)))))))))))))))))))))))..)))))).....**********							
.....AGGTCATCCCGTATCTAAAAACCAATA.....	27	0	14	0.07	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:9927418-9927599 +	dmo_3148	TCTT-AATG-AATTTTTAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGATTTTTGGTT----------ATTTCATCTTTAGTCGGAGTTCTGGTAAGTAAACCGATAAAGGTGAA---ATAACCACTAAAAT------CAATAAATAATAAACTAGTGAGAGAGA----------GTGCTCTAGGCTAGACTGTTCGACTAGCA
droVir3	scaffold_12970:8381135-8381222 +		GTAAGAA--AACAAACAAATAAACTAAGACAAACACAAAAA------AAAAAAAAAAAAA---C-----AAGA----------ATACTCTAGCCGCACAAGCTCGACTAGCA
droGri2	scaffold_15203:1387667-1387756 +		TAGT-AATCTCAAATTTACAACAA----------GTAAAA---------TACTGCAATGAAAAGAAAAGTCAAACAAG---T-----ACGA----------GTATTCTAGTCGAGACAGTTCGACTGGAA
droWil2	scf2_1100000004762:4363338-4363479 +		TTTT-AACT----------AATATAGAGTATACCCATATTCTCAATTTGAATAGATTTGTGTTCAGACTTTCATTAGGATTTTAATTTTAATCAAAATTGTTTTACAAA----------AATT---AAAAGTAATTG------AAACAGTTTTTAAATAGATATAT---------------------------AAT
dp5	XR_group6:12059501-12059542 -		ACAACAA--GCTAAAA------CAATAAAAATAAACTAGAGAAAGAG----------------------------AG
droPer2	scaffold_40:156609-156669 +		AGAA-A--ATAAATAAAAAAAGATA---ATAAATAAAAA------ATACAAATAATAAATAAGTAATAT---------------------------AAA
droAna3	scaffold_13337:4355251-4355277 +		AATT-T---------TTAATAAATAATAATATAT---CC
droKik1	scf7180000298055:15006-15036 -		CCAG-TG--AGAGAGT----------GAGATTATCAAACTTACA
droFic1	scf7180000453912:1478054-1478073 -		GCTT-T---ATCGCTGCTCTAGCA
droEle1	scf7180000491087:49525-49571 -		AGCG-A--ATGAACAAAGGTGAT---TAAACATTAAAAT------TAACAA----------TAAAT----------AA
droBia1	scf7180000302402:8501515-8501553 +		ATAT-AGCA--AAA---ATGACCACTAAAAC------AAACAAATAAAA----------------------------AA
droEre2	scaffold_4845:8994517-8994595 -		CACA-A--GAAACCAAAAATAAAAAA---ATAACGA----------AGAAGATCTTTGCATTTATAATTTCATGGCAGAATTCCTCGATAAATT

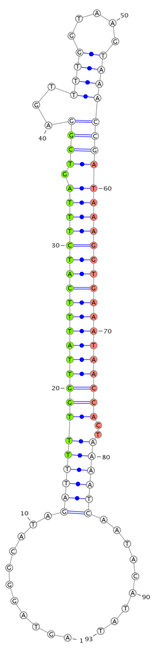
Generated: 09/08/2015 at 07:41 PM

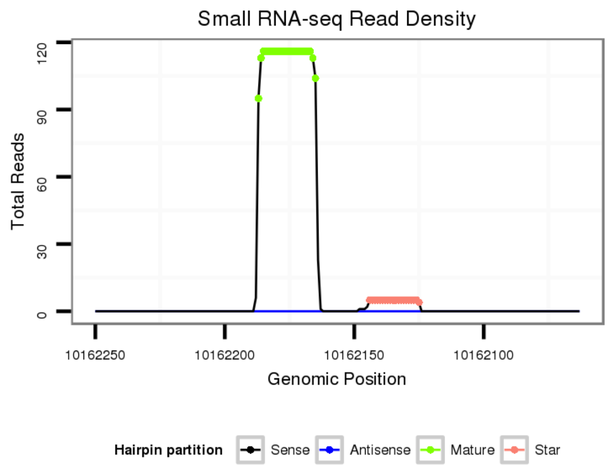
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

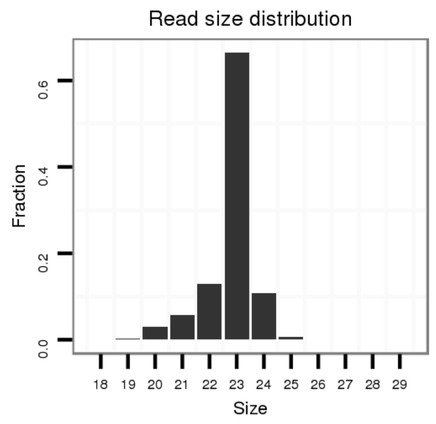
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3133	**scaffold_6473:10162113-10162200 -**	**confident**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

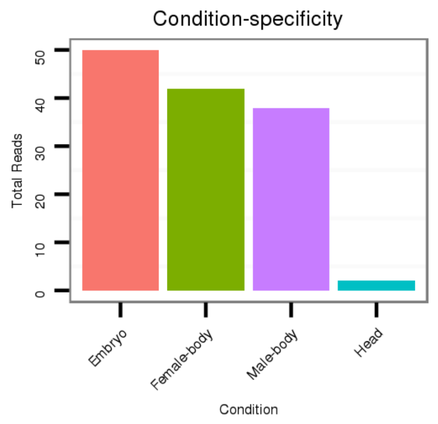
Legend: mature star mismatch in alignment mismatch in read

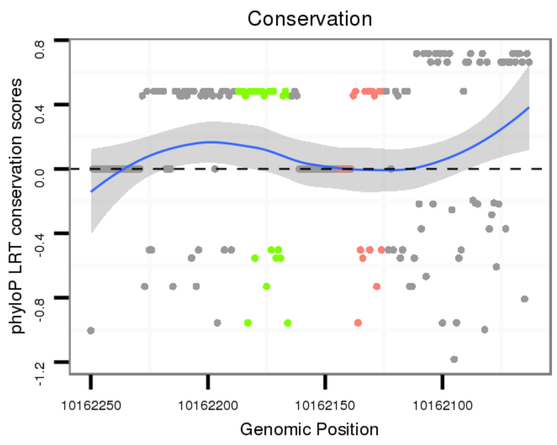
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [DmojGI15760-in]

No Repeatable elements found

mature	star
1. dmo_3141 scaffold_6473:8642796-8642818 + 2. dmo_3142 scaffold_6473:8643620-8643642 - 3. dmo_3138 scaffold_6473:8659793-8659815 + 4. dmo_3143 scaffold_6473:8660822-8660844 - 5. dmo_3150 scaffold_6473:9914890-9914912 - 6. scaffold_6473:9917724-9917746 + 7. dmo_3152 scaffold_6473:9919839-9919861 + 8. dmo_3148 scaffold_6473:9927476-9927498 + 9. scaffold_6473:9933776-9933798 + 10. scaffold_6473:9934446-9934468 - 11. dmo_3147 scaffold_6473:9937954-9937976 + 12. scaffold_6473:9938818-9938840 - 13. dmo_3146 scaffold_6473:9971832-9971854 - 14. dmo_3132 scaffold_6473:10161098-10161120 + 15. dmo_3133 scaffold_6473:10162165-10162187 - 16. dmo_3134 scaffold_6473:10167212-10167234 + 17. dmo_3136 scaffold_6473:10168425-10168447 - 18. scaffold_6473:10193224-10193246 +	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

CTTCTTCTTAATGAATTTTGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGATTTTTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATACATATTAAACTAGTGAGAGCGAGTGCTCTAGTAGAGACTGCTCGACTAGCAG **********.....(((((((((((((((((((((((.((((...((((.....))))))))))))))))))))))..))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
.....TTTGGTTATTTCATCTTTAGTCG.....	23	0	18	70.28	1265	258	545	378	69	11	4
.....TTGGTTATTTCATCTTTAGTCGG.....	23	0	19	13.16	250	97	37	103	10	2	1
.....TTTGGTTATTTCATCTTTAGTC.....	22	0	18	8.50	153	93	19	33	3	4	1
.....TTTGGTTATTTCATCTTTAGTCGG.....	24	0	18	8.44	152	82	14	48	7	0	1
.....TTGGTTATTTCATCTTTAGTCG.....	22	0	19	5.47	104	8	65	26	3	1	1
.....TTTTGGTTATTTCATCTTTAGTCGG.....	24	0	18	5.17	93	17	35	34	4	3	0
.....ATAAAGGTGAAATAACCACT.....	20	0	19	3.42	65	61	2	0	2	0	0
.....TTTGGTTATTTCATCTTTAGT.....	21	0	18	3.11	56	21	14	16	1	4	0
.....ACCGATAAAGGTGAAATAACCAC.....	23	0	15	1.67	25	25	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTCGG.....	22	0	20	1.65	33	14	0	16	2	1	0
.....TGGTTATTTCATCTTTAGTCG.....	21	0	20	1.35	27	0	0	21	6	0	0
.....TGGTTATTTCATCTTTAGTCGGA.....	23	0	20	1.35	27	21	0	5	1	0	0
.....GATAAAGGTGAAATAACCACT.....	21	0	18	1.11	20	17	2	0	1	0	0
.....TTGGTTATTTCATCTTTAGTCGGT.....	24	1	19	1.05	20	13	2	4	0	1	0
.....TTTTGGTTATTTCATCTTTAGTC.....	23	0	18	1.00	18	13	1	4	0	0	0
.....ATAAAGGTGAAATAACCACC.....	20	1	19	0.95	18	18	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGC.....	25	1	18	0.89	16	2	0	14	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGC.....	24	1	19	0.84	16	2	4	10	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGA.....	24	1	18	0.67	12	7	5	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCG.....	25	0	18	0.61	11	3	3	5	0	0	0
.....TTTGGTTATTTCATCTTTAGTCA.....	23	1	18	0.56	10	3	4	2	1	0	0
.....ACCGATAAAGGTGAAATAACC.....	21	0	20	0.50	10	9	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTC.....	21	0	19	0.47	9	6	2	1	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGC.....	24	1	18	0.44	8	2	1	5	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGT.....	24	1	18	0.39	7	1	1	5	0	0	0
.....GTTATTTCATCTTTAGTCGGA.....	21	0	20	0.35	7	7	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTTT.....	24	0	18	0.33	6	4	2	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCT.....	23	1	18	0.33	6	1	0	1	3	1	0
.....ACCGATAAAGGTGAAATAACCA.....	22	0	20	0.30	6	0	3	0	3	0	0
.....TTTGGTTATTTCATCTTTAGC.....	21	1	18	0.28	5	5	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCAA.....	24	2	18	0.28	5	0	5	0	0	0	0
.....CGATAAAGGTGAAATAACCACT.....	22	0	18	0.28	5	5	0	0	0	0	0
.....GATAAAGGTGAAATAACCACTA.....	22	0	18	0.28	5	4	0	0	0	1	0
.....ATAAAGGTGAAATAACCAC.....	19	0	19	0.26	5	5	0	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTC.....	24	0	18	0.22	4	3	1	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGT.....	22	0	18	0.22	4	0	1	2	0	1	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
.....CGATAAAGGTGAAATAACCACC.....	22	1	18	0.17	3	3	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCC.....	23	1	18	0.17	3	2	0	0	0	1	0
.....TTTGGTTATTTCATCTTTAG.....	20	0	18	0.17	3	2	1	0	0	0	0
.....TTTTGGTTATTTCATCTTTAG.....	21	0	18	0.17	3	0	3	0	0	0	0
.....TTATTTCATCTTTAGTCG.....	18	0	20	0.15	3	1	2	0	0	0	0
.....GTTATTTCATCTTTAGTCG.....	19	0	20	0.15	3	2	1	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGT.....	23	0	18	0.11	2	1	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGT.....	25	1	18	0.11	2	0	1	1	0	0	0
.....TTTGGTTATTTCATCTTTAGTT.....	22	1	18	0.11	2	2	0	0	0	0	0
.....CCGATAAAGGTGAAATAACCAC.....	22	0	18	0.11	2	2	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGG.....	25	0	18	0.11	2	2	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGAA.....	25	1	18	0.11	2	1	0	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGTC.....	25	2	19	0.11	2	1	0	1	0	0	0
.....TTGGTTATTTCATCTTTAGT.....	20	0	19	0.11	2	0	1	1	0	0	0
.....ATAAAGGTGAAATAACCACTT.....	21	1	19	0.11	2	1	0	0	1	0	0
.....TTGGTTATTTCATCTTTAGTCGA.....	23	1	19	0.11	2	2	0	0	0	0	0
.....AAACCGATAAAGGTGAAATAAC.....	22	0	20	0.10	2	2	0	0	0	0	0
.....CCGATAAAGGTGAAATAACCA.....	21	0	20	0.10	2	2	0	0	0	0	0
.....ACCGATAAAGGTGAAATAACCACA.....	24	1	15	0.07	1	0	1	0	0	0	0
.....ACCGATAAAGGTGAAATAACCACT.....	24	0	15	0.07	1	1	0	0	0	0	0
.....ATTTTTGGTTATTTCATCTTT.....	21	0	15	0.07	1	0	1	0	0	0	0
.....ATTTTTGGTTATTTCATCTTTAG.....	23	0	15	0.07	1	0	1	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCT.....	24	1	18	0.06	1	0	1	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCC.....	25	1	18	0.06	1	0	1	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCGA.....	26	1	18	0.06	1	0	0	1	0	0	0
.....CGATAAAGGTGAAATAACCACA.....	22	1	18	0.06	1	0	1	0	0	0	0
.....CATCCACATTTCCAGTAGGGC.....	21	0	18	0.06	1	0	0	1	0	0	0
.....TTTGGTTATTTCATCTTTAGTG.....	22	1	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCTT.....	24	2	18	0.06	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGA.....	24	0	18	0.06	1	0	0	1	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGA.....	25	1	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGA.....	25	0	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGAG.....	26	0	18	0.06	1	0	0	1	0	0	0
.....GAGTTTTGGTAAGTAAACCG.....	20	0	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGTC.....	25	2	18	0.06	1	1	0	0	0	0	0
.....ATTTCATCTTTAGTCGGAGTTT.....	22	0	18	0.06	1	1	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTTTTGGTA.....	29	0	18	0.06	1	1	0	0	0	0	0
.....TTTTTGGTTATTTCATCTTTA.....	21	0	18	0.06	1	0	1	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGT.....	25	1	18	0.06	1	0	0	1	0	0	0
.....TTTTGGTTATTTCATCTTTAGC.....	22	1	18	0.06	1	1	0	0	0	0	0
.....GATAAAGGTGAAATAACCAC.....	20	0	18	0.06	1	1	0	0	0	0	0
.....GATAAAGGTGAAATAACCACTAAC.....	24	1	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGC.....	25	1	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTA.....	22	1	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCA.....	24	1	18	0.06	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCA.....	22	1	19	0.05	1	0	1	0	0	0	0
.....AAAGGTGAAATAACCACT.....	18	0	19	0.05	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCAA.....	23	2	19	0.05	1	0	1	0	0	0	0
.....ATAAAGGTGAAATAACCACTGT.....	22	2	19	0.05	1	0	0	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCGC.....	23	1	19	0.05	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGT.....	23	1	19	0.05	1	0	0	0	1	0	0
.....ATAAAGGTGAAATAACCACTTT.....	22	2	19	0.05	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGTAA.....	26	3	19	0.05	1	0	1	0	0	0	0
.....TTATTTCATCTTTAGTCGGA.....	20	0	20	0.05	1	1	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTCGGT.....	23	1	20	0.05	1	1	0	0	0	0	0
.....CTCTAGTAGAGACTGCTCGAC.....	21	0	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCGG.....	21	0	20	0.05	1	0	0	0	0	0	1
.....GTTATTTCATCTTTAGTCGGC.....	21	1	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCG.....	20	0	20	0.05	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGC.....	20	1	20	0.05	1	0	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCGGC.....	22	1	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

GAAGAAGAATTACTTAAAACTTGTTTATTATTTATGTAGGTGTAAAGGTCATCCCGTATCTAAAAACCAATAAAGTAGAAATCAGCCTCAAAACCATTCATTTGGCTATTTCCACTTTATTGGTGATTTTAGTTATGTATAATTTGATCACTCTCGCTCACGAGATCATCTCTGACGAGCTGATCGTC **********.....(((((((((((((((((((((((.((((...((((.....))))))))))))))))))))))..))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	M060 embryo	V041 embryo
.....TCATCTCTGACGAGCTGATCG..	21	0	9	0.11	1	0	1	0	0
.....AGGTCATCCCGTATCTAAAAACCAATA.....	27	0	14	0.07	1	1	0	0	0
.....AAGAAATCAGCCTCAAAACCAT.....	22	1	18	0.06	1	1	0	0	0
.....AGATCATCTCTGACGAGCT.....	19	0	20	0.05	1	0	0	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:10162063-10162250 -	dmo_3133	CTTCTTCTTAATGAATTTTGAACAAATAATAAATACATCCACATT----------TCCAGTAGGGCATAGATTTTTGG--TTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATACA----------TATTAAACTAGTGAGAGCGAGTGCTCTAGTAGAGACTGCTCGACTAGCAG
droVir3	scaffold_12728:379342-379522 +		A----------CCAGCAATAA---AATCCACAATCATTTTTGTTTGTCAGTAG-CCACAGGTTTTTGCAATTTTTTCTTTACTGTGGGAG----------GTCGTATGACAATTAG-GTCTGTAACTAATTTTTAAAAAATGTTATTGATTTAATAATCACACTAGTAAGAAACTATGCTCTAGTCGGAAGTGCCGACTAGGAG
droGri2	scaffold_15110:19086589-19086634 +		T----------]----------]--]----------FAATAAACAAGTTAGAAG----GCTTCTGTTGAGGGAGCTCGACTAGCAG

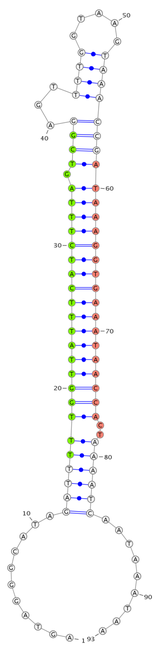
Generated: 09/08/2015 at 07:42 PM

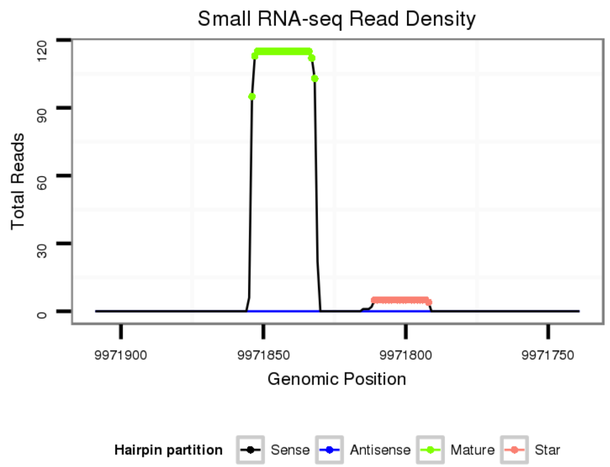
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

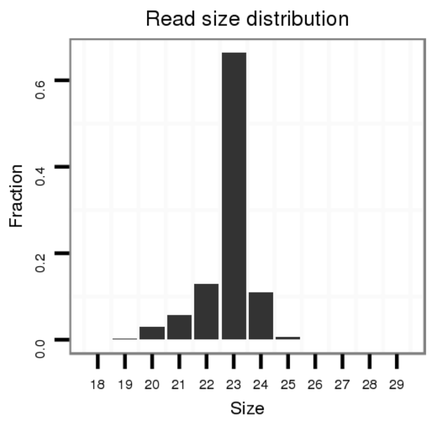
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3146	**scaffold_6473:9971789-9971859 -**	**confident**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

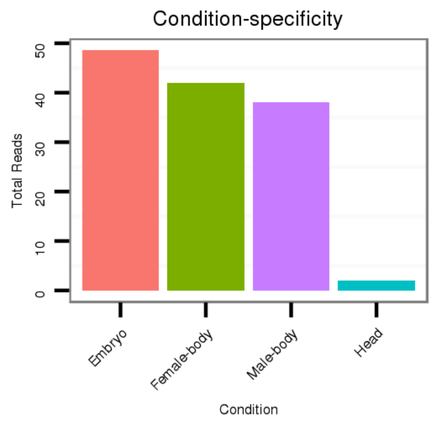
Legend: mature star mismatch in alignment mismatch in read

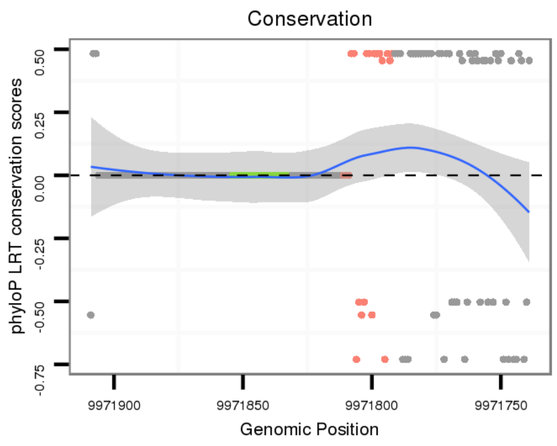
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [DmojGI15751-in]

No Repeatable elements found

mature	star
1. dmo_3141 scaffold_6473:8642796-8642818 + 2. dmo_3142 scaffold_6473:8643620-8643642 - 3. dmo_3138 scaffold_6473:8659793-8659815 + 4. dmo_3143 scaffold_6473:8660822-8660844 - 5. dmo_3150 scaffold_6473:9914890-9914912 - 6. scaffold_6473:9917724-9917746 + 7. dmo_3152 scaffold_6473:9919839-9919861 + 8. dmo_3148 scaffold_6473:9927476-9927498 + 9. scaffold_6473:9933776-9933798 + 10. scaffold_6473:9934446-9934468 - 11. dmo_3147 scaffold_6473:9937954-9937976 + 12. scaffold_6473:9938818-9938840 - 13. dmo_3146 scaffold_6473:9971832-9971854 - 14. dmo_3132 scaffold_6473:10161098-10161120 + 15. dmo_3133 scaffold_6473:10162165-10162187 - 16. dmo_3134 scaffold_6473:10167212-10167234 + 17. dmo_3136 scaffold_6473:10168425-10168447 - 18. scaffold_6473:10193224-10193246 +	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

TAATGAATTTTGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGATTTTTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATAAATAATAAACTAGTGAGAGAGAGTGCTCTAGTAGAGACTGCTC **********.....(((((((((((((((((((((((.((((...((((.....))))))))))))))))))))))..))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	M046 male body	V110 embryo	V041 head	V056 head	V049 head
...........TTTGGTTATTTCATCTTTAGTCG...........	23	0	18	70.28	1265	258	545	378	69	11	4	
...........TTGGTTATTTCATCTTTAGTCGG...........	23	0	19	13.16	250	97	37	103	10	2	1	
...........TTTGGTTATTTCATCTTTAGTC...........	22	0	18	8.50	153	93	19	33	3	4	1	
...........TTTGGTTATTTCATCTTTAGTCGG...........	24	0	18	8.44	152	82	14	48	7	0	1	
...........TTGGTTATTTCATCTTTAGTCG...........	22	0	19	5.47	104	8	65	26	3	1	1	
...........TTTTGGTTATTTCATCTTTAGTCG...........	24	0	18	5.17	93	17	35	34	4	3	0	
...........ATAAAGGTGAAATAACCACT...........	20	0	19	3.42	65	61	2	0	2	0	0	
...........TTTGGTTATTTCATCTTTAGT...........	21	0	18	3.11	56	21	14	16	1	4	0	
...........ACCGATAAAGGTGAAATAACCAC...........	23	0	15	1.67	25	25	0	0	0	0	0	
...........TGGTTATTTCATCTTTAGTCGG...........	22	0	20	1.65	33	14	0	16	2	1	0	
...........TGGTTATTTCATCTTTAGTCG...........	21	0	20	1.15	23	2	0	21	0	0	0	
...........GATAAAGGTGAAATAACCACT...........	21	0	18	1.11	20	17	2	0	1	0	0	
...........TTGGTTATTTCATCTTTAGTCGGT...........	24	1	19	1.05	20	13	2	4	0	1	0	
...........TTTTGGTTATTTCATCTTTAGTC...........	23	0	18	1.00	18	13	1	4	0	0	0	
...........ATAAAGGTGAAATAACCACC...........	20	1	19	0.95	18	18	0	0	0	0	0	
...........TTTGGTTATTTCATCTTTAGTCGGC...........	25	1	18	0.89	16	2	0	14	0	0	0	
...........TTGGTTATTTCATCTTTAGTCGGG...........	24	1	19	0.84	16	2	4	10	0	0	0	
...........TTGGTTATTTCATCTTTAGTCGA...........	24	1	18	0.67	12	7	5	0	0	0	0	
...........TTTTTGGTTATTTCATCTTTAGTCG...........	25	0	18	0.61	11	3	3	5	0	0	0	
...........TTTGGTTATTTCATCTTTAGTCA...........	23	1	18	0.56	10	3	4	2	1	0	0	
...........ACCGATAAAGGTGAAATAACC...........	21	0	20	0.50	10	9	1	0	0	0	0	
...........TTGGTTATTTCATCTTTAGTC...........	21	0	19	0.47	9	6	2	1	0	0	0	
...........TTTGGTTATTTCATCTTTAGTCGC...........	24	1	18	0.44	8	2	1	5	0	0	0	
...........TTTGGTTATTTCATCTTTAGTCGT...........	24	1	18	0.39	7	1	1	5	0	0	0	
...........GTTATTTCATCTTTAGTCGGA...........	21	0	20	0.35	7	7	0	0	0	0	0	
...........TGGTTATTTCATCTTTAGTCGGA...........	23	0	20	0.35	7	0	1	5	1	0	0	
...........TTATTTCATCTTTAGTCGGAGTTT...........	24	0	18	0.33	6	4	2	0	0	0	0	
...........TTTGGTTATTTCATCTTTAGTCT...........	23	1	18	0.33	6	1	0	1	3	1	0	
...........ACCGATAAAGGTGAAATAACCA...........	22	0	20	0.30	6	0	3	0	3	0	0	
...........CGATAAAGGTGAAATAACCACT...........	22	0	18	0.28	5	5	0	0	0	0	0	
...........TTTGGTTATTTCATCTTTAGTCAA...........	24	2	18	0.28	5	0	5	0	0	0	0	
...........TTTGGTTATTTCATCTTTAGC...........	21	1	18	0.28	5	5	0	0	0	0	0	
...........GATAAAGGTGAAATAACCACTA...........	22	0	18	0.28	5	4	0	0	0	1	0	
...........ATAAAGGTGAAATAACCAC...........	19	0	19	0.26	5	5	0	0	0	0	0	
...........TTTTTGGTTATTTCATCTTTAGTC...........	24	0	18	0.22	4	3	1	0	0	0	0	
...........TTTTGGTTATTTCATCTTTAGT...........	22	0	18	0.22	4	0	1	2	0	1	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	
...........TTTTGGTTATTTCATCTTTAG...........	21	0	18	0.17	3	0	3	0	0	0	0	
...........TTTGGTTATTTCATCTTTAGTCC...........	23	1	18	0.17	3	2	0	0	0	1	0	
...........CGATAAAGGTGAAATAACCACC...........	22	1	18	0.17	3	3	0	0	0	0	0	
...........TTTGGTTATTTCATCTTTAG...........	20	0	18	0.17	3	2	1	0	0	0	0	
...........CCGATAAAGGTGAAATAACCAC...........	22	0	18	0.11	2	2	0	0	0	0	0	
...........TTTTTGGTTATTTCATCTTTAGT...........	23	0	18	0.11	2	1	1	0	0	0	0	
...........TTTGGTTATTTCATCTTTAGTCGGT...........	25	1	18	0.11	2	0	1	1	0	0	0	
...........TTGGTTATTTCATCTTTAGTCGGAA...........	25	1	18	0.11	2	1	0	1	0	0	0	
...........TTTGGTTATTTCATCTTTAGTT...........	22	1	18	0.11	2	2	0	0	0	0	0	
...........TTTTGGTTATTTCATCTTTAGTCGG...........	25	0	18	0.11	2	2	0	0	0	0	0	
...........TTGGTTATTTCATCTTTAGTCGA...........	23	1	19	0.11	2	2	0	0	0	0	0	
...........TTGGTTATTTCATCTTTAGTCGGTC...........	25	2	19	0.11	2	1	0	1	0	0	0	
...........ATAAAGGTGAAATAACCACTT...........	21	1	19	0.11	2	1	0	0	1	0	0	
...........TTGGTTATTTCATCTTTAGT...........	20	0	19	0.11	2	0	1	1	0	0	0	
...........CCGATAAAGGTGAAATAACCA...........	21	0	20	0.10	2	2	0	0	0	0	0	
...........TTATTTCATCTTTAGTCG...........	18	0	20	0.10	2	0	2	0	0	0	0	
...........AAACCGATAAAGGTGAAATAAC...........	22	0	20	0.10	2	2	0	0	0	0	0	
...........ACCGATAAAGGTGAAATAACCACA...........	24	1	15	0.07	1	0	1	0	0	0	0	
...........ATTTTTGGTTATTTCATCTTTAG...........	23	0	15	0.07	1	0	1	0	0	0	0	
...........ATTTTTGGTTATTTCATCTTT...........	21	0	15	0.07	1	0	1	0	0	0	0	
...........ACCGATAAAGGTGAAATAACCACT...........	24	0	15	0.07	1	1	0	0	0	0	0	
...........TTTTGGTTATTTCATCTTTAGTCGA...........	25	1	18	0.06	1	1	0	0	0	0	0	
...........GATAAAGGTGAAATAACCAC...........	20	0	18	0.06	1	1	0	0	0	0	0	
...........TTTTGGTTATTTCATCTTTAGTCA...........	24	1	18	0.06	1	1	0	0	0	0	0	
...........TTTGGTTATTTCATCTTTAGTA...........	22	1	18	0.06	1	1	0	0	0	0	0	
...........TTTGGTTATTTCATCTTTAGTCGGA...........	25	0	18	0.06	1	1	0	0	0	0	0	
...........TTTTGGTTATTTCATCTTTAGTCT...........	24	1	18	0.06	1	0	1	0	0	0	0	
...........TTTGGTTATTTCATCTTTAGTCTT...........	24	2	18	0.06	1	1	0	0	0	0	0	
...........TTGGTTATTTCATCTTTAGTCGGA...........	24	0	18	0.06	1	0	0	1	0	0	0	
...........GATAAAGGTGAAATAACCACTAAC...........	24	1	18	0.06	1	1	0	0	0	0	0	
...CATCCACATTTCCAGTAGGGC...........	21	0	18	0.06	1	0	0	1	0	0	0	
...........GAGTTTTGGTAAGTAAACCG...........	20	0	18	0.06	1	1	0	0	0	0	0	
...........TTTGGTTATTTCATCTTTAGTCGGAG...........	26	0	18	0.06	1	0	0	1	0	0	0	
...........CGATAAAGGTGAAATAACCACA...........	22	1	18	0.06	1	0	1	0	0	0	0	
...........TTTTTGGTTATTTCATCTTTAGTCC...........	25	1	18	0.06	1	0	1	0	0	0	0	
...........TTTTTGGTTATTTCATCTTTA...........	21	0	18	0.06	1	0	1	0	0	0	0	
...........TTTTGGTTATTTCATCTTTAGTCGT...........	25	1	18	0.06	1	0	0	1	0	0	0	
...........TTTTTGGTTATTTCATCTTTAGTCGA...........	26	1	18	0.06	1	0	0	1	0	0	0	
...........TTATTTCATCTTTAGTCGGAGTTTTGGTA...........	29	0	18	0.06	1	1	0	0	0	0	0	
...........TTTTGGTTATTTCATCTTTAGTCGC...........	25	1	18	0.06	1	1	0	0	0	0	0	
...........TTTTGGTTATTTCATCTTTAGC...........	22	1	18	0.06	1	1	0	0	0	0	0	
...........TTTGGTTATTTCATCTTTAGTG...........	22	1	18	0.06	1	1	0	0	0	0	0	
...........TTTGGTTATTTCATCTTTAGTCGTC...........	25	2	18	0.06	1	1	0	0	0	0	0	
...........ATTTCATCTTTAGTCGGAGTTT...........	22	0	18	0.06	1	1	0	0	0	0	0	
...........AAAGGTGAAATAACCACT...........	18	0	19	0.05	1	1	0	0	0	0	0	
...........TTGGTTATTTCATCTTTAGTCGC...........	23	1	19	0.05	1	1	0	0	0	0	0	
...........ATAAAGGTGAAATAACCACTGT...........	22	2	19	0.05	1	0	0	1	0	0	0	
...........ATAAAGGTGAAATAACCACTTT...........	22	2	19	0.05	1	1	0	0	0	0	0	
...........TTGGTTATTTCATCTTTAGTCGT...........	23	1	19	0.05	1	0	0	0	1	0	0	
...........TTGGTTATTTCATCTTTAGTCAA...........	23	2	19	0.05	1	0	1	0	0	0	0	
...........TTGGTTATTTCATCTTTAGTCA...........	22	1	19	0.05	1	0	1	0	0	0	0	
...........TTGGTTATTTCATCTTTAGTCGGTAA...........	26	3	19	0.05	1	0	1	0	0	0	0	
...........TTGGTTATTTCATCTTTAGC...........	20	1	20	0.05	1	1	0	0	0	0	0	
...........TTATTTCATCTTTAGTCGGA...........	20	0	20	0.05	1	1	0	0	0	0	0	
...........GTTATTTCATCTTTAGTCGGC...........	21	1	20	0.05	1	1	0	0	0	0	0	
...........TTATTTCATCTTTAGTCGGAGTT...........	23	0	20	0.05	1	1	0	0	0	0	0	
...........GGTTATTTCATCTTTAGTCG...........	20	0	20	0.05	1	0	1	0	0	0	0	
...........GGTTATTTCATCTTTAGTCGGC...........	22	1	20	0.05	1	1	0	0	0	0	0	
...........GGTTATTTCATCTTTAGTCGG...........	21	0	20	0.05	1	0	0	0	0	0	1	
...........GTTATTTCATCTTTAGTCG...........	19	0	20	0.05	1	0	1	0	0	0	0	
...........TGGTTATTTCATCTTTAGTCGGT...........	23	1	20	0.05	1	1	0	0	0	0	0	

Anti-sense strand reads

ATTACTTAAAACTTGTTTATTATTTATGTAGGTGTAAAGGTCATCCCGTATCTAAAAACCAATAAAGTAGAAATCAGCCTCAAAACCATTCATTTGGCTATTTCCACTTTATTGGTGATTTTAGTTATTTATTATTTGATCACTCTCTCTCACGAGATCATCTCTGACGAG **********.....(((((((((((((((((((((((.((((...((((.....))))))))))))))))))))))..))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	M060 embryo
...........ACTCTCTCTCACGAGATCATCTC.......	23	0	2	0.50	1	1	0	0
...........AGGTCATCCCGTATCTAAAAACCAATA...........	27	0	14	0.07	1	1	0	0
...........AAGAAATCAGCCTCAAAACCAT...........	22	1	18	0.06	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:9971739-9971909 -	dmo_3146	TAATGAATTTTGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGATTTTTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATAAATAATAAACTAGTGAGAGAGAGTGCTCTAGTAGAGACTGCTC
droVir3	scaffold_13047:14612534-14612606 +		AAA----------AATAAAATTAAGAACTAAACGAATAAATAAATAATACAAGCAAGAGCGGCCCAGTCACCCATGACC

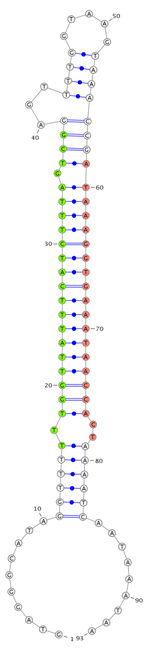
Generated: 09/08/2015 at 07:42 PM

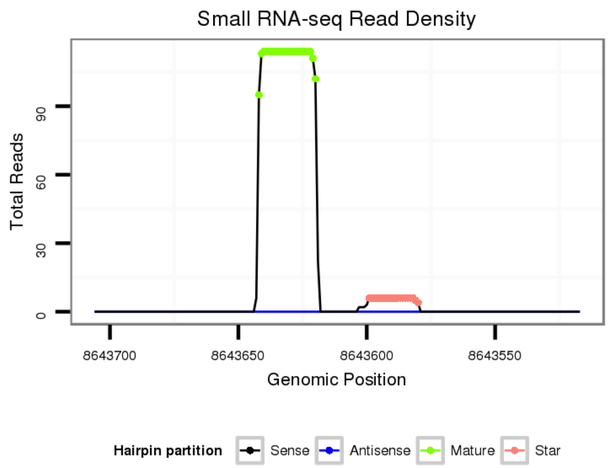
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

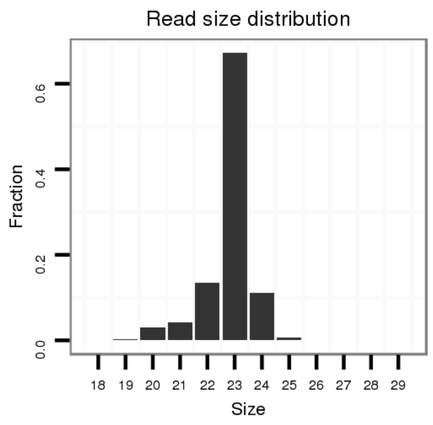
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3142	**scaffold_6473:8643567-8643656 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

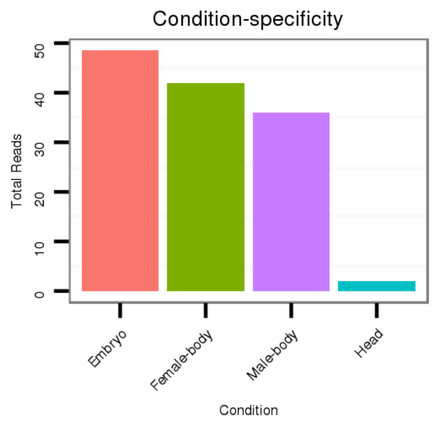
Legend: mature star mismatch in alignment mismatch in read

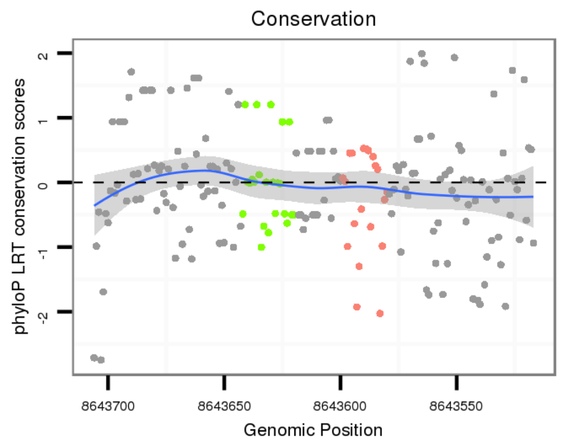
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dmo_3141 scaffold_6473:8642796-8642818 + 2. dmo_3142 scaffold_6473:8643620-8643642 - 3. dmo_3138 scaffold_6473:8659793-8659815 + 4. dmo_3143 scaffold_6473:8660822-8660844 - 5. dmo_3150 scaffold_6473:9914890-9914912 - 6. scaffold_6473:9917724-9917746 + 7. dmo_3152 scaffold_6473:9919839-9919861 + 8. dmo_3148 scaffold_6473:9927476-9927498 + 9. scaffold_6473:9933776-9933798 + 10. scaffold_6473:9934446-9934468 - 11. dmo_3147 scaffold_6473:9937954-9937976 + 12. scaffold_6473:9938818-9938840 - 13. dmo_3146 scaffold_6473:9971832-9971854 - 14. dmo_3132 scaffold_6473:10161098-10161120 + 15. dmo_3133 scaffold_6473:10162165-10162187 - 16. dmo_3134 scaffold_6473:10167212-10167234 + 17. dmo_3136 scaffold_6473:10168425-10168447 - 18. scaffold_6473:10193224-10193246 +	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

CGACTGCTTCATTAATTTAGAAAAAATAATATATACATCCACATTTCCAGTAGGGCATAGGTTTTTTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATAAATAAACTAGTGGGAGAGAGTGCTCTAGTAGAGACTGCTCGACTAGCAGATAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
**********.....(((((((.((((((((((((((((((.((((...((((.....)))))))))))))))))))))))))..)))))))).....**********											
.....TTTGGTTATTTCATCTTTAGTCG.....	23	0	18	70.28	1265	258	545	378	69	11	4
.....TTGGTTATTTCATCTTTAGTCGG.....	23	0	19	13.16	250	97	37	103	10	2	1
.....TTTGGTTATTTCATCTTTAGTC.....	22	0	18	8.50	153	93	19	33	3	4	1
.....TTTGGTTATTTCATCTTTAGTCGG.....	24	0	18	8.44	152	82	14	48	7	0	1
.....TTGGTTATTTCATCTTTAGTCG.....	22	0	19	5.47	104	8	65	26	3	1	1
.....TTTTGGTTATTTCATCTTTAGTCG.....	24	0	18	5.17	93	17	35	34	4	3	0
.....ATAAAGGTGAAATAACCACT.....	20	0	19	3.42	65	61	2	0	2	0	0
.....TTTGGTTATTTCATCTTTAGT.....	21	0	18	3.11	56	21	14	16	1	4	0
.....ACCGATAAAGGTGAAATAACCAC.....	23	0	15	1.67	25	25	0	0	0	0	0
.....ACCGATAAAGGTGAAATAACCA.....	22	0	20	1.20	24	17	3	1	3	0	0
.....GATAAAGGTGAAATAACCACT.....	21	0	18	1.11	20	17	2	0	1	0	0
.....TTGGTTATTTCATCTTTAGTCGGT.....	24	1	19	1.05	20	13	2	4	0	1	0
.....TTTTGGTTATTTCATCTTTAGTC.....	23	0	18	1.00	18	13	1	4	0	0	0
.....TGGTTATTTCATCTTTAGTCGG.....	22	0	20	1.00	20	14	6	0	0	0	0
.....ATAAAGGTGAAATAACCACC.....	20	1	19	0.95	18	18	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGC.....	25	1	18	0.89	16	2	0	14	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGC.....	24	1	19	0.84	16	2	4	10	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGA.....	24	1	18	0.67	12	7	5	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCG.....	25	0	18	0.61	11	3	3	5	0	0	0
.....TTTGGTTATTTCATCTTTAGTCA.....	23	1	18	0.56	10	3	4	2	1	0	0
.....TTGGTTATTTCATCTTTAGTC.....	21	0	19	0.47	9	6	2	1	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGC.....	24	1	18	0.44	8	2	1	5	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGT.....	24	1	18	0.39	7	1	1	5	0	0	0
.....TTATTTCATCTTTAGTCGGAGTTT.....	24	0	18	0.33	6	4	2	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCT.....	23	1	18	0.33	6	1	0	1	3	1	0
.....TTTGGTTATTTCATCTTTAGTCAA.....	24	2	18	0.28	5	0	5	0	0	0	0
.....TTTGGTTATTTCATCTTTAGC.....	21	1	18	0.28	5	5	0	0	0	0	0
.....CGATAAAGGTGAAATAACCACT.....	22	0	18	0.28	5	5	0	0	0	0	0
.....GATAAAGGTGAAATAACCACTA.....	22	0	18	0.28	5	4	0	0	0	1	0
.....ATAAAGGTGAAATAACCAC.....	19	0	19	0.26	5	5	0	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTC.....	24	0	18	0.22	4	3	1	0	0	0	0
.....GATAAAGGTGAAATAACCACC.....	21	1	18	0.22	4	4	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGT.....	22	0	18	0.22	4	0	1	2	0	1	0
.....ATAAAGGTGAAATAACCACTA.....	21	0	19	0.21	4	4	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAG.....	21	0	18	0.17	3	0	3	0	0	0	0
.....TTTGGTTATTTCATCTTTAG.....	20	0	18	0.17	3	2	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCC.....	23	1	18	0.17	3	2	0	0	0	1	0
.....CGATAAAGGTGAAATAACCACC.....	22	1	18	0.17	3	3	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTCG.....	21	0	20	0.15	3	2	0	0	0	1	0
.....TTTTTGGTTATTTCATCTTTAGT.....	23	0	18	0.11	2	1	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGT.....	25	1	18	0.11	2	0	1	1	0	0	0
.....CCGATAAAGGTGAAATAACCAC.....	22	0	18	0.11	2	2	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGAA.....	25	1	18	0.11	2	1	0	1	0	0	0
.....TTTGGTTATTTCATCTTTAGTTT.....	22	1	18	0.11	2	2	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGG.....	25	0	18	0.11	2	2	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGTC.....	25	2	19	0.11	2	1	0	1	0	0	0
.....TTGGTTATTTCATCTTTAGT.....	20	0	19	0.11	2	0	1	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCGA.....	23	1	19	0.11	2	2	0	0	0	0	0
.....ATAAAGGTGAAATAACCACTT.....	21	1	19	0.11	2	1	0	0	1	0	0
.....TGGTTATTTCATCTTTAGTCGGA.....	23	0	20	0.10	2	0	1	0	1	0	0
.....CCGATAAAGGTGAAATAACCA.....	21	0	20	0.10	2	2	0	0	0	0	0
.....TATTTCATCTTTAGTCGGAGTT.....	22	0	20	0.10	2	2	0	0	0	0	0
.....ACCGATAAAGGTGAAATAACCACT.....	24	0	15	0.07	1	1	0	0	0	0	0
.....ACCGATAAAGGTGAAATAACCACA.....	24	1	15	0.07	1	0	1	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGA.....	25	1	18	0.06	1	1	0	0	0	0	0
.....GAGTTTTGGTAAGTAAACCG.....	20	0	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTG.....	22	1	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCA.....	24	1	18	0.06	1	1	0	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCC.....	25	1	18	0.06	1	0	1	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCT.....	24	1	18	0.06	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGA.....	24	0	18	0.06	1	0	0	1	0	0	0
.....CATCCACATTTCCAGTAGGGC.....	21	0	18	0.06	1	0	0	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGA.....	25	0	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTA.....	22	1	18	0.06	1	1	0	0	0	0	0
.....GATAAAGGTGAAATAACCAC.....	20	0	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCTT.....	24	2	18	0.06	1	1	0	0	0	0	0
.....GATAAAGGTGAAATAACCACTAAC.....	24	1	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGT.....	25	1	18	0.06	1	0	0	1	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCG.....	22	1	18	0.06	1	1	0	0	0	0	0
.....ATTTCATCTTTAGTCGGAGTTT.....	22	0	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGTC.....	25	2	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGAG.....	26	0	18	0.06	1	0	0	1	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCGA.....	26	1	18	0.06	1	0	0	1	0	0	0
.....CGATAAAGGTGAAATAACCACA.....	22	1	18	0.06	1	0	1	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTTTTGGTA.....	29	0	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGC.....	25	1	18	0.06	1	1	0	0	0	0	0
.....TTTTTGGTTATTTCATCTTTA.....	21	0	18	0.06	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGTAA.....	26	3	19	0.05	1	0	1	0	0	0	0
.....ATAAAGGTGAAATAACCACTTT.....	22	2	19	0.05	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCAA.....	23	2	19	0.05	1	0	1	0	0	0	0
.....ATAAAGGTGAAATAACCACTGT.....	22	2	19	0.05	1	0	0	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCGT.....	23	1	19	0.05	1	0	0	0	1	0	0
.....AAAGGTGAAATAACCACT.....	18	0	19	0.05	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCA.....	22	1	19	0.05	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGC.....	23	1	19	0.05	1	1	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGA.....	20	0	20	0.05	1	1	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTT.....	23	0	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCG.....	20	0	20	0.05	1	0	1	0	0	0	0
.....GTTATTTCATCTTTAGTCG.....	19	0	20	0.05	1	0	1	0	0	0	0
.....GTTATTTCATCTTTAGTCGGC.....	21	1	20	0.05	1	1	0	0	0	0	0
.....CTCTAGTAGAGACTGCTCGAC.....	21	0	20	0.05	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGAA.....	22	1	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCGG.....	21	0	20	0.05	1	0	0	0	0	0	1
.....TTGGTTATTTCATCTTTAGC.....	20	1	20	0.05	1	1	0	0	0	0	0
.....CGATAAAGGTGAAATAACCC.....	20	1	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

GCTGACGAAGTAATTAAATCTTTTTTATTATATATGTAGGTGTAAAGGTCATCCCGTATCCAAAAAACCAATAAAGTAGAAATCAGCCTCAAAACCATTCATTTGGCTATTTCCACTTTATTGGTGATTTTAGTTATTTATTTGATCACCCTCTCTCACGAGATCATCTCTGACGAGCTGATCGTCTATG	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V041 embryo
**********.....(((((((.((((((((((((((((((.((((...((((.....)))))))))))))))))))))))))..)))))))).....**********									
.....TCATCTCTGACGAGCTGATCG.....	21	0	9	0.11	1	1	0	0	0
.....AAGAAATCAGCCTCAAAACCAT.....	22	1	18	0.06	1	0	1	0	0
.....AGATCATCTCTGACGAGCT.....	19	0	20	0.05	1	0	0	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:8643517-8643706 -	dmo_3142	CGACTGCTT-CATTA--ATTTAGAAAAAATAATATATACATCCACATTTCCAG-TAG----GGCATAGGTTTTTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAG---GT----------GAAATAAC------CACTAAAATCAATAAATAAACTAGTGGGAGAGAGTGCTCTAGTAGAGACTG-CTCGACTAGCAGATAC
droVir3	scaffold_12970:8707196-8707374 -		ATTATAT--------------TACAAATAATTCTGAGTTAATTCAACTTTCTATTTAG----GAGGTAGACTACTAGACTAGACTACTTTTTTTAGGAGATTAACAAATATATTTACTCCGTAATGC----------AC------ACGATATACGATTATAAAACGAACAAGTAAGAGTGCGCTTGTCGGAGTA-TCCAACTGGAGTTAC
droGri2	scaffold_15110:1885179-1885281 -		TTTTCTATTTTATTAAAGTTT----------TG-----------CAAA---AT----------TAAGT-TCAAAAAC----AAAGGAGAAAGTGAAAAATT--ACAAAGTGCTCTAAGCGAAAGTG-CTCGACTAGCAGATAC
droWil2	scf2_1100000003321:1876-1935 +		CGTCTGCGT-GTTTA--ATT----------CAT--------CAT--------CATTGATGAGGAGTGTCCTTAGTTCCG---GCCAGGTGTTGGCTTT
dp5	XL_group3a:114844-114847 -		CAAC----------AC----------CAT--------CAT--------CAT----------AT----------ATTTTTTTAAT----------T
droPer2	scaffold_94:207881-207928 -		AATATAT--------A----------CATACACATTTTTAG-TAA----GTAATAT----------AT----------ATTTTTTTAAT----------T
droAna3	scaffold_13337:21720750-21720795 +		AATTGAA----------CTGATGAAT---TT----------AAAACAAC-----AACAAAAATAAATAAATAAA----------
droBip1	scf7180000396768:15984-16024 +		ATTATT----------TTAGAAAAAATAATATATTGTGCCAAGTTTCCAG----------AT----------ATTTTTTTAAT----------T
droKik1	scf7180000302455:34556-34685 +		CATTAAT----------TTGGTAAAAACAAGGATATATAT----TTTTTTATATTTATATTTAGGTTTTTTTGTTTATTCATCATATT----------GTGAATTAGAAAATTCAAAAGTCGTCAAAATAAC-----CTGAAGTTTGCAAAATTAA----------
droEle1	scf7180000490470:7558-7618 +		AAATAAA----------CTGTTGAAA---GA----------GACAGTAC-----TGAAATAATGTAAAAATAAACTGTTGAAGAGAG----------
droRho1	scf7180000776945:11148-11234 +		AAATTT----------AA----------GAAA---AT----------GCAAT-AC-----AATAAAAATGAATAAATAAAAAAACAAGAGAGAACGCTATAGTCGAG--TGCCTCGACTATTAGATAC
droBia1	scf7180000298100:3999-4091 -		TTTTTAT----------AA----------GTA----------AGCCCACATTGT----------ACAAA-----TAAATAAATAAATAAATAAATTATAAAACAGAAAATGCTCGGAAAAAGGA---TGCATTATTAGAAAC
droEug1	scf7180000407611:1197-1250 -		AAGCCAT----------AAAG---TT----------GAAATACC-----CAAGATAATAAATACATAAATAAATAGCAAAAA----------
droSim2	21:20781195-20781247 +		AAAA----------AC----------AAATAGCAATAGAGAATGCTAAGGTCGGAGTTC-CCCGACTATCAGATAC
droEre2	scaffold_4784:25607109-25607215 +		TCATAAT----------TTTCGCAAAAATTATGAATATAAAAATTGTTTAG-TAG----GGCGAAGCTTACTTGGTTTTATAATT----------AT----------ATGATTTTCTTTGGGTTATTG-TAGCGTTAATCGT--G

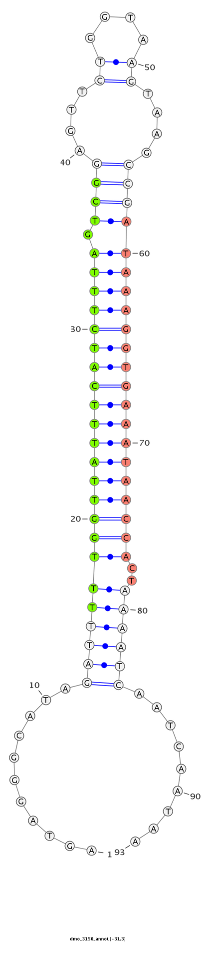
Generated: 09/08/2015 at 07:42 PM

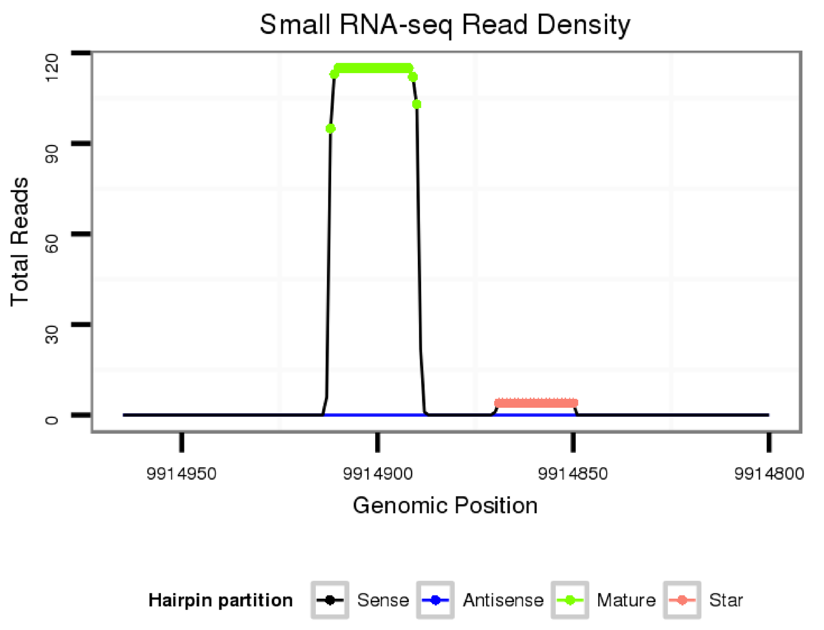
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

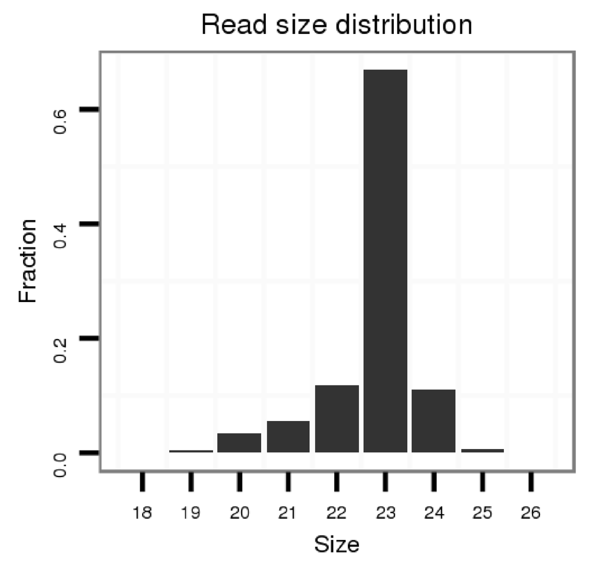
ID: dmo_3150	Coordinate: scaffold_6473:9914850-9914915 -	Confidence: confident	Class: Canonical miRNA	Genomic Locale: intergenic	[View on UCSC Genome Browser {Cornell Mirror}]

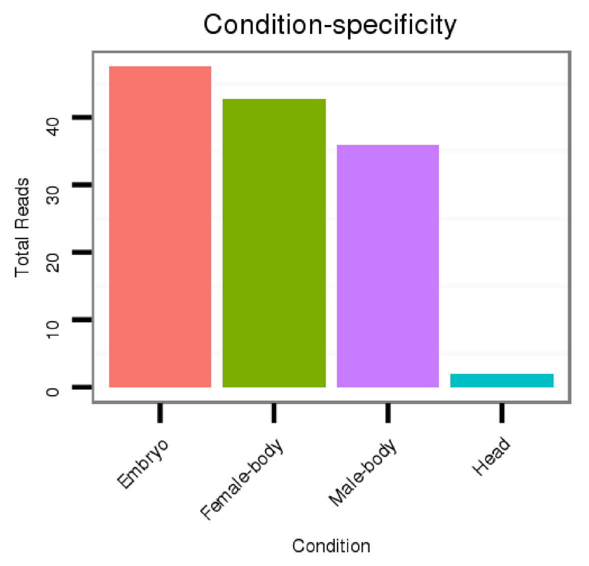
Legend: mature star mismatch in alignment mismatch in read

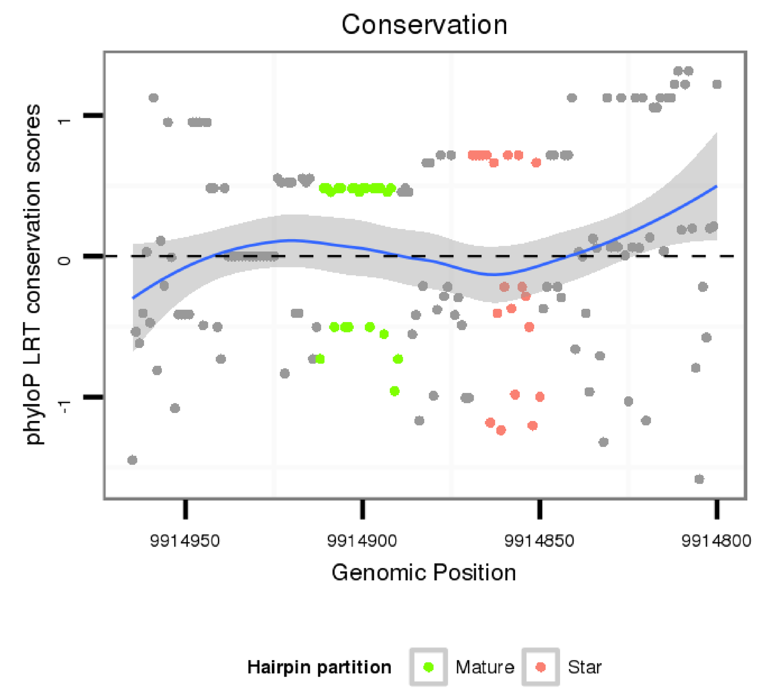
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
Homo6	DNA	hAT-Pegasus	+

mature	star
1. dmo_3141 scaffold_6473:8642796-8642818 +	1. dmo_3139 scaffold_6308:570088-570107 +
2. dmo_3142 scaffold_6473:8643620-8643642 -	2. dmo_3140 scaffold_6308:570824-570843 -
3. dmo_3138 scaffold_6473:8659793-8659815 +	3. dmo_3141 scaffold_6473:8642839-8642858 +
4. dmo_3143 scaffold_6473:8660822-8660844 -	4. dmo_3142 scaffold_6473:8643580-8643599 -
5. dmo_3150 scaffold_6473:9914890-9914912 -	5. dmo_69 scaffold_6473:8659160-8659179 -
6. scaffold_6473:9917724-9917746 +	6. dmo_3144 scaffold_6473:8660595-8660614 -
7. dmo_3152 scaffold_6473:9919839-9919861 +	7. dmo_3145 scaffold_6473:9912692-9912711 -
8. dmo_3148 scaffold_6473:9927476-9927498 +	8. dmo_3149 scaffold_6473:9914072-9914091 +
9. scaffold_6473:9933776-9933798 +	9. dmo_3150 scaffold_6473:9914850-9914869 -
10. scaffold_6473:9934446-9934468 -	10. dmo_3151 scaffold_6473:9918530-9918549 -
11. dmo_3147 scaffold_6473:9937954-9937976 +	11. dmo_3152 scaffold_6473:9919882-9919901 +
12. scaffold_6473:9938818-9938840 -	12. dmo_3148 scaffold_6473:9927519-9927538 +
13. dmo_3146 scaffold_6473:9971832-9971854 -	13. dmo_3147 scaffold_6473:9937997-9938016 +
14. dmo_3132 scaffold_6473:10161098-10161120 +	14. dmo_3146 scaffold_6473:9971792-9971811 -
15. dmo_3133 scaffold_6473:10162165-10162187 -	15. dmo_68 scaffold_6473:10161327-10161346 +
16. dmo_3134 scaffold_6473:10167212-10167234 +	16. dmo_3133 scaffold_6473:10162125-10162144 -
17. dmo_3136 scaffold_6473:10168425-10168447 -	17. dmo_3135 scaffold_6473:10167441-10167460 +
18. scaffold_6473:10193224-10193246 +	18. dmo_3137 scaffold_6473:10168232-10168251 -
	19. dmo_3153 scaffold_6473:10193453-10193472 +

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATGAATTTGGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGATTTTTGGTTATTTCATCTTTAGTCGGAGTTCTGGTAAGTAAGCCGATAAAGGTGAAATAACCACTAAAATCAATCAATAAACTAGTGACAGAGAGTGCTCTAGTAGAGACTGCTC *************************************...........((((((((((((((((((((((.((((....((....))....))))))))))))))))))))))..))))))........***************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
TTTGGTTATTTCATCTTTAGTCG	23	0	18	70.28	1265	258	545	378	69	11	4
TTGGTTATTTCATCTTTAGTCGG	23	0	19	13.16	250	97	37	103	10	2	1
TTTGGTTATTTCATCTTTAGTC	22	0	18	8.50	153	93	19	33	3	4	1
TTTGGTTATTTCATCTTTAGTCGG	24	0	18	8.44	152	82	14	48	7	0	1
TTGGTTATTTCATCTTTAGTCG	22	0	19	5.47	104	8	65	26	3	1	1
TTTTGGTTATTTCATCTTTAGTCG	24	0	18	5.17	93	17	35	34	4	3	0
ATAAAGGTGAAATAACCACT	20	0	19	3.42	65	61	2	0	2	0	0
TTTGGTTATTTCATCTTTAGT	21	0	18	3.11	56	21	14	16	1	4	0
TGGTTATTTCATCTTTAGTCG	21	0	20	1.50	30	0	24	0	6	0	0
GATAAAGGTGAAATAACCACT	21	0	18	1.11	20	17	2	0	1	0	0
TGGTTATTTCATCTTTAGTCGGA	23	0	20	1.10	22	21	0	0	1	0	0
TTGGTTATTTCATCTTTAGTCGGT	24	1	19	1.05	20	13	2	4	0	1	0
TTTTGGTTATTTCATCTTTAGTC	23	0	18	1.00	18	13	1	4	0	0	0
ATAAAGGTGAAATAACCACC	20	1	19	0.95	18	18	0	0	0	0	0
TTTGGTTATTTCATCTTTAGTCGGC	25	1	18	0.89	16	2	0	14	0	0	0
TTGGTTATTTCATCTTTAGTCGGC	24	1	19	0.84	16	2	4	10	0	0	0
TGGTTATTTCATCTTTAGTCGG	22	0	20	0.70	14	14	0	0	0	0	0
TTTGGTTATTTCATCTTTAGTCGA	24	1	18	0.67	12	7	5	0	0	0	0
TTTTTGGTTATTTCATCTTTAGTCG	25	0	18	0.61	11	3	3	5	0	0	0
TTTGGTTATTTCATCTTTAGTCA	23	1	18	0.56	10	3	4	2	1	0	0
GAGTTCTGGTAAGTAAGCCG	20	0	4	0.50	2	2	0	0	0	0	0
TTGGTTATTTCATCTTTAGTC	21	0	19	0.47	9	6	2	1	0	0	0
TTTGGTTATTTCATCTTTAGTCGC	24	1	18	0.44	8	2	1	5	0	0	0
TTTGGTTATTTCATCTTTAGTCGT	24	1	18	0.39	7	1	1	5	0	0	0
GTTATTTCATCTTTAGTCGGA	21	0	20	0.35	7	7	0	0	0	0	0
TTTGGTTATTTCATCTTTAGTCT	23	1	18	0.33	6	1	0	1	3	1	0
GATAAAGGTGAAATAACCACTA	22	0	18	0.28	5	4	0	0	0	1	0
TTTGGTTATTTCATCTTTAGTCAA	24	2	18	0.28	5	0	5	0	0	0	0
TTTGGTTATTTCATCTTTAGC	21	1	18	0.28	5	5	0	0	0	0	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
GAGTTCTGGTAAGTAAGCC	19	0	4	0.25	1	1	0	0	0	0	0
TTTTTGGTTATTTCATCTTTAGTC	24	0	18	0.22	4	3	1	0	0	0	0
GATAAAGGTGAAATAACCACC	21	1	18	0.22	4	4	0	0	0	0	0
TTTTGGTTATTTCATCTTTAGT	22	0	18	0.22	4	0	1	2	0	1	0
ATAAAGGTGAAATAACCACTA	21	0	19	0.21	4	4	0	0	0	0	0
TTATTTCATCTTTAGTCGGAGTTC	24	0	10	0.20	2	2	0	0	0	0	0
TTTGGTTATTTCATCTTTAG	20	0	18	0.17	3	2	1	0	0	0	0
CGATAAAGGTGAAATAACCACC	22	1	18	0.17	3	3	0	0	0	0	0
TTTGGTTATTTCATCTTTAGTCC	23	1	18	0.17	3	2	0	0	0	1	0
TTTTGGTTATTTCATCTTTAG	21	0	18	0.17	3	0	3	0	0	0	0
GTTATTTCATCTTTAGTCG	19	0	20	0.15	3	2	1	0	0	0	0
CCGATAAAGGTGAAATAACCA	21	0	20	0.15	3	2	1	0	0	0	0
TTTTGGTTATTTCATCTTTAGTCGG	25	0	18	0.11	2	2	0	0	0	0	0
TTGGTTATTTCATCTTTAGTCGGAA	25	1	18	0.11	2	1	0	1	0	0	0
TTTTTGGTTATTTCATCTTTAGT	23	0	18	0.11	2	1	1	0	0	0	0
TTTGGTTATTTCATCTTTAGTT	22	1	18	0.11	2	2	0	0	0	0	0
CCGATAAAGGTGAAATAACCAC	22	0	18	0.11	2	2	0	0	0	0	0
TTTGGTTATTTCATCTTTAGTCGGT	25	1	18	0.11	2	0	1	1	0	0	0
TTGGTTATTTCATCTTTAGTCGGTC	25	2	19	0.11	2	1	0	1	0	0	0
ATAAAGGTGAAATAACCACTT	21	1	19	0.11	2	1	0	0	1	0	0
TTGGTTATTTCATCTTTAGTCGA	23	1	19	0.11	2	2	0	0	0	0	0
TTGGTTATTTCATCTTTAGT	20	0	19	0.11	2	0	1	1	0	0	0
ATTTTTGGTTATTTCATCTTTAG	23	0	15	0.07	1	0	1	0	0	0	0
ATTTTTGGTTATTTCATCTTT	21	0	15	0.07	1	0	1	0	0	0	0
CGATAAAGGTGAAATAACCACA	22	1	18	0.06	1	0	1	0	0	0	0
TTGGTTATTTCATCTTTAGTCGGA	24	0	18	0.06	1	0	0	1	0	0	0
TTTGGTTATTTCATCTTTAGTCGTC	25	2	18	0.06	1	1	0	0	0	0	0
TTTGGTTATTTCATCTTTAGTA	22	1	18	0.06	1	1	0	0	0	0	0
CATCCACATTTCCAGTAGGGC	21	0	18	0.06	1	0	0	1	0	0	0
TTTTGGTTATTTCATCTTTAGTCT	24	1	18	0.06	1	0	1	0	0	0	0
TTTTGGTTATTTCATCTTTAGTCGC	25	1	18	0.06	1	1	0	0	0	0	0
TTTTGGTTATTTCATCTTTAGTCA	24	1	18	0.06	1	1	0	0	0	0	0
TTTTTGGTTATTTCATCTTTAGTCC	25	1	18	0.06	1	0	1	0	0	0	0
TTTTTGGTTATTTCATCTTTAGTCGA	26	1	18	0.06	1	0	0	1	0	0	0
TTTTGGTTATTTCATCTTTAGTCGT	25	1	18	0.06	1	0	0	1	0	0	0
TTTTGGTTATTTCATCTTTAGTCGA	25	1	18	0.06	1	1	0	0	0	0	0
GATAAAGGTGAAATAACCAC	20	0	18	0.06	1	1	0	0	0	0	0
TTTGGTTATTTCATCTTTAGTCGGA	25	0	18	0.06	1	1	0	0	0	0	0
TTTTTGGTTATTTCATCTTTA	21	0	18	0.06	1	0	1	0	0	0	0
TTTGGTTATTTCATCTTTAGTCGGAG	26	0	18	0.06	1	0	0	1	0	0	0
GATAAAGGTGAAATAACCACTAAC	24	1	18	0.06	1	1	0	0	0	0	0
TTTGGTTATTTCATCTTTAGTG	22	1	18	0.06	1	1	0	0	0	0	0
TTTTGGTTATTTCATCTTTAGC	22	1	18	0.06	1	1	0	0	0	0	0
TTTGGTTATTTCATCTTTAGTCTT	24	2	18	0.06	1	1	0	0	0	0	0
TTGGTTATTTCATCTTTAGTCAA	23	2	19	0.05	1	0	1	0	0	0	0
TTGGTTATTTCATCTTTAGTCGT	23	1	19	0.05	1	0	0	0	1	0	0
ATAAAGGTGAAATAACCACTGT	22	2	19	0.05	1	0	0	1	0	0	0
TTGGTTATTTCATCTTTAGTCGGTAA	26	3	19	0.05	1	0	1	0	0	0	0
AAAGGTGAAATAACCACT	18	0	19	0.05	1	1	0	0	0	0	0
ATAAAGGTGAAATAACCACTTT	22	2	19	0.05	1	1	0	0	0	0	0
TTGGTTATTTCATCTTTAGTCA	22	1	19	0.05	1	0	1	0	0	0	0
TTGGTTATTTCATCTTTAGTCGC	23	1	19	0.05	1	1	0	0	0	0	0
TTGGTTATTTCATCTTTAGC	20	1	20	0.05	1	1	0	0	0	0	0
GGTTATTTCATCTTTAGTCGG	21	0	20	0.05	1	0	0	0	0	0	1
GGTTATTTCATCTTTAGTCG	20	0	20	0.05	1	0	1	0	0	0	0
TTATTTCATCTTTAGTCGGA	20	0	20	0.05	1	1	0	0	0	0	0
GTTATTTCATCTTTAGTCGGC	21	1	20	0.05	1	1	0	0	0	0	0
TTATTTCATCTTTAGTCG	18	0	20	0.05	1	1	0	0	0	0	0
CGATAAAGGTGAAATAACCC	20	1	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

TACTTAAACCTTGTTTATTATTTATGTAGGTGTAAAGGTCATCCCGTATCTAAAAACCAATAAAGTAGAAATCAGCCTCAAGACCATTCATTCGGCTATTTCCACTTTATTGGTGATTTTAGTTAGTTATTTGATCACTGTCTCTCACGAGATCATCTCTGACGAG **********************************...........((((((((((((((((((((((.((((....((....))....))))))))))))))))))))))..))))))........************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body
AGGTCATCCCGTATCTAAAAACCAATA	27	0	14	0.07	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:9914800-9914965 -	dmo_3150	ATGAATTTGGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGA--TTTTTGGTTATTTCATCTTTAGTCGGAGTTCTG----GT-----AAGTAAGCCGATAAA-----------------GGTGAAATAACCACTAAAATCAATCAATAAACTAGTGACAGAGAGTGCTCTAGTAGAGACTGCTC
droVir3	scaffold_12963:13251043-13251230 +		GCGTATTGGGAAGGGGCAATTAATGAA--TTTCATTTGTTACAGCGCACTGTGCGGCGTTGATTGCTTCATTTTTGTGTGAGAATTGAGTGGA-----AAATATGAATATAAAATTGTGAAAATATTTATTG-CAAGCAGTTGCGGGAATCAATAACAGAAACAACAAGTAAAACTGCTCTAGTCGAAAATCTAC
droGri2	scaffold_15203:2504162-2504310 -		CACTTATTGA------------------------------AGCGCGCAGATTTATTGGAATTTAAAATTCCTTTGTTAGTCACCAGAGT-------------------------TGCG----GCTCTCCCAGAAATCTAATAAA-----------------CGCTTAAAAGC-CCAAGAAAAAATATAATAAAGAACAAGCAAGAAATGCTCTAGTCGAGCGAGCTC
droWil2	scf2_1100000004822:2917340-2917341 -		AT---
droRho1	scf7180000779710:5209-5273 -		ACAAAGTAAAATTAAATAATAA--TA--------------------------TTAATTTCCAAACAAGAAAGAACGCTATAGTCGAGTG-CCTC
droSim2	x:5708406-5708407 -		TC---
droYak3	X:18008264-18008276 -		A---GTCGAGCT-CCTC

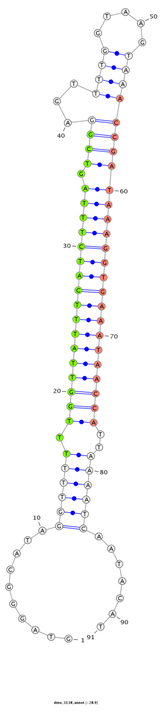
Generated: 09/08/2015 at 07:42 PM

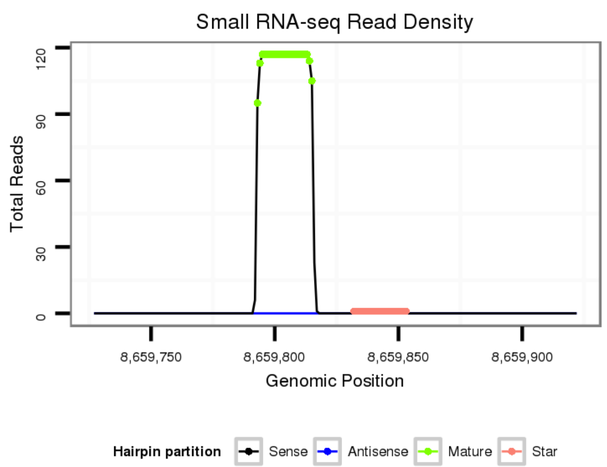
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

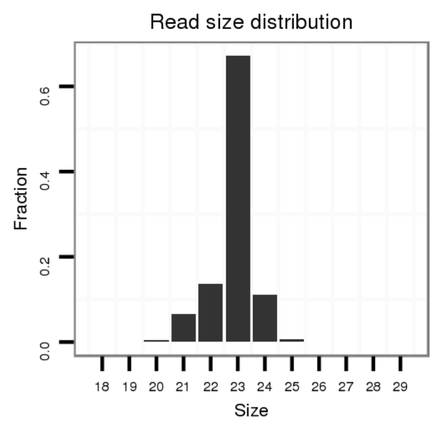
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3138	**scaffold_6473:8659777-8659872 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

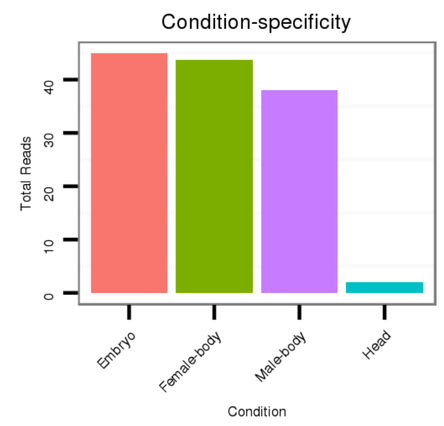
Legend: mature star **mismatch in alignment** mismatch in read

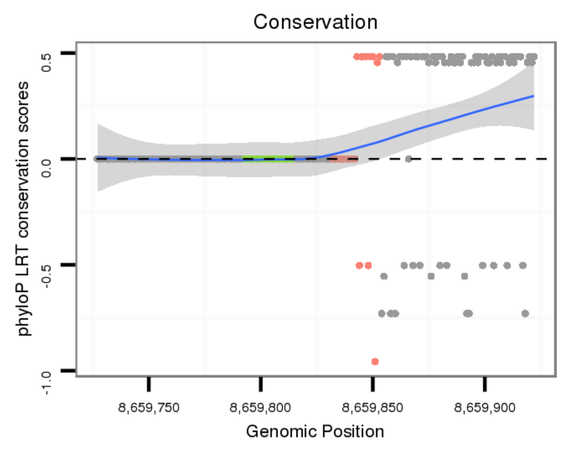
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dmo_3141 scaffold_6473:8642796-8642818 + 2. dmo_3142 scaffold_6473:8643620-8643642 - 3. dmo_3138 scaffold_6473:8659793-8659815 + 4. dmo_3143 scaffold_6473:8660822-8660844 - 5. dmo_3150 scaffold_6473:9914890-9914912 - 6. scaffold_6473:9917724-9917746 + 7. dmo_3152 scaffold_6473:9919839-9919861 + 8. dmo_3148 scaffold_6473:9927476-9927498 + 9. scaffold_6473:9933776-9933798 + 10. scaffold_6473:9934446-9934468 - 11. dmo_3147 scaffold_6473:9937954-9937976 + 12. scaffold_6473:9938818-9938840 - 13. dmo_3146 scaffold_6473:9971832-9971854 - 14. dmo_3132 scaffold_6473:10161098-10161120 + 15. dmo_3133 scaffold_6473:10162165-10162187 - 16. dmo_3134 scaffold_6473:10167212-10167234 + 17. dmo_3136 scaffold_6473:10168425-10168447 - 18. scaffold_6473:10193224-10193246 +	1. dmo_3139 scaffold_6308:570084-570105 + 2. dmo_3141 scaffold_6473:8642835-8642856 + 3. dmo_3142 scaffold_6473:8643582-8643603 - 4. dmo_3138 scaffold_6473:8659832-8659853 + 5. dmo_3143 scaffold_6473:8660784-8660805 - 6. dmo_3149 scaffold_6473:9914068-9914089 + 7. scaffold_6473:9917763-9917784 + 8. dmo_3152 scaffold_6473:9919878-9919899 + 9. dmo_3148 scaffold_6473:9927515-9927536 + 10. scaffold_6473:9933815-9933836 + 11. scaffold_6473:9934408-9934429 - 12. dmo_3147 scaffold_6473:9937993-9938014 + 13. scaffold_6473:9938780-9938801 - 14. dmo_3146 scaffold_6473:9971794-9971815 - 15. dmo_3132 scaffold_6473:10161137-10161158 + 16. dmo_68 scaffold_6473:10161323-10161344 + 17. dmo_3133 scaffold_6473:10162127-10162148 - 18. dmo_3134 scaffold_6473:10167251-10167272 + 19. dmo_3135 scaffold_6473:10167437-10167458 + 20. scaffold_6473:10193263-10193284 + 21. dmo_3140 scaffold_6308:570826-570847 - 22. dmo_69 scaffold_6473:8659162-8659183 - 23. dmo_3144 scaffold_6473:8660597-8660618 - 24. dmo_3137 scaffold_6473:10168234-10168255 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AGCGACTCCTTCATTAATTTAGAAAAAATAATAAATACATCCACATTTCCAGTAGGGCATAGGTTTTTTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCATTAAAATCAATACATAAGAAACTAGTGAGGGTGCTCTAGGCGAGACTGCTCGACTAGCAGATACACTGT	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
**********.....(((((((.((((((((((((((((((.((((...((((.....))))))))))))))))))))))))))..)))))))..**********											
.....TTTGGTTATTTCATCTTTAGTCG.....	23	0	18	70.28	1265	258	545	378	69	11	4
.....TTGGTTATTTCATCTTTAGTCGG.....	23	0	19	13.16	250	97	37	103	10	2	1
.....TTTGGTTATTTCATCTTTAGTC.....	22	0	18	8.50	153	93	19	33	3	4	1
.....TTTGGTTATTTCATCTTTAGTCGG.....	24	0	18	8.44	152	82	14	48	7	0	1
.....TTGGTTATTTCATCTTTAGTCG.....	22	0	19	5.47	104	8	65	26	3	1	1
.....TTTTGGTTATTTCATCTTTAGTCG.....	24	0	18	5.17	93	17	35	34	4	3	0
.....TTTGGTTATTTCATCTTTAGT.....	21	0	18	3.11	56	21	14	16	1	4	0
.....TGGTTATTTCATCTTTAGTCG.....	21	0	20	2.70	54	2	24	21	6	1	0
.....TGGTTATTTCATCTTTAGTCGGA.....	23	0	20	1.40	28	21	1	5	1	0	0
.....TGGTTATTTCATCTTTAGTCGG.....	22	0	20	1.25	25	0	6	16	2	1	0
.....ACCGATAAAGGTGAAATAACCA.....	22	0	20	1.20	24	17	3	1	3	0	0
.....TTGGTTATTTCATCTTTAGTCGGT.....	24	1	19	1.05	20	13	2	4	0	1	0
.....TTTTGGTTATTTCATCTTTAGTC.....	23	0	18	1.00	18	13	1	4	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGC.....	25	1	18	0.89	16	2	0	14	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGC.....	24	1	19	0.84	16	2	4	10	0	0	0
.....ATAAAGGTGAAATAACCATTA.....	21	0	10	0.80	8	8	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGA.....	24	1	18	0.67	12	7	5	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCG.....	25	0	18	0.61	11	3	3	5	0	0	0
.....TTTGGTTATTTCATCTTTAGTCA.....	23	1	18	0.56	10	3	4	2	1	0	0
.....GATAAAGGTGAAATAACCATTA.....	22	0	10	0.50	5	3	2	0	0	0	0
.....ACCGATAAAGGTGAAATAACC.....	21	0	20	0.50	10	9	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTC.....	21	0	19	0.47	9	6	2	1	0	0	0
.....ACCGATAAAGGTGAAATAACCAT.....	23	0	9	0.44	4	3	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGC.....	24	1	18	0.44	8	2	1	5	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGT.....	24	1	18	0.39	7	1	1	5	0	0	0
.....GTTATTTCATCTTTAGTCGGA.....	21	0	20	0.35	7	7	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCT.....	23	1	18	0.33	6	1	0	1	3	1	0
.....TTATTTCATCTTTAGTCGGAGTTT.....	24	0	18	0.33	6	4	2	0	0	0	0
.....TTTGGTTATTTCATCTTTAGC.....	21	1	18	0.28	5	5	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCAA.....	24	2	18	0.28	5	0	5	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTC.....	24	0	18	0.22	4	3	1	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGT.....	22	0	18	0.22	4	0	1	2	0	1	0
.....GATAAAGGTGAAATAACCATT.....	21	0	10	0.20	2	1	1	0	0	0	0
.....CGATAAAGGTGAAATAACCATT.....	22	0	10	0.20	2	1	1	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
.....TTTTGGTTATTTCATCTTTAG.....	21	0	18	0.17	3	0	3	0	0	0	0
.....TTTGGTTATTTCATCTTTAG.....	20	0	18	0.17	3	2	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCC.....	23	1	18	0.17	3	2	0	0	0	1	0
.....TTATTTCATCTTTAGTCG.....	18	0	20	0.15	3	1	2	0	0	0	0
.....CCGATAAAGGTGAAATAACCA.....	21	0	20	0.15	3	2	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTT.....	22	1	18	0.11	2	2	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGG.....	25	0	18	0.11	2	2	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGAA.....	25	1	18	0.11	2	1	0	1	0	0	0
.....TTTTTGGTTATTTCATCTTTAGT.....	23	0	18	0.11	2	1	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGT.....	25	1	18	0.11	2	0	1	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGTC.....	25	2	19	0.11	2	1	0	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCGA.....	23	1	19	0.11	2	2	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGT.....	20	0	19	0.11	2	0	1	1	0	0	0
.....GATAAAGGTGAAATAACCATTT.....	22	1	10	0.10	1	1	0	0	0	0	0
.....ATAAAGGTGAAATAACCATTAAAA.....	24	0	10	0.10	1	1	0	0	0	0	0
.....ATAAAGGTGAAATAACCATT.....	20	0	10	0.10	1	1	0	0	0	0	0
.....AAACCGATAAAGGTGAAATAAC.....	22	0	20	0.10	2	2	0	0	0	0	0
.....TATTTCATCTTTAGTCGGAGTT.....	22	0	20	0.10	2	2	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGC.....	25	1	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGA.....	25	0	18	0.06	1	1	0	0	0	0	0
.....CATCCACATTTCCAGTAGGGC.....	21	0	18	0.06	1	0	0	1	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCGA.....	26	1	18	0.06	1	0	0	1	0	0	0
.....GAGTTTTGGTAAGTAAACCG.....	20	0	18	0.06	1	1	0	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCC.....	25	1	18	0.06	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGA.....	24	0	18	0.06	1	0	0	1	0	0	0
.....TTTGGTTATTTCATCTTTAGTCG.....	22	1	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGTC.....	25	2	18	0.06	1	1	0	0	0	0	0
.....TTTTTGGTTATTTCATCTTTA.....	21	0	18	0.06	1	0	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGAG.....	26	0	18	0.06	1	0	0	1	0	0	0
.....TTTGGTTATTTCATCTTTAGTA.....	22	1	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCT.....	24	1	18	0.06	1	0	1	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTTTTGGTA.....	29	0	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCA.....	24	1	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGC.....	22	1	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGT.....	25	1	18	0.06	1	0	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCTT.....	24	2	18	0.06	1	1	0	0	0	0	0
.....ATTTCATCTTTAGTCGGAGTTT.....	22	0	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGA.....	25	1	18	0.06	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGTAA.....	26	3	19	0.05	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGT.....	23	1	19	0.05	1	0	0	0	1	0	0
.....TTGGTTATTTCATCTTTAGTCA.....	22	1	19	0.05	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCAA.....	23	2	19	0.05	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGC.....	23	1	19	0.05	1	1	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTT.....	23	0	20	0.05	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGAA.....	22	1	20	0.05	1	1	0	0	0	0	0
.....CGATAAAGGTGAAATAACCC.....	20	1	20	0.05	1	1	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTCGGT.....	23	1	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCG.....	20	0	20	0.05	1	0	1	0	0	0	0
.....GGTTATTTCATCTTTAGTCGGC.....	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
.....TTGGTTATTTCATCTTTAGC.....	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

Anti-sense strand reads

TCGCTGAGGAAGTAATTAAATCTTTTTTATTATTTATGTAGGTGTAAAGGTCATCCCGTATCCAAAAAACCAATAAAGTAGAAATCAGCCTCAAAACCATTCATTTGGCTATTTCCACTTTATTGGTAATTTTAGTTATGTATTCTTTGATCACTCCCACGAGATCCGCTCTGACGAGCTGATCGTCTATGTGACA	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_6473:8659727-8659922 +	dmo_3138	AGCGACTCCTTCATTAATTTAGAAAAAATAATAAATACATCCACATTTCCAGTAGGGCATAGGTTTTTTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCATTAAAATCAATACATAAGAAACTAGTGAGGGTGCTCTAGGCGAGACTGCTCGACTAGCAGATACACTGT
droVir3	scaffold_13047:13837445-13837523 +		----------TAAACAAGCAGAAACACCAACAC-ACAAAAAACAAGTAAGAGTGCTCTTTCGAGATTGCTTGACTAACAGATANCCTGT

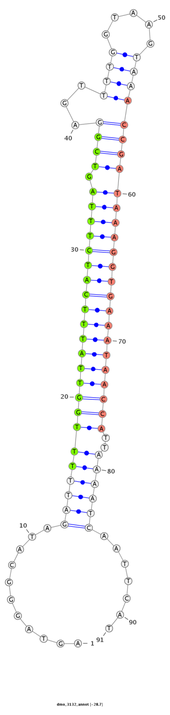
Generated: 09/08/2015 at 07:53 PM

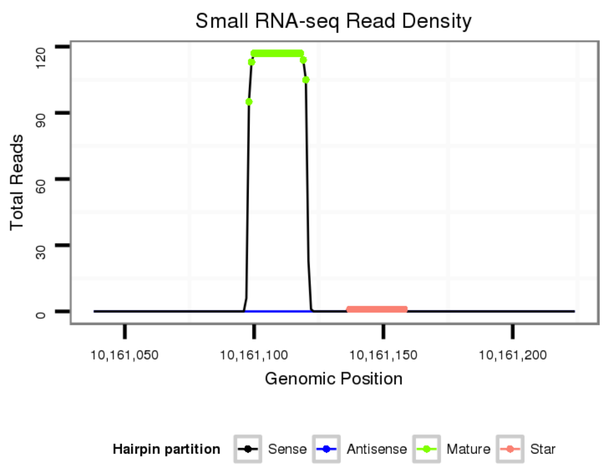
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

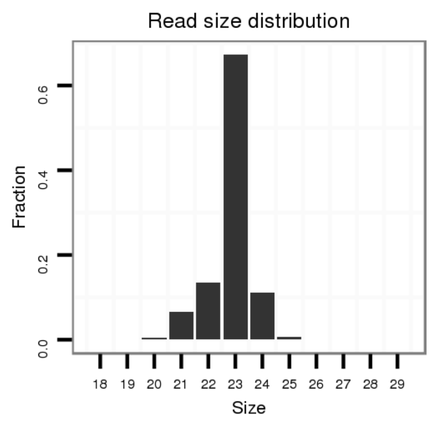
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3132	**scaffold_6473:10161088-10161174 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

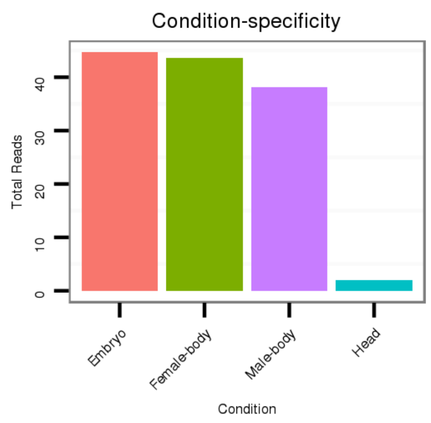
Legend: mature star **mismatch in alignment** mismatch in read

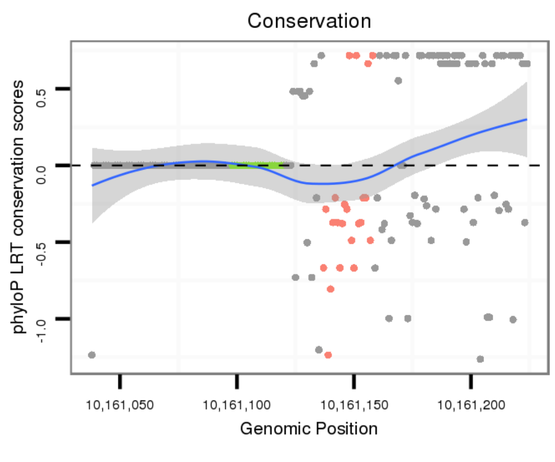
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI15760-in]

Repeatable elements

Name	Class	Family	Strand
Homo6	DNA	hAT-Pegasus	-

mature

1. dmo_3141 scaffold_6473:8642796-8642818 +
2. dmo_3142 scaffold_6473:8643620-8643642 -
3. dmo_3138 scaffold_6473:8659793-8659815 +
4. dmo_3143 scaffold_6473:8660822-8660844 -
5. dmo_3150 scaffold_6473:9914890-9914912 -
6. scaffold_6473:9917724-9917746 +
7. dmo_3152 scaffold_6473:9919839-9919861 +
8. dmo_3148 scaffold_6473:9927476-9927498 +
9. scaffold_6473:9933776-9933798 +
10. scaffold_6473:9934446-9934468 -
11. dmo_3147 scaffold_6473:9937954-9937976 +
12. scaffold_6473:9938818-9938840 -
13. dmo_3146 scaffold_6473:9971832-9971854 -
14. dmo_3132 scaffold_6473:10161098-10161120 +
15. dmo_3133 scaffold_6473:10162165-10162187 -
16. dmo_3134 scaffold_6473:10167212-10167234 +
17. dmo_3136 scaffold_6473:10168425-10168447 -
18. scaffold_6473:10193224-10193246 +

star

1. dmo_3139 scaffold_6308:570084-570105 +
2. dmo_3141 scaffold_6473:8642835-8642856 +
3. dmo_3142 scaffold_6473:8643582-8643603 -
4. dmo_3138 scaffold_6473:8659832-8659853 +
5. dmo_3143 scaffold_6473:8660784-8660805 -
6. dmo_3149 scaffold_6473:9914068-9914089 +
7. scaffold_6473:9917763-9917784 +
8. dmo_3152 scaffold_6473:9919878-9919899 +
9. dmo_3148 scaffold_6473:9927515-9927536 +
10. scaffold_6473:9933815-9933836 +
11. scaffold_6473:9934408-9934429 -
12. dmo_3147 scaffold_6473:9937993-9938014 +
13. scaffold_6473:9938780-9938801 -
14. dmo_3146 scaffold_6473:9971794-9971815 -
15. dmo_3132 scaffold_6473:10161137-10161158 +
16. dmo_68 scaffold_6473:10161323-10161344 +
17. dmo_3133 scaffold_6473:10162127-10162148 -
18. dmo_3134 scaffold_6473:10167251-10167272 +
19. dmo_3135 scaffold_6473:10167437-10167458 +
20. scaffold_6473:10193263-10193284 +
21. dmo_3140 scaffold_6308:570826-570847 -
22. dmo_69 scaffold_6473:8659162-8659183 -
23. dmo_3144 scaffold_6473:8660597-8660618 -
24. dmo_3137 scaffold_6473:10168234-10168255 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	female body	V110 male body	V041 embryo	V056 head	V049 head
CTTCTTAATGAATTTTGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGATTTTTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCATTAAAATCAATTCATAAGAAATTAGTGAGAGTGCTCTAGGCGAGACTGTTCGACTAGCAGATACTC												
..........(((((((((((((((((((((((.((((...((((.....))))))))))))))))))))))))..))))))).......*												
.....TTTGGTTATTTCATCTTTAGTCG.....	23	0	18	70.28	1265	258	545	378	69	11	4
.....TTGGTTATTTCATCTTTAGTCGG.....	23	0	19	13.16	250	97	37	103	10	2	1
.....TTTGGTTATTTCATCTTTAGTC.....	22	0	18	8.50	153	93	19	33	3	4	1
.....TTTGGTTATTTCATCTTTAGTCGG.....	24	0	18	8.44	152	82	14	48	7	0	1
.....TTGGTTATTTCATCTTTAGTCG.....	22	0	19	5.47	104	8	65	26	3	1	1
.....TTTTGGTTATTTCATCTTTAGTCG.....	24	0	18	5.17	93	17	35	34	4	3	0
.....TTTGGTTATTTCATCTTTAGT.....	21	0	18	3.11	56	21	14	16	1	4	0
.....TGGTTATTTCATCTTTAGTCG.....	21	0	20	2.70	54	2	24	21	6	1	0
.....TGGTTATTTCATCTTTAGTCGGA.....	23	0	20	1.35	27	21	1	5	0	0	0
.....TGGTTATTTCATCTTTAGTCGG.....	22	0	20	1.25	25	0	6	16	2	1	0
.....TTGGTTATTTCATCTTTAGTCGGT.....	24	1	19	1.05	20	13	2	4	0	1	0
.....ACCGATAAAGGTGAAATAACCA.....	22	0	20	1.05	21	17	3	1	0	0	0
.....TTTTGGTTATTTCATCTTTAGTC.....	23	0	18	1.00	18	13	1	4	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGC.....	25	1	18	0.89	16	2	0	14	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGG.....	24	1	19	0.84	16	2	4	10	0	0	0
.....ATAAAGGTGAAATAACCATTA.....	21	0	10	0.80	8	8	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGA.....	24	1	18	0.67	12	7	5	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCG.....	25	0	18	0.61	11	3	3	5	0	0	0
.....TTTGGTTATTTCATCTTTAGTCA.....	23	1	18	0.56	10	3	4	2	1	0	0
.....GATAAAGGTGAAATAACCATTA.....	22	0	10	0.50	5	3	2	0	0	0	0
.....ACCGATAAAGGTGAAATAACC.....	21	0	20	0.50	10	9	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTC.....	21	0	19	0.47	9	6	2	1	0	0	0
.....ACCGATAAAGGTGAAATAACCAT.....	23	0	9	0.44	4	3	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGC.....	24	1	18	0.44	8	2	1	5	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGT.....	24	1	18	0.39	7	1	1	5	0	0	0
.....GTTATTTCATCTTTAGTCGGA.....	21	0	20	0.35	7	7	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTTT.....	24	0	18	0.33	6	4	2	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCT.....	23	1	18	0.33	6	1	0	1	3	1	0
.....TTTGGTTATTTCATCTTTAGTCAA.....	24	2	18	0.28	5	0	5	0	0	0	0
.....TTTGGTTATTTCATCTTTAGC.....	21	1	18	0.28	5	5	0	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTC.....	24	0	18	0.22	4	3	1	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGT.....	22	0	18	0.22	4	0	1	2	0	1	0
.....CGATAAAGGTGAAATAACCATT.....	22	0	10	0.20	2	1	1	0	0	0	0
.....GATAAAGGTGAAATAACCATT.....	21	0	10	0.20	2	1	1	0	0	0	0
.....ACCGATAAAGGTGAAATAACCG.....	22	1	20	0.20	4	4	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCC.....	23	1	18	0.17	3	2	0	0	0	1	0
.....TTTGGTTATTTCATCTTTAG.....	20	0	18	0.17	3	2	1	0	0	0	0
.....TTTTGGTTATTTCATCTTTAG.....	21	0	18	0.17	3	0	3	0	0	0	0
.....GTTATTTCATCTTTAGTCG.....	19	0	20	0.15	3	2	0	1	0	0	0
.....TTATTTCATCTTTAGTCG.....	18	0	20	0.15	3	1	2	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGG.....	25	0	18	0.11	2	2	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGT.....	25	1	18	0.11	2	0	1	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGAA.....	25	1	18	0.11	2	1	0	1	0	0	0
.....TTTTTGGTTATTTCATCTTTAGT.....	23	0	18	0.11	2	1	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTT.....	22	1	18	0.11	2	2	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGTC.....	25	2	19	0.11	2	1	0	1	0	0	0
.....TTGGTTATTTCATCTTTAGTCGA.....	23	1	19	0.11	2	2	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGT.....	20	0	19	0.11	2	0	1	1	0	0	0
.....GATAAAGGTGAAATAACCATTT.....	22	1	10	0.10	1	1	0	0	0	0	0
.....ATAAAGGTGAAATAACCATT.....	20	0	10	0.10	1	1	0	0	0	0	0
.....ATAAAGGTGAAATAACCATTAAAA.....	24	0	10	0.10	1	1	0	0	0	0	0
.....AAACCGATAAAGGTGAAATAAC.....	22	0	20	0.10	2	2	0	0	0	0	0
.....TATTTCATCTTTAGTCGGAGTT.....	22	0	20	0.10	2	2	0	0	0	0	0
.....ATTTTTGGTTATTTCATCTTT.....	21	0	15	0.07	1	0	1	0	0	0	0
.....ATTTTTGGTTATTTCATCTTTAG.....	23	0	15	0.07	1	0	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCTT.....	24	2	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGT.....	25	1	18	0.06	1	0	0	1	0	0	0
.....TTATTTCATCTTTAGTCGGAGTTTTGGTA.....	29	0	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGG.....	25	1	18	0.06	1	1	0	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGC.....	22	1	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTA.....	22	1	18	0.06	1	1	0	0	0	0	0
.....TTTTTGGTTATTTCATCTTTAGTCC.....	25	1	18	0.06	1	0	1	0	0	0	0
.....CATCCACATTTCCAGTAGGGC.....	21	0	18	0.06	1	0	0	1	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCA.....	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
.....TTTTTGGTTATTTCATCTTTAGTCGA.....	26	1	18	0.06	1	0	0	1	0	0	0
.....TTTGGTTATTTCATCTTTAGTG.....	22	1	18	0.06	1	1	0	0	0	0	0
.....TTTTTGGTTATTTCATCTTTA.....	21	0	18	0.06	1	0	1	0	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCGA.....	25	1	18	0.06	1	1	0	0	0	0	0
.....ATTTCATCTTTAGTCGGAGTTT.....	22	0	18	0.06	1	1	0	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGA.....	25	0	18	0.06	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGGA.....	24	0	18	0.06	1	0	0	1	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGGAG.....	26	0	18	0.06	1	0	0	1	0	0	0
.....TTTTGGTTATTTCATCTTTAGTCT.....	24	1	18	0.06	1	0	1	0	0	0	0
.....TTTGGTTATTTCATCTTTAGTCGTC.....	25	2	18	0.06	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCA.....	22	1	19	0.05	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGT.....	23	1	19	0.05	1	0	0	0	1	0	0
.....TTGGTTATTTCATCTTTAGTCGGTAA.....	26	3	19	0.05	1	0	1	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCGG.....	23	1	19	0.05	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGTCAA.....	23	2	19	0.05	1	0	1	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTT.....	23	0	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCGG.....	21	0	20	0.05	1	0	0	0	0	0	1
.....TTATTTCATCTTTAGTCGGA.....	20	0	20	0.05	1	1	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTC.....	20	0	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCGGC.....	22	1	20	0.05	1	1	0	0	0	0	0
.....CGATAAAGGTGAAATAACCC.....	20	1	20	0.05	1	1	0	0	0	0	0
.....TTGGTTATTTCATCTTTAGC.....	20	1	20	0.05	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGA.....	22	1	20	0.05	1	1	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTCGGT.....	23	1	20	0.05	1	1	0	0	0	0	0
.....CCGATAAAGGTGAAATAACCA.....	21	0	20	0.05	1	0	1	0	0	0	0

Anti-sense strand reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo
GAAGAATTACTTAAAACTTGTTTATTATTTATGTAGGTGTAAAGGTCATCCCGTATCTAAAAACCAATAAAGTAGAAATCAGCCTCAAAACCATTCATTTGGCTATTTCCACTTTATTGGTAATTTTAGTTAAGTATTCTTTAATCACTCTCACGAGATCCGCTCTGACAAGCTGATCGTCTATGAG							
..........(((((((((((((((((((((((.((((...((((.....))))))))))))))))))))))))..))))))).......*							
.....AGGTCATCCCGTATCTAAAAACCAATA.....	27	0	14	0.07	1	1	0
.....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_6473:10161038-10161224 +	dmo_3132	CTTCTTAATGAATTTTGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGATTTTTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAAC--CATTAAAATCAATTCATAAGAAATTAGTGAGAGTGCTCTAGGCGAGACTGTTCGACTAGCAGATACTC
droVir3	scaffold_13047:3094110-3094208 +		G----------TGTTGGCACGTCACTGCGTGCAATGCAACAAC--AAGTATAAGAAA---ACCCGAAACAAGTAAGAGTGCTCTAATCGGAGTGAACGACTAATATATACCC
droGri2	scaffold_15110:20278068-20278160 -		A----------GCCAACAGACAACAGTCAACTGGCAGCATCAACAACAAT--AACAACAACAACTGAGAGTGCTCTAGTCGAGGTTGCCCAAATAACAAATACTC

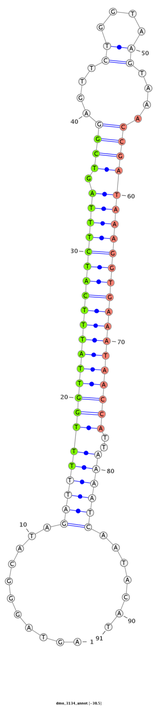
Generated: 09/08/2015 at 07:54 PM

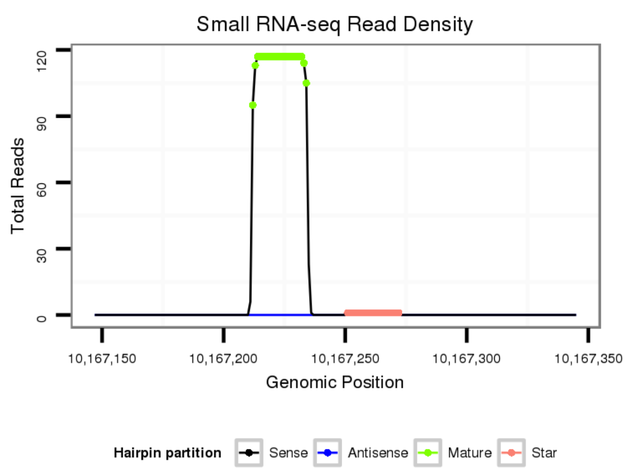
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

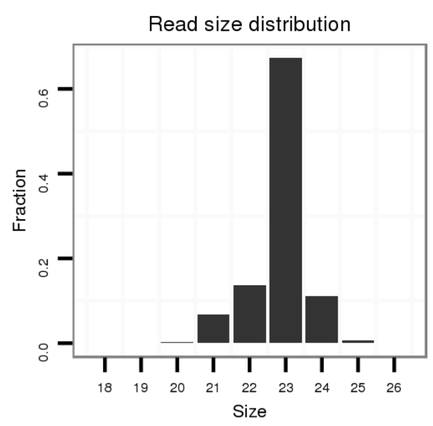
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3134	**scaffold_6473:10167197-10167295 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

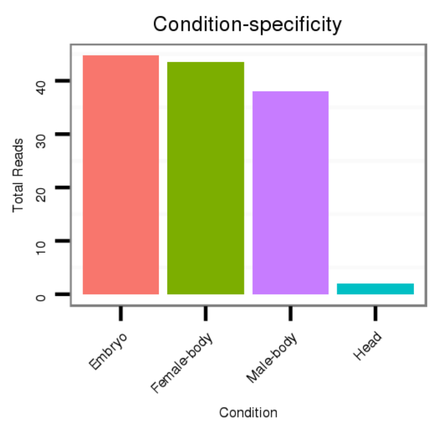
Legend: mature star **mismatch in alignment** mismatch in read

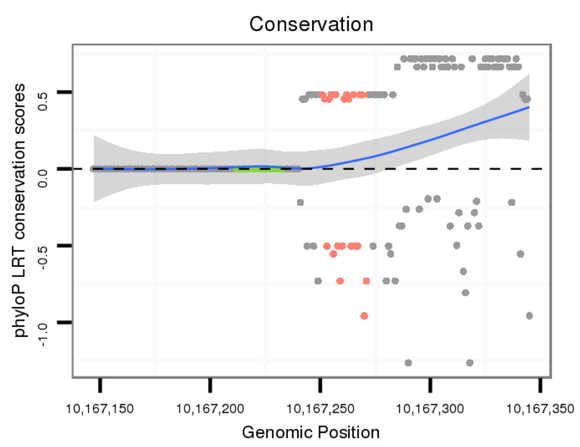
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI15760-in]

Repeatable elements

Name	Class	Family	Strand
Homo6	DNA	hAT-Pegasus	-

mature

1. dmo_3141 scaffold_6473:8642796-8642818 +
2. dmo_3142 scaffold_6473:8643620-8643642 -
3. dmo_3138 scaffold_6473:8659793-8659815 +
4. dmo_3143 scaffold_6473:8660822-8660844 -
5. dmo_3150 scaffold_6473:9914890-9914912 -
6. scaffold_6473:9917724-9917746 +
7. dmo_3152 scaffold_6473:9919839-9919861 +
8. dmo_3148 scaffold_6473:9927476-9927498 +
9. scaffold_6473:9933776-9933798 +
10. scaffold_6473:9934446-9934468 -
11. dmo_3147 scaffold_6473:9937954-9937976 +
12. scaffold_6473:9938818-9938840 -
13. dmo_3146 scaffold_6473:9971832-9971854 -
14. dmo_3132 scaffold_6473:10161098-10161120 +
15. dmo_3133 scaffold_6473:10162165-10162187 -
16. dmo_3134 scaffold_6473:10167212-10167234 +
17. dmo_3136 scaffold_6473:10168425-10168447 -
18. scaffold_6473:10193224-10193246 +

star

1. dmo_3139 scaffold_6308:570084-570105 +
2. dmo_3141 scaffold_6473:8642835-8642856 +
3. dmo_3142 scaffold_6473:8643582-8643603 -
4. dmo_3138 scaffold_6473:8659832-8659853 +
5. dmo_3143 scaffold_6473:8660784-8660805 -
6. dmo_3149 scaffold_6473:9914068-9914089 +
7. scaffold_6473:9917763-9917784 +
8. dmo_3152 scaffold_6473:9919878-9919899 +
9. dmo_3148 scaffold_6473:9927515-9927536 +
10. scaffold_6473:9933815-9933836 +
11. scaffold_6473:9934408-9934429 -
12. dmo_3147 scaffold_6473:9937993-9938014 +
13. scaffold_6473:9938780-9938801 -
14. dmo_3146 scaffold_6473:9971794-9971815 -
15. dmo_3132 scaffold_6473:10161137-10161158 +
16. dmo_68 scaffold_6473:10161323-10161344 +
17. dmo_3133 scaffold_6473:10162127-10162148 -
18. dmo_3134 scaffold_6473:10167251-10167272 +
19. dmo_3135 scaffold_6473:10167437-10167458 +
20. scaffold_6473:10193263-10193284 +
21. dmo_3140 scaffold_6308:570826-570847 -
22. dmo_69 scaffold_6473:8659162-8659183 -
23. dmo_3144 scaffold_6473:8660597-8660618 -
24. dmo_3137 scaffold_6473:10168234-10168255 -

Sense Strand Reads

hide 3p reads show mid mismatch reads

GACTTCTTCTTAATGAATTTTGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGATTTTTGGTTATTTCATCTTTAGTCGGAGTTCTGGTAAGTAAACCGATAAAGGTGAAATAACCATTAAAATCAATACATAAGAAACTAGTGAGAGTGCTCTAGGCGAGACTGTTCGACTAGCAGATACTCTGTAGCG **********..........((((((((((((((((((((((.((((....((....))....))))))))))))))))))))..))))))).....**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M060 embryo**	**M046 female body**	**V110 male body**	**V041 embryo**	**V056 head**	**V049 head**
..........TTTGGTTATTTCATCTTTAGTCG..........	23	0	18	70.28	1265	258	545	378	69	11	4
..........TTGGTTATTTCATCTTTAGTCGG..........	23	0	19	13.16	250	97	37	103	10	2	1
..........TTTGGTTATTTCATCTTTAGTC..........	22	0	18	8.50	153	93	19	33	3	4	1
..........TTTGGTTATTTCATCTTTAGTCGG..........	24	0	18	8.44	152	82	14	48	7	0	1
..........TTGGTTATTTCATCTTTAGTCG..........	22	0	19	5.47	104	8	65	26	3	1	1
..........TTTTGGTTATTTCATCTTTAGTCG..........	24	0	18	5.17	93	17	35	34	4	3	0
..........TTTGGTTATTTCATCTTTAGT..........	21	0	18	3.11	56	21	14	16	1	4	0
..........TGGTTATTTCATCTTTAGTCG..........	21	0	20	2.70	54	2	24	21	6	1	0
..........TGGTTATTTCATCTTTAGTCGGA..........	23	0	20	1.35	27	21	1	5	0	0	0
..........TGGTTATTTCATCTTTAGTCGG..........	22	0	20	1.25	25	0	6	16	2	1	0
..........ACCGATAAAGGTGAAATAACCA..........	22	0	20	1.20	24	17	3	1	3	0	0
..........TTGGTTATTTCATCTTTAGTCGGT..........	24	1	19	1.05	20	13	2	4	0	1	0
..........TTTTGGTTATTTCATCTTTAGTC..........	23	0	18	1.00	18	13	1	4	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGGC..........	25	1	18	0.89	16	2	0	14	0	0	0
..........TTGGTTATTTCATCTTTAGTCGGC..........	24	1	19	0.84	16	2	4	10	0	0	0
..........ATAAAGGTGAAATAACCATTA..........	21	0	10	0.80	8	8	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGA..........	24	1	18	0.67	12	7	5	0	0	0	0
..........TTTTTGGTTATTTCATCTTTAGTCG..........	25	0	18	0.61	11	3	3	5	0	0	0
..........TTTGGTTATTTCATCTTTAGTCA..........	23	1	18	0.56	10	3	4	2	1	0	0
..........GATAAAGGTGAAATAACCATTA..........	22	0	10	0.50	5	3	2	0	0	0	0
..........ACCGATAAAGGTGAAATAACC..........	21	0	20	0.50	10	9	1	0	0	0	0
..........TTGGTTATTTCATCTTTAGTC..........	21	0	19	0.47	9	6	2	1	0	0	0
..........ACCGATAAAGGTGAAATAACCAT..........	23	0	9	0.44	4	3	1	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCGC..........	24	1	18	0.44	8	2	1	5	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGT..........	24	1	18	0.39	7	1	1	5	0	0	0
..........GTTATTTCATCTTTAGTCGGA..........	21	0	20	0.35	7	7	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCT..........	23	1	18	0.33	6	1	0	1	3	1	0
..........TTTGGTTATTTCATCTTTAGC..........	21	1	18	0.28	5	5	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCAA..........	24	2	18	0.28	5	0	5	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGT..........	22	0	18	0.22	4	0	1	2	0	1	0
..........TTTTTGGTTATTTCATCTTTAGTC..........	24	0	18	0.22	4	3	1	0	0	0	0
..........TTATTTCATCTTTAGTCGGAGTTC..........	24	0	10	0.20	2	2	0	0	0	0	0
..........CGATAAAGGTGAAATAACCATT..........	22	0	10	0.20	2	1	1	0	0	0	0
..........GATAAAGGTGAAATAACCATT..........	21	0	10	0.20	2	1	1	0	0	0	0
..........ACCGATAAAGGTGAAATAACCG..........	22	1	20	0.20	4	4	0	0	0	0	0
..........TTTTGGTTATTTCATCTTTAG..........	21	0	18	0.17	3	0	3	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCG..........	23	1	18	0.17	3	2	0	0	0	1	0
..........TTTGGTTATTTCATCTTTAG..........	20	0	18	0.17	3	2	1	0	0	0	0
..........CCGATAAAGGTGAAATAACCA..........	21	0	20	0.15	3	2	1	0	0	0	0
..........GTTATTTCATCTTTAGTCG..........	19	0	20	0.15	3	2	0	1	0	0	0
..........TTATTTCATCTTTAGTCG..........	18	0	20	0.15	3	1	2	0	0	0	0
..........TTTTTGGTTATTTCATCTTTAGT..........	23	0	18	0.11	2	1	1	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTT..........	22	1	18	0.11	2	2	0	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCGG..........	25	0	18	0.11	2	2	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGGT..........	25	1	18	0.11	2	0	1	1	0	0	0
..........TTGGTTATTTCATCTTTAGTCGGAA..........	25	1	18	0.11	2	1	0	1	0	0	0
..........TTGGTTATTTCATCTTTAGTCGGTC..........	25	2	19	0.11	2	1	0	1	0	0	0
..........TTGGTTATTTCATCTTTAGTCGA..........	23	1	19	0.11	2	2	0	0	0	0	0
..........TTGGTTATTTCATCTTTAGT..........	20	0	19	0.11	2	0	1	1	0	0	0
..........ATAAAGGTGAAATAACCATT..........	20	0	10	0.10	1	1	0	0	0	0	0
..........ATAAAGGTGAAATAACCATTAAAA..........	24	0	10	0.10	1	1	0	0	0	0	0
..........GATAAAGGTGAAATAACCATTT..........	22	1	10	0.10	1	1	0	0	0	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
..........ATTTTTGGTTATTTCATCTTT..........	21	0	15	0.07	1	0	1	0	0	0	0
..........ATTTTTGGTTATTTCATCTTTAG..........	23	0	15	0.07	1	0	1	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGGA..........	25	0	18	0.06	1	1	0	0	0	0	0
..........TTTTTGGTTATTTCATCTTTAGTCGA..........	26	1	18	0.06	1	0	0	1	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCA..........	24	1	18	0.06	1	1	0	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCT..........	24	1	18	0.06	1	0	1	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTA..........	22	1	18	0.06	1	1	0	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGC..........	22	1	18	0.06	1	1	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCTT..........	24	2	18	0.06	1	1	0	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCGT..........	25	1	18	0.06	1	0	0	1	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGTC..........	25	2	18	0.06	1	1	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGGAG..........	26	0	18	0.06	1	0	0	1	0	0	0
..........TTTTTGGTTATTTCATCTTTA..........	21	0	18	0.06	1	0	1	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCGGA..........	24	0	18	0.06	1	0	0	1	0	0	0
..........TTTTTGGTTATTTCATCTTTAGTCC..........	25	1	18	0.06	1	0	1	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCGA..........	25	1	18	0.06	1	1	0	0	0	0	0
..........CATCCACATTTCCAGTAGGGC..........	21	0	18	0.06	1	0	0	1	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCGC..........	25	1	18	0.06	1	1	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTGG..........	22	1	18	0.06	1	1	0	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCAA..........	23	2	19	0.05	1	0	1	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCGGTAA..........	26	3	19	0.05	1	0	1	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCGT..........	23	1	19	0.05	1	0	0	0	1	0	0
..........TTGGTTATTTCATCTTTAGTCGG..........	23	1	19	0.05	1	1	0	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCA..........	22	1	19	0.05	1	0	1	0	0	0	0
..........CGATAAAGGTGAAATAACCG..........	20	1	20	0.05	1	1	0	0	0	0	0
..........GGTTATTTCATCTTTAGTCGG..........	21	0	20	0.05	1	0	0	0	0	0	1
..........GTTATTTCATCTTTAGTCGGAA..........	22	1	20	0.05	1	1	0	0	0	0	0
..........TTATTTCATCTTTAGTCGGAGTT..........	23	0	20	0.05	1	1	0	0	0	0	0
..........GGTTATTTCATCTTTAGTCGGC..........	22	1	20	0.05	1	1	0	0	0	0	0
..........TGGTTATTTCATCTTTAGTC..........	20	0	20	0.05	1	1	0	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCG..........	20	1	20	0.05	1	1	0	0	0	0	0
..........TTATTTCATCTTTAGTCGGA..........	20	0	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

CTGAAGAAGAATTACTTAAAACTTGTTTATTATTTATGTAGGTGTAAAGGTCATCCCGTATCTAAAAACCAATAAAGTAGAAATCAGCCTCAAGACCATTCATTTGGCTATTTCCACTTTATTGGTAATTTTAGTTATGTATTCTTTGATCACTCTCACGAGATCCGCTCTGACAAGCTGATCGTCTATGAGACATCGC **********..........((((((((((((((((((((((.((((....((....))....))))))))))))))))))))..))))))).....**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M046 female body**
..........AGGTCATCCCGTATCTAAAAACCAATA..........	27	0	14	0.07	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:10167147-10167345 +	dmo_3134	GACTTCTTCTTAATGAATTTTGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGATTTTTGGTTATTTCATCTTTAGTCGGAGTTCTGGTAAGTAAACCGATAAAGGTGAAATAACCATTAAAATCAATACATA----------AGAAACTAGTGAGAGTGCTCTAGGCGAGACTGTTCGACTAGCAGATACTCTGTAGCG
droVir3	scaffold_13049:16282067-16282188 -		----------TGGCAAATCAACTGAAAGCAGTCGAGCAAGAATCAAAATAGTTCCGCATGCCTCAAAGCGGAAGTTCAAACAAGTGAGAGTGCTCCAGTTGCCGGTATCCGACTAGCAGATACCTGAAGCC
droGri2	scaffold_14853:6986509-6986565 +		----------A----------CATA----------TAAAACAAGTAAGAATGCTCTAGTCGAGATTGCTCGACTAGCAGATACCCTG-----

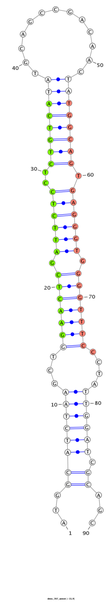
Generated: 09/08/2015 at 07:54 PM

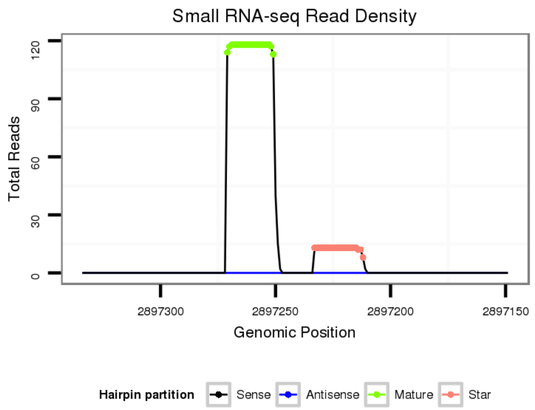
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

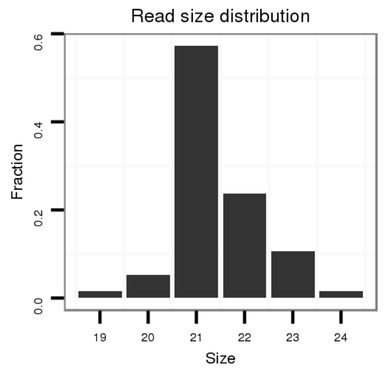
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_207	**scaffold_6328:2897199-2897284 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

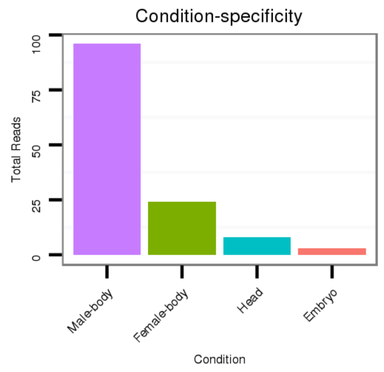
Legend: mature star mismatch in alignment mismatch in read

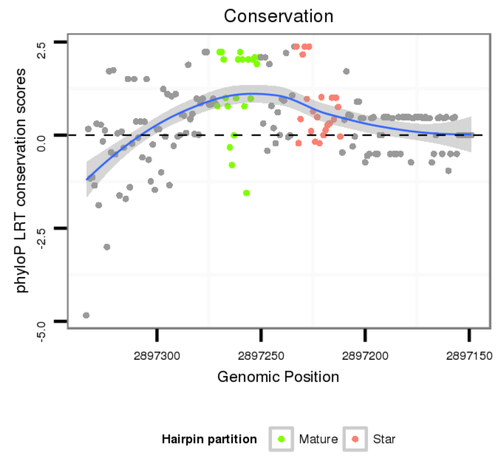
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TAACGATAACGATAACGATGACGATAACAAACATAAACGACGAAGATGATGGCATCTAAGCTGGAACTCGATTCTCCTCTGTCATATGCAGCCGACAACTATGGCAGTGAGGGTGGGGTTTCCCTATTGGATCGCAGCTTGGCAAATGTGTATTATCGATAACAGGAGCCAGCTCAGAGCTCACAG	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V049 head	V056 head	M060 embryo	V041 embryo
**********...(((((((((...(((((((.(((((((..(((((((((.............)))))))).)))))))..)))))))....)))))))..))...**********												
.....GAACTCGATTCTCCTCTGTCA.....	21	0	1	71.00	71	58	8	3	2	0	0
.....GAACTCGATTCTCCTCTGTCAT.....	22	0	1	24.00	24	14	8	1	1	0	0
.....GAACTCGATTCTCCTCTGTCATA.....	23	0	1	12.00	12	8	3	0	0	1	0
.....TGGCAGTGAGGGTGGGGTTTCC.....	22	0	1	6.00	6	4	0	0	1	1	0
.....GAACTCGATTCTCCTCTGTC.....	20	0	1	4.00	4	4	0	0	0	0	0
.....TGGCAGTGAGGGTGGGGTTTCC.....	21	0	1	4.00	4	4	0	0	0	0	0
.....TGGCAGTGAGGGTGGGGTTTCCCT.....	23	0	1	2.00	2	1	0	0	0	0	1
.....GAACTCGATTCTCCTCTGTCATAT.....	24	0	1	2.00	2	1	1	0	0	0	0
.....AACTCGATTCTCCTCTGTCA.....	20	0	1	2.00	2	0	2	0	0	0	0
.....GAACTCGATTCTCCTCTGTCG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....AACTCGATTCTCCTCTGTCATA.....	22	0	1	1.00	1	0	1	0	0	0	0
.....GGCAGTGAGGGTGGGGTTTCCTG.....	23	2	1	1.00	1	1	0	0	0	0	0
.....ACTCGATTCTCCTCTGTCAT.....	20	0	1	1.00	1	0	1	0	0	0	0
.....GGCAGTGAGGGTGGGGTTTCCCA.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TGGCAGTGAGGGTGGGGTTTCCCA.....	24	1	1	1.00	1	1	0	0	0	0	0
.....GAACTCGATTCTCCTCTGT.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TGGCAGTGAGGGTGGGGTTTCT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TGGCAGTGAGGGTGGGGTT.....	19	0	1	1.00	1	1	0	0	0	0	0
...CGATAACGATAACGATGACGAT.....	22	0	3	0.33	1	1	0	0	0	0	0
...CGATAACGATAACGATGAC.....	19	0	4	0.25	1	0	1	0	0	0	0

Anti-sense strand reads

ATTGCTATTGCTATTGCTACTGCTATTGTTTGTATTTGCTGCTTCTACTACCGTAGATTCGACCTTGAGCTAAGAGGAGACAGTATACGTCGGCTGTTGATACCGTCACTCCCACCCCAAAGGGATAACCTAGCGTCGAACCGTTTACACATAATAGCTATTGTCCTCGGTCGAGTCTCGAGTGTC	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_6328:2897149-2897334 -	dmo_207	TAACG----------ATAACGATAACGA----------TGACGATAACAAA---CATAAACGACGAAGATGATGGCATCTAAGCTGGAACTCGATTCTCCTCTGTCATATGCAGCCGACAACTATGGCAGTGAGGGTGGGGTTTCCCTATTGGAT-CGCAGCTTGGCAAATGTGTATTATCGATAA----------CAGGAGCCAGCTCAGAGCTCACAG
droVir3	scaffold_13042:902773-903026 -	dvi_76	CAGCATGTTACGAGTAATTGCACACAGCGACAGCCGGAGACAGATCCGGAGACAGATGAGTCTTGGATGATAACGCGAT----------G---------GTGGCATCTAAGCTGGAACTCGATTCTCCTCTGTCATATGCGACGATAACTATGGCAGTGAGGGTGGGGTTTCCTTATTAGATCGATACTCA--AAAGCATGTTATAGATAAACGATAAACGATAACCGATAACCGATAACACAAACATATATGGTACAGGCA-GAACTGGGAA------
droGri2	scaffold_15203:5172822-5172904 +		TAACA----------ATAACATATATAA----------TATTATATATAACAAACTATAAACAAAGCAAA-TGTTTTGTTCAAGACACAACTGAATTCTCACCC----------|----------|----------|----------
droWil2	scf2_1100000004909:7960960-7961040 +		G----|----------|----------|----------|----------TAACTAAACTGGAACTGATTTCTGATCTGTCATATAGATAGAATAGCTATAACAGTGAGACTAGGGTTTGTGGATTAAAT-|----------|----------|----------
dp5	XL_group1a:3370506-3370534 +		TAACG----------ATAAC-------|----------|----------|----------GATAACAGTAACGATAACA-|----------|----------|----------
droPer2	scaffold_39:597717-597764 -		CAACA----------ACAACGATAACGA----------TAACGATAATAAA---AGCGACG----------|----------|----------|----------|----------AACAAAGACG----|----------|----------
droAna3	scaffold_13417:2460723-2460806 -		GATT----------|----------|----------|----------GTTGTAACTAAACTGGAACTCGTTTCTGACTGTCATATAGATTCGATAGCTATAACAGTGAGGATGGGGTTTGTGGATT----|----------|----------
droBip1	scf7180000395874:32779-32866 -		CAACG----------ATT---------|----------|----------|----------GTTGTAACTAAACTGGAACTCGTTTCTGACTGTCATATAGATCGATAGCTATAACAGTGAGGATTGGGTTTGTGGATT----|----------|----------
droKik1	scf7180000302517:1186323-1186405 +		AT-T----------|----------|----------|----------GTTGCAACTAAACTGGAACTCGCTCTGATCTGTCATGTGCATTCGTTAGCTATTACAGTGAGGTTGGAGTTTGTGGATT----|----------|----------
droFic1	scf7180000454073:1735826-1735901 +		GATT----------|----------|----------|----------GTTGCAGCTAAACTGGAACTGAATTCTGACTGTCATATGCATTGAATAG-TATCGCAGTGCGGGTGGGTTCCT----------|----------|----------
droEle1	scf7180000491186:2837280-2837303 +		TAACG----------ATAACGATAACGA----------G----------|----------|----------|----------|----------|----------|----------ACG---A----------|----------|----------
droRho1	scf7180000761121:187451-187535 -		GACAA----------ACGATT-------|----------|----------|----------GTTGCAGCTAAACTGGAACTCATCTCTGACGTGTCATATAGATTTGATAGGTATAACAGTGAGGATGGGGTTTC---------|----------|----------
droBia1	scf7180000302069:1148323-1148393 -		G----|----------|----------|----------|----------CAGCTAAACTGGAACCTGGTCTCAACTGTCATGTGCATTTGATTATGTATAACAGTGAGGAGGGGGTTTG---------|----------|----------
droEug1	scf7180000409230:877540-877646 -		GGCGA----------GAAGCAAAACGA----------CTAGGACTGAGAA---TA----------GTTGCAGCTAAACTGGAACTCAACTCTGACGTGTCATATTGATTGATAGTTATGACAGTGAGGATGGGGTTTC---------|----------|----------
dm3	chr2R:15556553-15556590 +		AT--|----------|-------AATTTG----------TGACAATGACAAA---CATAAACAAAGAAA----------|----------|----------|----------|----------GCG---A----------|----------|----------
droSim2	4:53311-53346 -		TAATA----------ATAACAATAATAA----------TAATAATAACAAT---|----------|----------|----------|----------|----------|----------AATA---A----------|----------|----------
droSec2	scaffold_26:16365-16400 +		TAATA----------ATAATTATAAT---|----------|----------|----------|----------|----------|----------AATAATTATAACAATAATAA----------|----------|----------
droYak3	X:1662412-1662421 -		CAACG----------GCAGC---|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------
droEre2	scaffold_4690:16157275-16157323 +		CAAGA----------ATAACAACAGCAA----------CAACATAACAAA---AAAACGCAATGAAA----------|----------|----------|----------|----------ATG---A----------|----------|----------

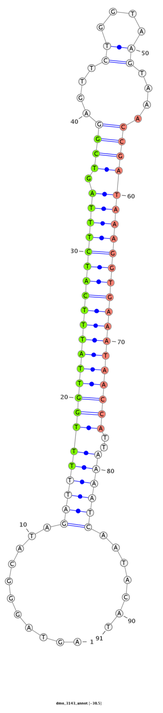
Generated: 09/08/2015 at 08:05 PM

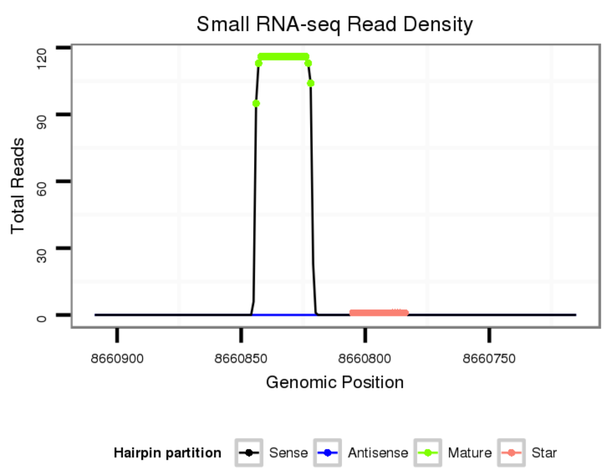
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	4
rescue.candidate	0

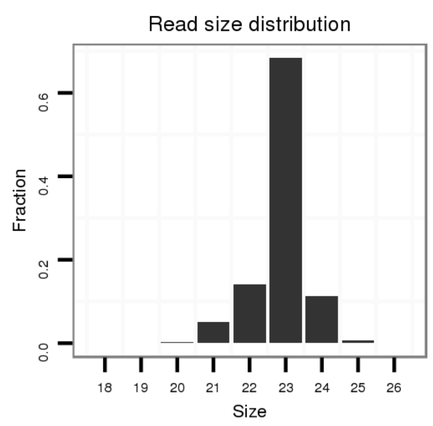
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3143	**scaffold_6473:8660765-8660859 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

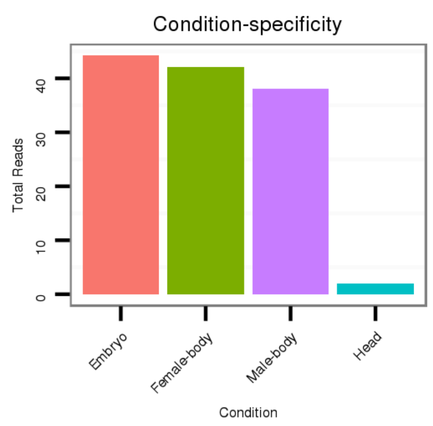
Legend: mature star **mismatch in alignment** mismatch in read

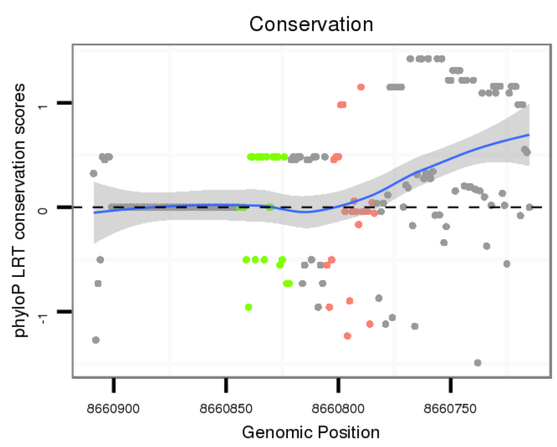
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
Homo6	DNA	hAT-Pegasus	+

mature

1. dmo_3141 scaffold_6473:8642796-8642818 +
2. dmo_3142 scaffold_6473:8643620-8643642 -
3. dmo_3138 scaffold_6473:8659793-8659815 +
4. dmo_3143 scaffold_6473:8660822-8660844 -
5. dmo_3150 scaffold_6473:9914890-9914912 -
6. scaffold_6473:9917724-9917746 +
7. dmo_3152 scaffold_6473:9919839-9919861 +
8. dmo_3148 scaffold_6473:9927476-9927498 +
9. scaffold_6473:9933776-9933798 +
10. scaffold_6473:9934446-9934468 -
11. dmo_3147 scaffold_6473:9937954-9937976 +
12. scaffold_6473:9938818-9938840 -
13. dmo_3146 scaffold_6473:9971832-9971854 -
14. dmo_3132 scaffold_6473:10161098-10161120 +
15. dmo_3133 scaffold_6473:10162165-10162187 -
16. dmo_3134 scaffold_6473:10167212-10167234 +
17. dmo_3136 scaffold_6473:10168425-10168447 -
18. scaffold_6473:10193224-10193246 +

star

1. dmo_3139 scaffold_6308:570084-570105 +
2. dmo_3141 scaffold_6473:8642835-8642856 +
3. dmo_3142 scaffold_6473:8643582-8643603 -
4. dmo_3138 scaffold_6473:8659832-8659853 +
5. dmo_3143 scaffold_6473:8660784-8660805 -
6. dmo_3149 scaffold_6473:9914068-9914089 +
7. scaffold_6473:9917763-9917784 +
8. dmo_3152 scaffold_6473:9919878-9919899 +
9. dmo_3148 scaffold_6473:9927515-9927536 +
10. scaffold_6473:9933815-9933836 +
11. scaffold_6473:9934408-9934429 -
12. dmo_3147 scaffold_6473:9937993-9938014 +
13. scaffold_6473:9938780-9938801 -
14. dmo_3146 scaffold_6473:9971794-9971815 -
15. dmo_3132 scaffold_6473:10161137-10161158 +
16. dmo_68 scaffold_6473:10161323-10161344 +
17. dmo_3133 scaffold_6473:10162127-10162148 -
18. dmo_3134 scaffold_6473:10167251-10167272 +
19. dmo_3135 scaffold_6473:10167437-10167458 +
20. scaffold_6473:10193263-10193284 +
21. dmo_3140 scaffold_6308:570826-570847 -
22. dmo_69 scaffold_6473:8659162-8659183 -
23. dmo_3144 scaffold_6473:8660597-8660618 -
24. dmo_3137 scaffold_6473:10168234-10168255 -

Sense Strand Reads

hide 3p reads show mid mismatch reads

GACTTCTTCTTAATGAATTTTGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGATTTTTGGTTATTTCATCTTTAGTCGGAGTTCTGGTAAGTAAACCGATAAAGGTGAAATAACCATTAAAATCAATACATAAGAAACTAGTGAGAGTGCTCTAGGCGAGACTGTTCGACTAGCAGATACTCTGC	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
**********											
..........(((((((((((((((((((((((.((((....((....))....)))))))))))))))))))))..)))))).....											
..........TTTGGTTATTTCATCTTTAGTCG..........	23	0	18	70.28	1265	258	545	378	69	11	4
..........TTGGTTATTTCATCTTTAGTCGG..........	23	0	19	13.16	250	97	37	103	10	2	1
..........TTTGGTTATTTCATCTTTAGTC..........	22	0	18	8.50	153	93	19	33	3	4	1
..........TTTGGTTATTTCATCTTTAGTCGG..........	24	0	18	8.44	152	82	14	48	7	0	1
..........TTGGTTATTTCATCTTTAGTCG..........	22	0	19	5.47	104	8	65	26	3	1	1
..........TTTTGGTTATTTCATCTTTAGTCG..........	24	0	18	5.17	93	17	35	34	4	3	0
..........TTTGGTTATTTCATCTTTAGT..........	21	0	18	3.11	56	21	14	16	1	4	0
..........TGGTTATTTCATCTTTAGTCGG..........	22	0	20	1.65	33	14	0	16	2	1	0
..........TGGTTATTTCATCTTTAGTCGGA..........	23	0	20	1.35	27	21	0	5	1	0	0
..........ACCGATAAAGGTGAAATAACCA..........	22	0	20	1.20	24	17	3	1	3	0	0
..........TTGGTTATTTCATCTTTAGTCGGTT..........	24	1	19	1.05	20	13	2	4	0	1	0
..........TGGTTATTTCATCTTTAGTCG..........	21	0	20	1.05	21	0	0	21	0	0	0
..........TTTTGGTTATTTCATCTTTAGTC..........	23	0	18	1.00	18	13	1	4	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGGC..........	25	1	18	0.89	16	2	0	14	0	0	0
..........TTGGTTATTTCATCTTTAGTCGGC..........	24	1	19	0.84	16	2	4	10	0	0	0
..........ATAAAGGTGAAATAACCATTA..........	21	0	10	0.80	8	8	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGA..........	24	1	18	0.67	12	7	5	0	0	0	0
..........TTTTTGGTTATTTCATCTTTAGTCG..........	25	0	18	0.61	11	3	3	5	0	0	0
..........TTTGGTTATTTCATCTTTAGTCA..........	23	1	18	0.56	10	3	4	2	1	0	0
..........GATAAAGGTGAAATAACCATTA..........	22	0	10	0.50	5	3	2	0	0	0	0
..........TTGGTTATTTCATCTTTAGTC..........	21	0	19	0.47	9	6	2	1	0	0	0
..........ACCGATAAAGGTGAAATAACCAT..........	23	0	9	0.44	4	3	1	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGC..........	24	1	18	0.44	8	2	1	5	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGT..........	24	1	18	0.39	7	1	1	5	0	0	0
..........GTTATTTCATCTTTAGTCGGA..........	21	0	20	0.35	7	7	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCT..........	23	1	18	0.33	6	1	0	1	3	1	0
..........TTTGGTTATTTCATCTTTAGC..........	21	1	18	0.28	5	5	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCAA..........	24	2	18	0.28	5	0	5	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGT..........	22	0	18	0.22	4	0	1	2	0	1	0
..........TTTTTGGTTATTTCATCTTTAGTC..........	24	0	18	0.22	4	3	1	0	0	0	0
..........CGATAAAGGTGAAATAACCATT..........	22	0	10	0.20	2	1	1	0	0	0	0
..........GATAAAGGTGAAATAACCATT..........	21	0	10	0.20	2	1	1	0	0	0	0
..........TTATTTCATCTTTAGTCGGAGTTC..........	24	0	10	0.20	2	2	0	0	0	0	0
..........ACCGATAAAGGTGAAATAACCC..........	22	1	20	0.20	4	4	0	0	0	0	0
..........TTTTGGTTATTTCATCTTTAG..........	21	0	18	0.17	3	0	3	0	0	0	0
..........TTGGTTATTTCATCTTTAG..........	20	0	18	0.17	3	2	1	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCC..........	23	1	18	0.17	3	2	0	0	0	1	0
..........CCGATAAAGGTGAAATAACCA..........	21	0	20	0.15	3	2	1	0	0	0	0
..........TTATTTCATCTTTAGTCG..........	18	0	20	0.15	3	1	2	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCGGAA..........	25	1	18	0.11	2	1	0	1	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCGG..........	25	0	18	0.11	2	0	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGGT..........	25	1	18	0.11	2	0	1	1	0	0	0
..........TTTTTGGTTATTTCATCTTTAGT..........	23	0	18	0.11	2	1	1	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTT..........	22	1	18	0.11	2	2	0	0	0	0	0
..........TTGGTTATTTCATCTTTAGT..........	20	0	19	0.11	2	0	1	1	0	0	0
..........TTGGTTATTTCATCTTTAGTCGA..........	23	1	19	0.11	2	2	0	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCGGTC..........	25	2	19	0.11	2	1	0	1	0	0	0
..........GATAAAGGTGAAATAACCATTT..........	22	1	10	0.10	1	1	0	0	0	0	0
..........ATAAAGGTGAAATAACCATT..........	20	0	10	0.10	1	1	0	0	0	0	0
..........ATAAAGGTGAAATAACCATTAAAA..........	24	0	10	0.10	1	1	0	0	0	0	0
..........ATTTTTGGTTATTTCATCTTT..........	21	0	15	0.07	1	0	1	0	0	0	0
..........ATTTTTGGTTATTTCATCTTTAG..........	23	0	15	0.07	1	0	1	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCGT..........	25	1	18	0.06	1	0	0	1	0	0	0
..........TTTGGTTATTTCATCTTTAGTTG..........	22	1	18	0.06	1	1	0	0	0	0	0
..........TTTTTGGTTATTTCATCTTTA..........	21	0	18	0.06	1	0	1	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCT..........	24	1	18	0.06	1	0	1	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGGAG..........	26	0	18	0.06	1	0	0	1	0	0	0
..........TTTGGTTATTTCATCTTTAGTCTT..........	24	2	18	0.06	1	1	0	0	0	0	0
..........TTTTTGGTTATTTCATCTTTAGTCC..........	25	1	18	0.06	1	0	1	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGC..........	22	1	18	0.06	1	1	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGTC..........	25	2	18	0.06	1	1	0	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCGA..........	25	1	18	0.06	1	1	0	0	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCGC..........	25	1	18	0.06	1	1	0	0	0	0	0
..........TTTTTGGTTATTTCATCTTTAGTCGA..........	26	1	18	0.06	1	0	0	1	0	0	0
..........TTTTGGTTATTTCATCTTTAGTCA..........	24	1	18	0.06	1	1	0	0	0	0	0
..........TTTGGTTATTTCATCTTTAGTA..........	22	1	18	0.06	1	1	0	0	0	0	0
..........CATCCACATTTCCAGTAGGGC..........	21	0	18	0.06	1	0	0	1	0	0	0
..........TTTGGTTATTTCATCTTTAGTCGGA..........	25	0	18	0.06	1	1	0	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCGGA..........	24	0	18	0.06	1	0	0	1	0	0	0
..........TTGGTTATTTCATCTTTAGTCAA..........	23	2	19	0.05	1	0	1	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCA..........	22	1	19	0.05	1	0	1	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCGC..........	23	1	19	0.05	1	1	0	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCGGTAA..........	26	3	19	0.05	1	0	1	0	0	0	0
..........TTGGTTATTTCATCTTTAGTCGT..........	23	1	19	0.05	1	0	0	0	1	0	0
..........GGTTATTTCATCTTTAGTCGG..........	21	0	20	0.05	1	0	0	0	0	0	1
..........GGTTATTTCATCTTTAGTCG..........	20	0	20	0.05	1	0	1	0	0	0	0
..........TGGTTATTTCATCTTTAGTCGGT..........	23	1	20	0.05	1	1	0	0	0	0	0
..........GGTTATTTCATCTTTAGTCGGC..........	22	1	20	0.05	1	1	0	0	0	0	0
..........GTTATTTCATCTTTAGTCG..........	19	0	20	0.05	1	0	1	0	0	0	0
..........TTGGTTATTTCATCTTTAGC..........	20	1	20	0.05	1	1	0	0	0	0	0
..........TTATTTCATCTTTAGTCGGA..........	20	0	20	0.05	1	1	0	0	0	0	0
..........GTTATTTCATCTTTAGTCGGC..........	21	1	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

CTGAAGAAGAATTACTTAAAACTTGTTTATTATTTATGTAGGTGTAAAGGTCATCCCGTATCTAAAAACCAATAAAGTAGAAATCAGCCTCAAGACCATTCATTTGGCTATTTCCACTTTATTGGTAATTTTAGTTATGTATTCTTTGATCACTCTCACGAGATCCGCTCTGACAAGCTGATCGTCTATGAGACG	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body
**********						
..........(((((((((((((((((((((((.((((....((....))....)))))))))))))))))))))..)))))).....						
..........AGGTCATCCCGTATCTAAAAACCAATA..........	27	0	14	0.07	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:8660715-8660909 -	dmo_3143	GACTTCTTCTTAATGAATTTTGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGATTTTTGGTTATTTCATCTTTAGTCGGAGTTCTGGTAAGTAAACCGATAAAGGTGAAATAACCATTAAAATCAATACATAAGAAA--CTAGTGAGAGTGCTCTAGGCGAGACTGTTCGACTAGCAGATACTCTGC
droVir3	scaffold_13052:1526695-1526823 +		AAAGTCTT----------ACTTGTTTTA--TTTTAATATGAGTTAAGGCAACACATGTGATAAGCACGTCACTGACATCTATATTAATATTTAAGAAATACAAGTAAGAGTGCTCTAGTCAGGAGTGCCCCACTAGGGATA-----
droGri2	scaffold_14853:6986509-6985918 +		AC----------ATAAAA--CAAGTAAGAATGCTCTAGTCGAGATTGCTCGACTAGCAGATACCCTG-
droRho1	scf7180000771295:2998-3045 +		AA----------AGTTGAAATAAAATTCAACTTAAATACATAAAAAA--TAATGAAAGT----------
droTak1	scf7180000415263:30117-30149 -		AT----------AACAAA--CAAGTGAGAACGCTATAGTCGAGAC----------
droYak3	2R:14899312-14899394 +		AC----------AAAAATAAAATAACAAAATATTGAATACAAATGCAA--GAAGAGAAAAGCTATAGTCGAGTTGCC-CGACTAACTGATAGCC---

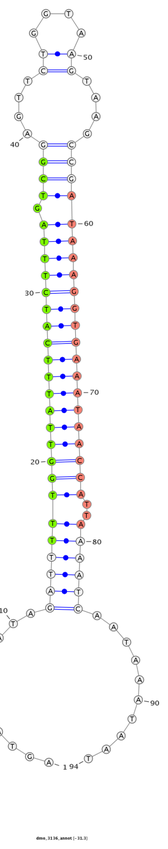
Generated: 09/08/2015 at 07:54 PM

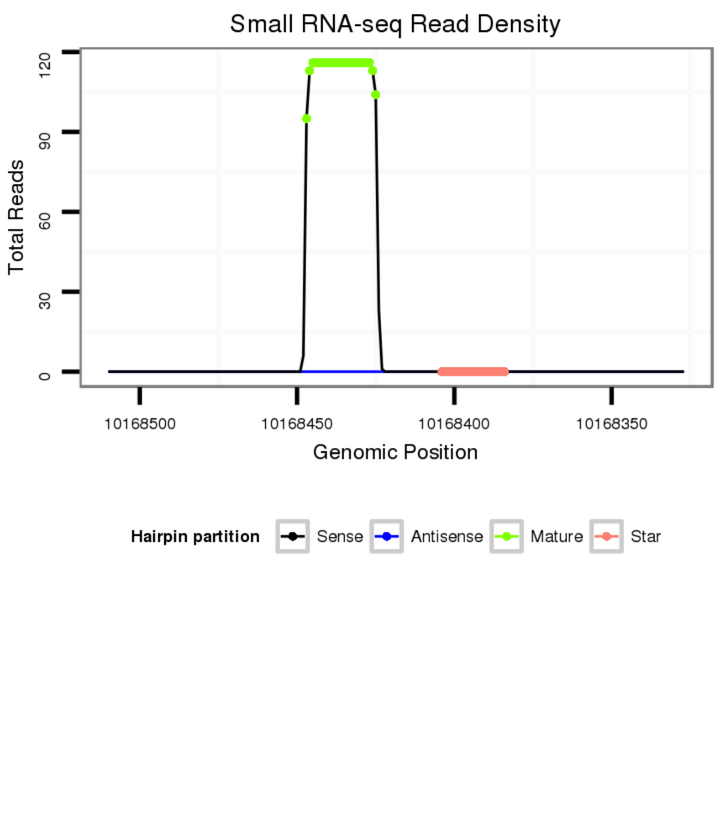
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

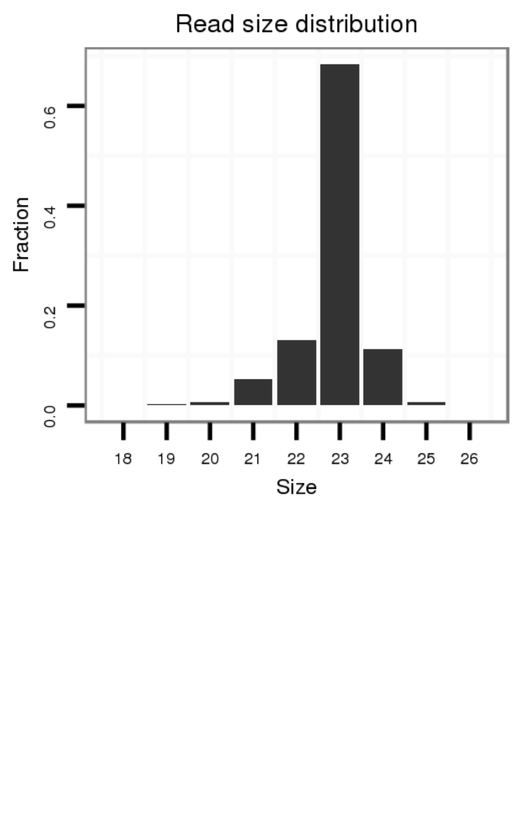
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3136	**scaffold_6473:10168377-10168460 -**	**confident-exception**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

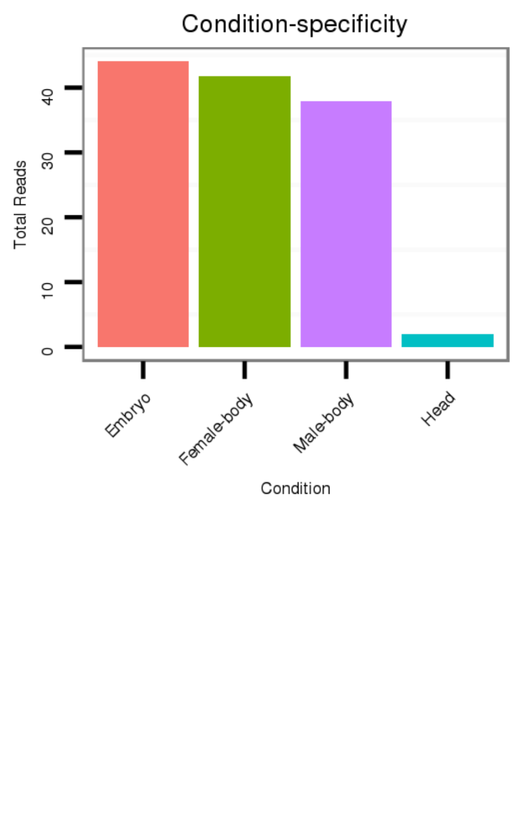
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dmoj\GI15760-in]

No Repeatable elements found

mature	star
1. dmo_3141 scaffold_6473:8642796-8642818 + 2. dmo_3142 scaffold_6473:8643620-8643642 - 3. dmo_3138 scaffold_6473:8659793-8659815 + 4. dmo_3143 scaffold_6473:8660822-8660844 - 5. dmo_3150 scaffold_6473:9914890-9914912 - 6. scaffold_6473:9917724-9917746 + 7. dmo_3152 scaffold_6473:9919839-9919861 + 8. dmo_3148 scaffold_6473:9927476-9927498 + 9. scaffold_6473:9933776-9933798 + 10. scaffold_6473:9934446-9934468 - 11. dmo_3147 scaffold_6473:9937954-9937976 + 12. scaffold_6473:9938818-9938840 - 13. dmo_3146 scaffold_6473:9971832-9971854 - 14. dmo_3132 scaffold_6473:10161098-10161120 + 15. dmo_3133 scaffold_6473:10162165-10162187 - 16. dmo_3134 scaffold_6473:10167212-10167234 + 17. dmo_3136 scaffold_6473:10168425-10168447 - 18. scaffold_6473:10193224-10193246 +	1. dmo_3138 scaffold_6473:8659836-8659856 + 2. dmo_3143 scaffold_6473:8660781-8660801 - 3. scaffold_6473:9917767-9917787 + 4. scaffold_6473:9933819-9933839 + 5. scaffold_6473:9934405-9934425 - 6. scaffold_6473:9938777-9938797 - 7. dmo_3132 scaffold_6473:10161141-10161161 + 8. dmo_3134 scaffold_6473:10167255-10167275 + 9. dmo_3136 scaffold_6473:10168384-10168404 - 10. scaffold_6473:10193267-10193287 +

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTTCTTCTTAATGAATTTTGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGATTTTTGGTTATTTCATCTTTAGTCGGAGTTCTGGTAAGTAAGCCGATAAAGGTGAAATAACCATTAAAATCAATAAATAATAAACTAGTAAGAGTGCTCTAGGCGAGACTGCTCGACTAGCCA **********…….(((((((((((((((((((((.((((….((….))….))))))))))))))))))))..))))))……..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
……TTTGGTTATTTCATCTTTAGTCG……	23	0	18	70.28	1265	258	545	378	69	11	4
……TTGGTTATTTCATCTTTAGTCGG……	23	0	19	13.16	250	97	37	103	10	2	1
……TTTGGTTATTTCATCTTTAGTC……	22	0	18	8.50	153	93	19	33	3	4	1
……TTTGGTTATTTCATCTTTAGTCGG……	24	0	18	8.44	152	82	14	48	7	0	1
……TTGGTTATTTCATCTTTAGTCG……	22	0	19	5.47	104	8	65	26	3	1	1
……TTTTGGTTATTTCATCTTTAGTCG……	24	0	18	5.17	93	17	35	34	4	3	0
……TTTGGTTATTTCATCTTTAGT……	21	0	18	3.11	56	21	14	16	1	4	0
……TGGTTATTTCATCTTTAGTCGG……	22	0	20	1.60	32	14	0	16	2	0	0
……TGGTTATTTCATCTTTAGTCG……	21	0	20	1.35	27	0	0	21	6	0	0
……TGGTTATTTCATCTTTAGTCGGA……	23	0	20	1.35	27	21	0	5	1	0	0
……TTGGTTATTTCATCTTTAGTCGGT……	24	1	19	1.05	20	13	2	4	0	1	0
……TTTTGGTTATTTCATCTTTAGTC……	23	0	18	1.00	18	13	1	4	0	0	0
……TTTGGTTATTTCATCTTTAGTCGGC……	25	1	18	0.89	16	2	0	14	0	0	0
……TTGGTTATTTCATCTTTAGTCGGC……	24	1	19	0.84	16	2	4	10	0	0	0
……ATAAAGGTGAAATAACCATTA……	21	0	10	0.80	8	8	0	0	0	0	0
……TTTGGTTATTTCATCTTTAGTCGA……	24	1	18	0.67	12	7	5	0	0	0	0
……TTTTTGGTTATTTCATCTTTAGTCG……	25	0	18	0.61	11	3	3	5	0	0	0
……TTTGGTTATTTCATCTTTAGTCA……	23	1	18	0.56	10	3	4	2	1	0	0
……GAGTTCTGGTAAGTAAGCCG……	20	0	4	0.50	2	2	0	0	0	0	0
……GATAAAGGTGAAATAACCATTA……	22	0	10	0.50	5	3	2	0	0	0	0
……TTGGTTATTTCATCTTTAGTC……	21	0	19	0.47	9	6	2	1	0	0	0
……TTTGGTTATTTCATCTTTAGTCGC……	24	1	18	0.44	8	2	1	5	0	0	0
……TTTGGTTATTTCATCTTTAGTCGT……	24	1	18	0.39	7	1	1	5	0	0	0
……GTTATTTCATCTTTAGTCGGA……	21	0	20	0.35	7	7	0	0	0	0	0
……TTTGGTTATTTCATCTTTAGTCT……	23	1	18	0.33	6	1	0	1	3	1	0
……TTTGGTTATTTCATCTTTAGC……	21	1	18	0.28	5	5	0	0	0	0	0
……TTTGGTTATTTCATCTTTAGTCAA……	24	2	18	0.28	5	0	5	0	0	0	0
……GAGTTCTGGTAAGTAAGCC……	19	0	4	0.25	1	1	0	0	0	0	0
……TTTTGGTTATTTCATCTTTAGT……	22	0	18	0.22	4	0	1	2	0	1	0
……TTTTTGGTTATTTCATCTTTAGTC……	24	0	18	0.22	4	3	1	0	0	0	0
……GATAAAGGTGAAATAACCATT……	21	0	10	0.20	2	1	1	0	0	0	0
……TTATTTCATCTTTAGTCGGAGTTC……	24	0	10	0.20	2	2	0	0	0	0	0
……CGATAAAGGTGAAATAACCATT……	22	0	10	0.20	2	1	1	0	0	0	0
……TTTGGTTATTTCATCTTTAG……	20	0	18	0.17	3	2	1	0	0	0	0
……TTTGGTTATTTCATCTTTAGTCC……	23	1	18	0.17	3	2	0	0	0	1	0
……TTTTGGTTATTTCATCTTTAG……	21	0	18	0.17	3	0	3	0	0	0	0
……CCGATAAAGGTGAAATAACCA……	21	0	20	0.15	3	2	1	0	0	0	0
……GTTATTTCATCTTTAGTCG……	19	0	20	0.15	3	2	1	0	0	0	0
……TTATTTCATCTTTAGTCG……	18	0	20	0.15	3	1	2	0	0	0	0
……TTTTTGGTTATTTCATCTTTAGT……	23	0	18	0.11	2	1	1	0	0	0	0
……TTTGGTTATTTCATCTTTAGTT……	22	1	18	0.11	2	2	0	0	0	0	0
……TTTTGGTTATTTCATCTTTAGTCGG……	25	0	18	0.11	2	2	0	0	0	0	0
……TTGGTTATTTCATCTTTAGTCGGAA……	25	1	18	0.11	2	1	0	1	0	0	0
……TTTGGTTATTTCATCTTTAGTCGGT……	25	1	18	0.11	2	0	1	1	0	0	0
……TTGGTTATTTCATCTTTAGTCGGTC……	25	2	19	0.11	2	1	0	1	0	0	0
……TTGGTTATTTCATCTTTAGT……	20	0	19	0.11	2	0	1	1	0	0	0
……TTGGTTATTTCATCTTTAGTCGA……	23	1	19	0.11	2	2	0	0	0	0	0
……ATAAAGGTGAAATAACCATTAAAA……	24	0	10	0.10	1	1	0	0	0	0	0
……GATAAAGGTGAAATAACCATTT……	22	1	10	0.10	1	1	0	0	0	0	0
……ATAAAGGTGAAATAACCATT……	20	0	10	0.10	1	1	0	0	0	0	0
……ATTTTTGGTTATTTCATCTTT……	21	0	15	0.07	1	0	1	0	0	0	0
……ATTTTTGGTTATTTCATCTTTAG……	23	0	15	0.07	1	0	1	0	0	0	0
……TTTTGGTTATTTCATCTTTAGC……	22	1	18	0.06	1	1	0	0	0	0	0
……TTTGGTTATTTCATCTTTAGTCGGA……	25	0	18	0.06	1	1	0	0	0	0	0
……TTGGTTATTTCATCTTTAGTCGGA……	24	0	18	0.06	1	0	0	1	0	0	0
……TTTGGTTATTTCATCTTTAGTCGTC……	25	2	18	0.06	1	1	0	0	0	0	0
……TTTTGGTTATTTCATCTTTAGTCT……	24	1	18	0.06	1	0	1	0	0	0	0
……TTTTTGGTTATTTCATCTTTA……	21	0	18	0.06	1	0	1	0	0	0	0
……CATCCACATTTCCAGTAGGGC……	21	0	18	0.06	1	0	0	1	0	0	0
……TTTTGGTTATTTCATCTTTAGTCGA……	25	1	18	0.06	1	1	0	0	0	0	0
……TTTTGGTTATTTCATCTTTAGTCGC……	25	1	18	0.06	1	1	0	0	0	0	0
……TTTGGTTATTTCATCTTTAGTG……	22	1	18	0.06	1	1	0	0	0	0	0
……TTTGGTTATTTCATCTTTAGTCGGAG……	26	0	18	0.06	1	0	0	1	0	0	0
……TTTTTGGTTATTTCATCTTTAGTCGA……	26	1	18	0.06	1	0	0	1	0	0	0
……TTTGGTTATTTCATCTTTAGTCTT……	24	2	18	0.06	1	1	0	0	0	0	0
……TTTTGGTTATTTCATCTTTAGTCA……	24	1	18	0.06	1	1	0	0	0	0	0
……TTTGGTTATTTCATCTTTAGTA……	22	1	18	0.06	1	1	0	0	0	0	0
……TTTTGGTTATTTCATCTTTAGTCGT……	25	1	18	0.06	1	0	0	1	0	0	0
……TTTTTGGTTATTTCATCTTTAGTCC……	25	1	18	0.06	1	0	1	0	0	0	0
……TTGGTTATTTCATCTTTAGTCAA……	23	2	19	0.05	1	0	1	0	0	0	0
……TTGGTTATTTCATCTTTAGTCGT……	23	1	19	0.05	1	0	0	0	1	0	0
……TTGGTTATTTCATCTTTAGTCGC……	23	1	19	0.05	1	1	0	0	0	0	0
……TTGGTTATTTCATCTTTAGTCA……	22	1	19	0.05	1	0	1	0	0	0	0
……TTGGTTATTTCATCTTTAGTCGGTAA……	26	3	19	0.05	1	0	1	0	0	0	0
……GTTATTTCATCTTTAGTCGGC……	21	1	20	0.05	1	1	0	0	0	0	0
……GGTTATTTCATCTTTAGTCG……	20	0	20	0.05	1	0	1	0	0	0	0
……TTATTTCATCTTTAGTCGGA……	20	0	20	0.05	1	1	0	0	0	0	0
……TGGTTATTTCATCTTTAGTCGGT……	23	1	20	0.05	1	1	0	0	0	0	0
……GGTTATTTCATCTTTAGTCGG……	21	0	20	0.05	1	0	0	0	0	0	1
……TTGGTTATTTCATCTTTAGC……	20	1	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

GAAGAAGAATTACTTAAAACTTGTTTATTATTTATGTAGGTGTAAAGGTCATCCCGTATCTAAAAACCAATAAAGTAGAAATCAGCCTCAAGACCATTCATTCGGCTATTTCCACTTTATTGGTAATTTTAGTTATTTATTATTTGATCATTCTCACGAGATCCGCTCTGACGAGCTGATCGGT **********…….(((((((((((((((((((((.((((….((….))….))))))))))))))))))))..))))))……..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body
……AGGTCATCCCGTATCTAAAAACCAATA……	27	0	14	0.07	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:10168327-10168510 -	dmo_3136	CTTCTTCTTAATGAATTTTGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGATTTTTGGTTATTTCATCTTTAGTCGGAGTTCTGGTAAGTAAGCCGATAAAGGTGAAATAACCATTAAAATCAATAAATAATAAACTAGTAAGAGTGCTCTAGGCGAGACTGCTCGACTAGCCA

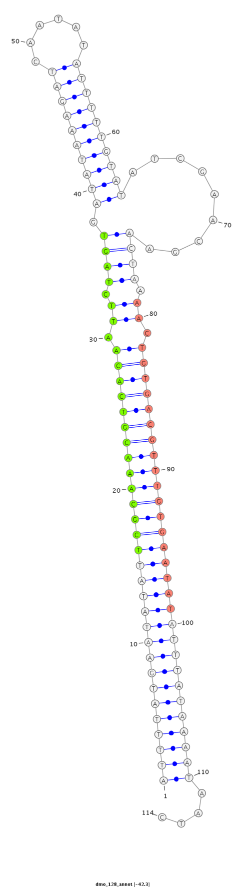
Generated: 09/08/2015 at 07:55 PM

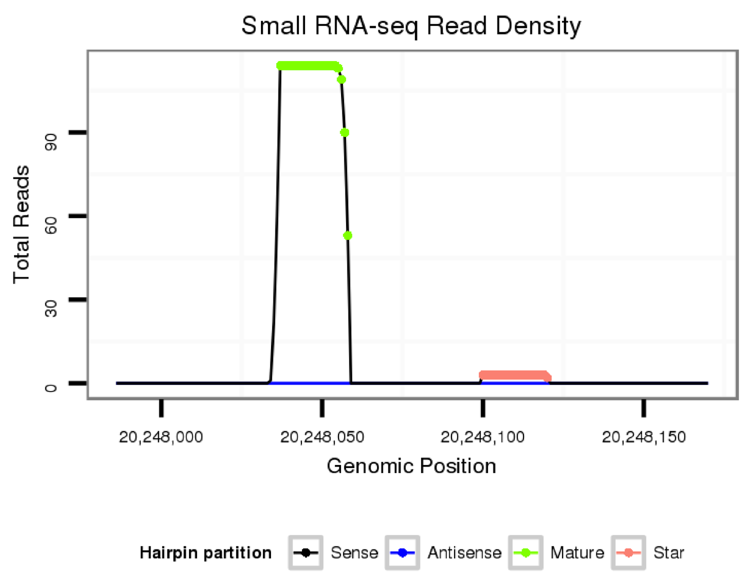
	PASS/FAIL
crit.star	0
crit.loop	1
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

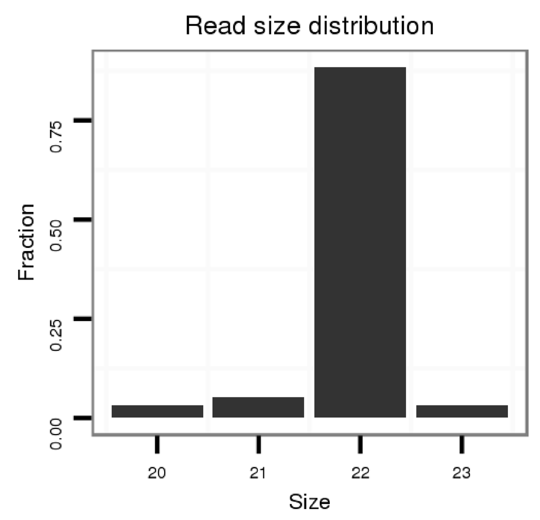
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_128	**scaffold_6496:20248036-20248120 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

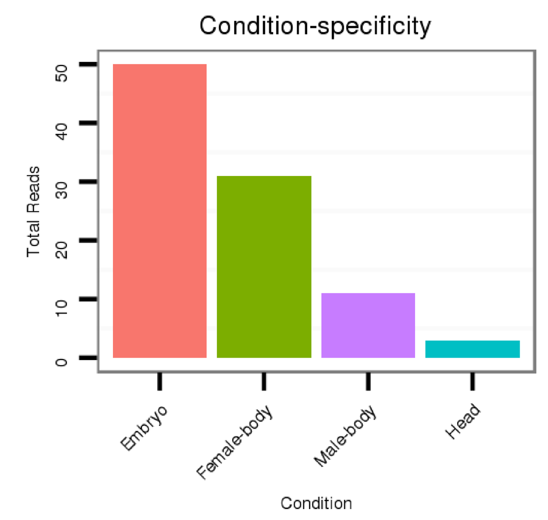
Legend: mature star mismatch in alignment mismatch in read

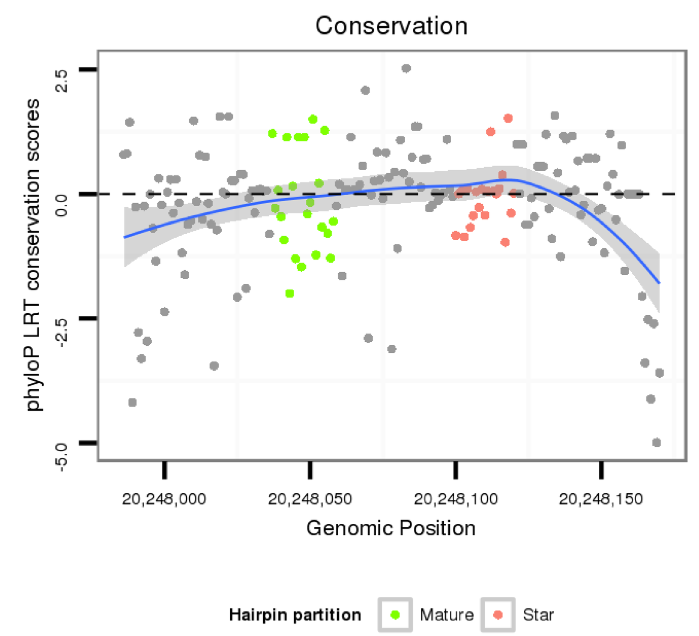
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI21040-in]

Repeatable elements

Name	Class	Family	Strand
AT_rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

TATTTGAAAAAATGTATATTATTTTATATAATTTATATTTTATGAATATATTCGCAAACGTCACAATTCTAGTGATATAAAGATCAATATATTTTTGTATATCGAACGAACTAAAACTGTGACGTTTGTGAATATATTTATAAAATAATCCTCGACGATATTTTCGCTCCTTCCAAATCCGTTTC ***********************************((((((((((((((((((((((((((((((.((.((((.((((((((((......))))))))))).........)))).)).)))))))))))))))))))))))))))))))....***********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
....TCGCAAACGTCACAATTCTAGT..	22	0	1	50.00	50	28	14	4	2	1	1
....TTCGCAAACGTCACAATTCTAG...	22	0	1	34.00	34	18	11	4	0	1	0
....ATTCGCAAACGTCACAATTCTA..	22	0	1	18.00	18	2	15	1	0	0	0
....TCGCAAACGTCACAATTCTAG...	21	0	1	3.00	3	0	3	0	0	0	0
....TTCGCAAACGTCACAATTCTAGT..	23	0	1	3.00	3	2	1	0	0	0	0
....ATTCGCAAACGTCACAATTCT...	21	0	1	2.00	2	0	2	0	0	0	0
....TCGCAAACGTCACAATTCTAGC..	22	1	1	2.00	2	2	0	0	0	0	0
....AACTGTGACGTTTGTGAATAT..	21	0	1	2.00	2	0	1	1	0	0	0
....TTCGCAAACGTCACAATTCTAC...	22	1	1	1.00	1	1	0	0	0	0	0
....TCGCAAACGTCACAATTCTA..	20	0	1	1.00	1	0	1	0	0	0	0
....AACTGTGACGTTTGTGAATA...	20	0	1	1.00	1	0	0	1	0	0	0
....TTCGCAAACGTCACAATTCT...	20	0	1	1.00	1	0	0	1	0	0	0
....TTCGCAAACGTCACAATTCTAGC..	23	1	1	1.00	1	0	1	0	0	0	0
....ATTCGCAAACGTCACAATTC..	20	0	1	1.00	1	0	1	0	0	0	0
....ATTCGCAAACGTCACAATTCTC..	22	1	1	1.00	1	0	1	0	0	0	0
....TATTCGCAAACGTCACAATTCT...	22	0	1	1.00	1	1	0	0	0	0	0
....ATTCGCAAACGTCACAATTCC...	21	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

ATAAACTTTTTTACATATAATAAAATATATTAAATATAAAATACTTATATAAGCGTTTGCAGTGTTAAGATCACTATATTTCTAGTTATATAAAAACATATAGCTTGCTTGATTTTGACACTGCAAACACTTATATAAATATTTTATTAGGAGCTGCTATAAAAGCGAGGAAGGTTTAGGCAAAG ***********************************((((((((((((((((((((((((((((((.((.((((.((((((((((......))))))))))).........)))).)).)))))))))))))))))))))))))))))))....***********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V049 head	V056 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6496:20247986-20248170 +	dmo_128	TATTTGAAAAA---ATGTATATTATTTTATATAAT------------------------------------TTATAT-T--------TTATGAATATATTC--------GCAAACGTCA----------------CAAT----TCTAGTGATATAAA------G-----------------A-------------TCAATATATTTTTGT-AT--ATC----GAACGAACTA---AAACTGTGACGTTTGTG----------------------AATATATTTATAA---AATAATCCTCGACGATATTTTCGCT-------------------------------------C--CTTCCAAATC--CG-TTTC
droVir3	scaffold_13036:31797-31957 +		TATGCCATCCG---TCAATTTCATAATTTCACATACATATATATATATATATATATATATATATATATATATATTAT--A-TATATATA-----------------------------TATATATA------------------------------T--ATATATATATATCAATACGGCTTTAAGTAT----------TGTAT-ATATATATA-----T--TATTCTATGTTATATGCTCT-------------------------------------C--------------CT
droGri2	scaffold_15203:1197089-1197260 +		TATAGATATAG---ATATATGTAGATGTATTTAACATGTTACTATTGTCAAAGGTGAC------------------A-AAAGTGAC-----------------------------TATAGAAA------------------------------TACGAT----CTT----AAA-------------TATTAAGAAATGCCT---T--------------------------------------AAAAGGCTACAGCTTGG----------------------AATTTATTGCTTATTTAATTCTAGTCTACGAAATGTGACC-------------------------------------AC--ATTC-----C--AAATGTGT
droWil2	scaf2_1100000009134:549-729 -		TATTTATATAT---TTATATATTTATATATTATATATTTATATATTTATGTTGAAAA------------------T-ACCATATG-----------------------------TTTCTGTT------------------------------TGCAGC----CCT----GTA-------------TTTATCCCTGGTTAT---ATC----GATTGTACTAAGCTTGTAGGTTATCGATATAAGATGCT--------------------------------TTGTAACTCTGT---ATA-----------------------------TTTTGGCTTCT-TCTT--C-----CTTTTCCGCC
dp5	2:21913829-21913930 +		TAGCTGAACAT---TTGCATTAATTA----------TGCTATTTTTT---------------------------CTACATAT--------GTACGAGTATA-------------TGTAGGCATACAATTCCCAAC---TCTA--------------ATGATACATACATAC-ATAT---A---TTCT
droPer2	scaffold_55:75716-75856 +		TATTTATTTTA---GTATACATATGTATATATATTTTTTCTTATAT--TATATAT--TTAGAT--ACATCATTGTTTTGCATAATTT-T------------T----------------------------------ATA--------------------------------ATTTATAATAAACCTGTTTAAAATAA------GGAAATAAATTTGTG-------------------------ATT---A--TA--T-----TATTGTAATA
droAna3	scaffold_13767:424581-424725 +		TATTATA-TAT---ATA--ATTTATAATATATAAT-------------------------------------ATATA-------------AATATAATA-------G---AAAAAATATATAAGGTGTT---------------------CTAAAATTCTAGATTTT------AAATCA-TA-AAAAACAGATTTTACATACACTAGTAACATTTACTGTAAATACAATTAG---A---AAATAAT
droBip1	scf7180000393098:7345-7512 +		TATTTATATTT---ATATTATATTTATATTATATTTATTTATATTTATATTTATATTTAT------------------A-TTTATATT-----------------------------TATATTTA------------------------------TATTTA----TAT----TTA-------------TATTTATATTTATAT-TTATATTTA----TATTTATATTTA--TATTT--------------ATAT-TTAT---ATATTCATA-----------------------------------ACCTTTTTT-------------------------TTT---G--AA--A-----CCCCCAAACC
droKik1	scf7180000302592:405216-405408 +		TATATATATAT---ATATATATATATATATATATATATATATATATATATATATATATAT------------------A-TATATATA-----------------------------TATATATA------------------------------TATATA----TAT----ATA-------------TATATATATATAT-ATATATATA----TATATATATATA--TATAT--------------ATAT-ATAT---ATATTAA--TTAATTAATTAAATTAATTAATTTTATATTC-AATAATTTT--AATT-----T-TAATTTTA
droFic1	scf7180000454105:206637-206756 +		TATATGGCAAA---AAAAAGATAACATCGTTGTTT-------------------------------------TTTTAT-T--------CCACGAACATTCTTACAA------------------------CTAT----TCTAACTA------TATATAT--TAA---AATAATTTGCCCAAC--------------------------------AGATCTTTA-------------------------ACT---G--TG--G-----CTCTTGAAAA
droEle1	scf7180000491044:1188791-1188975 -		CATTTAATAATCTGTTTAATAGAAATTTGTGTATT--T---ATAAGGATATA-----TGCTAGAGTTTAA--------------TTAG----TTTTATTAAATAAAGCTCAGAC--TCAAATACATATTAGTAAGGTATAGAATAT---AAGTA--AGTATATAATGATTTTATATATGGGCGTGACA----------------TTGTA---------------------------CTCTAGTTACC-TACG--T-----GTCTGCCAAA
droRho1	scf7180000770833:752-877 +		TATATACATAT---ATACATATATACATATATACATATATACATATATACATATATAC------------------A-TATATACA-----------------------------TATATACA------------------------------TATATA----CAT----ATA-------------TACATATATATGTAT-ATACATATA----TAGATATATAC--AAAAAAT
droBia1	scf7180000301129:929-1066 +		TATATAAATAT---ATAAATATATAAATATATAAATATATAAATATATAAATATATAA------------------A-TATATAAA-----------------------------TATATAAA------------------------------TATATA----AAT----ATA-------------TAAATATATAAATAT-ATAAATATA----TAAATATATAAA--TATAT--------------AAAT-ATAT---A--AATA
droTak1	scf7180000415809:1135929-1136037 +		GTTTCAAAGGG---G---ATATTATTATATATTAT-------------------------------------TTTCAT-T--------TTATTAAAACAATTATAAATGCTAAACTGTAA-----------------TTAT----AATTCTCCCATAAA-------------------------------ACTCTAT-A---AATCAA-----A---C--ATAGTAA
droEug1	scf7180000407462:614-779 +		TATATGTATAT---ATGTATATATGTATATATGTATATATGTATATATGTATATATGT------------------A-TATATGTA-----------------------------TATATGTA------------------------------TATATG----TAT----ATA-------------TGTATATATGTATAT-ATGTATATA----TGTATATATGTA--TATAT--------------GTAT-ATAT---AG--TGACA---------------------T----ATCTAC--------------------------------AATAACCT--CG--T-----C--ACCTCCA
dm3	chr4:119131-119297 +		TATTTATATAT---ACATATATATATATGTATATATATATATATATATATATATATAT------------------A-TATATATA-----------------------------TATACATA------------------------------AATATA----TAG--C-AGA-------------TGTATATATTTGTAT-ACAT--CTATTATTTATTTAT--ATAATCATTCATATATATTA---------T---ATGTTCA--CTGA--------------TACAT--AA--G-----C--CATTCAG
droSim2	x:3389329-3389438 -		TATTTAAACACTTAGTAGGTATTAATTTGTTTAGC--------TTT-------------------------ATACGC--------TTGCGTGTGTG--------TTCTTGAGTGTGA----------------CAAC----TTTCTCTATGAAAA---ACTCAATAAAATCGA-----A---G--AATTAAA
droSec2	scaffold_2801:594-732 -		TATATCTATAT---ATCTATATATCTATATATCTATATATCTATATATCTATATATCT------------------A-TATATCTA-----------------------------TATATCTA------------------------------TATATC----TAT----ATA-------------TCTATATATCTATAT-ATCTATATA----TCTATAT--------------ATGCTATATATCTAT-ATAT---C--TATA
droYak3	X:3128232-3128372 -		TATATTTATAT---TTATATTTATATTTATATTTATATTTAGCTTTATATTTATATTT------------------A-TATTAAAA-----------------------------TGAATATT------------------------------GAGG----AT----------------TATAT-TTATC-GGA----TTTTTAT-----------------------------ATCTTAG------------------------------AATTATTTT--ATA-----------------------------CATAAACATCT-TAAA--C-----GT-TATCTTC
droEre2	scaffold_4690:7558875-7559053 +		TTTTCATTA-T---ATATTTTTAT-TATAAATTTTCAT-TATATATTTTTATT--------------------------------ATGAATTTTCA-----TTGTAAATTTTA------------------TTATACATTTTCATTAAATATTTTT---TATTATATATTTTTGTTATATATTATAT-TTATTAATATATTATTATTATA----TATTTTT--------------ATGATATATTTTTATGATAT---A--TTTT

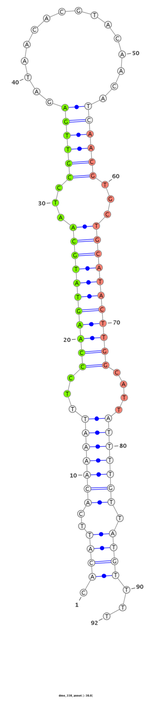
Generated: 09/08/2015 at 07:53 PM

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

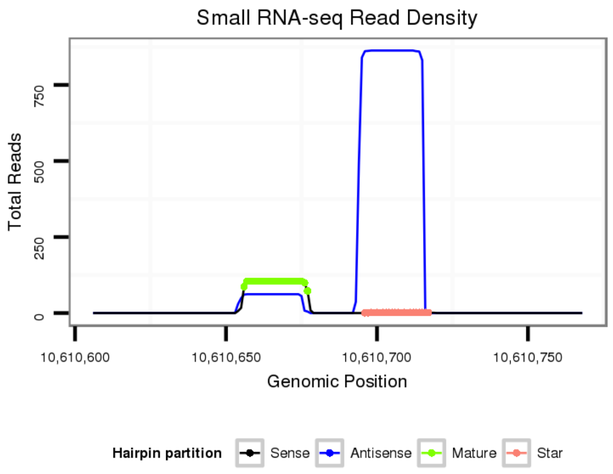
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_330	**scaffold_6500:10610656-10610718 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

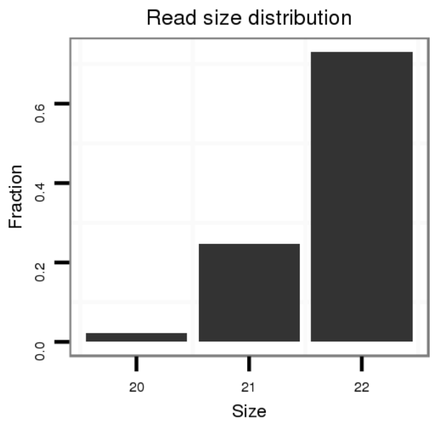
Legend: mature star mismatch in alignment mismatch in read

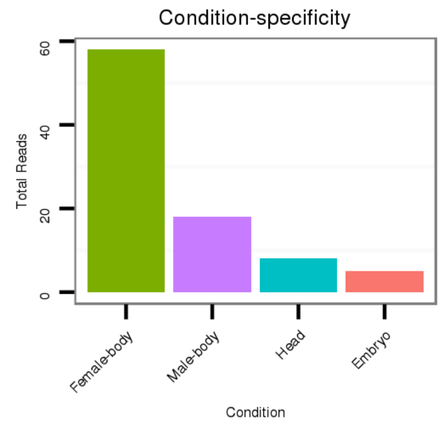
Predicted structure

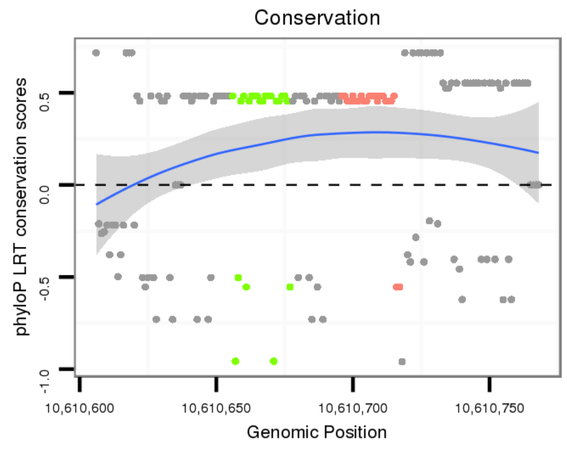


Show Alternate Folds









Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TAACATAAGTTTTTATGCACATCAGCAACATAATACACATTCACAAAATTTCCCAAGTATGCAATCCGTTGAGATAACACGTACAACATCAACGTGCTGCATACTTGGCATTATTTTGTTATGTTTTTGCTATTGTTAATTGTGATTTGCTAAAATATTATCA	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	V049 head	M060 embryo	V056 head	V041 embryo
**********.((((..(((((((...((((((((((...(((((.....))))))...))))))))))....)))))))....))))...**********											
.....TCCCAAGTATGCAATCCGTTGA.....	22	0	1	55.00	55	34	9	4	4	3	1
.....TCCCAAGTATGCAATCCGTTG.....	21	0	1	15.00	15	11	3	1	0	0	0
.....CCCAAGTATGCAATCCGTTGAG.....	22	0	1	9.00	9	5	4	0	0	0	0
.....TTCCCAAGTATGCAATCCGTTG.....	22	0	1	9.00	9	6	3	0	0	0	0
.....CCCAAGTATGCAATCCGTTGA.....	21	0	1	7.00	7	7	0	0	0	0	0
.....TTTCCCAAGTATGCAATCCGTT.....	22	0	1	5.00	5	4	1	0	0	0	0
.....CCCAAGTATGCAATCCGTTG.....	20	0	1	2.00	2	0	2	0	0	0	0
.....TCCCAAGTATGCAATCCGTTGAA.....	23	1	1	2.00	2	2	0	0	0	0	0
.....AACGTGCTGCATACTTGGCATT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....CCCAAGTATGCAATCCGTTTTT.....	21	2	1	1.00	1	0	0	0	0	1	0
.....CGTGCTGCATACTTGGCATTAT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TTTCCCAAGTATGCAATCCGTTGA.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TTTCCCAAGTATGCAATCCGTTG.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TTCCCAAGTATGCAATCCGTTGA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....AACGTGCTGCATACTTGGCATTAA.....	24	1	1	1.00	1	0	0	0	1	0	0

Anti-sense strand reads

ATTGTATTCAAAAATACGTGTAGTCGTTGTATTATGTGTAAGTGTTTTAAAGGGTTCATACGTTAGGCAACTCTATTGTGCATGTTGTAGTTGCACGACGTATGAACCGTAATAAAACAATACAAAAACGATAACAATTAACACTAAACGATTTTATAATAGT	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V041 embryo	V049 head	V056 head
**********.((((..(((((((...((((((((((...(((((.....))))))...))))))))))....)))))))....))))...**********											
.....AGTTGCACGACGTATGAACCGT.....	22	0	1	436.00	436	285	91	21	19	10	10
.....GTTGCACGACGTATGAACCGT.....	21	0	1	342.00	342	254	73	2	2	6	5
.....TAGTTGCACGACGTATGAACCGT.....	23	0	1	29.00	29	25	2	1	0	0	1
.....AAAGGGTTCATACGTTAGGCAA.....	22	0	1	25.00	25	14	2	7	2	0	0
.....TTGCACGACGTATGAACCGT.....	20	0	1	20.00	20	18	1	0	0	0	1
.....CTAGTTGCACGACGTATGAACCGT.....	24	1	1	18.00	18	18	0	0	0	0	0
.....AAGGGTTCATACGTTAGGCAA.....	21	0	1	16.00	16	5	4	7	0	0	0
.....AGTTGCACGACGTATGAACCG.....	21	0	1	15.00	15	6	9	0	0	0	0
.....AAGTTGCACGACGTATGAACCGT.....	23	1	1	11.00	11	10	1	0	0	0	0
.....TAGTTGCACGACGTATGAACCG.....	22	0	1	8.00	8	6	0	2	0	0	0
.....CAGTTGCACGACGTATGAACCGT.....	23	1	1	7.00	7	5	2	0	0	0	0
.....TGTTGCACGACGTATGAACCGT.....	22	1	1	7.00	7	5	1	1	0	0	0
.....AGGGTTCATACGTTAGGCAA.....	20	0	1	6.00	6	3	1	2	0	0	0
.....GTTGCACGACGTATGAACCG.....	20	0	1	6.00	6	0	6	0	0	0	0
.....TAAGGGTTCATACGTTAGGCAA.....	22	1	1	5.00	5	5	0	0	0	0	0
.....AAAGGGTTCATACGTTAGGCA.....	21	0	1	4.00	4	4	0	0	0	0	0
.....TTAGTTGCACGACGTATGAACCGT.....	24	1	1	4.00	4	3	0	1	0	0	0
.....TAGGGTTCATACGTTAGGCA.....	20	1	1	4.00	4	4	0	0	0	0	0
.....AGGGTTCATACGTTAGGCAACT.....	22	0	1	4.00	4	3	0	0	0	0	1
.....AAAAGGGTTCATACGTTAGGCAA.....	23	1	1	3.00	3	3	0	0	0	0	0
.....AAAGTTGCACGACGTATGAACCGT.....	24	2	1	3.00	3	2	0	0	0	0	1
.....CTAGTTGCACGACGTATGAACCG.....	23	1	1	2.00	2	2	0	0	0	0	0
.....AGGGTTCATACGTTAGGCAAC.....	21	0	1	2.00	2	2	0	0	0	0	0
.....TAGGGTTCATACGTTAGGCAA.....	21	1	1	2.00	2	2	0	0	0	0	0
.....AAGGGTTCATACGTTAGGCA.....	20	0	1	2.00	2	1	1	0	0	0	0
.....TAGGGTTCATACGTTAGGCAAC.....	22	1	1	2.00	2	2	0	0	0	0	0
.....GGTTGCACGACGTATGAACCGT.....	22	1	1	2.00	2	2	0	0	0	0	0
.....TTAGTTGCACGACGTATGAACC.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TTAGTTGCACGACGTATGAACCG.....	23	1	1	1.00	1	1	0	0	0	0	0
.....AAAGTTGCACGACGTATGAACCGT.....	25	3	1	1.00	1	0	0	1	0	0	0
.....TTTGCACGACGTATGAACCGT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TGCACGACGTATGAACCGT.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TAAAGGGTTCATACGTTAGGCAA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....AGTTGCACGACGTATGAAC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....CGTTGCACGACGTATGAACCGT.....	22	1	1	1.00	1	0	1	0	0	0	0
.....AGTTGCACGACGTATGAACCGTA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TCCGGGTTCATACGTTAGGCAACT.....	24	3	1	1.00	1	1	0	0	0	0	0
.....TTGGGTTCATACGTTAGGCAA.....	21	2	1	1.00	1	1	0	0	0	0	0
.....CTGTTGCACGACGTATGAACCGT.....	23	2	1	1.00	1	0	1	0	0	0	0
.....GCACGACGTATGAACCGT.....	18	0	1	1.00	1	0	1	0	0	0	0
.....CAAGTTGCACGACGTATGAACCGT.....	24	2	1	1.00	1	1	0	0	0	0	0
.....AATAGTTGCACGACGTATGAACCGT.....	25	2	1	1.00	1	0	1	0	0	0	0
.....AAAAGGGTTCATACGTTAGGCA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....GTAGGGTTCATACGTTAGGCA.....	21	2	1	1.00	1	1	0	0	0	0	0
.....GTTGCACGACGTATGAAC.....	18	0	1	1.00	1	0	1	0	0	0	0
.....CAGTTGCACGACGTATGAACCG.....	22	1	1	1.00	1	0	1	0	0	0	0
.....AGTTGCACGACGTATGAACC.....	20	0	1	1.00	1	0	1	0	0	0	0
.....GGGTTCATACGTTAGGCAACT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....AATGTTGCACGACGTATGAACCGT.....	24	3	1	1.00	1	1	0	0	0	0	0
.....AAAAAGGGTTCATACGTTAGGCAA.....	24	2	1	1.00	1	1	0	0	0	0	0
.....TAAGGGTTCATACGTTAGGCA.....	21	1	1	1.00	1	1	0	0	0	0	0
.....CTAGGGTTCATACGTTAGGCA.....	21	2	1	1.00	1	1	0	0	0	0	0
.....AAGGGTTCATACGTTAGGCAAC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TTGCACGACGTATGAACCGTA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CCTGGTTCATACGTTAGGCAA.....	21	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_6500:10610606-10610768 +	dmo_330	TAACATAAGT-TTTTATGCACATCAGCAACATAATACACATTCACAAAATTTCCCAAGTATGCAATCCGTTGAGATAACACGTACAACATCAACGTGCTGCATACTTGGCATTATTTTGTTATGTTTTTGCTATTGTTAATTGTGATTTGCTAAAATATTATCA
droVir3	scaffold_12723:4640725-4640849 +	dvi_24640	TATTATAATTTACTTTATGTTTACAAGCAGA---ATACAAATTAGCAAAATTTGTCATGTATGCAATGCGTTGTGACAAGGAGAAAACATCAACGTGCTGCATACTTGGCAAATTTATATTTGTGTTTT----------
droGri2	scaffold_15203:4252192-4252254 -		TGTTTGTTTGGCTTTT----------GTGTTGTTATATTCTTGCTGTATTTAATTATAATCTGATGCAATATT----

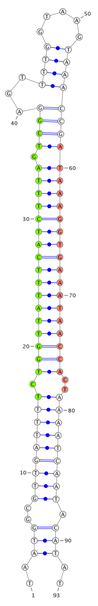
Generated: 08/18/2015 at 05:25 PM

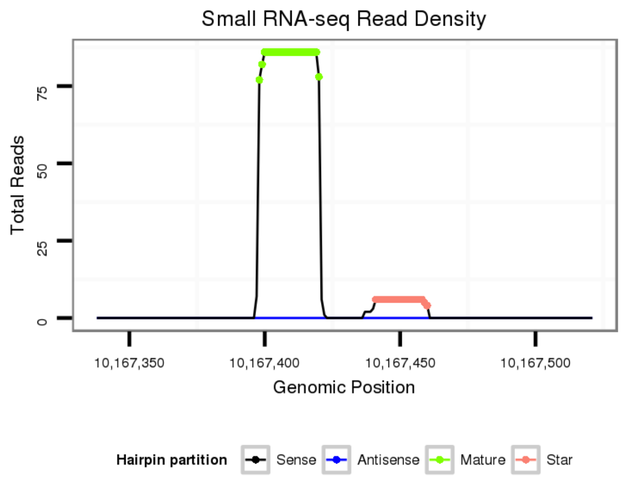
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

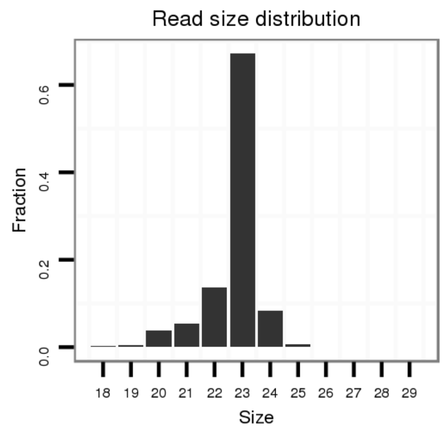
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3135	**scaffold_6473:10167388-10167471 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

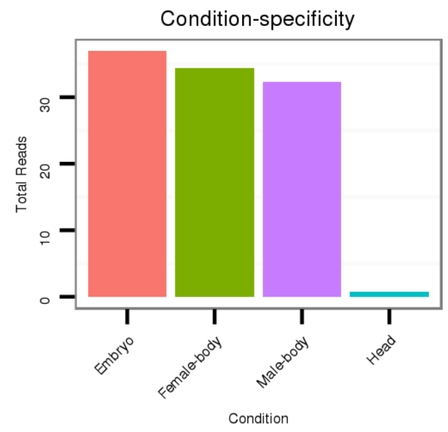
Legend: mature star mismatch in alignment mismatch in read

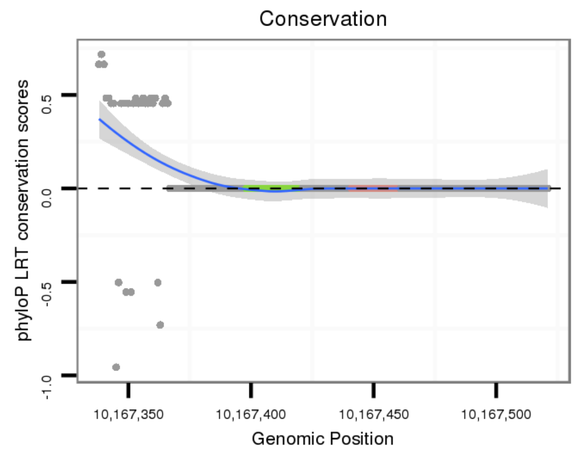
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI15760-in]

No Repeatable elements found

mature	star
1. dmo_3139 scaffold_6308:570045-570067 + 2. dmo_3140 scaffold_6308:570864-570886 - 3. dmo_3144 scaffold_6473:8660635-8660657 - 4. dmo_3145 scaffold_6473:9912732-9912754 - 5. dmo_3149 scaffold_6473:9914029-9914051 + 6. dmo_3151 scaffold_6473:9918570-9918592 - 7. dmo_3135 scaffold_6473:10167398-10167420 + 8. dmo_3137 scaffold_6473:10168272-10168294 - 9. dmo_3153 scaffold_6473:10193410-10193432 +	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

CTGTAGCGTGCAGTGAGCTGCTGTGCCACTCGTTCTCAGGCTGTTTAATGGCGTTGATTTTCTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATACATATTAAACTAGTGAGAGCGAGTGCTCTAGTAGAGACTGCTCGACTAGCA **..(((..(((((((((.(((((((((((((((((.((((...((((.....))))))))))))))))))))))))..)))))))))..))))..***	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
.....TCTGGTTATTTCATCTTTAGTCG.....	23	0	9	62.56	563	82	227	226	25	2	1
.....TCTGGTTATTTCATCTTTAGTC.....	22	0	9	7.00	63	50	6	6	1	0	0
.....TTCTGGTTATTTCATCTTTAGTCG.....	24	0	9	6.33	57	9	25	19	4	0	0
.....ATAAAGGTGAAATAACCACT.....	20	0	19	3.42	65	61	2	0	2	0	0
.....CTGGTTATTTCATCTTTAGTCGG.....	23	0	11	3.00	33	10	5	16	1	0	1
.....CTGGTTATTTCATCTTTAGTCG.....	22	0	11	2.82	31	4	19	7	1	0	0
.....TGGTTATTTCATCTTTAGTCG.....	21	0	20	2.70	54	2	24	21	6	1	0
.....TGGTTATTTCATCTTTAGTCGG.....	22	0	20	1.95	39	14	6	16	2	1	0
.....ACCGATAAAGGTGAAATAACCAC.....	23	0	15	1.67	25	25	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGG.....	24	0	9	1.44	13	10	2	0	1	0	0
.....TGGTTATTTCATCTTTAGTCGGA.....	23	0	20	1.40	28	21	1	5	1	0	0
.....TTCTGGTTATTTCATCTTTAGTC.....	23	0	9	1.22	11	7	3	0	1	0	0
.....ACCGATAAAGGTGAAATAACCA.....	22	0	20	1.20	24	17	3	1	3	0	0
.....GATAAAGGTGAAATAACCACT.....	21	0	18	1.11	20	17	2	0	1	0	0
.....TCTGGTTATTTCATCTTTAGTCGA.....	24	1	9	1.00	9	4	1	4	0	0	0
.....ATAAAGGTGAAATAACCACG.....	20	1	19	0.95	18	18	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGT.....	21	0	9	0.67	6	5	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTCG.....	25	0	9	0.67	6	2	4	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTC.....	24	0	9	0.56	5	4	1	0	0	0	0
.....ACCGATAAAGGTGAAATAACC.....	21	0	20	0.50	10	9	1	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCA.....	23	1	9	0.44	4	1	2	1	0	0	0
.....TCTGGTTATTTCATCTTTAG.....	20	0	9	0.44	4	4	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGA.....	21	0	20	0.35	7	7	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCT.....	23	1	9	0.33	3	1	0	1	0	1	0
.....TTATTTCATCTTTAGTCGGAGTTT.....	24	0	18	0.33	6	4	2	0	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
.....TTGATTTTCTGGTTATTTCATC.....	22	0	4	0.25	1	1	0	0	0	0	0
.....TAATGGCGTTGATTTTCTGG.....	20	0	4	0.25	1	0	1	0	0	0	0
.....TCTGGTTATTTCATCTTTAGC.....	21	1	9	0.22	2	2	0	0	0	0	0
.....TTCTGGTTATTTCATCTTTAGTCGC.....	25	1	9	0.22	2	0	0	2	0	0	0
.....TTCTGGTTATTTCATCTTTAGT.....	22	0	9	0.22	2	1	0	0	0	1	0
.....TCTGGTTATTTCATCTTTAGTCTT.....	24	2	9	0.22	2	2	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGC.....	24	1	9	0.22	2	0	0	2	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGT.....	24	1	9	0.22	2	0	0	2	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
.....CTGGTTATTTCATCTTTAGTCGGT.....	24	1	11	0.18	2	1	1	0	0	0	0
.....ATTTTCTGGTTATTTCATCTTTA.....	23	0	6	0.17	1	1	0	0	0	0	0
.....CGATAAAGGTGAAATAACCACC.....	22	1	18	0.17	3	3	0	0	0	0	0
.....GTTATTTCATCTTTAGTCG.....	19	0	20	0.15	3	2	0	1	0	0	0
.....TTATTTCATCTTTAGTCG.....	18	0	20	0.15	3	1	2	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCAA.....	24	2	9	0.11	1	0	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTCGA.....	26	1	9	0.11	1	0	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGC.....	23	1	9	0.11	1	0	1	0	0	0	0
.....TTCTGGTTATTTCATCTTTAG.....	21	0	9	0.11	1	0	0	1	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGGC.....	25	1	9	0.11	1	1	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGGAA.....	26	1	9	0.11	1	0	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGT.....	23	0	9	0.11	1	0	1	0	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	0	1	0	0	0
.....CTGGTTATTTCATCTTTAGTCAA.....	23	2	11	0.09	1	0	1	0	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGC.....	24	1	11	0.09	1	0	0	1	0	0	0
.....ACCGATAAAGGTGAAATAACCACA.....	24	1	15	0.07	1	0	1	0	0	0	0
.....ACCGATAAAGGTGAAATAACCACT.....	24	0	15	0.07	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	1	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTTTTGGTA.....	29	0	18	0.06	1	1	0	0	0	0	0
.....GATAAAGGTGAAATAACCACTAAC.....	24	1	18	0.06	1	1	0	0	0	0	0
.....ATTTCATCTTTAGTCGGAGTTT.....	22	0	18	0.06	1	1	0	0	0	0	0
.....GATAAAGGTGAAATAACCAC.....	20	0	18	0.06	1	1	0	0	0	0	0
.....ATAAAGGTGAAATAACCACTGT.....	22	2	19	0.05	1	0	0	1	0	0	0
.....AAAGGTGAAATAACCACT.....	18	0	19	0.05	1	1	0	0	0	0	0
.....ATAAAGGTGAAATAACCACTTT.....	22	2	19	0.05	1	1	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTC.....	20	0	20	0.05	1	1	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTT.....	23	0	20	0.05	1	1	0	0	0	0	0
.....CGATAAAGGTGAAATAACCC.....	20	1	20	0.05	1	1	0	0	0	0	0
.....CCGATAAAGGTGAAATAACCA.....	21	0	20	0.05	1	0	1	0	0	0	0
.....TGGTTATTTCATCTTTAGTCGGT.....	23	1	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCGGC.....	22	1	20	0.05	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGAA.....	22	1	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

GACATCGCACGTCACTCGACGACACGGTGAGCAAGAGTCCGACAAATTACCGCAACTAAAAGACCAATAAAGTAGAAATCAGCCTCAAAACCATTCATTTGGCTATTTCCACTTTATTGGTGATTTTAGTTATGTATAATTTGATCACTCTCGCTCACGAGATCATCTCTGACGAGCTGATCGT **..(((..(((((((((.(((((((((((((((((.((((...((((.....))))))))))))))))))))))))..)))))))))..))))..***	Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head	V110 male body	V049 head	M046 female body	M060 embryo	V041 embryo
.....TCATCTCTGACGAGCTGATCG.	21	0	9	0.11	1	0	1	0	0	0	0
.....AAGAAATCAGCCTCAAAACCAT.....	22	1	18	0.06	1	0	0	0	1	0	0
.....AGATCATCTCTGACGAGCT.....	19	0	20	0.05	1	0	0	0	0	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:10167338-10167521 +	dmo_3135	CTGTAGCGTGCAGTGAGCTGCTGTGCCACTCGTTCTCAGGCTGTTTAATGGCGTTGATTTTCTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATACATATTAAACTAGTGAGAGCGAGTGCTCTAGTAGAGACTGCTCGACTAGCA
droVir3	scaffold_13047:13837520-13837548 +		CTGTAGCCCGGTGAGAGCTGCTGTAACAC----------
droGri2	scaffold_14853:6986563-6986565 +		CTG----------

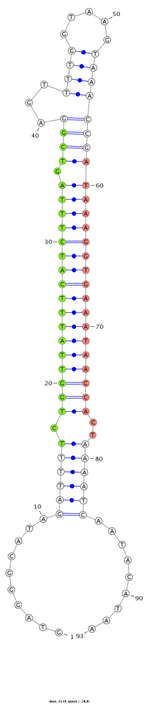
Generated: 09/08/2015 at 07:45 PM

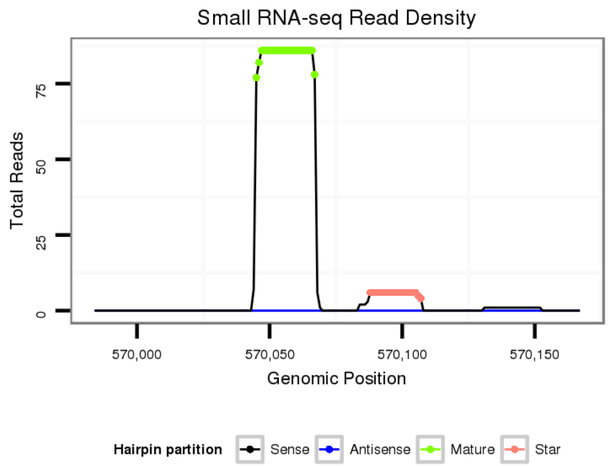
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

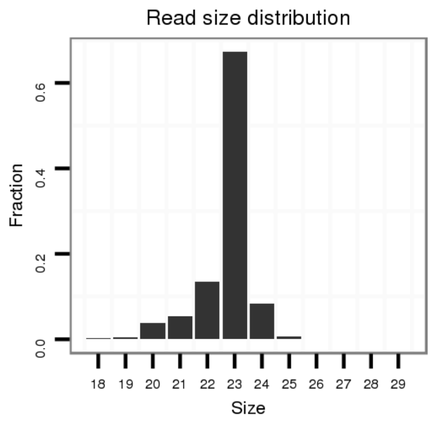
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3139	**scaffold_6308:570034-570117 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

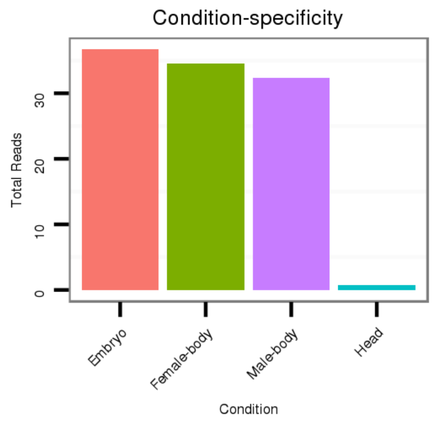
Legend: mature star mismatch in alignment mismatch in read

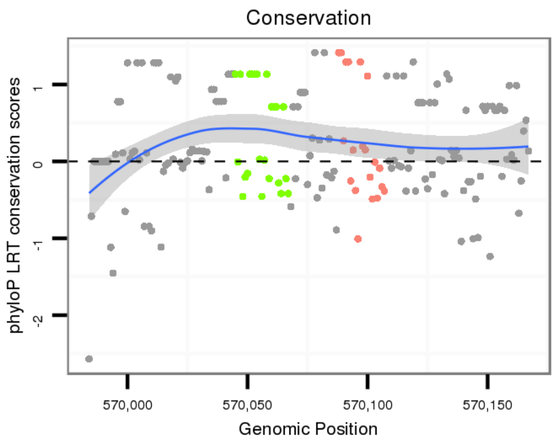
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dmo_3139 scaffold_6308:570045-570067 + 2. dmo_3140 scaffold_6308:570864-570886 - 3. dmo_3144 scaffold_6473:8660635-8660657 - 4. dmo_3145 scaffold_6473:9912732-9912754 - 5. dmo_3149 scaffold_6473:9914029-9914051 + 6. dmo_3151 scaffold_6473:9918570-9918592 - 7. dmo_3135 scaffold_6473:10167398-10167420 + 8. dmo_3137 scaffold_6473:10168272-10168294 - 9. dmo_3153 scaffold_6473:10193410-10193432 +	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

CTTCCTCATTATTTTTAAACAATTAATAAATACATCCACACTTCCAGTAGGGCATAGATTTTCTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATACATAATATACTAGTGAGAGTGCTCATGGTGAGACTGCTCGACTAGCAGAT **********.....(((((((.((((((((((((((((((.((((...((((.....))))))))))))))))))))))))..)))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
.....TCTGGTTATTTCATCTTTAGTCG.....	23	0	9	62.56	563	82	227	226	25	2	1
.....TCTGGTTATTTCATCTTTAGTC.....	22	0	9	7.00	63	50	6	6	1	0	0
.....TTCTGGTTATTTCATCTTTAGTCG.....	24	0	9	6.33	57	9	25	19	4	0	0
.....ATAAAGGTGAAATAACCACT.....	20	0	19	3.42	65	61	2	0	2	0	0
.....CTGGTTATTTCATCTTTAGTCGG.....	23	0	11	3.00	33	10	5	16	1	0	1
.....CTGGTTATTTCATCTTTAGTCG.....	22	0	11	2.82	31	4	19	7	1	0	0
.....TGGTTATTTCATCTTTAGTCG.....	21	0	20	2.70	54	2	24	21	6	1	0
.....TGGTTATTTCATCTTTAGTCGG.....	22	0	20	1.95	39	14	6	16	2	1	0
.....ACCGATAAAGGTGAAATAACCAC.....	23	0	15	1.67	25	25	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGG.....	24	0	9	1.44	13	10	2	0	1	0	0
.....TGGTTATTTCATCTTTAGTCGGA.....	23	0	20	1.40	28	21	1	5	1	0	0
.....TTCTGGTTATTTCATCTTTAGTC.....	23	0	9	1.22	11	7	3	0	1	0	0
.....ACCGATAAAGGTGAAATAACCA.....	22	0	20	1.20	24	17	3	1	3	0	0
.....GATAAAGGTGAAATAACCACT.....	21	0	18	1.11	20	17	2	0	1	0	0
.....TGAGAGTGCTCATGGTGAGACT.....	22	0	1	1.00	1	0	0	1	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGA.....	24	1	9	1.00	9	4	1	4	0	0	0
.....ATAAAGGTGAAATAACCACC.....	20	1	19	0.95	18	18	0	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTCG.....	25	0	9	0.67	6	2	4	0	0	0	0
.....TCTGGTTATTTCATCTTTAGT.....	21	0	9	0.67	6	5	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTC.....	24	0	9	0.56	5	4	1	0	0	0	0
.....ACCGATAAAGGTGAAATAACC.....	21	0	20	0.50	10	9	1	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCA.....	23	1	9	0.44	4	1	2	1	0	0	0
.....TCTGGTTATTTCATCTTTAG.....	20	0	9	0.44	4	4	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGA.....	21	0	20	0.35	7	7	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCT.....	23	1	9	0.33	3	1	0	1	0	1	0
.....TTATTTCATCTTTAGTCGGAGTTT.....	24	0	18	0.33	6	4	2	0	0	0	0
.....CGATAAAGGTGAAATAACCACT.....	22	0	18	0.28	5	5	0	0	0	0	0
.....GATAAAGGTGAAATAACCACTA.....	22	0	18	0.28	5	4	0	0	0	1	0
.....ATAAAGGTGAAATAACCAC.....	19	0	19	0.26	5	5	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGC.....	24	1	9	0.22	2	0	0	2	0	0	0
.....TTCTGGTTATTTCATCTTTAGT.....	22	0	9	0.22	2	1	0	0	0	1	0
.....TTCTGGTTATTTCATCTTTAGTCGC.....	25	1	9	0.22	2	0	0	2	0	0	0
.....TCTGGTTATTTCATCTTTAGTCTT.....	24	2	9	0.22	2	2	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGT.....	24	1	9	0.22	2	0	0	2	0	0	0
.....TCTGGTTATTTCATCTTTAGC.....	21	1	9	0.22	2	2	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	1	0	0	0	0
.....ATTTTCTGGTTATTTCATCTTTA.....	23	0	6	0.17	1	1	0	0	0	0	0
.....CGATAAAGGTGAAATAACCACC.....	22	1	18	0.17	3	3	0	0	0	0	0
.....TTATTTCATCTTTAGTCG.....	18	0	20	0.15	3	1	2	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTCGA.....	26	1	9	0.11	1	0	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGT.....	23	0	9	0.11	1	0	1	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGGAA.....	26	1	9	0.11	1	0	1	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCAA.....	24	2	9	0.11	1	0	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGC.....	23	1	9	0.11	1	0	1	0	0	0	0
.....TTCTGGTTATTTCATCTTTAG.....	21	0	9	0.11	1	0	0	1	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGGC.....	25	1	9	0.11	1	1	0	0	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
.....CTGGTTATTTCATCTTTAGTCGGC.....	24	1	11	0.09	1	0	0	1	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGAG.....	25	0	11	0.09	1	0	0	1	0	0	0
.....CTGGTTATTTCATCTTTAGTCAA.....	23	2	11	0.09	1	0	1	0	0	0	0
.....ACCGATAAAGGTGAAATAACCACA.....	24	1	15	0.07	1	0	1	0	0	0	0
.....ACCGATAAAGGTGAAATAACCACT.....	24	0	15	0.07	1	1	0	0	0	0	0
.....GAGTTTTGGTAAGTAAACCG.....	20	0	18	0.06	1	1	0	0	0	0	0
.....ATTTCATCTTTAGTCGGAGTTT.....	22	0	18	0.06	1	1	0	0	0	0	0
.....GATAAAGGTGAAATAACCAC.....	20	0	18	0.06	1	1	0	0	0	0	0
.....CGATAAAGGTGAAATAACCACA.....	22	1	18	0.06	1	0	1	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTTTTGGTA.....	29	0	18	0.06	1	1	0	0	0	0	0
.....GATAAAGGTGAAATAACCACTAAC.....	24	1	18	0.06	1	1	0	0	0	0	0
.....ATAAAGGTGAAATAACCACTGT.....	22	2	19	0.05	1	0	0	1	0	0	0
.....AAAGGTGAAATAACCACT.....	18	0	19	0.05	1	1	0	0	0	0	0
.....ATAAAGGTGAAATAACCACTTT.....	22	2	19	0.05	1	1	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTCGGT.....	23	1	20	0.05	1	1	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTT.....	23	0	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCG.....	20	0	20	0.05	1	0	1	0	0	0	0
.....GGTTATTTCATCTTTAGTCGGC.....	22	1	20	0.05	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGAA.....	22	1	20	0.05	1	1	0	0	0	0	0
.....CGATAAAGGTGAAATAACCC.....	20	1	20	0.05	1	1	0	0	0	0	0
.....CCGATAAAGGTGAAATAACCA.....	21	0	20	0.05	1	0	1	0	0	0	0
.....TGGTTATTTCATCTTTAGTC.....	20	0	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

GAAGGAGTAATAAAAATTTGTTAATTATTTATGTAGGTGTGAAGGTCATCCCGTATCTAAAAGACCAATAAAGTAGAAATCAGCCTCAAAACCATTCATTTGGCTATTTCCACTTTATTGGTGATTTTAGTTATGTATTATATGATCACTCTCACGAGTACCACTCTGACGAGCTGATCGTCTA **********.....(((((((.((((((((((((((((((.((((...((((.....))))))))))))))))))))))))..)))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V049 head	M046 female body	M060 embryo
.....AAGAAATCAGCCTCAAAACCAT.....	22	1	18	0.06	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:569984-570167 +	dmo_3139	CTTCCTCATTATTTTTAAACAATTAATAAATACATCCACACTTCCAGTAGGGCATAGATTTTCTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAG----------TAAACCGATAAAGGTGAAATAACCACTAAAATCAATACATAATATACTAGTGAGAGTGCTCATGGTGAGACTGCTCGACTAGCAGAT
droVir3	scaffold_13049:24408128-24408225 -		GG------AGT----------TTTAGTAAGTCCATTGAAACTTGCAGGCCTTAATCAAAGTTAAGCATAATAACCATA----------GAGAGTGGTCTATTAGAGACTGCTCGACTAGAAGAT
droGri2	scaffold_15245:18234579-18234668 +		TT------TTC----------GTACACCAC---------CAGACAAAAAAAAAA--------AATGATAATAAAAAATAAA----------TAA--------AGTTAGAATGCGCTAAGCAAGAATGCTTGACTGGCAGAT
droWil2	scf2_1100000004909:10627472-10627594 -		TT------AA---AAACTTAATGTCGAAAGTTATCCATGTTACTAATAGA-------TTTTTTTATATATTTTGTTTTTTTTTCAATTTTAATATG----------TATAACAATTAAGAACAATTATGTTGAGAAGGTCTAGGCA----------TGAT
droPer2	scaffold_28:787529-787540 +		CG----------CAAGTGGAT
droRho1	scf7180000778986:11087-11130 -		AT------AT---TTAAACATTAATCAAAAATTTTCACACCTCCAGCAGAGG----------A
droBia1	scf7180000301359:5484-5554 +		TT------GG----------AAAG----------TAAAGTAATAAAAATGATATCTCAAATAGAGTATATACATAATTGATTAAAAGGGCTA----------TCAT
droTak1	scf7180000415914:501913-501913 -		T----------
droYak3	3R:13378371-13378412 +		CA------TAT----------TTTTTGTGTGGCATAGTTTTCTTGTTATTCAGT----------CCT
droEre2	scaffold_4820:2633342-2633366 -		AT------TATTTTCAAACAATTAATAAAC----------A

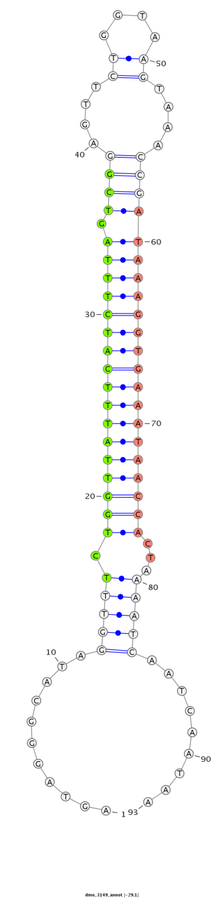
Generated: 09/08/2015 at 07:45 PM

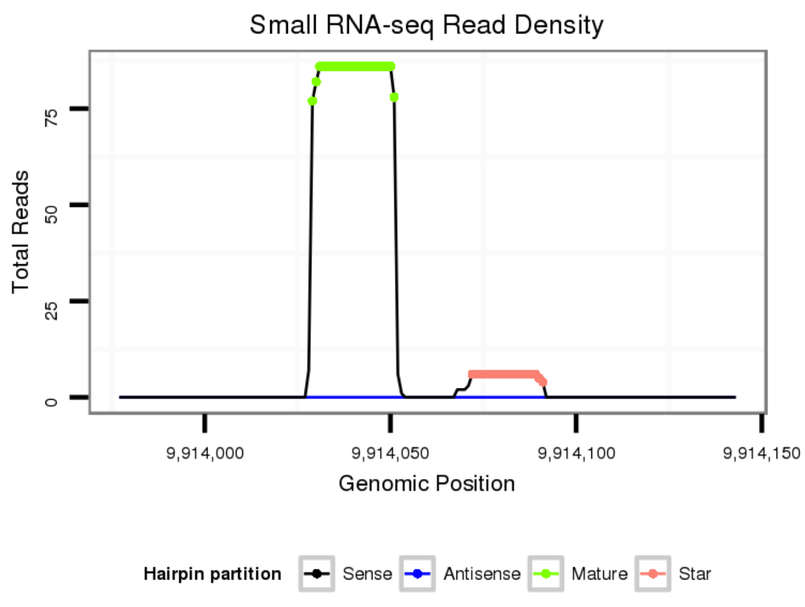
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

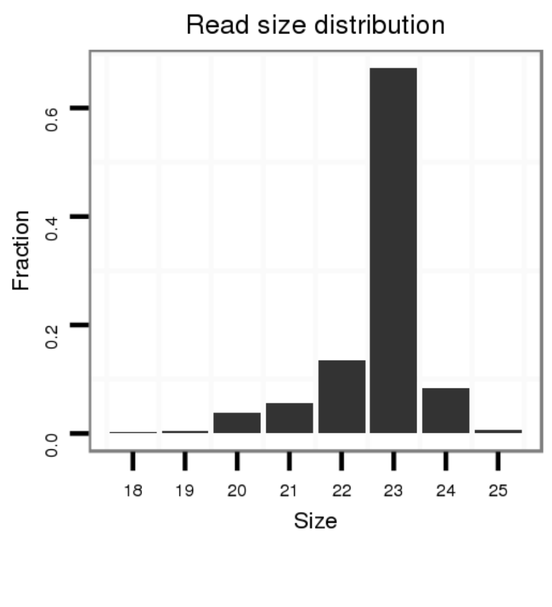
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3149	**scaffold_6473:9914027-9914093 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

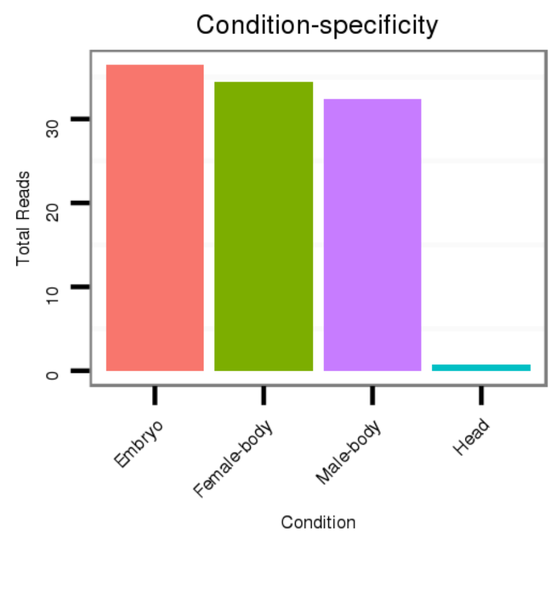
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
Homo6	DNA	hAT-Pegasus	-

mature

1. dmo_3139 scaffold_6308:570045-570067 +
2. dmo_3140 scaffold_6308:570864-570886 -
3. dmo_3144 scaffold_6473:8660635-8660657 -
4. dmo_3145 scaffold_6473:9912732-9912754 -
5. dmo_3149 scaffold_6473:9914029-9914051 +
6. dmo_3151 scaffold_6473:9918570-9918592 -
7. dmo_3135 scaffold_6473:10167398-10167420 +
8. dmo_3137 scaffold_6473:10168272-10168294 -
9. dmo_3153 scaffold_6473:10193410-10193432 +

star

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

TAAATTTTTAACAAATAATAAATATATCCACATTTCCAGTAGGGCATAGGTTTCTGGTTATTTCATCTTTAGTCGGAGTTCTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATCAATAAACTAGTGAGAGTGCTCTAGTAGAGACTGCTCGACTAC **********.....(((((.(((((((((((((((((.((((....((....))....)))))))))))))))))))...)))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
.....TCTGGTTATTTCATCTTTAGTCG.....	23	0	9	62.56	563	82	227	226	25	2	1
.....TCTGGTTATTTCATCTTTAGTC.....	22	0	9	7.00	63	50	6	6	1	0	0
.....TTCTGGTTATTTCATCTTTAGTCG.....	24	0	9	6.33	57	9	25	19	4	0	0
.....ATAAAGGTGAAATAACCACT.....	20	0	19	3.42	65	61	2	0	2	0	0
.....CTGGTTATTTCATCTTTAGTCGG.....	23	0	11	3.00	33	10	5	16	1	0	1
.....CTGGTTATTTCATCTTTAGTCG.....	22	0	11	2.82	31	4	19	7	1	0	0
.....TGGTTATTTCATCTTTAGTCG.....	21	0	20	2.70	54	2	24	21	6	1	0
.....TGGTTATTTCATCTTTAGTCGG.....	22	0	20	1.95	39	14	6	16	2	1	0
.....ACCGATAAAGGTGAAATAACCAC.....	23	0	15	1.67	25	25	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGG.....	24	0	9	1.44	13	10	2	0	1	0	0
.....TGGTTATTTCATCTTTAGTCGGA.....	23	0	20	1.40	28	21	1	5	1	0	0
.....TTCTGGTTATTTCATCTTTAGTC.....	23	0	9	1.22	11	7	3	0	1	0	0
.....ACCGATAAAGGTGAAATAACCA.....	22	0	20	1.20	24	17	3	1	3	0	0
.....GATAAAGGTGAAATAACCACT.....	21	0	18	1.11	20	17	2	0	1	0	0
.....TCTGGTTATTTCATCTTTAGTCGA.....	24	1	9	1.00	9	4	1	4	0	0	0
.....ATAAAGGTGAAATAACCACC.....	20	1	19	0.95	18	18	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGT.....	21	0	9	0.67	6	5	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTCG.....	25	0	9	0.67	6	2	4	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTC.....	24	0	9	0.56	5	4	1	0	0	0	0
.....ACCGATAAAGGTGAAATAACC.....	21	0	20	0.50	10	9	1	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCA.....	23	1	9	0.44	4	1	2	1	0	0	0
.....TCTGGTTATTTCATCTTTAG.....	20	0	9	0.44	4	4	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGA.....	21	0	20	0.35	7	7	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCT.....	23	1	9	0.33	3	1	0	1	0	1	0
.....CGATAAAGGTGAAATAACCACT.....	22	0	18	0.28	5	5	0	0	0	0	0
.....GATAAAGGTGAAATAACCACTA.....	22	0	18	0.28	5	4	0	0	0	1	0
.....ATAAAGGTGAAATAACCAC.....	19	0	19	0.26	5	5	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGC.....	24	1	9	0.22	2	0	0	2	0	0	0
.....ATAAAGGTGAAATAACCAC.....	19	0	19	0.26	5	5	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGC.....	24	1	9	0.22	2	0	0	2	0	0	0
.....TCTGGTTATTTCATCTTTAGC.....	21	1	9	0.22	2	2	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCTT.....	24	2	9	0.22	2	2	0	0	0	0	0
.....TTCTGGTTATTTCATCTTTAGTCGC.....	25	1	9	0.22	2	0	0	2	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGT.....	24	1	9	0.22	2	0	0	2	0	0	0
.....TTCTGGTTATTTCATCTTTAGT.....	22	0	9	0.22	2	1	0	0	0	1	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
.....TTATTTCATCTTTAGTCGGAGTTC.....	24	0	10	0.20	2	2	0	0	0	0	0
.....GTTATTTCATCTTTAGTCG.....	19	0	20	0.20	4	2	1	1	0	0	0
.....ACCGATAAAGGTGAAATAACCC.....	22	1	20	0.20	4	4	0	0	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGT.....	24	1	11	0.18	2	1	1	0	0	0	0
.....CGATAAAGGTGAAATAACCACC.....	22	1	18	0.17	3	3	0	0	0	0	0
.....TTATTTCATCTTTAGTCG.....	18	0	20	0.15	3	1	2	0	0	0	0
.....CCGATAAAGGTGAAATAACCA.....	21	0	20	0.15	3	2	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGC.....	23	1	9	0.11	1	0	1	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGGC.....	25	1	9	0.11	1	1	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGGAA.....	26	1	9	0.11	1	0	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTCGA.....	26	1	9	0.11	1	0	1	0	0	0	0
.....TTCTGGTTATTTCATCTTTAG.....	21	0	9	0.11	1	0	0	1	0	0	0
.....TTTCTGGTTATTTCATCTTTAGT.....	23	0	9	0.11	1	0	1	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCAA.....	24	2	9	0.11	1	0	1	0	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
.....AAACCGATAAAGGTGAAATAAC.....	22	0	20	0.10	2	2	0	0	0	0	0
.....TATTTCATCTTTAGTCGGAGTT.....	22	0	20	0.10	2	2	0	0	0	0	0
.....CTGGTTATTTCATCTTTAGTCAA.....	23	2	11	0.09	1	0	1	0	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGAG.....	25	0	11	0.09	1	0	0	1	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGC.....	24	1	11	0.09	1	0	0	1	0	0	0
.....ACCGATAAAGGTGAAATAACCACA.....	24	1	15	0.07	1	0	1	0	0	0	0
.....ACCGATAAAGGTGAAATAACCACT.....	24	0	15	0.07	1	1	0	0	0	0	0
.....GATAAAGGTGAAATAACCACTAAC.....	24	1	18	0.06	1	1	0	0	0	0	0
.....CGATAAAGGTGAAATAACCACA.....	22	1	18	0.06	1	0	1	0	0	0	0
.....GATAAAGGTGAAATAACCAC.....	20	0	18	0.06	1	1	0	0	0	0	0
.....AAAGGTGAAATAACCACT.....	18	0	19	0.05	1	1	0	0	0	0	0
.....ATAAAGGTGAAATAACCACTGT.....	22	2	19	0.05	1	0	0	1	0	0	0
.....ATAAAGGTGAAATAACCACTTT.....	22	2	19	0.05	1	1	0	0	0	0	0
.....CGATAAAGGTGAAATAACCC.....	20	1	20	0.05	1	1	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTCGGT.....	23	1	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCG.....	20	0	20	0.05	1	0	1	0	0	0	0
.....GTTATTTCATCTTTAGTCGGC.....	21	1	20	0.05	1	1	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTT.....	23	0	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCGGC.....	22	1	20	0.05	1	1	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTC.....	20	0	20	0.05	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGAA.....	22	1	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

ATTTAAAAATTGTTTATTATTTATATAGGTGTAAAGGTCATCCCGTATCCAAAGACCAATAAAGTAGAAATCAGCCTCAAGACCATTCATTTGGCTATTTCCACTTTATTGGTGATTTTAGTTAGTTATTTGATCACTCTCACGAGATCATCTCTGACGAGCTGATG **********.....(((((.(((((((((((((((((.((((....((....))....)))))))))))))))))))...)))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V049 head	M060 embryo	V110 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:9913977-9914143 +	dmo_3149	TAAATTTTTAACAAATAATAAATATATCCACATTTCCAGTAGGGCATAGGTTTCTGGTTATTTCATCTTTAGTCGGAGTTCTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATCAATAAACTAGTGAGAGTGCTCTAGTAGAGACTGCTCGACTAC

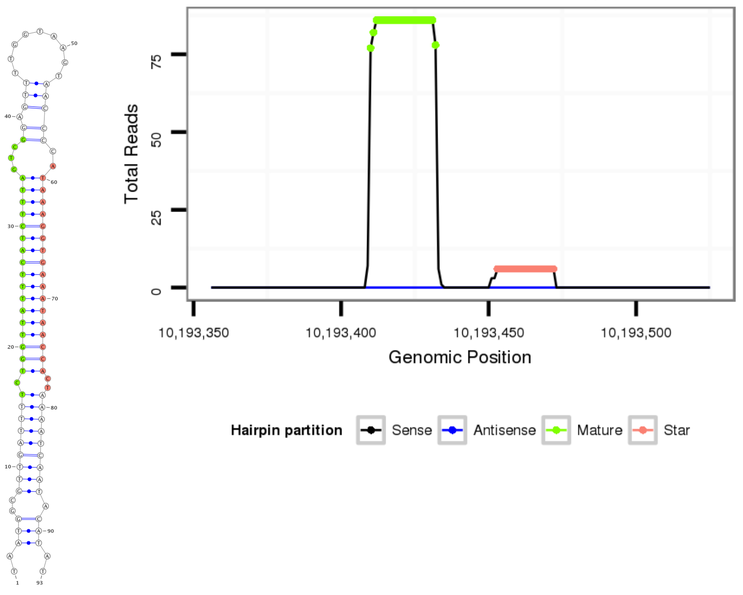
Generated: 09/08/2015 at 07:45 PM

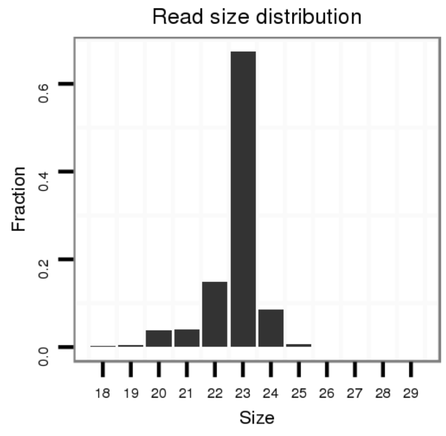
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

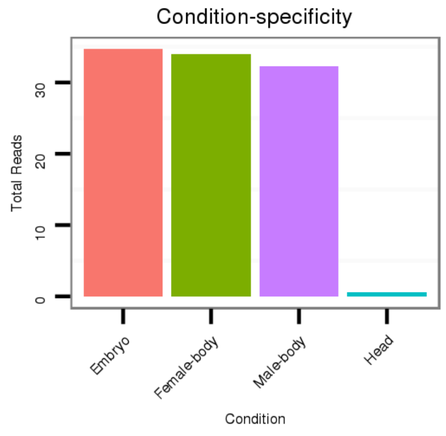
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3153	**scaffold_6473:10193406-10193475 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

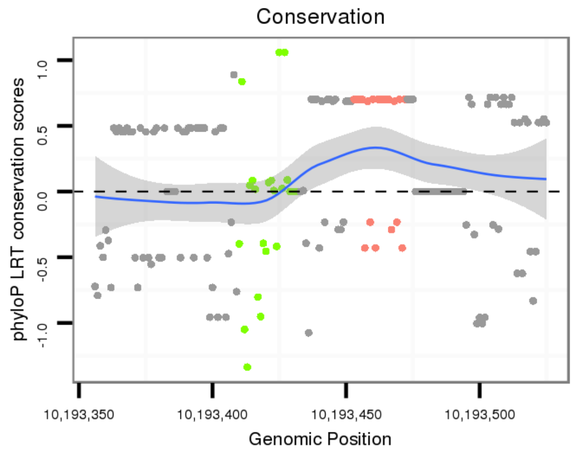
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dmo_3139 scaffold_6308:570045-570067 + 2. dmo_3140 scaffold_6308:570864-570886 - 3. dmo_3144 scaffold_6473:8660635-8660657 - 4. dmo_3145 scaffold_6473:9912732-9912754 - 5. dmo_3149 scaffold_6473:9914029-9914051 + 6. dmo_3151 scaffold_6473:9918570-9918592 - 7. dmo_3135 scaffold_6473:10167398-10167420 + 8. dmo_3137 scaffold_6473:10168272-10168294 - 9. dmo_3153 scaffold_6473:10193410-10193432 +	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

CGTGCAGTGAGCTGCTGTGCCACTCATTCTCAGGCTTTTTAATGGCGTTGATTTTCTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAACCCCATAAAGGTGAAATAACCACTAAAATCAATACATATTAAACTAGTGAGAGCGAGTGCTCCAGGCTAGACTGCTC **********..(((..(((((((((.(((((((((((((((((...((.(((.........)))))..)))))))))))))))))..)))))))))..)))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
.....TCTGGTTATTTCATCTTTAGTCG.....	23	0	9	62.56	563	82	227	226	25	2	1
.....TCTGGTTATTTCATCTTTAGTC.....	22	0	9	7.00	63	50	6	6	1	0	0
.....TTCTGGTTATTTCATCTTTAGTCG.....	24	0	9	6.33	57	9	25	19	4	0	0
.....ATAAAGGTGAAATAACCACT.....	20	0	19	3.42	65	61	2	0	2	0	0
.....CCATAAAGGTGAAATAACCACT.....	22	0	1	3.00	3	3	0	0	0	0	0
.....CTGGTTATTTCATCTTTAGTCGG.....	23	0	11	3.00	33	10	5	16	1	0	1
.....CTGGTTATTTCATCTTTAGTCG.....	22	0	11	2.82	31	4	19	7	1	0	0
.....TGGTTATTTCATCTTTAGTCG.....	21	0	20	2.70	54	2	24	21	6	1	0
.....TGGTTATTTCATCTTTAGTCGG.....	22	0	20	1.95	39	14	6	16	2	1	0
.....TCTGGTTATTTCATCTTTAGTCGG.....	24	0	9	1.44	13	10	2	0	1	0	0
.....TGGTTATTTCATCTTTAGTCGGA.....	23	0	20	1.40	28	21	1	5	1	0	0
.....TTCTGGTTATTTCATCTTTAGTC.....	23	0	9	1.22	11	7	3	0	1	0	0
.....TCTGGTTATTTCATCTTTAGTCGA.....	24	1	9	1.00	9	4	1	4	0	0	0
.....ATAAAGGTGAAATAACCACC.....	20	1	19	0.95	18	18	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGT.....	21	0	9	0.67	6	5	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTCG.....	25	0	9	0.67	6	2	4	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTC.....	24	0	9	0.56	5	4	1	0	0	0	0
.....TCTGGTTATTTCATCTTTAG.....	20	0	9	0.44	4	4	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCA.....	23	1	9	0.44	4	1	2	1	0	0	0
.....GTTATTTCATCTTTAGTCGGA.....	21	0	20	0.35	7	7	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCT.....	23	1	9	0.33	3	1	0	1	0	1	0
.....TTATTTCATCTTTAGTCGGAGTTT.....	24	0	18	0.33	6	4	2	0	0	0	0
.....ATAAAGGTGAAATAACCAC.....	19	0	19	0.26	5	5	0	0	0	0	0
.....TTGATTTTCTGGTTATTTCATC.....	22	0	4	0.25	1	1	0	0	0	0	0
.....TAATGGCGTTGATTTTCTGG.....	20	0	4	0.25	1	0	1	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCTT.....	24	2	9	0.22	2	2	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGT.....	24	1	9	0.22	2	0	0	2	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGC.....	24	1	9	0.22	2	0	0	2	0	0	0
.....TCTGGTTATTTCATCTTTAGC.....	21	1	9	0.22	2	2	0	0	0	0	0
.....TTCTGGTTATTTCATCTTTAGTCGC.....	25	1	9	0.22	2	0	0	2	0	0	0
.....TTCTGGTTATTTCATCTTTAGT.....	22	0	9	0.22	2	1	0	0	0	1	0
.....ATAAAGGTGAAATAACCACTA.....	21	0	19	0.21	4	4	0	0	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGT.....	24	1	11	0.18	2	1	1	0	0	0	0
.....ATTTTCTGGTTATTTCATCTTTA.....	23	0	6	0.17	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCG.....	19	0	20	0.15	3	2	0	1	0	0	0
.....TTATTTCATCTTTAGTCG.....	18	0	20	0.15	3	1	2	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGGAA.....	26	1	9	0.11	1	0	1	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGGC.....	25	1	9	0.11	1	1	0	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGT.....	23	0	9	0.11	1	0	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTCGA.....	26	1	9	0.11	1	0	1	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCAA.....	24	2	9	0.11	1	0	1	0	0	0	0
.....TTCTGGTTATTTCATCTTTAG.....	21	0	9	0.11	1	0	0	1	0	0	0
.....TTTCTGGTTATTTCATCTTTAGC.....	23	1	9	0.11	1	0	1	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
.....CTGGTTATTTCATCTTTAGTCGGAG.....	25	0	11	0.09	1	0	0	1	0	0	0
.....CTGGTTATTTCATCTTTAGTCAA.....	23	2	11	0.09	1	0	1	0	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGC.....	24	1	11	0.09	1	0	0	1	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
.....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
.....ATAAAGGTGAAATAACCACTGT.....	22	2	19	0.05	1	0	0	1	0	0	0
.....TGGTTATTTCATCTTTAGTC.....	20	0	20	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
.....GGTTATTTCATCTTTAGTCGGC.....	22	1	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

GCACGTCACTCGACGACACGGTGAGTAAGAGTCCGAAAAATTACCGCAACTAAAAGACCAATAAAGTAGAAATCAGCCTCAAAACCATTCATTGGGGTATTTCCACTTTATTGGTGATTTTAGTTATGTATAATTTGATCACTCTCGCTCACGAGGTCCGATCTGACGAG **********..(((..(((((((((.(((((((((((((((((...((.(((.........)))))..)))))))))))))))))..)))))))))..)))..**********	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_6473:10193356-10193525 +	dmo_3153	CGTGCAGTGAGCTGCTGTGCCACTCATTCTCAGGCTTTTTAATGGCGTTGATTTTCTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAACCCCATAAAGGTGAAATAACCACTAAAATCAATACATATTAAACTAGTGAGA--GCGAGT-GCTCCAGGCTAGACTGCTC
droVir3	scaffold_13047:8479673-8479764 +		CCCGGGTTGAGCTGCTTACTTCTTGT----AAGCTTCTTAACCTCGTTCT-TCCCATATTTCCACACTTTA-----GAG----------ATGCTTTCTTGAATAACTCCA----------
droGri2	scaffold_15245:7258984-7259040 -		ACTAAA----------GCATCGACACATCTATA-----AAA----------ATGCAC--AAGAAT-GCTCCAGACGAGTGAGCTC
droPer2	scaffold_60:107040-107108 +		GTCT----------ACTATCTGAATGATTTTTTTTG-----AGTTTTTGCAAGTTTTCCCATAACGATTAAATATCTAATAAA-----------------------------------

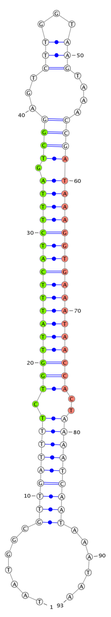
Generated: 09/08/2015 at 07:46 PM

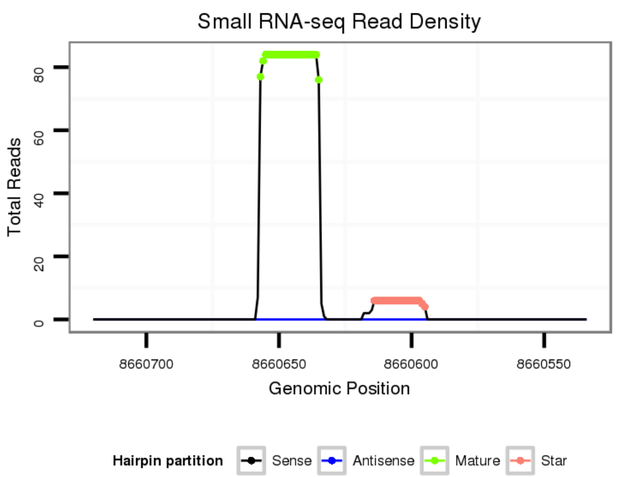
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

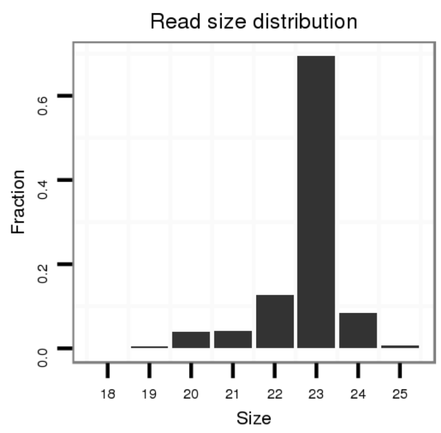
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3144	**scaffold_6473:8660584-8660670 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

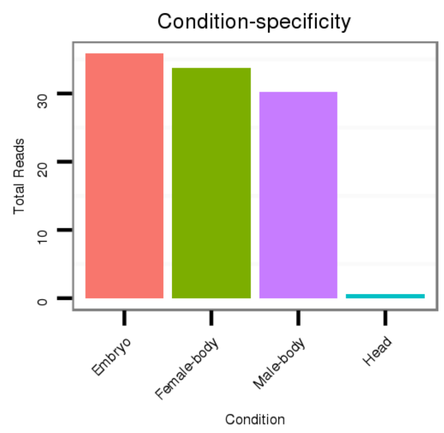
Legend: mature star mismatch in alignment mismatch in read

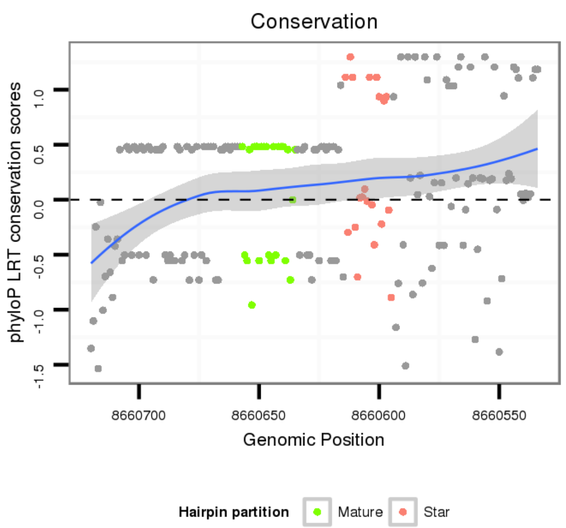
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dmo_3139 scaffold_6308:570045-570067 + 2. dmo_3140 scaffold_6308:570864-570886 - 3. dmo_3144 scaffold_6473:8660635-8660657 - 4. dmo_3145 scaffold_6473:9912732-9912754 - 5. dmo_3149 scaffold_6473:9914029-9914051 + 6. dmo_3151 scaffold_6473:9918570-9918592 - 7. dmo_3135 scaffold_6473:10167398-10167420 + 8. dmo_3137 scaffold_6473:10168272-10168294 - 9. dmo_3153 scaffold_6473:10193410-10193432 +	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

CTCTGCAGCGTGCAGTGGAGCTGCTGTGCCACTCATTCTCAGGCTGTTTAATGGCGTTGATTTTCTGGTTATTTCATCTTTAGTCGGAGTCTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATAAATAAACTAGTGAGAGAGAGTGCTCTAGTAGAGACTGCTCGACTAGCAGAT **********.....(((((((((.(((((((((((((((((.((((...(((...)))....)))))))))))))))))))..)))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
..........TCTGGTTATTTCATCTTTAGTCG..........	23	0	9	62.56	563	82	227	226	25	2	1
..........TCTGGTTATTTCATCTTTAGTC..........	22	0	9	7.00	63	50	6	6	1	0	0
..........TTCTGGTTATTTCATCTTTAGTCG..........	24	0	9	6.33	57	9	25	19	4	0	0
..........ATAAAGGTGAAATAACCACT..........	20	0	19	3.42	65	61	2	0	2	0	0
..........CTGGTTATTTCATCTTTAGTCGG..........	23	0	11	3.00	33	10	5	16	1	0	1
..........CTGGTTATTTCATCTTTAGTCG..........	22	0	11	2.82	31	4	19	7	1	0	0
..........ACCGATAAAGGTGAAATAACCAC..........	23	0	15	1.67	25	25	0	0	0	0	0
..........TGGTTATTTCATCTTTAGTCG..........	21	0	20	1.50	30	0	24	0	6	0	0
..........TCTGGTTATTTCATCTTTAGTCGG..........	24	0	9	1.44	13	10	2	0	1	0	0
..........TTCTGGTTATTTCATCTTTAGTC..........	23	0	9	1.22	11	7	3	0	1	0	0
..........GATAAAGGTGAAATAACCACT..........	21	0	18	1.11	20	17	2	0	1	0	0
..........TGGTTATTTCATCTTTAGTCGGA..........	23	0	20	1.10	22	21	0	0	1	0	0
..........ACCGATAAAGGTGAAATAACCA..........	22	0	20	1.05	21	17	0	1	3	0	0
..........TCTGGTTATTTCATCTTTAGTCGA..........	24	1	9	1.00	9	4	1	4	0	0	0
..........ATAAAGGTGAAATAACCACG..........	20	1	19	0.95	18	18	0	0	0	0	0
..........TGGTTATTTCATCTTTAGTCGG..........	22	0	20	0.70	14	14	0	0	0	0	0
..........TTTCTGGTTATTTCATCTTTAGTCG..........	25	0	9	0.67	6	2	4	0	0	0	0
..........TCTGGTTATTTCATCTTTAGT..........	21	0	9	0.67	6	5	1	0	0	0	0
..........TTTCTGGTTATTTCATCTTTAGTC..........	24	0	9	0.56	5	4	1	0	0	0	0
..........ACCGATAAAGGTGAAATAACC..........	21	0	20	0.45	9	9	0	0	0	0	0
..........TCTGGTTATTTCATCTTTAG..........	20	0	9	0.44	4	4	0	0	0	0	0
..........TCTGGTTATTTCATCTTTAGTCA..........	23	1	9	0.44	4	1	2	1	0	0	0
..........TCTGGTTATTTCATCTTTAGTCT..........	23	1	9	0.33	3	1	0	1	0	1	0
..........CGATAAAGGTGAAATAACCACT..........	22	0	18	0.28	5	5	0	0	0	0	0
..........GATAAAGGTGAAATAACCACTA..........	22	0	18	0.28	5	4	0	0	0	1	0
..........ATAAAGGTGAAATAACCAC..........	19	0	19	0.26	5	5	0	0	0	0	0
..........TAATGGCGTTGATTTTCTGG..........	20	0	4	0.25	1	0	1	0	0	0	0
..........TTGATTTTCTGGTTATTTCATC..........	22	0	4	0.25	1	1	0	0	0	0	0
..........TTCTGGTTATTTCATCTTTAGT..........	22	0	9	0.22	2	1	0	0	0	1	0
..........TCTGGTTATTTCATCTTTAGC..........	21	1	9	0.22	2	2	0	0	0	0	0
..........TCTGGTTATTTCATCTTTAGTCGC..........	24	1	9	0.22	2	0	0	2	0	0	0
..........TCTGGTTATTTCATCTTTAGTCTT..........	24	2	9	0.22	2	2	0	0	0	0	0
..........TTCTGGTTATTTCATCTTTAGTCGC..........	25	1	9	0.22	2	0	0	2	0	0	0
..........TCTGGTTATTTCATCTTTAGTCGT..........	24	1	9	0.22	2	0	0	2	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
..........GTTATTTCATCTTTAGTCG..........	19	0	20	0.20	4	2	1	1	0	0	0
..........ACCGATAAAGGTGAAATAACCC..........	22	1	20	0.20	4	4	0	0	0	0	0
..........CTGGTTATTTCATCTTTAGTCGGT..........	24	1	11	0.18	2	1	1	0	0	0	0
..........ATTTTCTGGTTATTTCATCTTTA..........	23	0	6	0.17	1	1	0	0	0	0	0
..........CGATAAAGGTGAAATAACCACG..........	22	1	18	0.17	3	3	0	0	0	0	0
..........CCGATAAAGGTGAAATAACCA..........	21	0	20	0.15	3	2	1	0	0	0	0
..........TCTGGTTATTTCATCTTTAGTCGGAA..........	26	1	9	0.11	1	0	1	0	0	0	0
..........TTTCTGGTTATTTCATCTTTAGC..........	23	1	9	0.11	1	0	1	0	0	0	0
..........TCTGGTTATTTCATCTTTAGTCGGC..........	25	1	9	0.11	1	1	0	0	0	0	0
..........TTTCTGGTTATTTCATCTTTAGT..........	23	0	9	0.11	1	0	1	0	0	0	0
..........TTCTGGTTATTTCATCTTTAG..........	21	0	9	0.11	1	0	0	1	0	0	0
..........TCTGGTTATTTCATCTTTAGTCAA..........	24	2	9	0.11	1	0	1	0	0	0	0
..........TTTCTGGTTATTTCATCTTTAGTCGA..........	26	1	9	0.11	1	0	1	0	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
..........CTGGTTATTTCATCTTTAGTCGGAG..........	25	0	11	0.09	1	0	0	1	0	0	0
..........CTGGTTATTTCATCTTTAGTCGGC..........	24	1	11	0.09	1	0	0	1	0	0	0
..........CTGGTTATTTCATCTTTAGTCAA..........	23	2	11	0.09	1	0	1	0	0	0	0
..........ACCGATAAAGGTGAAATAACCACT..........	24	0	15	0.07	1	1	0	0	0	0	0
..........ACCGATAAAGGTGAAATAACCACA..........	24	1	15	0.07	1	0	1	0	0	0	0
..........CGATAAAGGTGAAATAACCACA..........	22	1	18	0.06	1	0	1	0	0	0	0
..........GATAAAGGTGAAATAACCAC..........	20	0	18	0.06	1	1	0	0	0	0	0
..........GATAAAGGTGAAATAACCACTAAC..........	24	1	18	0.06	1	1	0	0	0	0	0
..........ATAAAGGTGAAATAACCACTGT..........	22	2	19	0.05	1	0	0	1	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
..........GGTTATTTCATCTTTAGTCGG..........	21	0	20	0.05	1	0	0	0	0	0	1
..........TTATTTCATCTTTAGTCGGA..........	20	0	20	0.05	1	1	0	0	0	0	0
..........GTTATTTCATCTTTAGTCGGG..........	21	1	20	0.05	1	1	0	0	0	0	0
..........CTCTAGTAGAGACTGCTCGAC.....	21	0	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	1	0	0	0	0

Anti-sense strand reads

GAGACGTCGCACGTCACCTCGACGACACGGTGAGTAAGAGTCCGACAAATTACCGCAACTAAAAGACCAATAAAGTAGAAATCAGCCTCAGAACCATTCATTTGGCTATTTCCACTTTATTGGTGATTTTAGTTATTTATTTGATCACTCTCTCTCACGAGATCATCTCTGACGAGCTGATCGTCTA **********.....(((((((((.(((((((((((((((((.((((...(((...)))....)))))))))))))))))))..)))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V041 embryo
..........ACTCTCTCTCACGAGATCATCTC.....	23	0	2	0.50	1	0	1	0
..........TCATCTCTGACGAGCTGATCG....	21	0	9	0.11	1	1	0	0
..........AGATCATCTCTGACGAGCT.....	19	0	20	0.05	1	0	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:8660534-8660720 -	dmo_3144	CTCTGCAGC--GTGCAGTGGAGCTGCTGTGCCACT------CATTCTCAGGCTGTTTAATGGCG--TTGATTTTCTGGTTA----------TTTCATCTTTAGTCGGAGTCTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAA------TAAATAAACTAGTGAGAGAGAGTGCTCTAGTAGAGACTGCTCGACTAGCAGAT
droVir3	scaffold_12855:134563-134699 -		GCCTTGATATCCTCACTATGAAGTTGTTGCGCCATAAATATCTTATCATATGTTTCTAAATTTCGTTTTGATTTTTAGCTTTAAGATAGATGTTTTTTTTTTTGG-GGGTTCGGGAAAGTTATCCAA--AAAGTGAAATA---
droGri2	scaffold_14906:5923695-5923759 +		AAAAAA---TA----------ACTAAAAAAAAAGCACA---AAACA----AGAATGCTGCAGTCGAGACGCTCGACTTGCAGAT
droRho1	scf7180000780147:1253-1331 +		GTAGAG---CGACAACGGGAAAGAAAGCAAAACAAAGAG------CAAATAAACAAGCGAGGGGAGTCCCCGATGTCGATTGATTG----------
droTak1	scf7180000415059:24491-24576 +		AAAC---CAAAAAAAAGAGAAGAAGCAACAGCACTAA------CAATAAAAAAAACAAGAGAGAACGCTATAGTCGAGTGC-CTCGACTATTAGAT
droYak3	chrXh:62904-62976 -		TAAAATGAACGCTA--CA----------ACCAA------AAAAAAATAAAACAAGAGAGAACGCTATAGTCGAGTTC-CCCGACCATCTGAT

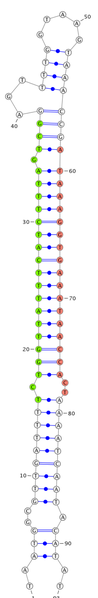
Generated: 09/08/2015 at 07:46 PM

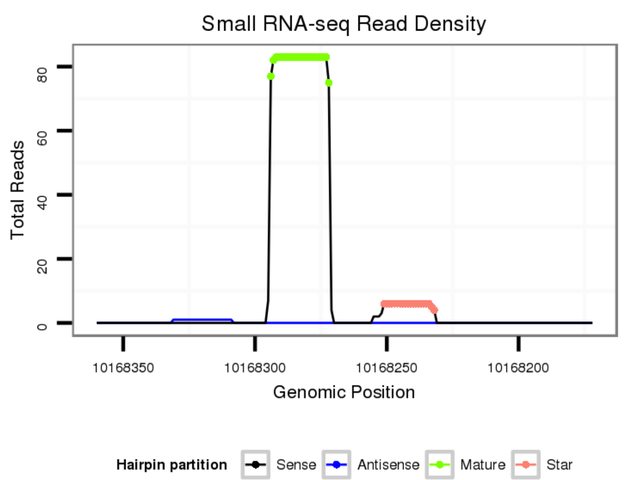
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

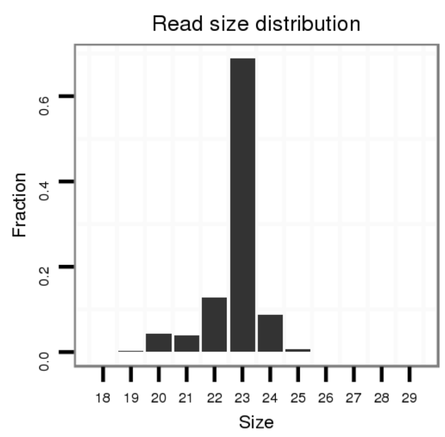
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3137	**scaffold_6473:10168222-10168310 -**	**confident**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

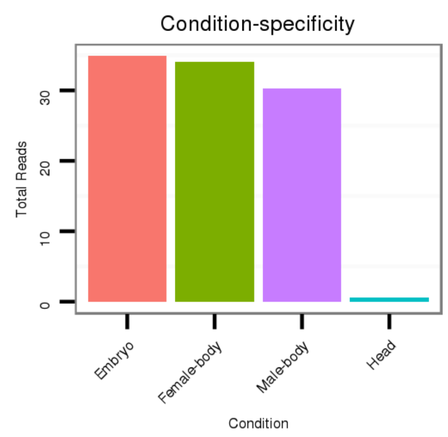
Legend: mature star mismatch in alignment mismatch in read

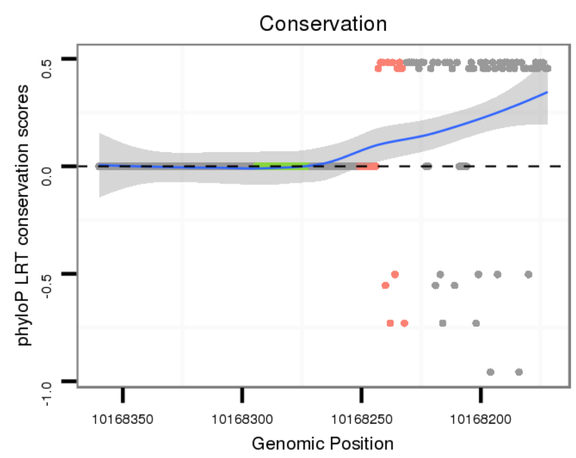
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dmoj\GI15760-in]

No Repeatable elements found

mature	star
1. dmo_3139 scaffold_6308:570045-570067 + 2. dmo_3140 scaffold_6308:570864-570886 - 3. dmo_3144 scaffold_6473:8660635-8660657 - 4. dmo_3145 scaffold_6473:9912732-9912754 - 5. dmo_3149 scaffold_6473:9914029-9914051 + 6. dmo_3151 scaffold_6473:9918570-9918592 - 7. dmo_3135 scaffold_6473:10167398-10167420 + 8. dmo_3137 scaffold_6473:10168272-10168294 - 9. dmo_3153 scaffold_6473:10193410-10193432 +	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

AAGAGTGCTCTAGGCGAGACTGCTCGACTAGCCACTCATTCTCAGGCTGTTTAATGGCGTTGATTTTCTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATACATATTAAACTAGTGAGAGCGAGTGCTCTAGTAGAGACTGCTCGACTAGC **********..(((..(((((((((.(((((((((((((((((.((((...((((.....))))))))))))))))))))))))..)))))))))..)))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
...TCTGGTTATTTCATCTTTAGTCG...	23	0	9	62.56	563	82	227	226	25	2	1
...TCTGGTTATTTCATCTTTAGTC...	22	0	9	7.00	63	50	6	6	1	0	0
...TTCTGGTTATTTCATCTTTAGTCG...	24	0	9	6.33	57	9	25	19	4	0	0
...ATAAAGGTGAAATAACCACT...	20	0	19	3.42	65	61	2	0	2	0	0
...CTGGTTATTTCATCTTTAGTCGG...	23	0	11	3.00	33	10	5	16	1	0	1
...CTGGTTATTTCATCTTTAGTCG...	22	0	11	2.82	31	4	19	7	1	0	0
...ACCGATAAAGGTGAAATAACCAC...	23	0	15	1.67	25	25	0	0	0	0	0
...TCTGGTTATTTCATCTTTAGTCGG...	24	0	9	1.44	13	10	2	0	1	0	0
...TTCTGGTTATTTCATCTTTAGTC...	23	0	9	1.22	11	7	3	0	1	0	0
...TGGTTATTTCATCTTTAGTCG...	21	0	20	1.20	24	0	24	0	0	0	0
...GATAAAGGTGAAATAACCACT...	21	0	18	1.11	20	17	2	0	1	0	0
...TCTGGTTATTTCATCTTTAGTCGA...	24	1	9	1.00	9	4	1	4	0	0	0
...ACCGATAAAGGTGAAATAACCA...	22	0	20	1.00	20	17	0	0	3	0	0
...ATAAAGGTGAAATAACCACC...	20	1	19	0.95	18	18	0	0	0	0	0
...TGGTTATTTCATCTTTAGTCGG...	22	0	20	0.70	14	14	0	0	0	0	0
...TCTGGTTATTTCATCTTTAGT...	21	0	9	0.67	6	5	1	0	0	0	0
...TTTCTGGTTATTTCATCTTTAGTCG...	25	0	9	0.67	6	2	4	0	0	0	0
...TTTCTGGTTATTTCATCTTTAGTC...	24	0	9	0.56	5	4	1	0	0	0	0
...ACCGATAAAGGTGAAATAACC...	21	0	20	0.50	10	9	1	0	0	0	0
...TCTGGTTATTTCATCTTTAG...	20	0	9	0.44	4	4	0	0	0	0	0
...TCTGGTTATTTCATCTTTAGTCA...	23	1	9	0.44	4	1	2	1	0	0	0
...TCTGGTTATTTCATCTTTAGTCT...	23	1	9	0.33	3	1	0	1	0	1	0
...TTATTTCATCTTTAGTCGGAGTTT...	24	0	18	0.33	6	4	2	0	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
...TTGATTTTCTGGTTATTTCATC...	22	0	4	0.25	1	1	0	0	0	0	0
...TAATGGCGTTGATTTTCTGG...	20	0	4	0.25	1	0	1	0	0	0	0
...TCTGGTTATTTCATCTTTAGTCTT...	24	2	9	0.22	2	2	0	0	0	0	0
...TCTGGTTATTTCATCTTTAGC...	21	1	9	0.22	2	2	0	0	0	0	0
...TTCTGGTTATTTCATCTTTAGTCGC...	25	1	9	0.22	2	0	0	2	0	0	0
...TTCTGGTTATTTCATCTTTAGT...	22	0	9	0.22	2	1	0	0	0	1	0
...TCTGGTTATTTCATCTTTAGTCGT...	24	1	9	0.22	2	0	0	2	0	0	0
...TCTGGTTATTTCATCTTTAGTCGC...	24	1	9	0.22	2	0	0	2	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
...ACCGATAAAGGTGAAATAACCG...	22	1	20	0.20	4	4	0	0	0	0	0
...CTGGTTATTTCATCTTTAGTCGGT...	24	1	11	0.18	2	1	1	0	0	0	0
...ATTTTCTGGTTATTTCATCTTTA...	23	0	6	0.17	1	1	0	0	0	0	0
...CGATAAAGGTGAAATAACCACC...	22	1	18	0.17	3	3	0	0	0	0	0
...TCTGGTTATTTCATCTTTAGTCGGAA...	26	1	9	0.11	1	0	1	0	0	0	0
...TTTCTGGTTATTTCATCTTTAGT...	23	0	9	0.11	1	0	1	0	0	0	0
...TCTGGTTATTTCATCTTTAGTCAA...	24	2	9	0.11	1	0	1	0	0	0	0
...TTTCTGGTTATTTCATCTTTAGTCGA...	26	1	9	0.11	1	0	1	0	0	0	0
...TTTCTGGTTATTTCATCTTTAGC...	23	1	9	0.11	1	0	1	0	0	0	0
...TTCTGGTTATTTCATCTTTAG...	21	0	9	0.11	1	0	0	1	0	0	0
...TCTGGTTATTTCATCTTTAGTCGGC...	25	1	9	0.11	1	1	0	0	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
...CCGATAAAGGTGAAATAACCA...	21	0	20	0.10	2	2	0	0	0	0	0
...GTTATTTCATCTTTAGTCG...	19	0	20	0.10	2	0	1	1	0	0	0
...AAACCGATAAAGGTGAAATAAC...	22	0	20	0.10	2	2	0	0	0	0	0
...CTGGTTATTTCATCTTTAGTCAA...	23	2	11	0.09	1	0	1	0	0	0	0
...CTGGTTATTTCATCTTTAGTCGGC...	24	1	11	0.09	1	0	0	1	0	0	0
...CTGGTTATTTCATCTTTAGTCGGAG...	25	0	11	0.09	1	0	0	1	0	0	0
...ACCGATAAAGGTGAAATAACCACT...	24	0	15	0.07	1	1	0	0	0	0	0
...ACCGATAAAGGTGAAATAACCACA...	24	1	15	0.07	1	0	1	0	0	0	0
...CGATAAAGGTGAAATAACCACA...	22	1	18	0.06	1	0	1	0	0	0	0
...GAGTTTTGGTAAGTAAACCG...	20	0	18	0.06	1	1	0	0	0	0	0
...ATTTCATCTTTAGTCGGAGTTT...	22	0	18	0.06	1	1	0	0	0	0	0
...GATAAAGGTGAAATAACCACTAAG...	24	1	18	0.06	1	1	0	0	0	0	0
...TTATTTCATCTTTAGTCGGAGTTTTGGTA...	29	0	18	0.06	1	1	0	0	0	0	0
...GATAAAGGTGAAATAACCAC...	20	0	18	0.06	1	1	0	0	0	0	0
...ATAAAGGTGAAATAACCACTTT...	22	2	19	0.05	1	1	0	0	0	0	0
...ATAAAGGTGAAATAACCACTGT...	22	2	19	0.05	1	0	0	1	0	0	0
...AAAGGTGAAATAACCACT...	18	0	19	0.05	1	1	0	0	0	0	0
...TGGTTATTTCATCTTTAGTC...	20	0	20	0.05	1	1	0	0	0	0	0
...TGGTTATTTCATCTTTAGTCGGA...	23	0	20	0.05	1	0	0	0	1	0	0
...CTCTAGTAGAGACTGCTCGAC....	21	0	20	0.05	1	1	0	0	0	0	0
...GTTATTTCATCTTTAGTCGGC...	21	1	20	0.05	1	1	0	0	0	0	0
...GGTTATTTCATCTTTAGTCGG...	21	0	20	0.05	1	0	0	0	0	0	1
...GGTTATTTCATCTTTAGTCG...	20	0	20	0.05	1	0	1	0	0	0	0
...TTATTTCATCTTTAGTCGGA...	20	0	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

TTCTCACGAGATCCGCTCTGACGAGCTGATCGGTGAGTAAGAGTCCGACAAATTACCGCAACTAAAAGACCAATAAAGTAGAAATCAGCCTCAAAACCATTCATTTGGCTATTTCCACTTTATTGGTGATTTTAGTTATGTATAATTTGATCACTCTCGCTCACGAGATCATCTCTGACGAGCTGATCG **********..(((..(((((((((.(((((((((((((((((.((((...((((.....))))))))))))))))))))))))..)))))))))..)))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V041 embryo
...TCGGTGAGTAAGAGTCCGACAAA...	23	0	1	1.00	1	1	0	0	0
...TCATCTCTGACGAGCTGATCG	21	0	9	0.11	1	1	0	0	0
...AAGAAATCAGCCTCAAAACCAT...	22	1	18	0.06	1	0	1	0	0
...AGATCATCTCTGACGAGCT.....	19	0	20	0.05	1	0	0	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:10168172-10168360 -	dmo_3137	AAGAGTGCTCTAGGCGAGACTGCTCGACTAGCCACTCATTCTCAGGCTGTTTAATGGCGTTGATTTTCTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAA-TCAATACATATTAAACTAGTGAGAGCGAGTGCTCTAGTAGAGACTGCTCGACTAGC
droVir3	scaffold_13049:121860-121926 -		----------GAATTCATCACGAAAACTCAA--CAAACGAAACAA----GAGAAAGTGCTCCAGTAGAGACTGCCCGACTAGC

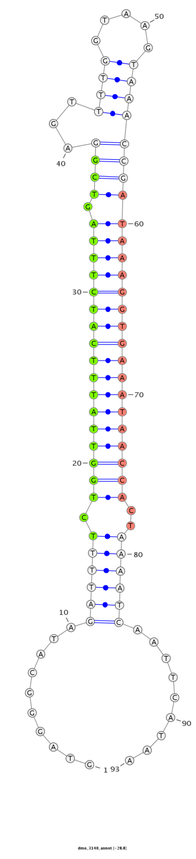
Generated: 09/08/2015 at 07:46 PM

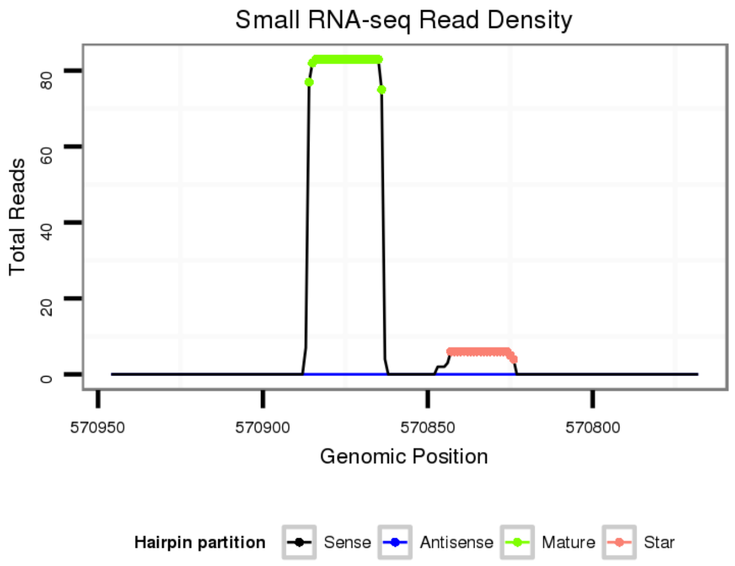
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

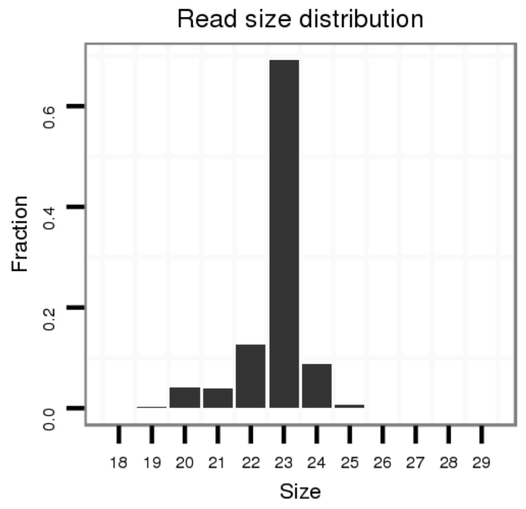
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3140	**scaffold_6308:570818-570896 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

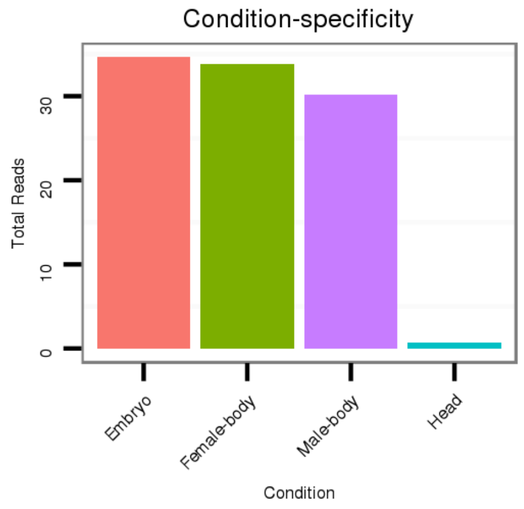
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
Homo6	DNA	hAT-Pegasus	+

mature

1. dmo_3139 scaffold_6308:570045-570067 +
2. dmo_3140 scaffold_6308:570864-570886 -
3. dmo_3144 scaffold_6473:8660635-8660657 -
4. dmo_3145 scaffold_6473:9912732-9912754 -
5. dmo_3149 scaffold_6473:9914029-9914051 +
6. dmo_3151 scaffold_6473:9918570-9918592 -
7. dmo_3135 scaffold_6473:10167398-10167420 +
8. dmo_3137 scaffold_6473:10168272-10168294 -
9. dmo_3153 scaffold_6473:10193410-10193432 +

star

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

TTCCTCATTAATTTTGAACAATTAATAAATACATCCACACTTCCAGTAGGGCATAGATTTTCTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATTCATAATAAACCAGTAAGAGAGAGTGCTCTAGGCGAGACTGCTCGAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
..........TCTGGTTATTTCATCTTTAGTCG..........	23	0	9	62.56	563	82	227	226	25	2	1
..........TCTGGTTATTTCATCTTTAGTC..........	22	0	9	7.00	63	50	6	6	1	0	0
..........TTCTGGTTATTTCATCTTTAGTCG..........	24	0	9	6.33	57	9	25	19	4	0	0
..........ATAAAGGTGAAATAACCACT..........	20	0	19	3.42	65	61	2	0	2	0	0
..........CTGGTTATTTCATCTTTAGTCGG..........	23	0	11	3.00	33	10	5	16	1	0	1
..........CTGGTTATTTCATCTTTAGTCG..........	22	0	11	2.82	31	4	19	7	1	0	0
..........ACCGATAAAGGTGAAATAACCAC..........	23	0	15	1.67	25	25	0	0	0	0	0
..........TCTGGTTATTTCATCTTTAGTCGG..........	24	0	9	1.44	13	10	2	0	1	0	0
..........TGGTTATTTCATCTTTAGTCG..........	21	0	20	1.25	25	0	24	0	0	1	0
..........TTCTGGTTATTTCATCTTTAGTC..........	23	0	9	1.22	11	7	3	0	1	0	0
..........GATAAAGGTGAAATAACCACT..........	21	0	18	1.11	20	17	2	0	1	0	0
..........TCTGGTTATTTCATCTTTAGTCGA..........	24	1	9	1.00	9	4	1	4	0	0	0
..........ACCGATAAAGGTGAAATAACCA..........	22	0	20	1.00	20	17	0	0	3	0	0
..........ATAAAGGTGAAATAACCACC..........	20	1	19	0.95	18	18	0	0	0	0	0
..........TGGTTATTTCATCTTTAGTCGG..........	22	0	20	0.70	14	14	0	0	0	0	0
..........TCTGGTTATTTCATCTTTAGT..........	21	0	9	0.67	6	5	1	0	0	0	0
..........TTTCTGGTTATTTCATCTTTAGTCG..........	25	0	9	0.67	6	2	4	0	0	0	0
..........TTTCTGGTTATTTCATCTTTAGTC..........	24	0	9	0.56	5	4	1	0	0	0	0
..........ACCGATAAAGGTGAAATAACC..........	21	0	20	0.50	10	9	1	0	0	0	0
..........TCTGGTTATTTCATCTTTAG..........	20	0	9	0.44	4	4	0	0	0	0	0
..........TCTGGTTATTTCATCTTTAGTCA..........	23	1	9	0.44	4	1	2	1	0	0	0
..........TCTGGTTATTTCATCTTTAGTCT..........	23	1	9	0.33	3	1	0	1	0	1	0
..........TTATTTCATCTTTAGTCGGAGTTT..........	24	0	18	0.33	6	4	2	0	0	0	0
..........CGATAAAGGTGAAATAACCACT..........	22	0	18	0.28	5	5	0	0	0	0	0
..........GATAAAGGTGAAATAACCACTA..........	22	0	18	0.28	5	4	0	0	0	1	0
..........ATAAAGGTGAAATAACCAC..........	19	0	19	0.26	5	5	0	0	0	0	0
..........TTCTGGTTATTTCATCTTTAGT..........	22	0	9	0.22	2	1	0	0	0	1	0
..........TCTGGTTATTTCATCTTTAGC..........	21	1	9	0.22	2	2	0	0	0	0	0
..........TTCTGGTTATTTCATCTTTAGTCGC..........	25	1	9	0.22	2	0	0	2	0	0	0
..........TCTGGTTATTTCATCTTTAGTCGT..........	24	1	9	0.22	2	0	0	2	0	0	0
..........TCTGGTTATTTCATCTTTAGTCTT..........	24	2	9	0.22	2	2	0	0	0	0	0
..........TCTGGTTATTTCATCTTTAGTCGC..........	24	1	9	0.22	2	0	0	2	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
..........CTGGTTATTTCATCTTTAGTCGGT..........	24	1	11	0.18	2	1	1	0	0	0	0
..........ATTTTCTGGTTATTTCATCTTTA..........	23	0	6	0.17	1	1	0	0	0	0	0
..........CGATAAAGGTGAAATAACCACC..........	22	1	18	0.17	3	3	0	0	0	0	0
..........TCTGGTTATTTCATCTTTAGTCAA..........	24	2	9	0.11	1	0	1	0	0	0	0
..........TCTGGTTATTTCATCTTTAGTCGGC..........	25	1	9	0.11	1	1	0	0	0	0	0
..........TTTCTGGTTATTTCATCTTTAGC..........	23	1	9	0.11	1	0	1	0	0	0	0
..........TTTCTGGTTATTTCATCTTTAGT..........	23	0	9	0.11	1	0	1	0	0	0	0
..........TCTGGTTATTTCATCTTTAGTCGGAA..........	26	1	9	0.11	1	0	1	0	0	0	0
..........TTCTGGTTATTTCATCTTTAG..........	21	0	9	0.11	1	0	0	1	0	0	0
..........TTTCTGGTTATTTCATCTTTAGTCGA..........	26	1	9	0.11	1	0	1	0	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
..........AAACCGATAAAGGTGAAATAAC..........	22	0	20	0.10	2	2	0	0	0	0	0
..........GTTATTTCATCTTTAGTCG..........	19	0	20	0.10	2	0	1	1	0	0	0
..........CCGATAAAGGTGAAATAACCA..........	21	0	20	0.10	2	2	0	0	0	0	0
..........CTGGTTATTTCATCTTTAGTCAA..........	23	2	11	0.09	1	0	1	0	0	0	0
..........CTGGTTATTTCATCTTTAGTCGGC..........	24	1	11	0.09	1	0	0	1	0	0	0
..........CTGGTTATTTCATCTTTAGTCGGAG..........	25	0	11	0.09	1	0	0	1	0	0	0
..........ACCGATAAAGGTGAAATAACCACT..........	24	0	15	0.07	1	1	0	0	0	0	0
..........ACCGATAAAGGTGAAATAACCACA..........	24	1	15	0.07	1	0	1	0	0	0	0
..........GAGTTTTGGTAAGTAAACCG..........	20	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
..........GATAAAGGTGAAATAACCAC..........	20	0	18	0.06	1	1	0	0	0	0	0
..........CGATAAAGGTGAAATAACCACA..........	22	1	18	0.06	1	0	1	0	0	0	0
..........TTATTTCATCTTTAGTCGGAGTTTTGGTA..........	29	0	18	0.06	1	1	0	0	0	0	0
..........AAAGGTGAAATAACCACT..........	18	0	19	0.05	1	1	0	0	0	0	0
..........ATAAAGGTGAAATAACCACTTT..........	22	2	19	0.05	1	1	0	0	0	0	0
..........ATAAAGGTGAAATAACCACTGT..........	22	2	19	0.05	1	0	0	1	0	0	0
..........GTTATTTCATCTTTAGTCGGC..........	21	1	20	0.05	1	1	0	0	0	0	0
..........TGGTTATTTCATCTTTAGTC..........	20	0	20	0.05	1	1	0	0	0	0	0
..........TGGTTATTTCATCTTTAGTCGGA..........	23	0	20	0.05	1	0	0	0	1	0	0
..........GGTTATTTCATCTTTAGTCG..........	20	0	20	0.05	1	0	1	0	0	0	0
..........GTTATTTCATCTTTAGTCGGAA..........	22	1	20	0.05	1	1	0	0	0	0	0
..........GGTTATTTCATCTTTAGTCGG..........	21	0	20	0.05	1	0	0	0	0	0	1
..........TTATTTCATCTTTAGTCGGA..........	20	0	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

AAGGAGTAATTAAAACTTGTTAATTATTTATGTAGGTGTGAAGGTCATCCCGTATCTAAAAGACCAATAAAGTAGAAATCAGCCTCAAAACCATTCATTTGGCTATTTCCACTTTATTGGTGATTTTAGTTAAGTATTATTTGGTCATTCTCTCTCACGAGATCCGCTCTGACGAGCTG	Read size	# Mismatch	Hit Count	Total Norm	Total	V049 head	V110 male body	M046 female body	M060 embryo
..........AAGAAATCAGCCTCAAAACCAT..........	22	1	18	0.06	1	0	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:570768-570946 -	dmo_3140	TTCCTCATTAATTTTGAACAATTAATAAATACATCCACACTTCCAGTAGGGCATAGATTTTCTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATTCATAATAAACCAGTAAGAGAGAGTGCTCTAGGCGAGACTGCTCGAC

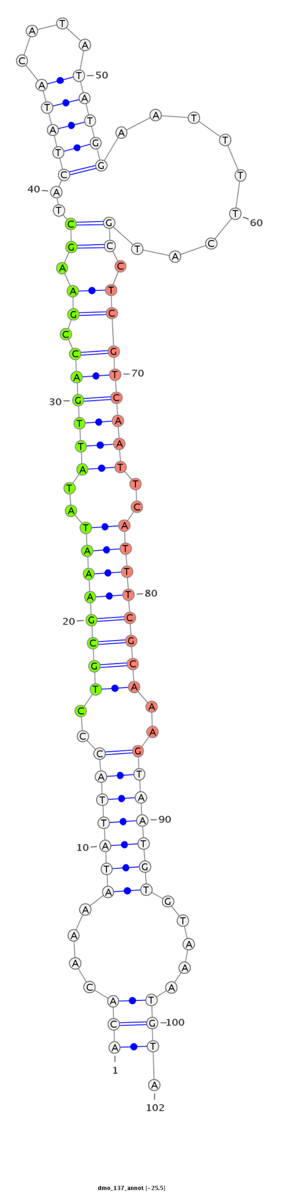
Generated: 09/08/2015 at 07:46 PM

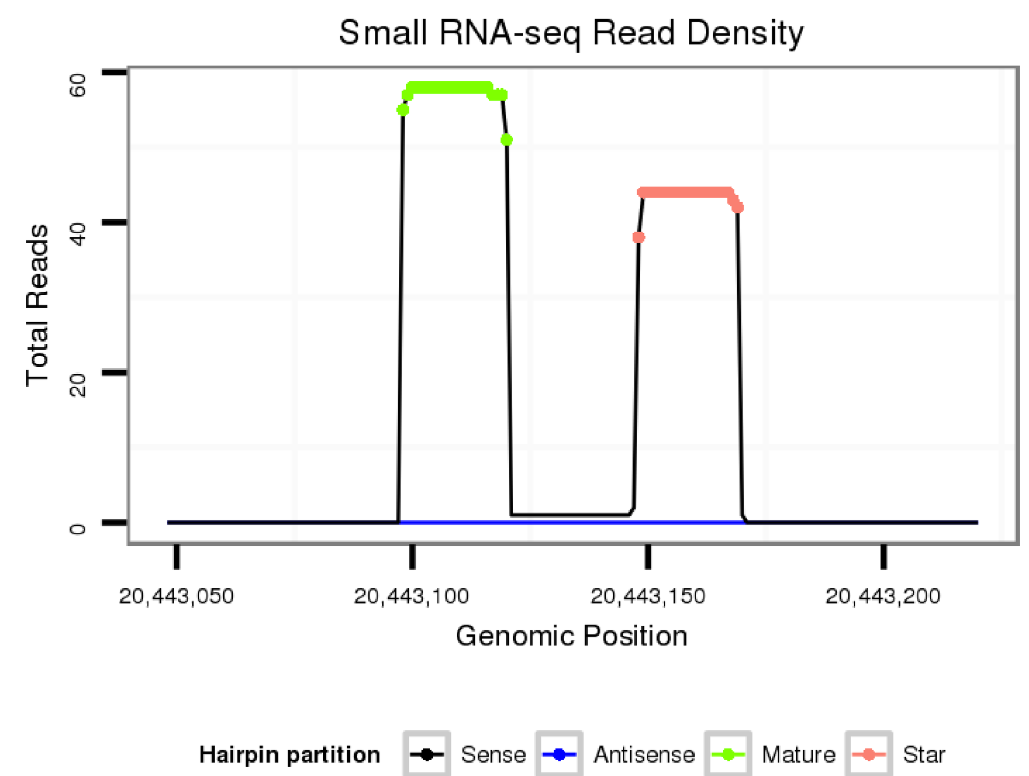
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

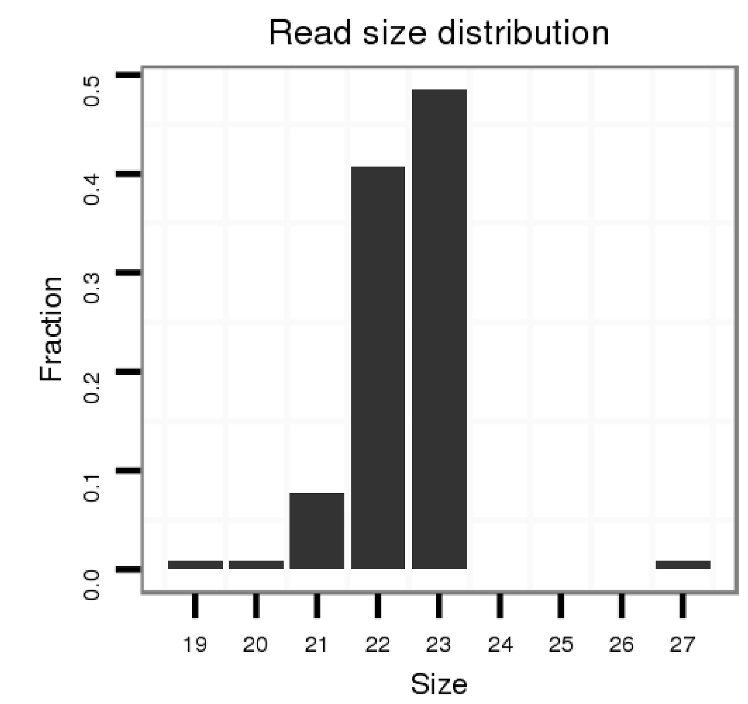
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_137	**scaffold_6500:20443098-20443170 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

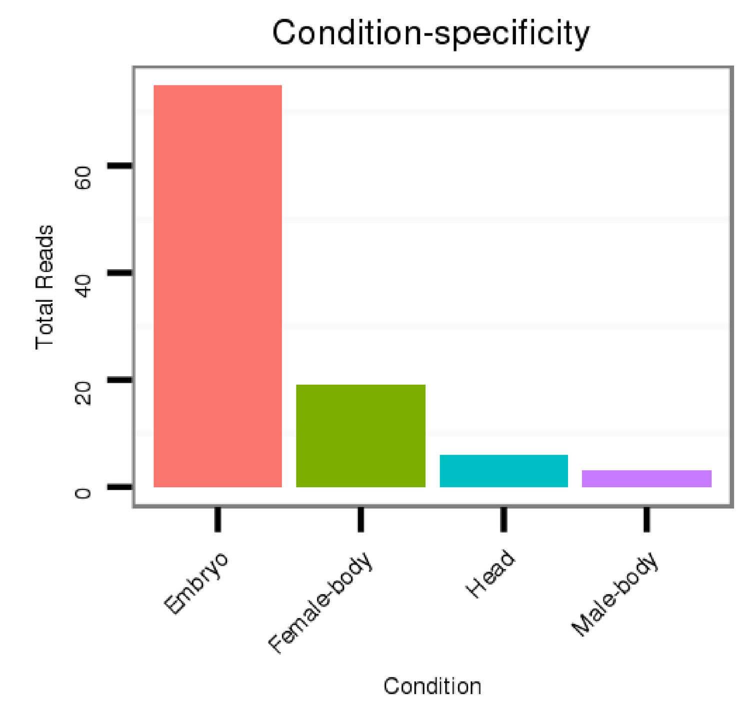
Legend: mature star mismatch in alignment mismatch in read

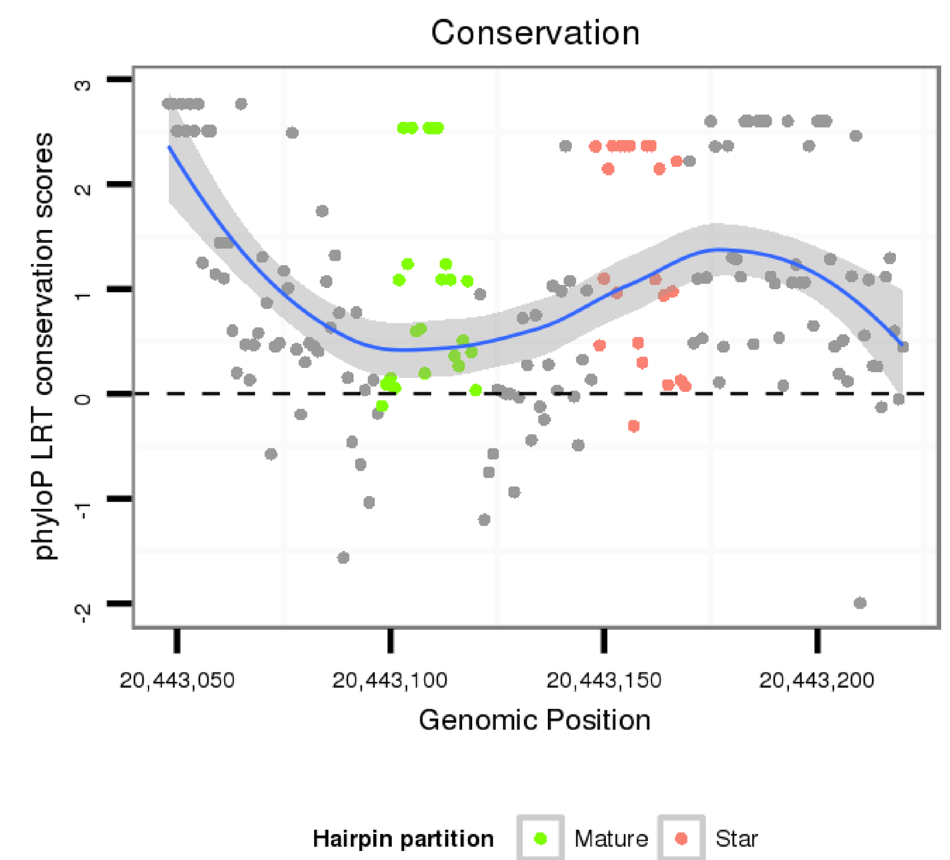
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI17886-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTGTCTGTCCCCTCACCAACCAAACACACAAACACACACAAAATATTACCCTGCGAAATATATTGACCGAAGCTACTATACATATATGGAATTTTCATGCCTCGTCAATTCATTTCGCAAAGTAATGTGTAAATGTATATAGAAGTGAGGAATTAACAACCTATTCTTGTCTT ***********************************(((....(((((((..((((((((..((((((.((.((..(((((....))))).........)).))))))))..))))))))..))))))).....))).************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V056 head	V041 embryo	V110 male body	V049 head
....CTGCGAAATATATTGACCGAAGC..	23	0	1	48.00	48	40	4	1	1	1	1
....CTCGTCAATTCATTTCGCAAAG...	22	0	1	34.00	34	24	7	1	1	1	0
....CTGCGAAATATATTGACCGAAG...	22	0	1	6.00	6	1	2	1	1	1	0
....TCGTCAATTCATTTCGCAAAG...	21	0	1	6.00	6	1	5	0	0	0	0
....TGCGAAATATATTGACCGAAGC..	22	0	1	2.00	2	1	0	0	1	0	0
....CTCGTCAATTCATTTCGCAAAGT..	23	0	1	1.00	1	0	1	0	0	0	0
....CTCGTCAATTCATTTCGCAA...	20	0	1	1.00	1	0	0	1	0	0	0
....CTGCGAAATATATTGACCG..	19	0	1	1.00	1	0	0	1	0	0	0
....GCGAAATATATTGACCGAAGC..	21	0	1	1.00	1	1	0	0	0	0	0
....TACTATACATATATGGAATTTTCATGC...	27	0	1	1.00	1	1	0	0	0	0	0
....CCTCGTCAATTCATTTCGCAAAG...	23	0	1	1.00	1	0	0	0	1	0	0
....CTCGTCAATTCATTTCGCAAA..	21	0	1	1.00	1	1	0	0	0	0	0
....CTCGTCAATTCATTTCGCAAAGA..	23	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

AACAGACAGGGGAGTGGTTGGTTTGTGTGTTTGTGTGTGTTTTATAATGGGACGCTTTATATAACTGGCTTCGATGATATGTATATACCTTAAAAGTACGGAGCAGTTAAGTAAAGCGTTTCATTACACATTTACATATATCTTCACTCCTTAATTGTTGGATAAGAACAGAA ***********************************(((....(((((((..((((((((..((((((.((.((..(((((....))))).........)).))))))))..))))))))..))))))).....))).************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V110 male body
........................GTGTGTTTGTGTGTGTTTTA...	20	0	4	0.25	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6500:20443048-20443220 +	dmo_137	TTGTCTGTCCCCTCACCAACCAA------------------------A-C-ACA--CAAAC--ACAC------------------ACAA--------------------------AATA--TTACCCTGCGAAATATATTGACCGAAGC--TAC-TATACATATATGGA-ATTT-TCATGCCTCGTCAATTCATTTC----GCAAAGTAATGTGTAAATGTATATAGAAGTGAGGAATTAACAACCTATTCTTGTCT-------T
droVir3	scaffold_12963:11747773-11747931 +		TTGTCTGTCCCCTCAACA-----------------------------A--ACAA----GCACACAC------------------ACAA--------------------------ACTA--TTACTTGGCGAAATATATTGACCGAAGC--CAA-TAC--TCCA------AATT-TCGTGCCTTGTCAATTTATTTC-CC-G--ATATATTGTGTAAATGTATATAAAAGTGAGGAATTAACAATCTGTTCTCGTAT-------T
droGri2	scaffold_15126:5300878-5301036 +		TTGTCTGTTCCCTCACCA-----------------------------A--ACAATCACAC----AC------------------ACAA--------------------------TTGA--TTTCCTAGCGAGATATATTGACCAAAGA--CACTTCC----------CAGAATT-TCATGCCGTGTCAATATATTTC-CTCACA-TA--TTGTGTAAATGTATATAGAAATGAGGAATTAACAATCTATTCTTGAAT-------A
droWil2	scf2_1100000004516:2656211-2656350 +		TTGTCTGTCCCAC-GCAACAAA-----TT----------------AAAA-AAACAAAAATTC----CCAAGGAAATTTATAT----ATATTTACTGACCAACAGCCAATTCATAATAAAAATTAC--CAC--------------------------------GTGT--AAATACATAGGACTTCT--TTTATAAAGCTATTGCAATTG-------T
dp5	4_group3:11306972-11307033 +		TTGTCTGTCCCCTCACAAGAAA------CACAAAA--AT------T-------------------------T-A--------------------------CCCGATTTACCCGACGAAATATATTGAC--
droAna3	scaffold_12943:3292738-3292916 +		TTGTCTGTCCCCTCACCAAGCAAAAAAAC----------------AA----ATAAATAAAT-------------------ACAA--------------------------TCAACCGCATAGGAGGAAAGACATTGGCCAAGAC--CCT-TTC--TCCT------G-T-CAGCGCCTTGTCAATATTTTTC-CTCGCGATGT-TTGTGTAAATGTACATAGGACTGAGAAATTAAACGCCTGTACGGGTACAGGGTTCC
droBip1	scf7180000396433:195977-196159 +		TTGTCTGTCCCCTCACCAAGCAA------AAAAA--AAT-----TAA----ATAAATAAAT-------------------ACAA--------------------------CCGATCGCCAACGGGAAACACATTGGCCAAGAC--CCC---------TGTCC--TGTT-CGGCGCCTTGTCAATATTTTTCCCCGCGATGT-TTGTGTAAATGTACATAGGACTGAGAAATTAACCGCCTGTACGGGTACAGGGTTCC
droKik1	scf7180000302472:3211534-3211729 -		TTGTCTGTCCCCTCACAAAAAA-----------A--AAT-----TAAAA-TAAAAATAAAAA---A--AGAACCTCAACCGATCGCAA--------------------------ACAAATCAGCACGAGAAAATACATTGACCGAAGCGCCGCCTAC--ACCTTTTAATGTT-TCAGGTCTTGTCAATTATTTTC-CTAGAAATGT-TTGTGCAAATGTACATAGGACTGAGAAATTAACTGCC------CGTAC-------C
droFic1	scf7180000453842:1705110-1705286 +		TTGTCTGTCCCCTCACAAAAAC-----------------------CAAA-CAGCGATAAAGC----A-------------------CAA--------------------------GCAAAT-ATCCCGTCGAAATGTATTGACCAAAGC--CGTCCAC--ACCTGTTTAATGTT-TCGGGCCATGTCAATCTGTTTC-CTCGAAATGT-TTGTGTCAATGTACATAGGACTGAGAAGTTAACTGCCTGTAGCCGTAT-------C
droEle1	scf7180000491046:2187236-2187413 -		TTGTCTGTCCCCTCACAAAAAAA-----------------------GAAA-AAGCGATAAAGC----A-------------------CAA--------------------------ACAAATATTTCCGACGAAATATATTGACGAAAGA--CCTTACC--ATCTGTTTAATGTT-TCGGGCCTTGTCAATCTGTTTC-CTAGAAATTT-TGTTGTAAATGTACATAGGTCTGAGAAATTAACTGCATTTAGCCGTAT-------C
droRho1	scf7180000777227:336397-336574 -		TTGTCTGTCCCCTCACAAAAAG-----------------------AAAA-CAGCGATAAAGC----A-------------------CAA--------------------------ACAAATGTTTCCGACGAAATATATTGACGACAAA--CCTTCAT--TCCTGTCTAATGTT-TCTGGTCTTGTCAATCTGTTTC-CTCGAAATGT-TATTGTAAATGTATATAGGTCTGAGAAATTAACTGCCTCTAGCCGTAT-------C
droBia1	scf7180000302188:1097683-1097865 -		TTGTCTGTCCCCTCACGAAAAA-----------A--TG------TAAAA-CAGCGATAAAGC----AC------------------ACTT--------------------------GCAAATTTGCCCGACGAAATATATTGACCAAAGC--CATCCAC--ACCTGTTTAATG-T-TCGGGCCTTGTCAATCTGTTTC-CGCGCAACGT-TTGTGCCAATGTACATAGGTCTGAGAAATTAACTACCTGCAGCCGTAT-------C
droTak1	scf7180000415264:647651-647834 -		TTGTCTGTCCC-TCAAAAAAAAA-----AAAAAAA--A------AAAAACAAGCGATAAAGC----AC------------------ACAA--------------------------GC-AATATGCCCGACGAAATACATTGATCAAAGC--CAA--AG--TCC-A--TTATGTT-TCGGGCCTTGTCAATCTGTTTC-CTCGCAATGT-TTGTGCCAATGTACATAGGACTGAGAAATTAACTGCCTCTAGCCGTAT-------C
droEug1	scf7180000409005:424449-424635 -		TTGTCTGTCCCCTCACAAAAAA-----------ACCTA------AAAAA-CAGCGATAAAGG----C------------------ACAA--------------------------ACAAATATGCGTAATGAAATATATTAACAAGAGT--CATCTAC--ATCTATTGAATGTTATTGGGCCTTGTTAATTTGTTGC-ATCGCAATGT-TTGTGCAAATGTACATAGGTCTGAGAAATTAACTGCCTAGAGCCGTAC-------C
dm3	chr2L:4547680-4547874 -		TTGTCTGTCCCCTTACAAAAAAA------AAAAAA--ACATAAATATAT-CAGCGATAAAGC----AC------------------ACAA--------------------------GCCCATTTGCCCGACGAAATGTATTGACCAAAGC--CCCGTAC--TCCTGATTAGTCCT-TTGGGCCTTGTCAATCTGTTTC-CTCGCAAGGT-TTGTGGAAGTGTACATAGGTCTGAGAAATTAACAGCCTGTAGCCGTAT-------C
droSim2	2L:4384033-4384219 -		TTGTCTGTCCCCTTACAAAAAA------CCA--A--AA------TATAT-CAGCGATAAAGC----AC------------------ACAA--------------------------GCCAATTTGCCCGACGAAATGTATTGACCAAAGC--CCCGTAC--TCCCGATTAGTCCT-TTGGGCCTTGTCAATCTGTTTC-CTCGCAAGGT-TTGTGGAAGTGTACATAGGTCTGAGAAATTAACAGCCTGTAGCCGTAT-------C
droYak3	2L:4565122-4565305 -		TTGTCTGTCCCCTTACAAACAA-----------A--AA------TATAA-CAGCGATAAAGC----AC------------------ACAA--------------------------ACCAATTTGCCCGACGAAATGTATTGACCAAAGC--CGCGCAC--TCCTGATTTGTCCT-TCCGGCCTTGTCAATCTGTTTC-CTTGCAATGT-TTGTGGAAGTGTACATAGGTTTGAGAAATTAACAGCCTGTAGCCGTAT-------C
droEre2	scaffold_4929:4631168-4631348 -		TTGTCTGTCCCCTTACAAAAAA-----------------------TATAA-CAGCGATAAAGC----AC------------------ACAA--------------------------ACCAATTTGCCCGACGAAATGTATTGACCAAAGC--CGCGTAC--TCCTGATTAGTCCT-TTGGGCCTTGTCAATCTGTTTC-CTTGCAATGT-TTGTGGAAGTGTACATAGGTCTGAGAAATTAACAGCCTGTAGCCGTAT-------C

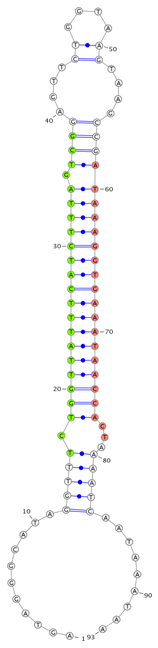
Generated: 09/08/2015 at 07:43 PM

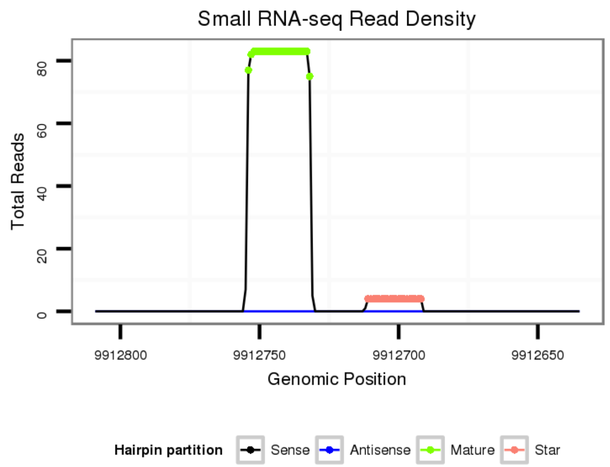
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

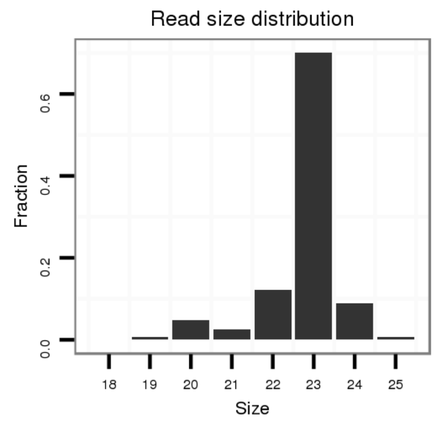
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3145	**scaffold_6473:9912685-9912759 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

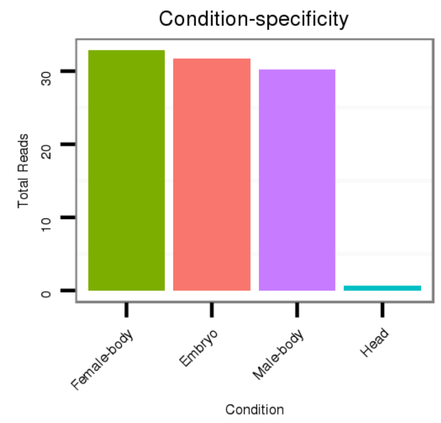
Legend: mature star mismatch in alignment mismatch in read

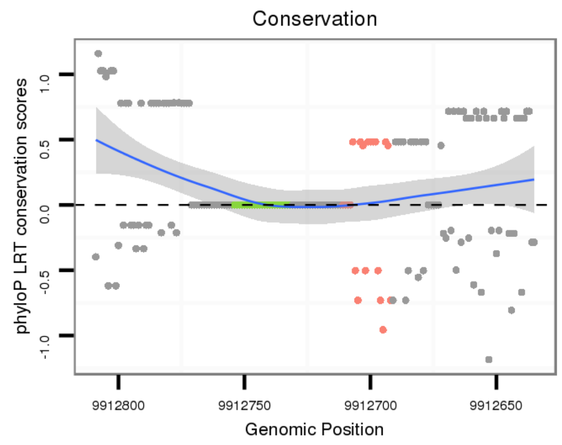
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dmo_3139 scaffold_6308:570045-570067 + 2. dmo_3140 scaffold_6308:570864-570886 - 3. dmo_3144 scaffold_6473:8660635-8660657 - 4. dmo_3145 scaffold_6473:9912732-9912754 - 5. dmo_3149 scaffold_6473:9914029-9914051 + 6. dmo_3151 scaffold_6473:9918570-9918592 - 7. dmo_3135 scaffold_6473:10167398-10167420 + 8. dmo_3137 scaffold_6473:10168272-10168294 - 9. dmo_3153 scaffold_6473:10193410-10193432 +	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

TAATGAATTTTTAACAAATAATAAATATATCCACATTTCCAGTAGGGCATAGGTTTCTGGTTATTTCATCTTTAGTCGGAGTTCTGGTAAGTAAGCCGATAAAGGTGAAATAACCACTAAAATCAATAAATAAACTGGTGAGAGAGAGCGGTCTAGGCGAGAGTACTCGACTAGC **********.....(((((.((((((((((((((((((.((((....((....))....))))))))))))))))))))...)))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
.....TCTGGTTATTTCATCTTTAGTCG.....	23	0	9	62.56	563	82	227	226	25	2	1
.....TCTGGTTATTTCATCTTTAGTC.....	22	0	9	7.00	63	50	6	6	1	0	0
.....TTCTGGTTATTTCATCTTTAGTCG.....	24	0	9	6.33	57	9	25	19	4	0	0
.....ATAAAGGTGAAATAACCACT.....	20	0	19	3.42	65	61	2	0	2	0	0
.....CTGGTTATTTCATCTTTAGTCGG.....	23	0	11	3.00	33	10	5	16	1	0	1
.....CTGGTTATTTCATCTTTAGTCG.....	22	0	11	2.82	31	4	19	7	1	0	0
.....TCTGGTTATTTCATCTTTAGTCGG.....	24	0	9	1.44	13	10	2	0	1	0	0
.....TTCTGGTTATTTCATCTTTAGTC.....	23	0	9	1.22	11	7	3	0	1	0	0
.....GATAAAGGTGAAATAACCACT.....	21	0	18	1.11	20	17	2	0	1	0	0
.....TCTGGTTATTTCATCTTTAGTCGA.....	24	1	9	1.00	9	4	1	4	0	0	0
.....TGGTTATTTCATCTTTAGTCGG.....	22	0	20	1.00	20	14	6	0	0	0	0
.....ATAAAGGTGAAATAACCACC.....	20	1	19	0.95	18	18	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGT.....	21	0	9	0.67	6	5	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTCG.....	25	0	9	0.67	6	2	4	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTC.....	24	0	9	0.56	5	4	1	0	0	0	0
.....GAGTTCTGGTAAGTAAGCCG.....	20	0	4	0.50	2	2	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAG.....	20	0	9	0.44	4	4	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCA.....	23	1	9	0.44	4	1	2	1	0	0	0
.....TCTGGTTATTTCATCTTTAGTCT.....	23	1	9	0.33	3	1	0	1	0	1	0
.....CGATAAAGGTGAAATAACCACT.....	22	0	18	0.28	5	5	0	0	0	0	0
.....GATAAAGGTGAAATAACCACTA.....	22	0	18	0.28	5	4	0	0	0	1	0
.....ATAAAGGTGAAATAACCAC.....	19	0	19	0.26	5	5	0	0	0	0	0
.....GAGTTCTGGTAAGTAAGCC.....	19	0	4	0.25	1	1	0	0	0	0	0
.....TTCTGGTTATTTCATCTTTAGT.....	22	0	9	0.22	2	1	0	0	0	1	0
.....TCTGGTTATTTCATCTTTAGTCGC.....	24	1	9	0.22	2	0	0	2	0	0	0
.....TCTGGTTATTTCATCTTTAGC.....	21	1	9	0.22	2	2	0	0	0	0	0
.....TTCTGGTTATTTCATCTTTAGTCGC.....	25	1	9	0.22	2	0	0	2	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGT.....	24	1	9	0.22	2	0	0	2	0	0	0
.....TCTGGTTATTTCATCTTTAGTCTT.....	24	2	9	0.22	2	2	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
.....TTATTTCATCTTTAGTCGGAGTTC.....	24	0	10	0.20	2	2	0	0	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGT.....	24	1	11	0.18	2	1	1	0	0	0	0
.....CGATAAAGGTGAAATAACCACC.....	22	1	18	0.17	3	3	0	0	0	0	0
.....CCGATAAAGGTGAAATAACCA.....	21	0	20	0.15	3	2	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGC.....	23	1	9	0.11	1	0	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTCGA.....	26	1	9	0.11	1	0	1	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCAA.....	24	2	9	0.11	1	0	1	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGGC.....	25	1	9	0.11	1	1	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGGAA.....	26	1	9	0.11	1	0	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGT.....	23	0	9	0.11	1	0	1	0	0	0	0
.....TTCTGGTTATTTCATCTTTAG.....	21	0	9	0.11	1	0	0	1	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
.....GTTATTTCATCTTTAGTCG.....	19	0	20	0.10	2	0	1	1	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGAG.....	25	0	11	0.09	1	0	0	1	0	0	0
.....CTGGTTATTTCATCTTTAGTCAA.....	23	2	11	0.09	1	0	1	0	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGC.....	24	1	11	0.09	1	0	0	1	0	0	0
.....GATAAAGGTGAAATAACCACTAAC.....	24	1	18	0.06	1	1	0	0	0	0	0
.....GATAAAGGTGAAATAACCAC.....	20	0	18	0.06	1	1	0	0	0	0	0
.....CGATAAAGGTGAAATAACCACA.....	22	1	18	0.06	1	0	1	0	0	0	0
.....ATAAAGGTGAAATAACCACTGT.....	22	2	19	0.05	1	0	0	1	0	0	0
.....AAAGGTGAAATAACCACT.....	18	0	19	0.05	1	1	0	0	0	0	0
.....ATAAAGGTGAAATAACCACTTT.....	22	2	19	0.05	1	1	0	0	0	0	0
.....CGATAAAGGTGAAATAACCC.....	20	1	20	0.05	1	1	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTCGGA.....	23	0	20	0.05	1	0	0	0	1	0	0
.....GGTTATTTCATCTTTAGTCGG.....	21	0	20	0.05	1	0	0	0	0	0	1
.....TTATTTCATCTTTAGTCGGA.....	20	0	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCG.....	20	0	20	0.05	1	0	1	0	0	0	0
.....TGGTTATTTCATCTTTAGTC.....	20	0	20	0.05	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGC.....	21	1	20	0.05	1	1	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTCG.....	21	0	20	0.05	1	0	0	0	0	1	0
.....GTTATTTCATCTTTAGTCGGAA.....	22	1	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

ATTACTTAAAAATTGTTTATTATTTATATAGGTGTAAAGGTCATCCCGTATCCAAAGACCAATAAAGTAGAAATCAGCCTCAAGACCATTCATTCGGCTATTTCCACTTTATTGGTGATTTTAGTTATTTATTTATTTGACCACTCTCTCTCGCCAGATCCGCTCTCATGAGCTGATCG **********.....(((((.((((((((((((((((((.((((....((....))....))))))))))))))))))))...)))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V049 head	V110 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:9912635-9912809 -	dmo_3145	TAATGAATTTTTAACAAATAATAAATATATCCACATTTCCAGTAGGGCATAGGTTTCTGGTTATTTCATCTTTAGTCGGAGTTCTGGTAAGTAAGCCGATAAAGGTGAAATAACCACTAAAATCAATAAATAAACTGGTGAGAG----------AGAGCGGTCTAGGCGAGAGTACTCGACTAGC
droVir3	scaffold_12970:4011786-4011855 +		AA----------AATTGGAATAGAGAGCCAAATAGATATACA-----GCAGAT----------AAAGTGCTCGAGTCGGGAGTGGCCGCCTAAT
droGri2	scaffold_14853:6237421-6237487 -		AAATGCATGC----------CAAAATATTTGAAAAAAGAGAGTATAAGAGTGCTCTAGCTGAAAGTGCCCGACTAGC
dm3	chr2R:8701636-8701673 -		GAATGAATTTTCAATGCGTCGCAAATTTATTCTCATTT----------|----------|

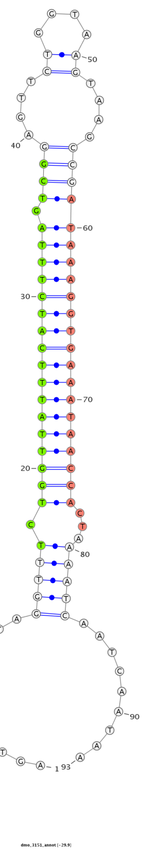
Generated: 09/08/2015 at 07:48 PM

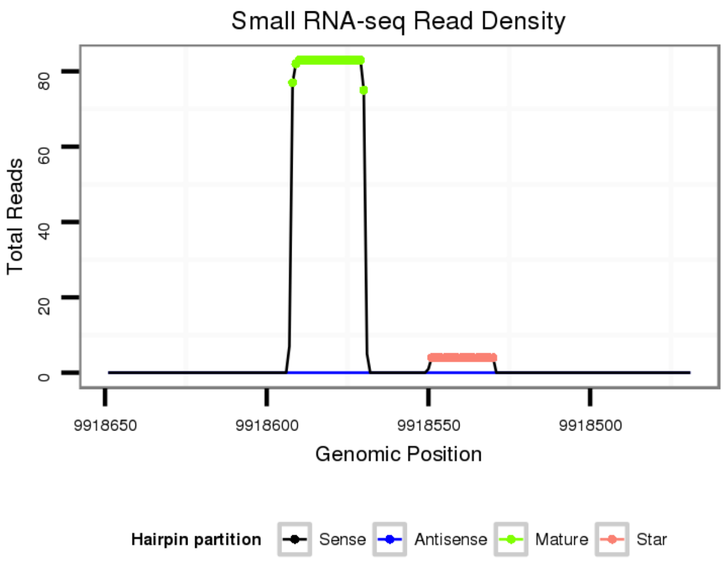
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

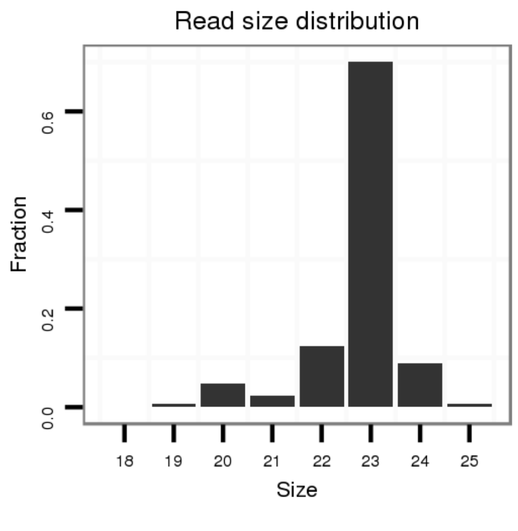
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3151	**scaffold_6473:9918519-9918599 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

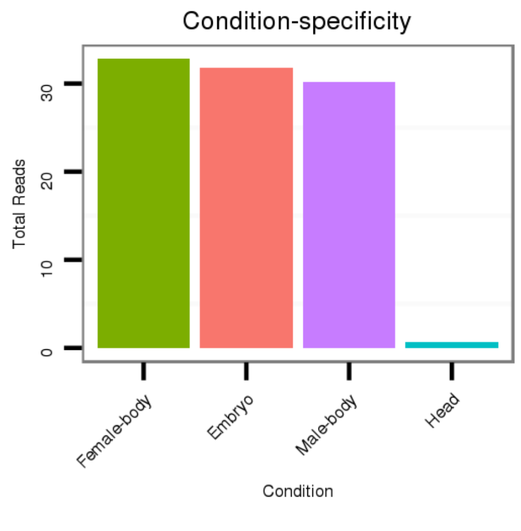
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
Homo6	DNA	hAT-Pegasus	+

mature

1. dmo_3139 scaffold_6308:570045-570067 +
2. dmo_3140 scaffold_6308:570864-570886 -
3. dmo_3144 scaffold_6473:8660635-8660657 -
4. dmo_3145 scaffold_6473:9912732-9912754 -
5. dmo_3149 scaffold_6473:9914029-9914051 +
6. dmo_3151 scaffold_6473:9918570-9918592 -
7. dmo_3135 scaffold_6473:10167398-10167420 +
8. dmo_3137 scaffold_6473:10168272-10168294 -
9. dmo_3153 scaffold_6473:10193410-10193432 +

star

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

CTTAATGAATTTTGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGGTTTCTGGTTATTTCATCTTTAGTCGGAGTTCTGGTAAGTAAGCCGATAAAGGTGAAATAACCACTAAAATCAATCAATAAACTAGTGACGGAGAGTGCTCTAGTAGAGACTGCTCGACTAGCAGAT **********.....(((((.((((((((((((((((.((((....((....))....))))))))))))))))))...)))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
.....TCTGGTTATTTCATCTTTAGTCG.....	23	0	9	62.56	563	82	227	226	25	2	1
.....TCTGGTTATTTCATCTTTAGTC.....	22	0	9	7.00	63	50	6	6	1	0	0
.....TTCTGGTTATTTCATCTTTAGTCG.....	24	0	9	6.33	57	9	25	19	4	0	0
.....ATAAAGGTGAAATAACCACT.....	20	0	19	3.42	65	61	2	0	2	0	0
.....CTGGTTATTTCATCTTTAGTCGG.....	23	0	11	3.00	33	10	5	16	1	0	1
.....CTGGTTATTTCATCTTTAGTCG.....	22	0	11	2.82	31	4	19	7	1	0	0
.....TCTGGTTATTTCATCTTTAGTCGG.....	24	0	9	1.44	13	10	2	0	1	0	0
.....TTCTGGTTATTTCATCTTTAGTC.....	23	0	9	1.22	11	7	3	0	1	0	0
.....GATAAAGGTGAAATAACCACT.....	21	0	18	1.11	20	17	2	0	1	0	0
.....TCTGGTTATTTCATCTTTAGTCGA.....	24	1	9	1.00	9	4	1	4	0	0	0
.....TGGTTATTTCATCTTTAGTCGG.....	22	0	20	1.00	20	14	6	0	0	0	0
.....ATAAAGGTGAAATAACCACC.....	20	1	19	0.95	18	18	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGT.....	21	0	9	0.67	6	5	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTCG.....	25	0	9	0.67	6	2	4	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTC.....	24	0	9	0.56	5	4	1	0	0	0	0
.....GAGTTCTGGTAAGTAAGCCG.....	20	0	4	0.50	2	2	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCA.....	23	1	9	0.44	4	1	2	1	0	0	0
.....TCTGGTTATTTCATCTTTAG.....	20	0	9	0.44	4	4	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCT.....	23	1	9	0.33	3	1	0	1	0	1	0
.....CGATAAAGGTGAAATAACCACT.....	22	0	18	0.28	5	5	0	0	0	0	0
.....GATAAAGGTGAAATAACCACTA.....	22	0	18	0.28	5	4	0	0	0	1	0
.....ATAAAGGTGAAATAACCAC.....	19	0	19	0.26	5	5	0	0	0	0	0
.....GAGTTCTGGTAAGTAAGCC.....	19	0	4	0.25	1	1	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGC.....	24	1	9	0.22	2	0	0	2	0	0	0
.....TCTGGTTATTTCATCTTTAGTCTT.....	24	2	9	0.22	2	2	0	0	0	0	0
.....TTCTGGTTATTTCATCTTTAGT.....	22	0	9	0.22	2	1	0	0	0	1	0
.....TCTGGTTATTTCATCTTTAGTCGT.....	24	1	9	0.22	2	0	0	2	0	0	0
.....TCTGGTTATTTCATCTTTAGC.....	21	1	9	0.22	2	2	0	0	0	0	0
.....TTCTGGTTATTTCATCTTTAGTCGC.....	25	1	9	0.22	2	0	0	2	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
.....TTATTTCATCTTTAGTCGGAGTTC.....	24	0	10	0.20	2	2	0	0	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGT.....	24	1	11	0.18	2	1	1	0	0	0	0
.....CGATAAAGGTGAAATAACCACC.....	22	1	18	0.17	3	3	0	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGT.....	23	0	9	0.11	1	0	1	0	0	0	0
.....TTCTGGTTATTTCATCTTTAG.....	21	0	9	0.11	1	0	0	1	0	0	0
.....TTTCTGGTTATTTCATCTTTAGC.....	23	1	9	0.11	1	0	1	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGGC.....	25	1	9	0.11	1	1	0	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCAA.....	24	2	9	0.11	1	0	1	0	0	0	0
.....TTTCTGGTTATTTCATCTTTAGTCGA.....	26	1	9	0.11	1	0	1	0	0	0	0
.....TCTGGTTATTTCATCTTTAGTCGGAA.....	26	1	9	0.11	1	0	1	0	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
.....CCGATAAAGGTGAAATAACCA.....	21	0	20	0.10	2	2	0	0	0	0	0
.....TATTTCATCTTTAGTCGGAGTT.....	22	0	20	0.10	2	2	0	0	0	0	0
.....GTTATTTCATCTTTAGTCG.....	19	0	20	0.10	2	0	1	1	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGC.....	24	1	11	0.09	1	0	0	1	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGAG.....	25	0	11	0.09	1	0	0	1	0	0	0
.....CTGGTTATTTCATCTTTAGTCAA.....	23	2	11	0.09	1	0	1	0	0	0	0
.....GATAAAGGTGAAATAACCACTAAC.....	24	1	18	0.06	1	1	0	0	0	0	0
.....GATAAAGGTGAAATAACCAC.....	20	0	18	0.06	1	1	0	0	0	0	0
.....CGATAAAGGTGAAATAACCACA.....	22	1	18	0.06	1	0	1	0	0	0	0
.....CATCCACATTTCCAGTAGGGC.....	21	0	18	0.06	1	0	0	1	0	0	0
.....ATAAAGGTGAAATAACCACTTT.....	22	2	19	0.05	1	1	0	0	0	0	0
.....ATAAAGGTGAAATAACCACTGT.....	22	2	19	0.05	1	0	0	1	0	0	0
.....AAAGGTGAAATAACCACT.....	18	0	19	0.05	1	1	0	0	0	0	0
.....CTCTAGTAGAGACTGCTCGAC.....	21	0	20	0.05	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGAA.....	22	1	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCGG.....	21	0	20	0.05	1	0	0	0	0	0	1
.....GTTATTTCATCTTTAGTCGGC.....	21	1	20	0.05	1	1	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGA.....	20	0	20	0.05	1	1	0	0	0	0	0
.....GGTTATTTCATCTTTAGTCG.....	20	0	20	0.05	1	0	1	0	0	0	0
.....TGGTTATTTCATCTTTAGTCG.....	21	0	20	0.05	1	0	0	0	0	1	0
.....TGGTTATTTCATCTTTAGTCGGA.....	23	0	20	0.05	1	0	0	0	1	0	0
.....CGATAAAGGTGAAATAACCC.....	20	1	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

GAATTACTTAAAACTTGTTTATTATTTATGTAGGTGTAAAGGTCATCCCGTATCCAAAGACCAATAAAGTAGAAATCAGCCTCAAGACCATTCATTCGGCTATTTCCACTTTATTGGTGATTTTAGTTAGTTATTTGATCACTGCCTCTCACGAGATCATCTCTGACGAGCTGATCGTCTA **********.....(((((.((((((((((((((((.((((....((....))....))))))))))))))))))...)))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	V041 embryo
.....TCATCTCTGACGAGCTGATCG....	21	0	9	0.11	1	1	0
.....AGATCATCTCTGACGAGCT.....	19	0	20	0.05	1	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:9918469-9918649 -	dmo_3151	CTTAATGAATTTTGAACAAATAATAAATACATCCACATTTCCAGTAGGGCATAGGTTTCTGGTTATTTCATCTTTAGTCGGAGTTCTGGTAAGTAAGCCGATAAAGGTGAAATAACCACTAAAATCAATCAATAAACTAGTGACGGAGAGTGCTCTAGTAGAGACTGCTCGACTAGCAGAT

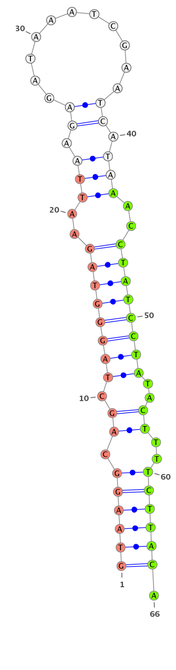
Generated: 09/08/2015 at 07:49 PM

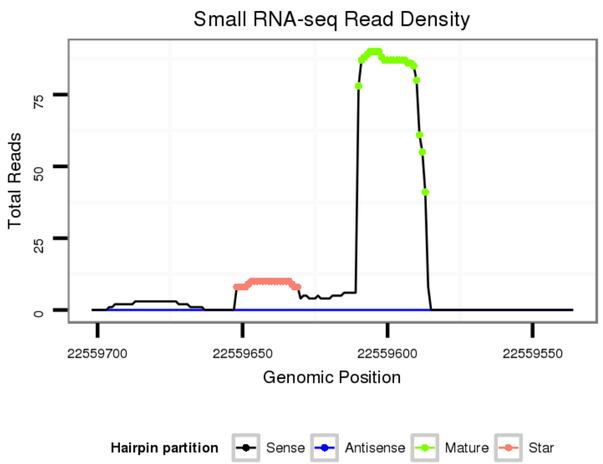
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

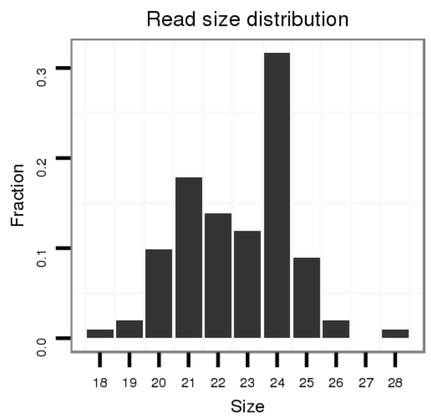
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_161	**scaffold_6496:22559586-22559652 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

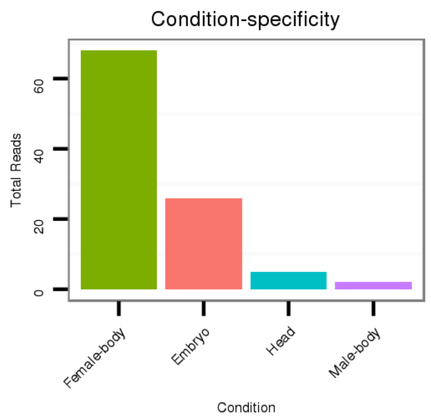
Legend: mature star **mismatch in alignment** mismatch in read

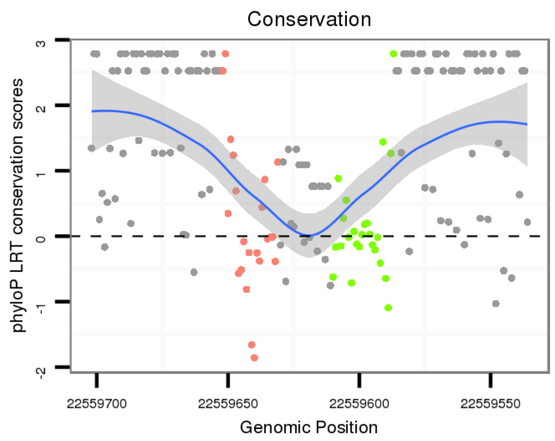
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI18489-in]; CDS [Dmoj\GI18489-cds]; CDS [Dmoj\GI18489-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GATCGCACGGGAGTCCAAGTGCATCATTGAGATGAGTGGGGCTACAACGGGTAAGGCAGCTAGGGTAGAATTAAGAGATAAATCGAATCATAAACCTATCCTATACTTTTCTTACAGCCATTACCAATCCGAAGGTGCCACCAAACACGAGCGAGTCCGTCAAGCGC **********(((((((.((.(((((((((..(((.((..........)).)))..)))))))))..))).)))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V110 male body	V041 embryo	V056 head	V049 head
..........AACCTATCCTATACTTTTCTTACA..........	24	0	1	29.00	29	21	5	1	0	2	0
..........AACCTATCCTATACTTTTCTT..........	21	0	1	16.00	16	14	0	0	0	1	1
..........AACCTATCCTATACTTTTCTTAC..........	23	0	1	10.00	10	8	2	0	0	0	0
..........AACCTATCCTATACTTTTCTTACAG..........	25	0	1	7.00	7	5	2	0	0	0	0
..........AACCTATCCTATACTTTTCTTA..........	22	0	1	6.00	6	6	0	0	0	0	0
..........GTAAGGCAGCTAGGGTAGAATT..........	22	0	1	4.00	4	0	3	0	1	0	0
..........AACCTATCCTATACTTTTCT..........	20	0	1	4.00	4	3	0	0	0	0	1
..........ACCTATCCTATACTTTTCTT..........	20	0	1	3.00	3	3	0	0	0	0	0
..........ACCTATCCTATACTTTTCTTAC..........	22	0	1	3.00	3	2	1	0	0	0	0
..........ACCTATCCTATACTTTTCTTACA..........	23	0	1	2.00	2	2	0	0	0	0	0
..........GTAAGGCAGCTAGGGTAGA..........	19	0	1	2.00	2	0	1	0	1	0	0
..........CTATCCTATACTTTTCTTAC..........	20	0	1	1.00	1	0	1	0	0	0	0
........GGGAGTCCAAGTGCATCATTGA..........	22	0	1	1.00	1	0	0	1	0	0	0
..........GATAAATCGAATCATAAACCTATC..........	24	0	1	1.00	1	1	0	0	0	0	0
..........GCAGCTAGGGTAGAATTAAGA..........	21	0	1	1.00	1	0	0	0	1	0	0
..........TATCCTATACTTTTCTTACA..........	20	0	1	1.00	1	1	0	0	0	0	0
..........CCTATCCTATACTTTTCT..........	18	0	1	1.00	1	0	1	0	0	0	0
..........ATTAAGAGATAAATCGAATCATAAAC..........	26	0	1	1.00	1	0	1	0	0	0	0
..............CAAGTGCATCATTGAGATGAGTGG..........	24	0	1	1.00	1	1	0	0	0	0	0
..........ACCTATCCTATACTTTTCTTACAG..........	24	0	1	1.00	1	1	0	0	0	0	0
..........GTAAGGCAGCTAGGGTAGAA..........	20	0	1	1.00	1	0	0	0	1	0	0
..........AGAGATAAATCGAATCATAAACCTATCC..........	28	0	1	1.00	1	0	1	0	0	0	0
..........TAAATCGAATCATAAACCTATC..........	22	0	1	1.00	1	0	1	0	0	0	0
..........TCATAAACCTATCCTATACTTTTC..........	24	0	1	1.00	1	0	1	0	0	0	0
..........CTATCCTATACTTTTCTTACA..........	21	0	1	1.00	1	0	1	0	0	0	0
......ACGGGAGTCCAAGTGCATCATTGAGATG..........	28	0	1	1.00	1	0	0	1	0	0	0
..........CGAATCATAAACCTATCCTATACTTT..........	26	0	1	1.00	1	1	0	0	0	0	0
..........GTAAGGCAGCTAGGGTAGAATTAAG..........	25	0	1	1.00	1	0	0	1	0	0	0
..........GGCAGCTAGGGTAGAATTAAGAGAT..........	25	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

CTAGCGTGCCCTCAGGTTCACGTAGTAACTCTACTCACCCCGATGTTGCCCATTCCGTCGATCCCATCTTAATTCTCTATTTAGCTTAGTATTTGGATAGGATATGAAAAGAATGTCGGTAATGGTTAGGCTTCCACGGTGGTTTGTGCTCGCTCAGGCAGTTCGCG **********(((((((.((.(((((((((..(((.((..........)).)))..)))))))))..))).)))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V041 embryo	V049 head
..........AACCTATCCTATACTTTTCTTACA..........	24	0	1	29.00	29	21	5	1
..........AACCTATCCTATACTTTTCTT..........	21	0	1	16.00	16	14	0	0
..........AACCTATCCTATACTTTTCTTAC..........	23	0	1	10.00	10	8	2	0
..........AACCTATCCTATACTTTTCTTACAG..........	25	0	1	7.00	7	5	2	0
..........AACCTATCCTATACTTTTCTTA..........	22	0	1	6.00	6	6	0	0
..........GTAAGGCAGCTAGGGTAGAATT..........	22	0	1	4.00	4	0	3	0
..........AACCTATCCTATACTTTTCT..........	20	0	1	4.00	4	3	0	0
..........ACCTATCCTATACTTTTCTT..........	20	0	1	3.00	3	3	0	0
..........ACCTATCCTATACTTTTCTTAC..........	22	0	1	3.00	3	2	1	0
..........ACCTATCCTATACTTTTCTTACA..........	23	0	1	2.00	2	2	0	0
..........GTAAGGCAGCTAGGGTAGA..........	19	0	1	2.00	2	0	1	0
..........CTATCCTATACTTTTCTTAC..........	20	0	1	1.00	1	0	1	0
........GGGAGTCCAAGTGCATCATTGA..........	22	0	1	1.00	1	0	0	1
..........GATAAATCGAATCATAAACCTATC..........	24	0	1	1.00	1	1	0	0
..........GCAGCTAGGGTAGAATTAAGA..........	21	0	1	1.00	1	0	0	1
..........TATCCTATACTTTTCTTACA..........	20	0	1	1.00	1	1	0	0
..........CCTATCCTATACTTTTCT..........	18	0	1	1.00	1	0	1	0
..........ATTAAGAGATAAATCGAATCATAAAC..........	26	0	1	1.00	1	0	1	0
..............CAAGTGCATCATTGAGATGAGTGG..........	24	0	1	1.00	1	1	0	0
..........ACCTATCCTATACTTTTCTTACAG..........	24	0	1	1.00	1	1	0	0
..........GTAAGGCAGCTAGGGTAGAA..........	20	0	1	1.00	1	0	0	1
..........AGAGATAAATCGAATCATAAACCTATCC..........	28	0	1	1.00	1	0	1	0
..........TAAATCGAATCATAAACCTATC..........	22	0	1	1.00	1	0	1	0
..........TCATAAACCTATCCTATACTTTTC..........	24	0	1	1.00	1	0	1	0
..........CTATCCTATACTTTTCTTACA..........	21	0	1	1.00	1	0	1	0
......ACGGGAGTCCAAGTGCATCATTGAGATG..........	28	0	1	1.00	1	0	0	1
..........CGAATCATAAACCTATCCTATACTTT..........	26	0	1	1.00	1	1	0	0
..........GTAAGGCAGCTAGGGTAGAATTAAG..........	25	0	1	1.00	1	0	0	1
..........GGCAGCTAGGGTAGAATTAAGAGAT..........	25	0	1	1.00	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6496:22559536-22559702 -	dmo_161	GATCGCACGGGAGTCCAAGTGCATCATTGAGATGAGTGGGGCTACAACGGGTAAGGCAGCTAGG----------GTAG----------AATTAAGAGATAAATCGAATCATA---------AACCTAT--C-C-------T----ATACTTTTCTTACAGCCATTACCAATCCGAAGGTGCCACCAAACACGAGCGAGTCCGTCAAGCGC
droVir3	scaffold_12875:2669888-2670042 +		GATTGCACGGGAGTCCAATGCATCATCGAGATGAGCGGCGCCACAACGGGTAATGCAGCTAG----------AA-ATTGCGTT--------------------TAAAC------TAAACGTCTAAGCC-TCTA------TTTTACAGCCATTACCAATCCGAAAGTGCCGCCCAACACAAGCGAGTCCATCAAGCGC
droGri2	scaffold_15112:3503915-3504082 -		GATTGGCCCCGAGTCCAATGCATCATCGAGATGACCGGCGCCACAACGGGTGAGTCTGCCTCA-AATAT---ACAC---A------CA-----GCCTAAAG----------CAACTAATTT--------CGAATCCATTCTCA-----------TTTTTGATAGCCATTACCAATCCGAAGGTGCCACCGAACACAAGCGAGTCCGTCGAAACGC
droWil2	scf2_1100000004382:567408-567569 +		AATAGCCAGAGAATCGAAATGCATCATCGAGATGACCGGGGCTACAACGGGTAAGAAATA----------T---ATA-CGAACCT--G--TATTTAA--------------------------TATTT------CATTTATTTCATCA-TTTA------TATTGCAGCCATTACCAATCCAAAAGTTCCACCCAATACCAGTGATTCGGTGAAACGC
dp5	3:19061236-19061394 +		AATAGGCAGGGAGTCGAAATGCATCATCGAGATGACCGGGGCCACCACGGGTAAGACCCAGCACA-A-CAG---ACAC---A------T--C-------ACC----AGAGA----------------------------CTCTCAT--C-C-------T---TGTGATTCTTTTGCAGCCATAACCAATCCGAAGGTGCCGCCCAACACAAGTGAGGCGGTGAAGCGC
droPer2	scaffold_37:64036-64194 +		AATAGGCAGGGAGTCGAAATGCATCATCGAGATGACCGGGGCCACCACGGGTAAGACCCACACA-A-CAG---ACAC---A------C--C-------ACC----ACAGA----------------------------CTCTCAT--C-C-------T---TGTGATTCTTCTGCAGCCATAACCAATCCGAAGGTGCCGCCCAACACAAGTGAGGCGGTGAAGCGC
droAna3	scaffold_13266:13940577-13940738 +		AATAGCCAGGGAGTCGAAATGCATTATCGAGATGAGCGGGGCCACAACGGGTAAGAACATTTGA-AA----------A-----ATAA-ATTGCAATAA----------AAATAAAAACTAAATT--------------------------GAAATCGTGTTTCAGCCATTACCAACCCAAAGTACCGCCAAACACAAGCGAGTCGGTGAAGCGA
droBip1	scf7180000396759:2196176-2196338 -		AATAGCCAGGGAGTCGAAATGCATTATCGAGATGAGCGGGGCCACAACGGGTAAGACACTGAA-AA----------AA--CA--AA-ATTGCAATAA----------AAATAAAAACTAAATT--------------------------GAAATCGTGTTTCAGCCATTACCAATCCAAAGTACCGCCAAACACAAGCGATCAGTGAAGCGC
droKik1	scf7180000302470:1057973-1058132 -		AATAAGCAGGGAGTCGAAATGCATCATCGAGATGAGCGGGGCCACCACGGGTAAGAGAT-----------------G--TCCTAG-ATGTCTAC--------------------------AAATT------CACATTTTT--ATAA-CACG-AAAACCCCTTGCAGCCATTACCAACCCAAAGGTACCACCAAACACAAGTGATTCGGTAAACGCA
droFic1	scf7180000453851:864445-864610 -		AATAGCCAGGGAGTCGAAATGCATCATCGAGATGCAGGAGCCACAACGGGTAGGAGTCTCAAA-AG----------TG--TTCTAACATTCTACT--------------------------AAGCC------CAATATAATAAAATATATTTT-----TTTCTAACAGCCATACCAATCCAAAGGTGCCGCCAACACAAGCGAGTCAGTAAAGCGC
droEle1	scf7180000491214:1731864-1732031 +		AATCAGCAGGGAGTCGAAATGCATCATCGAGATGCAGGAGCCACAACGGGTAAGAGTCCTATC-TATAG---AT------CTATAG-ATTA-----TC----AGGGGTGCTCAGAACT----------T---------------AATAA-TA-----TTTTTTTTCAGCCATCACCAATCCAAAGGTGCCGCCCAACACAAGCGATTCAGTAAAGCGC
droRho1	scf7180000780084:701830-701992 +		AATAGGCAGGGAGTCGAAATGCATCATCGAGATGCAGGCGCCACAACGGGTAAGATTCTTTA--AC----------CA--CTCGAA-ATTTATT--------------------------AAACC------CAATACACTTATGCAA-AATC-------TTTTGGCAGCCATCACCAATCCAAAGGTGCCGCCCAACACAAGCGACTCAGTAAAGCGT
droBia1	scf7180000301506:2048767-2048929 -		AATAGCCAGGGAGTCGAAATGCATCATCGAGATGGCTGGGGCCACAACGGGTAAGAGTCTCCTT-AA----------AA--CTCAG--AGT-----------------------------GATTCCTTAATT------CAAA--CTTGAACAT-TATG-------ACTTGACAGCCATCACCAATCCAAAGGTGCCGCCCAACACAAGCGACTCGGTAAAGCGC
droTak1	scf7180000414504:35970-36133 -		AATAGCCAGGGAGTCGAAATGCATCATCGAGATGCAGGGGCCACAACGGGTAAGAGACTCTAA-GA----------CA--CTGTAG-ATTTTTCT--------------------------ACATT------CAATATACTTTTAATG-CATC-------CCCTCGCAGCCATCACCAATCCAAAGGTGCCGCCCAACACAAGCGACTCAGTGAAGCGC
droEug1	scf7180000409672:2496656-2496822 +		AATAGCCAGGGAGTCGAAATGCATCATCGAGAATGCTGGAGCCACAACGGGTAAGAGTCCCTTAGAA----------AA--CTTTAC-ATTTTTCT--------------------------AAGCT------CAATTTATAAATAT-GAAA-----CCTACTTTCAGCTATCACCAATCCAAAGGTGCCGCCCAACACAAGCGACTCAGTGAAGCGC
dm3	chr2R:12650589-12650752 -		AATAGCCAGGGAGTCGAAATGCATCATCGAGATGCAGGAGCCACAACGGGTGAGAATCCCATA-AA----------CA--CTCTAG-ATTTCTCT--------------------------TAATT------CAATATACTTCAATCT-TATG-------TCCTGACAGCCATCACCAATCCAAAGGTGCCGCCCAACACAAGCGATTCAGTAAAGCGC
droSim2	2r:13322273-13322436 -		AATAGCCAGGGAGTCGAAATGCATCATCGAGATGCAGGAGCCACAACGGGTGAGAATCTCATA-AA----------CA--CTCTAG-ATTTTGCT--------------------------TAATT------CAATATACTTCAATCT-TATG-------TCCTGACAGCCATCACCAATCCAAAGGTGCCGCCCAACACAAGCGATTCAGTAAAGCGC
droSec2	scaffold_1:10156041-10156204 -		AATAGCCAGGGAGTCGAAATGCATCATCGAGATGCAGGAGCCACAACGGGTGAGAATCCCATA-AA----------CA--CTTTAT-ATTTTGCT--------------------------TAATT------CAATGTACTTTAATCT-TATG-------TCCTGACAGCCATAACCAATCCAAAGGTGCCGCCCAACACAAGCGATTCAGTAAAGCGC
droYak3	2R:16327262-16327429 +		AATAGCCAGGGAGTCGAAATGCATCATCGAGATGCAGGAGCCACAACGGGTTAGAATC------AACACTCTCTA-CA--CTCCAG-ATTTTTCT--------------------------TAATT------CAATATTATTCGATAT-TATG-------TCCTGACAGCCATCACCAATCCAAAGGTGCCGCCCAACACAAGCGATTCGGTGAAGCGC
droEre2	scaffold_4845:13200985-13201148 +		AATAGCCAGGGAGTCGAAATGCATCATCGAGATGCAGGAGCCACAACGGGTTAGAATCTCATG-AG----------CA--CTTTGG-GTTTTTCT--------------------------TAATT------CAATATTATTCGATAT-TATG-------TCCTGACAGCCATACCAATCCAAAGGTGCCGCCCAACACAAGCGATTCGGTGAAGCGC

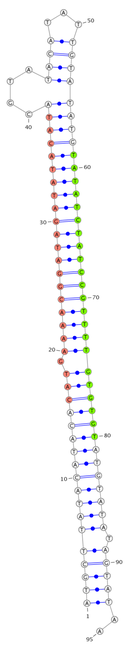
Generated: 09/08/2015 at 10:36 PM

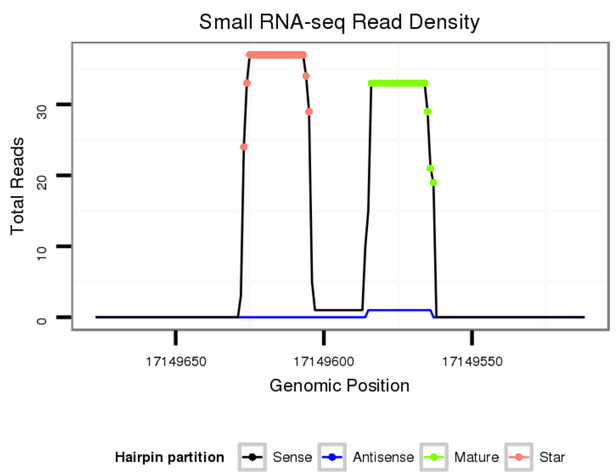
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

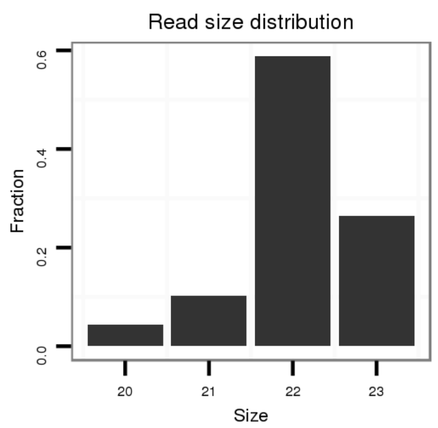
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_119	**scaffold_6496:17149562-17149627 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

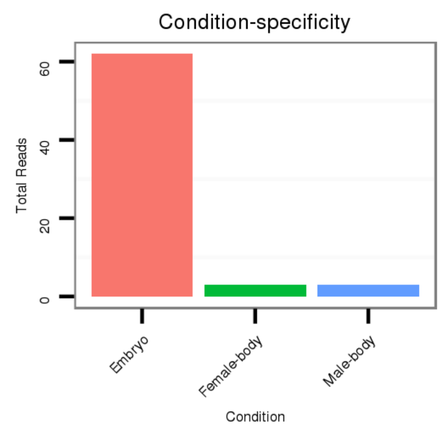
Legend: mature star mismatch in alignment mismatch in read

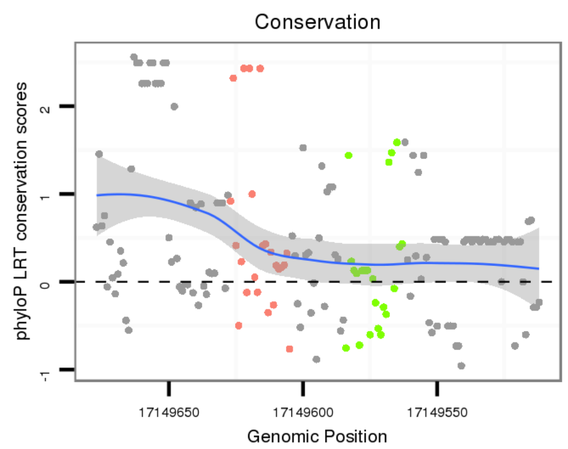
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
(CATATA)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTCAACGTTAAAATTTTGGGTTGGGTTTAGAGCACATGCTTATACATACACATGAAAACGGATAGATATACATACGTATACATATTGTATATGTATATCTATCCGTTTTGTGTGTATGTATATAGTATAACTAATCGGAAGAACAACCCTAAGATCCGCTCGAATA **********(((((((((((((((((.(((((((((((((((((((....((((...))))))))))))))))))))))))))))))))).)))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V041 embryo	V110 male body	M046 female body	V049 head
..........TATATCTATCCGTTTTGTGTGT..........	22	0	1	19.00	19	14	4	0	1	0
..........CATGAAAACGGATAGATATACAT..........	23	0	1	16.00	16	6	8	2	0	0
..........TGTATATCTATCCGTTTTGTGT..........	22	0	1	8.00	8	5	3	0	0	0
..........ATGAAAACGGATAGATATACAT..........	22	0	1	6.00	6	3	3	0	0	0
..........TATATCTATCCGTTTTGTGTGC..........	22	1	1	5.00	5	5	0	0	0	0
..........TGTATATCTATCCGTTTTGTGC..........	22	1	1	5.00	5	5	0	0	0	0
..........CATGAAAACGGATAGATATACATT..........	24	1	1	4.00	4	1	3	0	0	0
..........GTATATCTATCCGTTTTGTG..........	20	0	1	3.00	3	2	1	0	0	0
..........CATGAAAACGGATAGATATACA..........	22	0	1	3.00	3	3	0	0	0	0
..........ACATGAAAACGGATAGATATACA..........	23	0	1	2.00	2	2	0	0	0	0
..........TGAAAACGGATAGATATACAT..........	21	0	1	2.00	2	0	2	0	0	0
..........GTATATCTATCCGTTTTGTGTG..........	22	0	1	2.00	2	0	0	0	2	0
..........CATGAAAACGGATAGATATAC..........	21	0	1	2.00	2	2	0	0	0	0
..........TGAAAACGGATAGATATACATA..........	22	0	1	2.00	2	2	0	0	0	0
..........ATGAAAACGGATAGATATACATA..........	23	0	1	2.00	2	1	0	1	0	0
..........TACGTATACATATTGTATATG..........	21	0	1	1.00	1	1	0	0	0	0
..........ATGAAAACGGATAGATATACA..........	21	0	1	1.00	1	1	0	0	0	0
..........GTATATCTATCCGTTTTGTGTC..........	22	1	1	1.00	1	0	0	1	0	0
..........ACATGAAAACGGATAGATATAC..........	22	0	1	1.00	1	1	0	0	0	0
..........GTATATCTATCCGTTTTGTGC..........	21	1	1	1.00	1	1	0	0	0	0
..........TCTATCCGTTTTGTGTGTC..........	19	1	1	1.00	1	1	0	0	0	0
..........TGTATATCTATCCGTTTTGTG..........	21	0	1	1.00	1	0	1	0	0	0
..........CATGAAAACGGATAGATATACATC..........	24	1	1	1.00	1	1	0	0	0	0
..........TATATCTATCCGTTTTGTGTGTT..........	23	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

GAGTTGCAATTTTAAAACCCAACCCAAATCTCGTGTACGAATATGTATGTGTACTTTTGCCTATCTATATGTATGCATATGTATAACATATACATATAGATAGGCAAAACACACATACATATATCATATTGATTAGCCTTCTTGTTGGGATTCTAGGCGAGCTTAT **********(((((((((((((((((.(((((((((((((((((((....((((...))))))))))))))))))))))))))))))))).)))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V049 head	V110 male body
..........CATATAGATAGGCAAAACACAC..........	22	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6496:17149512-17149677 -	dmo_119	CTCAACGTTAA-------AA-TTTTGGGTTGGGTTT----------AGA-----GCACATGCTTATACATA----------CA--------CA----TGAAAAC-----GGATAGATATACATACGTATACATATTGTATATG------TATATCTATCCGTTT----------TGTGTGTATGTA--TATAGTATAACTAATCGGAAGAACAACCCTAAGATCCGCTCGAATA
droVir3	scaffold_12875:9886470-9886613 +		CTCAACGTCGAAT-----**--**-TTTTGGGTTGGGTTT---------AGA-----GCACATGCTTATACATACAAACGGATATATAA------**--**--------**-**----**--**ATAC-----ACACA--------CACACACACACAC----------**-**----**-**ATGTATGTA--TGTATGCACAACCGGGACGAAGAACAACCCTA-GATCAGC------
droGri2	scaffold_15245:3087174-3087259 +		CTCATCTTTGGG------**-**T-TTTTGGGTTGGGTTT---------AGAGTTAAGT--------GT-----GC------ATATAC-TTA--AC--------CA----TATACAGAAAACGGATGCAC----AAT----------**-**----**-**----------**-**----CGTATATA-----**--**----------
droWil2	scf2_1100000004963:886476-886567 +		GATATACAT**--**-------**--**----------**-**----------**-**-----**-**---------ATACATA----------CA--------CA----TGTACAT-----ATACATATATACATAGATATATATA-----TATATGTATGTATATACATT-----**-**----------CATGTATGCATATGTATATA----------
dp5	3:8887138-8887231 +		TTCAACGTTGGGTTTTC-GG-TTTTGGGTTGGGTTG-----GCTATAGA-----GGGTAGGGTAGGGT---**-**----A----GGGTATAGGGTATA--------CA----T--ATAC-----ACATT----------**-**CGGCT-------**-**----------**-**----------**-**----------**--**----------GGATAG
droPer2	scaffold_4:2772503-2772586 +		TTCAACGTTGGGTTTTC-GG-TTTTGGGTTGGGTTG-----GCTATAGA-----GGGTAGG----------GTA----GGGTATAGGG---TATACATATACA----T--ATAC-----ACATT----------**-**----**-**----------**-**----------**-**----------**--**----------
droAna3	scaffold_13266:2328159-2328178 -		TTCAG------**-**-------**-**T-TTTTGGGTTGGGTT----------**-**----**-**----------**-**----------**-**--------**-**----**-**-------**-**----------**-**----**-**----------**-**----------**-**----------**--**----------
droBip1	scf7180000396759:1372989-1373007 -		TTCGG------**-**-------**-**--TTTTGGGTTGGGTT----------**-**----**-**----------**-**----------**-**--------**-**----**-**-------**-**----------**-**----**-**----------**-**----------**-**----------**--**----------
droKik1	scf7180000302367:116300-116382 -		TTCAGCGCTGGGTTTTC-GG-TTTTGGGTTGGGTT----GTCTT-GG-----GC--------AC-----ATGT----ACTCGTATGA---TATACATATATA----TATATAC-----GGATAG----------**-**----**-**----------**-**----------**-**----------**--**----------
droFic1	scf7180000453342:903490-903557 -		TTCAGCGCGGGGTT-TTC-GG-TTTTGGGTTGGGTTG---TGTCTT-GGG-----TT--------AT-----**-**----------ATGTATTA---TA--------CA----TATATAC-----GGA----------**-**----**-**----------**-**----------**-**----------**--**----------
droEle1	scf7180000490546:1064163-1064245 +		ATACATATATATA-TAT-AT-AT----------**-**----------**-**----------**-**----------**-**--------**-**----**-**-------**-**----**-**ATATATATATATATATATATTGTATGTA------TATATATATATATAT----------TGTATGTATATA--TATA----------
droRho1	scf7180000776849:832392-832452 -		TTCAGCGCGGGGTTTTC-AG-TTTTGGGTTGGGTT----GTCTT-GG-----GT--------AT-----**-**----------ATGTATTA---TA--------CA----T--ATAC-----**-**----------**-**----**-**----------**-**----------**-**----------**--**----------
droBia1	scf7180000302143:1482574-1482651 +		TTCAGCGCGGGGTT-TTC-GG-TTTTGGGTTGGGTTGGGTTGTCTT-GG-----T--------GT-----GTGT----GTGTGTGTGG--CA--------CA----CGTACAC-----GGATAG----------**-**----**-**----------**-**----------**-**----------**--**----------
droTak1	scf7180000415389:187555-187632 -		TTCAGCGCGGGGTTTTC-AG-TTTTGGGTTGGGTTGGGTTGTCTT-GG-----GT--------AT-----**-**----------ACGTATTG---TA--------CATATACATATAC----GGATAG----------**-**----**-**----------**-**----------**-**----------**--**----------
droEug1	scf7180000409462:135160-135239 -		TTCAGCGCGGGGTTTTC-AGTTTTGGGTTGGGTT----GTCTT-GG-----AT--------AT-----ATACGAGTATATGTATTA---TA--------CA----TATATAC-----GGATAG----------**-**----**-**----------**-**----------**-**----------**--**----------
dm3	chr2R:11019308-11019406 +		TTCAGCGAGGGGTTT-CGGT-TTTTGGGTTGGGTTGGGTTGTCTT-GG-----CT--------AT-----**-**----------ATGTATTA---TA--------CA----CGAATAC-----GGATAGGCTGGCCCACGGATTGGGATGGTAT----**-**----------**-**----------**-**----------**--**----------
droSim2	2r:11690207-11690353 +		TTCAGCGAGGGGTTT-CGGT-TTTTGGGTTGGGTTGGGTTGTCTT-GG-----CT--------AT-----**-**----------ATGTATTA---TA--------CA----CGAATAC-----GGATAGGCTGGCCCACGGATTGGGATGGTATGAT-----GATGGCTGCTTGGGCTGTGGCATTTCTCGTGTGTAGGTAGG--TGGT----------
droSec2	scaffold_1:8513712-8513853 +		TTCAGCGAGGGGTTT-CGGT-TTTTGGGTTGGGTT----GTCTT-GG-----CT--------AT-----**-**----------ATGTATTA---TA--------CA----CGAATAC-----GGATAGCTGGCCCACGGATTGGGATGGTATGAT-----GATGGCTGCTTGGGCTGTGGCATTTCTCGTGTGTAGGTAGG--TGGT----------
droYak3	2R:10939594-10939698 +		TTCAGCGAGGGGTTT-CGGT-TTTTGGGTTGGGTTGGGCTGTCTT-GG-----CT--------GC-----CTCT----ATATGTATTA---TA--------CA----CGAATAC-----GGATAGGCTGGCCCACGGATTGGGATGGTAT----**-**----------**-**----------**-**----------**--**----------
droEre2	scaffold_4845:14854905-14854937 -		TTCAGCGAGGGGTTT-CGGT-TTTTGGGTTGGGTT----------**-**----**-**----------**-**----------**-**--------**-**----**-**-------**-**----------**-**----**-**----------**-**----------**-**----------**--**----------

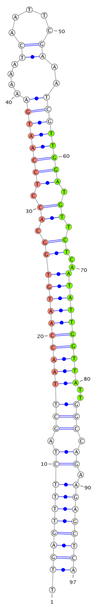
Generated: 09/08/2015 at 07:46 PM

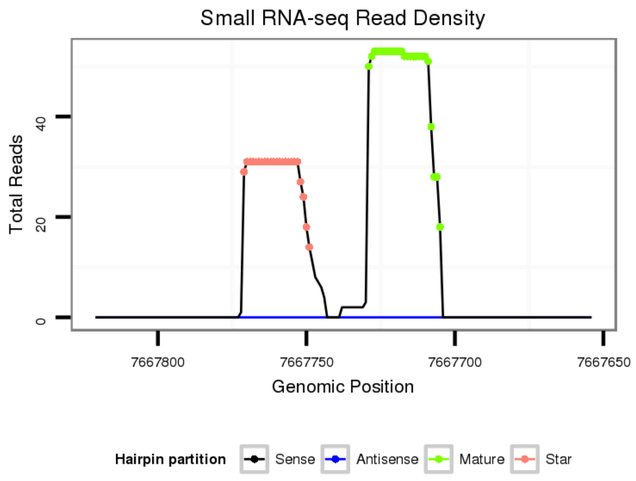
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

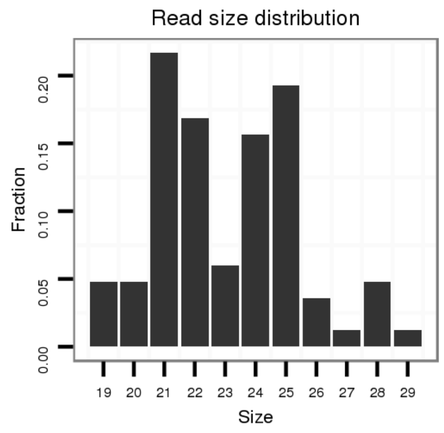
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_270	**scaffold_6540:7667704-7667771 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

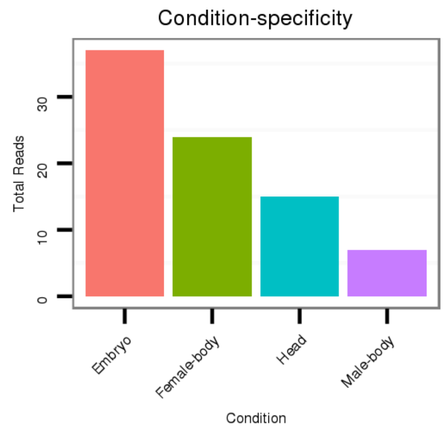
Legend: mature star mismatch in alignment mismatch in read

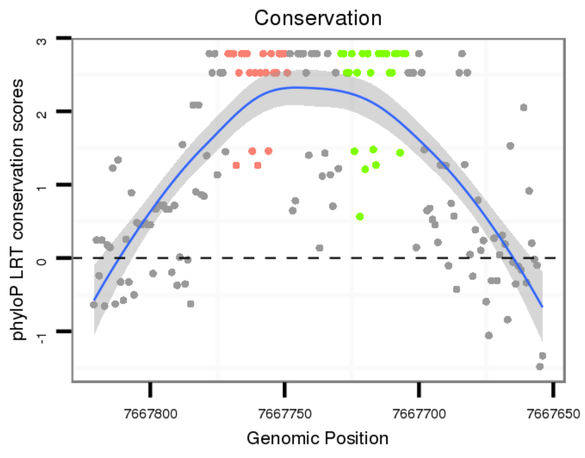
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GAGAGGAGGTGAACCCTCGACGACAAAGCGAACGATTGAGTTTTCTAGCTTAACCAATGTGGCACCTCCAATGAAAAATCAATTCGAAATCGTTGGATGTTCTCAATATTGGTTATTGGCCAGAAGAGCTCAAACACAGCTATAAGAAACGAAACCATCAAATATATG **********.((((((((((.((((((((((((((((.((.((((((((....((.....))..))))))))).))..))..))))))))))..))))..))..))))))))********** **Read size**	**#Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M060 embryo**	**M046 female body**	**V049 head**	**V056 head**	**V110 male body**	**V041 embryo**
.....TTGGATGTTCTCAATATTGGTTATT.....	25	0	1	15.00	15	9	3	0	0	1	2
.....TTGGATGTTCTCAATATTGGT.....	21	0	1	13.00	13	1	4	4	2	2	0
.....TTGGATGTTCTCAATATTGGTT.....	22	0	1	10.00	10	0	2	3	4	1	0
.....TTGGATGTTCTCAATATTGGTTAT.....	24	0	1	9.00	9	4	1	0	1	2	1
.....TAACCAATGTGGCACCTCC.....	19	0	1	4.00	4	1	3	0	0	0	0
.....TTGGATGTTCTCAATATTGGTTATC.....	25	1	1	4.00	4	3	1	0	0	0	0
.....TAACCAATGTGGCACCTCCAATGAAAAA.....	28	0	1	4.00	4	3	1	0	0	0	0
.....TAACCAATGTGGCACCTCCAA.....	21	0	1	4.00	4	4	0	0	0	0	0
.....TAACCAATGTGGCACCTCCAAT.....	22	0	1	4.00	4	3	0	0	1	0	0
.....TAACCAATGTGGCACCTCCA.....	20	0	1	3.00	3	2	1	0	0	0	0
.....TAACCAATGTGGCACCTCCAATGA.....	24	0	1	3.00	3	2	1	0	0	0	0
.....TAACCAATGTGGCACCTCCAATG.....	23	0	1	3.00	3	1	2	0	0	0	0
.....TCGAAATCGTTGGATGTTCTCAATATTGG.....	29	0	1	1.00	1	0	1	0	0	0	0
.....TAACCAATGTGGCACCTCCAATGAA.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TAACCAATGTGGCACCTCCAATGAAAA.....	27	0	1	1.00	1	0	1	0	0	0	0
.....TAACCAATGTGGCACCTCCAATC.....	23	1	1	1.00	1	0	1	0	0	0	0
.....TTGGATGTTCTCAATATTGGTC.....	22	1	1	1.00	1	0	1	0	0	0	0
.....TAACCAATGTGGCACCTCCAATGAAA.....	26	0	1	1.00	1	0	1	0	0	0	0
.....GGATGTTCTCAATATTGGTTATT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....AACCAATGTGGCACCTCCAA.....	20	0	1	1.00	1	0	1	0	0	0	0
.....GTTGGATGTTCTCAATATTGGTTATT.....	26	0	1	1.00	1	0	0	0	0	1	0
.....TCGAAATCGTTGGATGTTCTC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TGGATGTTCTCAATATTGGTTATT.....	24	0	1	1.00	1	0	0	0	0	0	1
.....TGGATGTTCTCAATATTGGTTATC.....	24	1	1	1.00	1	1	0	0	0	0	0
.....AACCAATGTGGCACCTCCAATGAAAA.....	26	0	1	1.00	1	0	1	0	0	0	0
.....TTAACCAATGTGGCACCTCCAA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TGGATGTTCTCAATATTGGTTAT.....	23	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

CTCTCCTCCACTTGGGAGCTGCTGTTTCGCTTGCTAACTCAAAAGATCGAATTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC **********.((((((((((.((((((((((((((((.((.((((((((....((.....))..))))))))).))..))..))))))))))..))))..))..))))))))********** **Read size**	**#Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M046 female body**
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	25	0	1	15.00	15	9
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	21	0	1	13.00	13	1
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	22	0	1	10.00	10	0
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	24	0	1	9.00	9	4
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	19	0	1	4.00	4	1
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	25	1	1	4.00	4	3
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	28	0	1	4.00	4	3
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	21	0	1	4.00	4	4
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	22	0	1	4.00	4	3
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	20	0	1	3.00	3	2
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	24	0	1	3.00	3	2
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	23	0	1	3.00	3	1
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	29	0	1	1.00	1	0
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	25	0	1	1.00	1	1
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	27	0	1	1.00	1	0
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	23	1	1	1.00	1	0
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	22	1	1	1.00	1	0
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	26	0	1	1.00	1	0
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	23	0	1	1.00	1	1
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	20	0	1	1.00	1	0
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	26	0	1	1.00	1	0
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	21	0	1	1.00	1	1
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	24	0	1	1.00	1	0
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	24	1	1	1.00	1	1
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	26	0	1	1.00	1	0
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	22	0	1	1.00	1	1
.....AGTTGGTTACACCGTGGAGGTTACTTTTTAGTTAAGCTTTAGCAACCTACAAGAGTTATAACCAATAACCGGTCTTCTCGAGTTTGTGTCGATATTCTTTGCTTTGGTAGTTTATATAC.....	23	0	1	1.00	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:7667654-7667821 -	dmo_270	GAGAGGAG------GTGAA---------CC---CTCGACGACAAAGCGAAC----------GATTGAGTTTTCTAGCTTAACCAATGTGGCACCTCCAATGAAAAATCAATTCGAAATCGTTGGATGTTCTCAATATTGGTTATTGGCCAGAAGAGCTCAAACACAGCTATAAGAAACG----------AAACCA------TCA-AA---TATATG
droVir3	scaffold_13047:9559466-9559645 -	dvi_24635	GAGAGGAG------CTTCTCGAAAGCCAATCCCTTTCGACGACAAAGCGAGC----------GATTGGTTTTCTAGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTCGAAATCGTTGGATGTTCTCAGTATTGGTTATTGGCCAGAAGAAGCCAAACACAGCTATAAGAAA--CCA---------AA----A----ATAAAA---TAAACA
droGri2	scaffold_14906:2448935-2449115 -	dgr_463	AAAGAGAG------ATTAA---------------GCAAAGCAAAAAAGGGCGTTCAGTTCGTAAATAGATTGGGTTTTCTAGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTGCAATCGTTGGATGTTCTCAGTATTGGTTATTGGCCAGATGAATCCAAACACAGCAATAATTAAAACCA---------AATA--------CCA-AC---AACAAA
droWil2	scf2_1100000004902:9400242-9400354 +		---TTCTAGCTTAATCAATCGACACTTCCAATGAGGAATCCATTCGAAATCGTTGGATGATATCAGTATTGGTTATTGGCGAGAAGCATCTAAAAGCAGCTTTAAGTTA--AC----------------AA----------AC
dp5	2:16675574-16675724 -	dps_3828	AAGAAACGTGAAAAGTGTA---------------C----------AAGTTGGGGGTCTCTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTTGGACGTTCTCAGTATTGGTTATTGGCAGAAGAGCCCACAGGCAGCTATAAGAG---------------TTACAATTGTAA----------AG
droPer2	scaffold_0:3721637-3721776 +	dpe_2482	AAA-----------GTGTA---------------C----------AAGTTGGGGGTCTCTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTTGGACGTTCTCAGTATTGGTTATTGGCAGAGAAGAGCCCACAGGCAGCTATAAGAG---------------TTACAATTGTAA----------AG
droAna3	scaffold_12911:3664274-3664396 -	dan_200	---TTCTGGCTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGTCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCGAGACAACTGTGTCCA--CCCACT----------CGT-AG---TCCGTT
droBip1	scf7180000396640:523330-523439 -		---TCTGGCCTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGTCCTTGGATGCTCTCAGTATTGGTTTTGGCGAGATTGGCCCGCGGCAACTGTGTCTA--------------------------CCCA
droKik1	scf7180000302810:681855-682005 +		GGGACGGG------GTGTA---------TC---------------------CGCCGCGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGGAATCAATTGCAAGTCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGAGGCAGCTATAGTGTT-T----------GTTCCG------CTT-AG---TCCGAG
droFic1	scf7180000454114:125810-125941 +		---GGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGCCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCGAGCAGCAGCGGTATTGGGCACTA----------GA----CC--CCT-AATAGT-TCCG
droEle1	scf7180000491194:1479877-1480015 +		---GGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGACGTTGGATGCTCTCAGTATTGGTTATTGGCAGATTGGCCCGAGACAGCAGTATTCTA--GGCA---------CTTG--GATACCAATCCAATAGTTC---
droRho1	scf7180000779322:264823-264952 -		C---GGGGGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATAGGCCCCTAGGCAGCAATATTAGGCA----------C----TGGTACCCA--------T
droBia1	scf7180000302035:101939-102073 +		---GGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCTGTATTGGTTATTGGCGAGATTGGCCCGAGGCAGCGTCACTAGG--------TCTAGGCAGTTCCG------ATC-AG---TCCG--
droTak1	scf7180000415712:510701-510817 +		---GGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGTTGGCCCGAGGCAGCATAACTATA--------T-------------CT----------AG
droEug1	scf7180000409488:463429-463564 -		C---GGCGGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCGAGACAGCAATTCTCTAAGCA----------GTTTCG------TTC-AG---TCCGAG
dm3	chr3R:27444091-27444220 +		---GGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCGGGGACAGCAATTACTAGCAGA----------GTTCCG------ATC-AG---TCCGC-
droSim2	3r:26724064-26724194 +	dsi_32457	---GGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCGGGGACAGCAATTACTAGCAGA----------GTTCCG------ATC-AG---TCCGCA
droSec2	scaffold_2807:1133-1263 +	dse_1845	---GGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCGGGGACAGCAATTACTAGCAGA----------GTTCCG------ATC-AG---TCCGCA
droYak3	3R:28380205-28380333 +	dya_1797	---GGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCGGGGACAGCAATTACCAGAC----------GTTCCG------ATT-AG---TCCG--
droEre2	scaffold_4820:530486-530616 -	der_1522	---GGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCGGGGCAGCATATACTAGCAGA----------GTTCCG------ATC-AG---TCCGCA

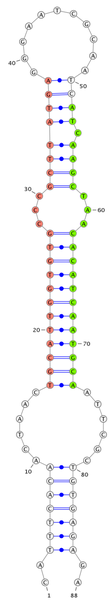
Generated: 09/08/2015 at 08:00 PM

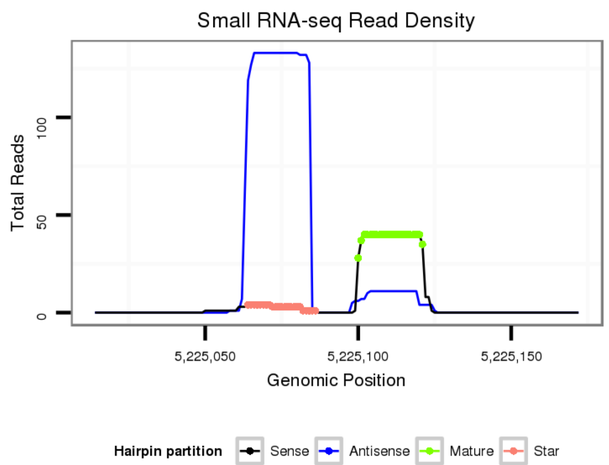
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	7
rescue.candidate	5

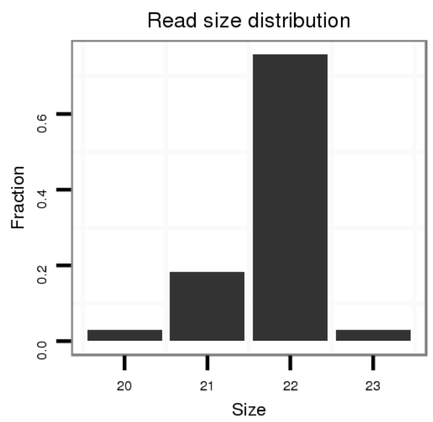
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_309	**scaffold_6540:5225064-5225122 +**	**confident**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

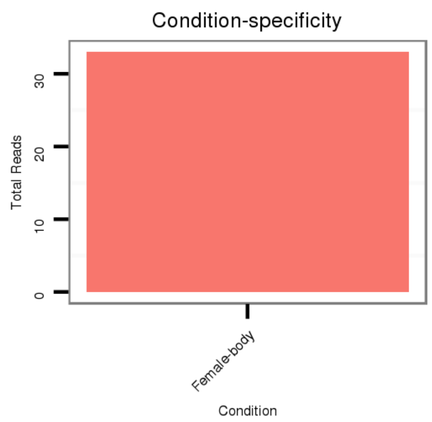
Legend: mature star mismatch in alignment mismatch in read

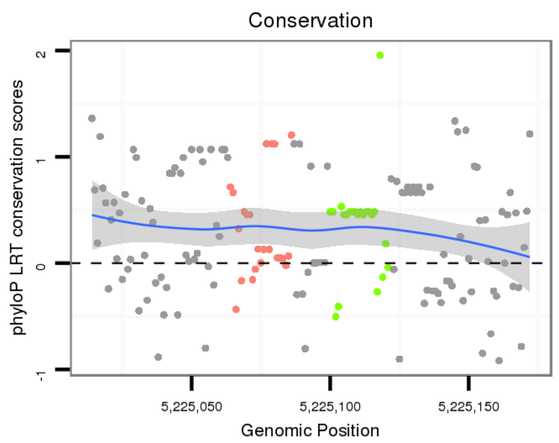
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dmoj\GI23565-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TACGTGCTAGTGTCTTGCCAATGCCTGCGGTCCGGCATTTCACAACTAACTGCATTGGTGTGCCCGCTTATGAGGGAATCGCAATCATCAAGCTAACACATCAATGCAATTCGCTGTGAGAGATTGATCCGAGTGATGCAATAGGTCTAACGTTGAAGC	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body
**********..(((((((.....(((((((((((...(((((((.....)))).)))))...)))))))))))).....)))))..**********							
.....ATCAAGCTAACACATCAATGCA.....	22	0	1	24.00	24	24	0
.....TCAAGCTAACACATCAATGCAAT.....	23	0	1	4.00	4	4	0
.....CAAGCTAACACATCAATGCAAT.....	22	0	1	3.00	3	3	0
.....TCAAGCTAACACATCAATGCA.....	21	0	1	3.00	3	3	0
.....ATCAAGCTAACACATCAATGC.....	21	0	1	3.00	3	3	0
.....AACTGCATTGGTGTGCCCGCT.....	21	0	1	2.00	2	2	0
.....ATTTCACAACTAACTGCATTGG.....	22	0	1	1.00	1	1	0
.....TCAAGCTAACACATCAATGCAATT.....	24	0	1	1.00	1	1	0
.....TCAAGCTAACACATCAATGC.....	20	0	1	1.00	1	1	0
.....TGCATTGGTGTGCCCGCTTATGA.....	23	0	1	1.00	1	1	0
.....CATCAAGCTAACACATCAATGC.....	22	0	1	1.00	1	1	0

Anti-sense strand reads

ATGCACGATCACAGAACGGTTACGGACGCCAGGCCGTAAAGTGTTGATTGACGTAACCACACGGGCGAATACTCCCTTAGCGTTAGTAGTTCGATTGTGTAGTTACGTTAAGCGACACTCTCTAACTAGGCTCACTACGTTATCCAGATTGCAACTTCG	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V049 head	V041 embryo	V056 head
**********..(((((((.....(((((((((((...(((((((.....)))).)))))...)))))))))))).....)))))..**********												
.....GACGTAACCACACGGGCGAATA.....	22	0	1	57.00	57	9	11	15	8	9	5
.....ACGTAACCACACGGGCGAATA.....	21	0	1	54.00	54	22	13	11	2	3	3
.....CGTAACCACACGGGCGAATA.....	20	0	1	7.00	7	2	5	0	0	0	0
.....GTAACCACACGGGCGAATA.....	19	0	1	6.00	6	1	2	1	0	0	2
.....AGTAGTTCGATTGTGTAGTTAC.....	22	0	1	5.00	5	0	3	0	0	1	1
.....TGACGTAACCACACGGGCGAAT.....	22	0	1	4.00	4	2	0	2	0	0	0
.....TTCGATTGTGTAGTTACGTTAA.....	22	0	1	3.00	3	0	1	2	0	0	0
.....AACGTAACCACACGGGCGAATA.....	22	1	1	3.00	3	2	1	0	0	0	0
.....TCGTAACCACACGGGCGAATA.....	21	1	1	2.00	2	1	0	1	0	0	0
.....TGACGTAACCACACGGGCGAATA.....	23	0	1	2.00	2	0	0	2	0	0	0
.....TGATTGACGTAACCACACGGGCG.....	23	0	1	1.00	1	1	0	0	0	0	0
.....AAGTAGTTCGATTGTGTAGTTAC.....	23	1	1	1.00	1	0	0	1	0	0	0
.....TCGATTGTGTAGTTACGTTAAG.....	22	0	1	1.00	1	0	1	0	0	0	0
.....TTAACCACACGGGCGAATA.....	19	1	1	1.00	1	0	0	1	0	0	0
.....GTCGATTGTGTAGTTACGTTAA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....GTAGTTCGATTGTGTAGTTAC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....CGTAACCACACGGGCGAATAC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GAACCACACGGGCGAATA.....	18	1	1	1.00	1	0	1	0	0	0	0
.....AGTTCGATTGTGTAGTTAC.....	19	0	1	1.00	1	0	1	0	0	0	0
.....ACGTAACCACACGGGCGAATAC.....	22	0	1	1.00	1	0	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:5225014-5225172 +	dmo_309	TACGTG----------CTAGTGT---------------CTTGCCAATGCC---TGCGGTC-CGGCATTTCACAACTAACTGCATTGGTGTGCCCGCTTATGAGGGAATCGCAATCATCAAGCTAACACATCAA--------------TGCAATT----------CGCTGTGAGAGATTGATC----CGAGTG---------ATGCAATAGGTCTAACGT----TGAAGC
droVir3	scaffold_13047:1194007-1194164 +	dvi_253	TACGTG----------GTGGTGT---------------CTTGCCAATGCA---CTTGGTA-CGGCATTTCACAATTAACTGCATTGGTGTGCCCGCTTATGAGGGACTCGCAATCATTAAGCTAACACATCAA--------------TACAATT----------CGCTGTGAGAAAAAGTA----CAAGTG---------ATACAAAAAGTCTA-CGT----TCCAGC
droGri2	scaffold_14906:5077569-5077681 -		TACGTG----------CTGGTGT---------------CTTGCTA-----------------------GGCATTTCACAATTAACTGCAT---T----------AA-------------GCCAACACA-TCAATGCAATTG-------CTAT-TTC----------TGCTGTGAGCAAAAGAAC----CGAGT---------GCATC---GATGATGACAAT
droWil2	scf2_1100000004921:442-496 +		TAAGTGAACGAATGCAACGCGAGTGATTCA---------A--TGAGCC---------AC--AT-CATCAT-----CTTCGCC
dp5	2:7233608-7233736 -		TACGTT----------CTTTGATTTGTGGCGGTGATGTGGTGAGGTTGTGTTCCTTGGTAGCGAAAGATCGTACTCAAC--TGA---ACTTGCCGGAAGGAAGTGT----------T----T--CCTTTCGCT-TC----------GTTTCGGAAGTAAT-------ACAAT-----TGTCGC
droPer2	scaffold_0:1094297-1094425 -		TACGTT----------CTTGATTTGTGGCGGTGATGTGGTGAGGTGTGTTCCTTGGTAACGAAAGATCGTACTCAAC--TGA---ACTTGCCGGAAGGAAGTGT----------T----T--CCTTTTGCT-TC----------GTTTCGGAAGTAAT-------ACAAT-----TGTCGC
droAna3	scaffold_13340:867471-867589 -		GATGCG----------CTGGCAGCGAAGTG---------GGGTGG-A-------CAT---------GGA---ACCTTGTGCTTATAAGAGCTGCATGGC----------AGATCTCCGGT----------TTTAGTT-TG----------ATTCCGGA---GTTACAAGCGACGCGGTCGGTCA-----GGAAGC
droKik1	scf7180000302475:1425663-1425728 +		TCTTGCTTGAAGGTGTCGCGATTGGTGGA---------AGATGT---GAAGAAAA-GT----------GCTC-------------GG-AGTCTC-----GATCGC
droFic1	scf7180000453800:2313426-2313513 +		TACGTG----------TCGCGTTGGTATC---------CACATTT-A-------C-----------------------------------C----------CTTTTGAAGAACCCAGTGGAACTC----------AT---T--TGTGCAGCA-TT----------GAATC-------------GG-AAACC-----GAACGC
droEle1	scf7180000490995:508689-508797 -		TTCGTT----------TCGCGGTTGGTAAA---------CTGGTGT-T-------C-----------CTG-ATT-----AGC---C----------C----------CTTTTGAAGGG-CCAGTGATATTATATATCCATCT-ATCAT----T--TGTGAAATA-TG----------GCCTC-------------GG-AACTTC-----GAACGC
droRho1	scf7180000777158:16593-16697 -		TTCGTG----------TCGCGGTTGGTAAA---------CTGGTGGC-T-------CCT-CTT-----GGC---C----------GC----------CTTGAATGG-CCAGTTAAAAGT-------CCCA-ACAGTTAATT--TGTGCAACA-CT----------GCCTC-------------GG-AACTTT-----GATCGC
droBia1	scf7180000302402:8322697-8322795 +		TACGTG----------TCGCGGTTGGTAAA---------CTGGTGT-T-------C-----------CTC---------AGC---C----------CC----------CTTGAGCAA-TCAGTGAAAATA-------ATCAAATGAC----T--TTTGCAATG-GC----------GCCTC-------------GG-AACTTG-----GATCGC
droTak1	scf7180000415380:1406303-1406404 -		TACGTG----------TCGCGATTGGTAAA---------CTGGTGC-T-------C-----------CAT---------AGC---C----------CC----------CTATTGAAGAG-CCAGTGAAAATA-------ATTTCATAAT----T--TGTGCAATTTGT----------GCTTT-------------GG-AACTTG-----GATCGC
droEug1	scf7180000409692:709969-710066 +		TACGTG----------TCGCGGTTGGTAAA---------CTGAAAT-A-------T-----------CA----------------------------------GTCTTGAAATA-TCAGTGAGAATA-------ATATAATAATC---CATTGTGCAACT-TC----------GCCTC-------------GG-AACTTT-----GAACGC
dm3	chr3R:6233746-6233846 +		TACGTG----------TCGCGGTTGGTAAA---------CTGGAGT-A-------C-----------TT---------GGA---T----------AC----------CCCGAGGAA-TCAGTTAAAATC-------ATAC-ATAAT----TGTTGACCACAA-TT----------GCCTC-------------GGGAACTTC-----GATCGC
droSim2	3r:14842999-14843098 -		TACGTG----------TCGCGGTTGGTAAA---------CTGGATGT-A-------C-----------TT---------GGA---T----------AC----------CCCGAGGAA-TCAGTTAAAATC-------ATAC-ATAAT----TGTTGACCACAA-TT----------GCCTC-------------GG-AACTTC-----GATCGC
droSec2	scaffold_0:15709568-15709667 -		TACGTG----------TCGCGGTTGGTAAA---------CAGGATGT-A-------C-----------TT---------GGA---T----------AC----------CCCGAGGAA-TCAGTTAAAATC-------ATAC-ATAAT----TGTTGACCACAA-TT----------GCCTC-------------GG-AACTTC-----GATCGC
droYak3	3R:10262261-10262361 +		TACGTG----------TCGCGGTTGGTAAA---------CTGGATGT-T-------C-----------TT---------GGA---T----------CC----------CTCGAAGAA-TCAGTTAAGATC-------ATAAAATATT----TGATGGCCACAA-TT----------GCCTC-------------GG-AACTTC-----GATCGC
droEre2	scaffold_4770:15384153-15384253 -		TACGTG----------TCGCGGTTGGTAAA---------CTGGATGT-T-------C-----------TT---------GGA---T----------CC----------CCCAACGAA-TCTGTTAGAATC-------ATACAATAAT----TGTTGCCCACAG-TT----------GCCTC-------------GG-AACTTC-----GATCGC

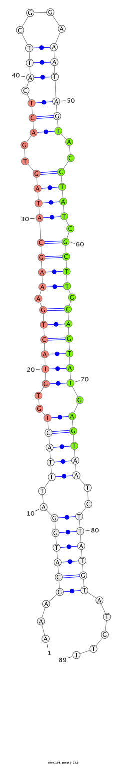
Generated: 09/08/2015 at 07:46 PM

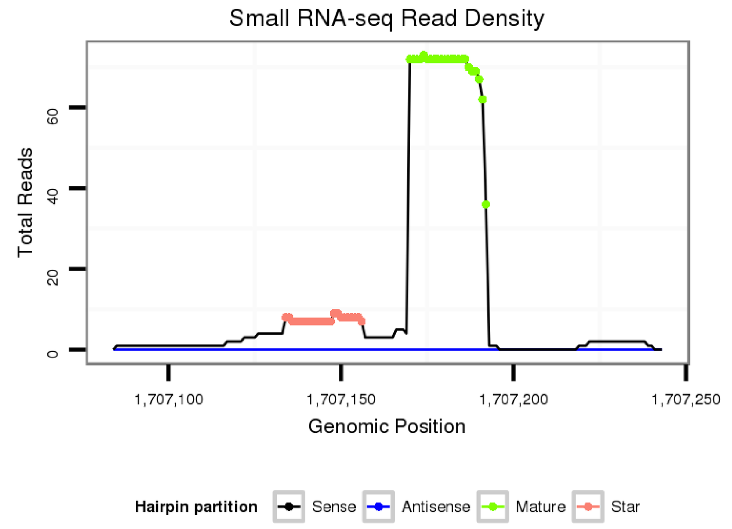
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

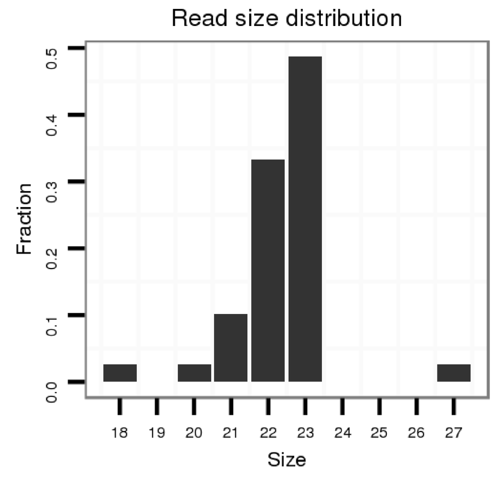
ID: dmo_108	Coordinate: scaffold_6541:1707134-1707193 +	Confidence: confident	Class: Canonical miRNA	Genomic Locale: intergenic	[View on UCSC Genome Browser {Cornell Mirror}]

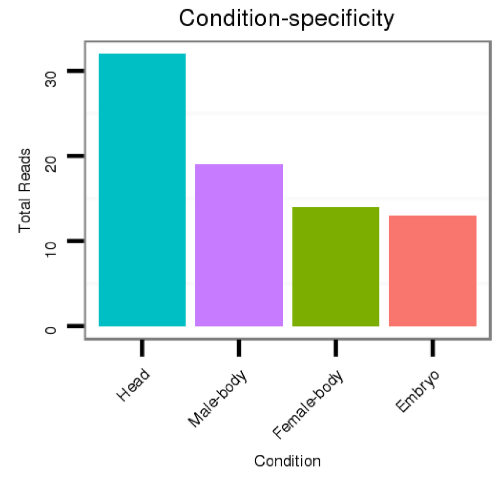
Legend: mature star mismatch in alignment mismatch in read

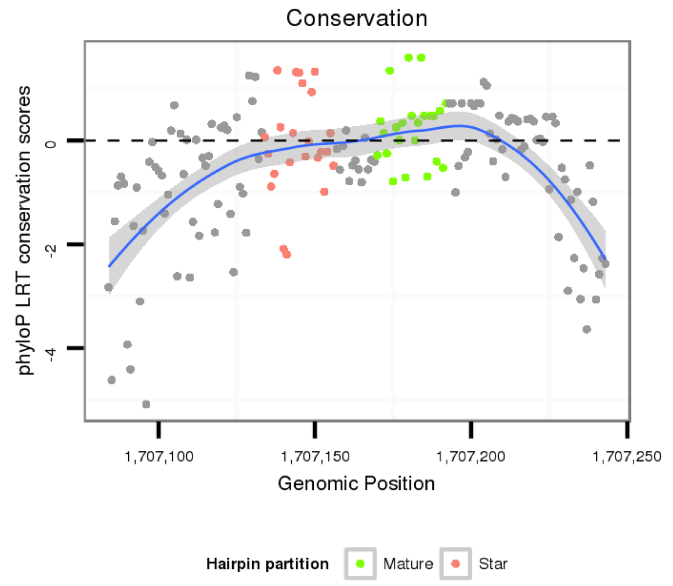
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGATTTACTTATCAAATGAGTTGATCTATGTGGATAAAGCATGGATTTACTGTGTACTGAAAGCATAGTGACTCATTCGGAAATAGTACCTATCGCTTGCAGTATGAGTAATCTTATGTATGTTTTATCTTCAGTTGCAACTCCTACAAATGCAACCAAA ***********************************...((((((..(((((..((((((.((((((((..(((.(((....))))))..)))).)))).)))))).)))))..))))))).....************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	V056 head	M046 female body	V049 head	M060 embryo	V041 embryo
...TACCTATCGCTTGCAGTATGAGT...	23	0	1	35.00	35	9	10	5	5	3	3
...TACCTATCGCTTGCAGTATGAG...	22	0	1	25.00	25	6	5	4	4	2	4
...TACCTATCGCTTGCAGTATGA...	21	0	1	5.00	5	0	2	0	3	0	0
...TACCTATCGCTTGCAGTATGAGTT...	24	1	1	4.00	4	2	1	0	0	1	0
...TGTGTACTGAAAGCATAGTGACT...	23	0	1	3.00	3	1	0	1	1	0	0
...ATAGTACCTATCGCTTGCAGT...	21	0	1	2.00	2	0	0	2	0	0	0
...TACCTATCGCTTGCAGTATG...	20	0	1	2.00	2	0	1	1	0	0	0
...ATAGTGACTCATTCGGAAATAGTACCT...	27	0	1	2.00	2	2	0	0	0	0	0
...TACCTATCGCTTGCAGTATGAGA...	23	1	1	1.00	1	0	1	0	0	0	0
...ATAAAGCATGGATTTACTG...	19	0	1	1.00	1	0	0	1	0	0	0
...TATCGCTTGCAGTATGAG...	18	0	1	1.00	1	0	0	0	0	1	0
...TACCTATCGCTTGCAGTATGAGC...	23	1	1	1.00	1	1	0	0	0	0	0
...ATCGCTTGCAGTATGAGTAAT...	21	0	1	1.00	1	0	0	1	0	0	0
...TACCTATCGCTTGCAGTA...	18	0	1	1.00	1	0	0	0	1	0	0
...TGTGTACTGAAAGCATAGTGACTT...	24	1	1	1.00	1	0	0	0	1	0	0
...GCATGGATTTACTGTGTACTGAAAGCAT...	28	0	1	1.00	1	0	0	1	0	0	0
...GGATTTACTGTGTACTGAAAGC...	22	0	1	1.00	1	0	0	1	0	0	0
...TGCAACTCCTACAAATGCAA...	20	0	1	1.00	1	0	0	1	0	0	0
...AACTCCTACAAATGCAACC...	19	0	1	1.00	1	0	0	0	0	1	0
...TACCTATCGCTTGCAGTATGAA...	22	1	1	1.00	1	0	1	0	0	0	0
...CTATGTGGATAAAGCATGG...	19	0	1	1.00	1	1	0	0	0	0	0
...ATAGTGACTCATTCGGAAATA...	21	0	1	1.00	1	1	0	0	0	0	0
...TGTGTACTGAAAGCATAGTGAC...	22	0	1	1.00	1	0	0	1	0	0	0
...ATTTACTGTGTACTGAAAGCATAGTGACT...	29	0	1	1.00	1	1	0	0	0	0	0
.GATTTACTTATCAAATGAGTTGAT...	24	0	1	1.00	1	1	0	0	0	0	0
....TTACTTATCAAATGAGTTG...	19	0	2	0.50	1	0	1	0	0	0	0

Anti-sense strand reads

ACTAAATGAATAGTTTACTCAACTAGATACACCTATTTCGTACCTAAATGACACATGACTTTCGTATCACTGAGTAAGCCTTTATCATGGATAGCGAACGTCATACTCATTAGAATACATACAAAATAGAAGTCAACGTTGAGGATGTTTACGTTGGTTT ***********************************...((((((..(((((..((((((.((((((((..(((.(((....))))))..)))).)))).)))))).)))))..))))))).....************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head	V049 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6541:1707084-1707243 +	dmo_108	TGAT---TTACTTA---TCAAATGAGTT---GATCT-ATGTGGATAAA---G---CATGG---ATTTAC---TGTGTACT---GAAAGCATAGTGACTCATTCGGAAATAGTACCTATCGCTTGCAGTATGAGTAATCTTATGTATGTTTT---ATCTTCAGTTG---CAACTCCTA--CAA---ATGCAA---CCAAA
droVir3	scaffold_13036:588437-588541 +		ACCG---ACAGTAT---ACCAGCAGTCTCTGTCAGAGTACCTTCTGCTTGCAATATGGGTAACCTGGTGTATGTAAT---ATCTTCAGTGG---CAACACCTA--CAA---CTCCGA---CCCTA
droGri2	scaffold_15203:4419951-4420034 -		TCTG---TAACC--- G ---GGCCTATTGTTTGCAAAATGAATAAAGTGGTGTATGTATT---TACCTCAGTTG---CATCGCCGG--TTG---GTGCAA---CAAAA
droWil2	scf2_1100000004521:1182334-1182479 -		GAAT---CTGTTCG---TCAAAAACGTT---GGTCA-A---ATATAAA---T---CAGTATT-CCTACCACAAAATTGGTTGAACATTCATTCTGAAATAGTTTTTGTCTTTTATGGAAGTCATCTAACAACCA---AATCCTCAACTGCAAT-TACTA---TTACAA---GCAAG
dp5	Unknown_group_103:1143-1237 -		AAAT---ATTGTCT---TTGATA---GGAGCTGA-AGCTTCAGAAGAAATATACG---AAT---TGTTCCG---TACA---GTAAG---CATTCTAAATCT---T-AAAGATTTATCCAGAAAT
droPer2	scaffold_2246:2162-2333 -		TTAT---TAATTTA---ATTTATTTATATTGGCGTGGACT---GGGCCCAT-AA---CCTATTGGTAGACTAGCTATGACAATTAGTA---AACGGAAGACAGTACCAAGTTATGTTTTCTTTAAAGATTAT---TTATGTATTTCTTGATT---ACTTTTGCTG---CAACACCGG--TCC---ACACAC---T-TG---AGATCA
droAna3	scaffold_13334:685267-685317 +		AGCC---TTTTGTT---TGCTTT---TTCTTCTATTG---ATTCTCTTG--AAA---ATAAAA---ACAAA
droBip1	scf7180000395142:32109-32178 -		TAAT---TTATTTC-TAGTTCTAAGAATAAGGCATTTGAGGCATACAAAAACATAATATT---AAT---TAAAAA---ATAAT
droKik1	scf7180000302590:78777-78933 +		TTCTTTAAA---TATC-CAGGCGAGTGAATCAAGCC---ATTT---TATAT-AAAT---CTATA--AGCTGGGGTTTATTTAAATAGAGCATGGTTTCAAAACTCATCAAGGGAAATCCAAATAATTTTTTTCATTATTAAAATGGAAATAT---AA---TTATATT---A--TATA-TTT---TTT
droFic1	scf7180000453769:5842-5916 -		AATT---TGGGG---TCAAATGGGT---CAAAA-AATAGAAAAA---G---AATGAA---TGGAT---CGGTTAAGTTCT---AAAA---GAA---TA-G---GTACT
droEle1	scf7180000490489:11078-11207 -		CTGTACCATTGACTTACCAAATTGAAAATA---ATGCAGTACAAG---T---GTTAAAAAATGTGTTCGAACGT---GTTAAAAACAC---G-AAATTTTATACATTGC---T---TGCTTAAAATACGAA---ATATTTT---AAGTGTC-TTT---TAT
droRho1	scf7180000759908:15346-15501 -		TAAC---TTATTTACAGACTTTTGAATAATGAT---TTCTAA---ATCATTTTATT---TAAAGCTTAATTACCGATTGATAACTGTTATTTCTTGTTTAAAATATCAA---ATATAA---AATTGAGAAAATCTTTACTCCGCTTATGATTTCTCTCA--GTG---CACACA---CCCAA
droBia1	scf7180000302433:9753-9865 -		ATAT---TTATATA---TCAAAAGAATT---CATAT-ATATAG---TAAAATTATTTATTACA---TTAA--TGAGTCGAACTAATGTCCCGTCATTTAAATTTTGATTTCACTTATTTAAGTTTTAG---TTT
droTak1	scf7180000415941:338694-338823 +		ATAT---TTCAAAA---A---TGAAATATAAATTAAGTTTATTAATGTTTGTTTGATGTGG---TTATTGTGTAGG---TAAAGTTTAATAACCGCTTCAAA--TTGCA---CTTTATAAATCTGATTTTTACAAATTTTATAAATGTTT
droEug1	scf7180000409027:17786-17905 +		TAAT---TATTTTG---TGTAATATTTT---AAAG---ATAAG---TGGAAAAAAATTAATTTATCTCTTTTGGCACAAGTTTAAGT---CGGTAAAAACGT---AGAGTAGTTTAAAGTATAGC-TTATCCTCGG---CTGTA
dm3	chr4:769657-769732 -		TAAT---CTTAATA---T---TGTTTGCCAAATGTGTT---TAAAT-GTTAAGCCAAA---G---CAGGT---T---TATA---GC--TGGACTGA---ACTGA---TAATG
droSim2	2L:21033289-21033441 -		TGGC---TTACTTA---AG---ACTAAGGAGCCA-AATACAAAAA---TTTCCAAAGCAGAAAATAGTTTTGAAATGTGTAA---ACTGAA---TGTACCTGGCA---AATAGT---CC---AATCAAAAACATTAACGTGTTATCATCGGCAGTTGGAGTATATTACTATGTATT-TTA---TCT
droSec2	scaffold_28:298602-298755 -		TGGC---TTACTTA---AG---ACTAAGGAGCCAAATACAAAAA---TTTCCAATGCAGAAAATAGTTTTGAAATGTGTAA---ACTGAA---TGTACCTGGCA---AATAGT---CC---AATCAAAAACATTAACGTGTTATCATCGGCAGTTGGAGTATATTACTATGTATT-TTA---TCT
droYak3	2R:10750491-10750547 +		AAAA---TTTAAAA---TTATAAAT---ATTTT---TGGGAATAAAGTAG---AT---TTAATT---TGAGTG---CTAAA
droEre2	scaffold_4784:23832881-23832949 -		AGAA---CTGCTTT---TCAACAGACTA---TAA---TTTATTTTGGTTGAA---G---CT---TGCCT---TGGTCAAATA---CAAAAA---CCATA

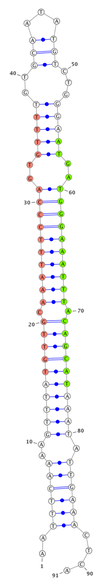
Generated: 09/08/2015 at 07:47 PM

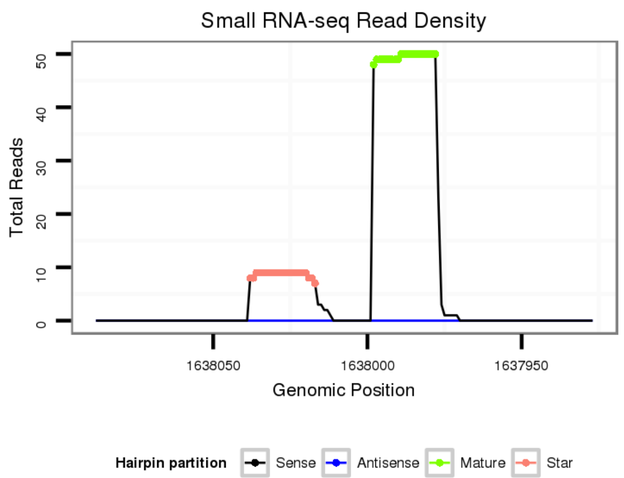
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

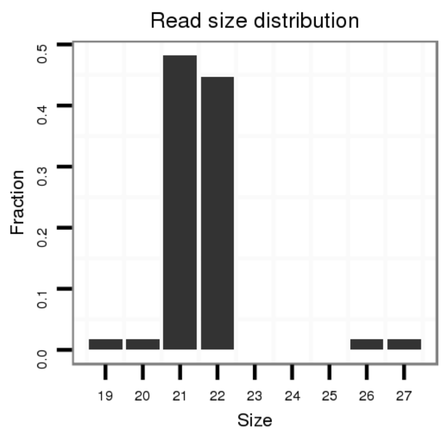
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_278	**scaffold_6654:1637977-1638038 -**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

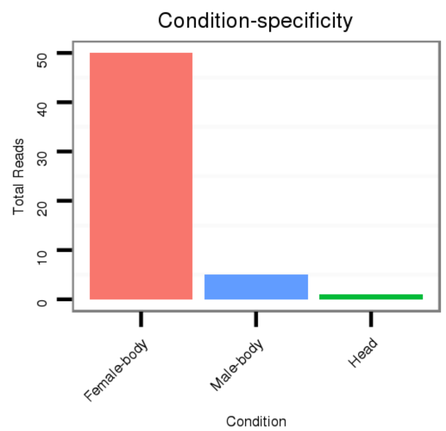
Legend: mature star mismatch in alignment mismatch in read

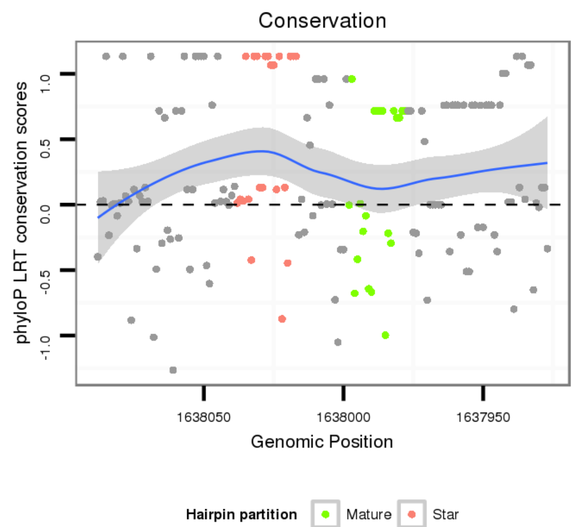
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI16601-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTTATTTCAAGTCGTTTAAAAATCCCTGAGAAGACAATTTCAAAAGTTTATGTTGCAAATTTCCCAGTGTTTTGTGCAATATGTCTGGGAATGATGGGAAATTTACAGCATAAATATTGAAACTCACTTAATGGATGCTAAATATTTTTTATTGCCGTTTTA	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	V049 head
**********..(((((((..((((((((((.((((((((((..(((((..(((...)))...)))))..))))))))))).)))))))))).))))))....**********								
.....ATGATGGGAAATTTACAGCAT.....	21	0	1	26.00	26	24	1	1
.....ATGATGGGAAATTTACAGCATA.....	22	0	1	20.00	20	16	4	0
.....TGTTGCAAATTTCCCAGTGTTT.....	22	0	1	4.00	4	4	0	0
.....ATGATGGGAAATTTACAGCATAA.....	23	0	1	2.00	2	2	0	0
.....AATTTACAGCATAAATATT.....	19	0	1	1.00	1	1	0	0
.....TGTTGCAAATTTCCCAGTGTTTTGTGC.....	27	0	1	1.00	1	1	0	0
.....TTGCAAATTTCCCAGTGTTTTG.....	22	0	1	1.00	1	1	0	0
.....TGTTGCAAATTTCCCAGTG.....	19	0	1	1.00	1	1	0	0
.....TGTTGCAAATTTCCCAGTGTT.....	21	0	1	1.00	1	1	0	0
.....TGATGGGAAATTTACAGCAT.....	20	0	1	1.00	1	1	0	0
.....TGTTGCAAATTTCCCAGTGTTTTGTG.....	26	0	1	1.00	1	1	0	0

Anti-sense strand reads

AAATAAAGTTCAGCAAATTTTTAGGGACTCTTCTGTTAAAGTTTTCAAATACAACGTTTAAAGGGTCACAAAACACGTTATACAGACCCTTACTACCCTTTAAATGTCGTATTTATAACTTTGAGTGAATTACCTACGATTTATAAAAAATAACGGCAAAAT	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_6654:1637927-1638088 -	dmo_278	TTTATTTCAAGTCGTTTAAAAAT----------CCCTGAGAAGACAATTTCAAAAGTTTATGTTGCAAATTTCCCAGTGTTTTGTGCAATATGT----------CTGGGAATGATGGGAAATTTACAGCATAAATATTGAAACTCACTTAATGGATGCTAAATATTTTTTATTGCCG----------TTTTA
droVir3	scaffold_13049:2226096-2226251 +		ATTATTTCGAAATGCAAATATTT----------CCCACAAAAGCAATTGA-GATGTGAACGTTGCAAATTTCCCAGTATTT-GTGCAATATG----------CGCAAAATACTGGTCAATTGACAGCATAAACGTTT----------AATTGCGT---------TTTATGGCTGA----------TATTGAGCGTTGTTAGCTTTG
droGri2	scaffold_15110:3266164-3266322 +		ACAAA---AAATAGCATAAAGATTCAATAGTGATGACTAAAAAAGCAATTGG-AAAGCTAATGATGAAAATTTCCCAGTATTT-GGG-------AAATTATAAGCATAAGCAT----------TTTTGATTGCGT---------TTTTTGGTTGTTTATATTTTCGATTACTGAAAGTTGTTGCTGTTG
droTak1	scf7180000415352:330557-330726 +		TTTAAACAAATTATATTAATT----------AATTAATTATAAAATTAGTTTTTAATATTCCTAAATTTTAT---CATTTATTTTTCAATCCTTTTTAAATTTACCTT----------CAATTATTCCATAGCAAAACTTTCCGAATTCCATAACTCTCTTCTAAG--AAA----------ACACCACTTTAATTAGTTAAA

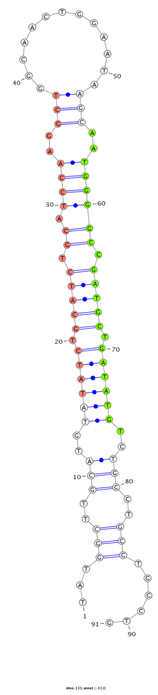
Generated: 09/08/2015 at 07:47 PM

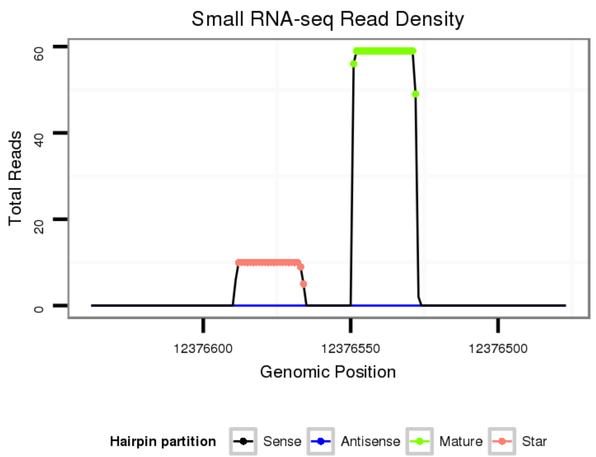
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

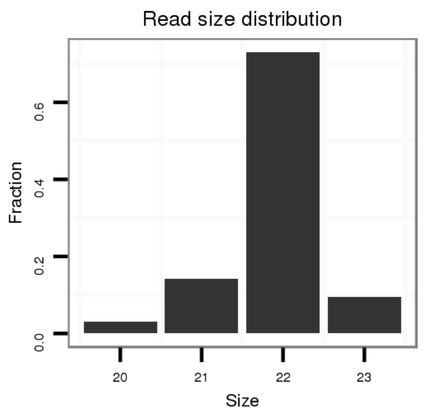
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_133	**scaffold_6473:12376527-12376588 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Comell Mirror}]

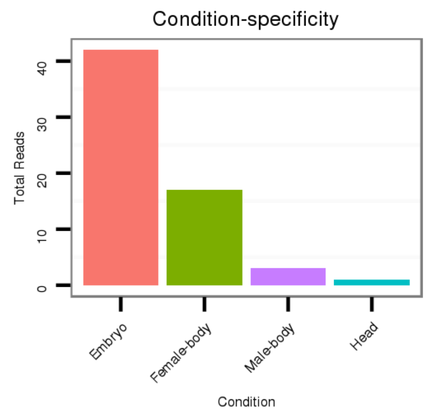
Legend: mature star mismatch in alignment mismatch in read

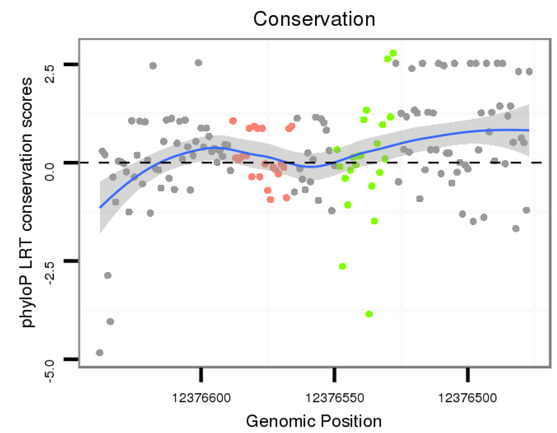
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
MINIME_DN	Unknown	Unknown	-

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TATAGTGCTGGGATATACGCAATGCTCTGCGGCTATATGGCTTGCATGTATATCTGCATCTGCATCCAAGGCTGGCAACTGGAATAAGCAATGGGGCCGATGCTGATATGTCTGCCTGCCTGCCTGCCTGCCTGCATATCTGTCTGTCTGTTCGTCCG **********...(((..(((..(((((((.(((((.((.((((..(((.............)))..)))))))..)))))..)))))))..)))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V041 embryo	V110 male body	V056 head
.....AATGGGGCCGATGCTGATATGT.....	22	0	1	46.00	46	26	6	11	3	0
.....AATGGGGCCGATGCTGATATGC.....	22	1	1	12.00	12	11	1	0	0	0
.....AATGGGGCCGATGCTGATATG.....	21	0	1	8.00	8	1	7	0	0	0
.....TATCTGCATCTGCATCCAAGGCT.....	23	0	1	4.00	4	2	1	1	0	0
.....ATATCTGCATCTGCATCCAAGGC.....	23	0	1	4.00	4	4	0	0	0	0
.....ATGGGGCCGATGCTGATATG.....	20	0	1	2.00	2	0	2	0	0	0
.....AATGGGGCCGATGCTGATATGTC.....	23	0	1	2.00	2	0	0	1	0	1
.....TATCTGCATCTGCATCCAAGGCC.....	23	1	1	1.00	1	1	0	0	0	0
.....ATATCTGCATCTGCATCCAAGG.....	22	0	1	1.00	1	0	1	0	0	0
.....ATATCTGCATCTGCATCCAAGGCT.....	24	0	1	1.00	1	1	0	0	0	0
.....ATGGGGCCGATGCTGATATGT.....	21	0	1	1.00	1	0	1	0	0	0
.....AATGGGGCCGATGCTGATATGTT.....	23	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

ATATCACGACCCTATATGCGTTACGAGACGCCGATATACCGAACGTACATATAGACGTAGACGTAGGTTCCGACCGTTGACCTTATTCGTTACCCCGGCTACGACTATACAGACGGACGGACGGACGGACGGACGTATAGACAGACAGACAGACAAGCAGGC **********...(((..(((..(((((((.(((((.((.((((..(((.............)))..)))))))..)))))..)))))))..)))).....**********	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_6473:12376477-12376638 -	dmo_133	TATAGTGCTG-------G-----------------GATATACGCAATGC-------------TCTGCGGCTATATGGCTTGCATGTATATCTG-----CAT-CTGCATCCAAGG-CTGGCAACTG-----------------------G-----AATAAGCAATGGGGCCGATGCTGATATGTCT-------GCCTGCCT--------GCCTG----CCTG---CCTGCATATCTGTCTGTCTGTCTGTTCGTCCG
droVir3	scaffold_1248:477-624 +		TATGTA----TGTAT---G--GTATATCTGTATGTCTGTATATCTGTATGTCTGTA---------TGTCTGTCTTAT----------------------GTCTGTCTGTCTGT---CTGTGTG-----------------TCTGGC--TGTCT-------GTCTGTCTGTCTCTCTGTCTG----TCTG---TCTGTCTATCTGTCTGTCTGTCTGTCTGTTG
droGri2	scaffold_14853:5347703-5347853 +		GATTGA----AGTG----G-----------------------CAGTG---------------ATTGCCCCTTGTC--GTCTGCCCGTTAGCCGGCGTT-CAGCTGGTGAGTCCTCGTTGCCAGGACGAGCT-----------------G-----------GCA-TG----TCTATCT-------GTCTGTCTATCTGTCTGTCTA----TCTG---CCTGCCTGTCTGTCTGTCTGTCTCTCTGTCCG
droWil2	scf2_1100000004909:8502481-8502616 -		TAGAATGTAG-------AATG-----------------TACATATGTAATTGCA-GTACGTGCGCAGTTATGGATTTTGT----------------GCTTG----G----------A---AAATTCGCCCAAAAGC---------AGCAAAGCGGTCTTGTCC-------GTCTGTCT--------GCCTG----TCTG---TCTGCCTGCTGCCTGCTGTCTGTCGT-------
dp5	2:18351980-18352104 +		AATCG-----------------G----------------------------TTCCGACCCAATAAAGTACATATATCTTGATCA----G----------G----------G-----CATCAATAGCCGAGTCGATTGAGCCCTGTCT-------GTCTGTCC----GTCTGTCGG----TCCG---TCTGTCCGTCGTCTGTCGTCCGTCGTTG
droPer2	scaffold_11:299226-299374 +		CATGTA----CATAT---G--GCA----------TG--TGTG----GT----------------GGTGTGGTATGTG-----CATTCTGTGCATAGTC-CTG-TGCT---------TCCTGCAGCA----G----------GCCAGTCCTGTCCGTACG----GTCTGGCCCTGTC-------CTGCCTGCCTG----CCTG---CCTGCCTGCTGCCTGCCGCCGCCTGCCGCCGTG
droAna3	scaffold_343:1489-1645 +		TATAATTTTG-------GTCA----------AAAGTGTGCAACGCA-GTGAAGGAGACATCTCGGACCCTATAAAGTATATATATCTTGATCA----G----------G----------G-----GATCACGTCCTGAGTCGATATAAGCATGTCC-------GTCTGTCC--------GTCTG----TCCG---TCTGTCCGTCTGTCGTCTGTCTGTCTGTCTG
droBip1	scf7180000396413:1815939-1816091 -		TATAATTTTG-------GTCA----------AAAGTGTGCAACGCA-GTGAAGGAGACATCTCGGACCCTATAAAGTATATATATCTTGATCA----G----------G----------G-----GATCACGTCCTGAGTTGATATGAGCATGTCC-------GTCTGTCC--------GTCTG----TCC----------GTCTGTCGTCTGTCGTCTGTCGTCTG
droKik1	scf7180000302344:137365-137529 +		TATAATTTCA-------GTCA----------GAAGTTTGCAACGCA-GTGAAGGAGACGTTTCGGACCCTATAAAGTATATATATCTTGATCA----G----------G----------G-----CATCAACAGCCGAGTCGATCTAGCCATGTCC-------GTCTGTCCGTCTGTCCGTCTG----TCCG---TCTGTCCGTCTGTCTGTCTGTCCGTCTGTCG
droFic1	scf7180000454073:1099803-1099960 +		TATATA----TATATA---TTCA----------CAGATGTAGAACCCC-T------AGA----------------------CATTTCTTAGACTC----G----------G---GGTTTGTAGTACGAGTATCTATCAACAATGCG-----------TCTCGCCG----------TCTGACTTCAGT----CTGACTCCCCGTGTGGATGTCTGGCATTGGTTTAACTGTCTGTCTGTCTGTCTGTCCGTCCG
droEle1	scf7180000487692:110-242 +		G---------------G----------------------CAACGCT----------CATCGCGTCCCTATAAAGTATATATATCTTGATCA----G----------G----------G-----CATCACTAGACGAGTCGATCTAGCCATGTCC-------GTCTGTCAGTCTGTCCGTCTG----TCCG---TCCGTCTGTCCGTCCGTCTGTCGTCCGTCTG
droRho1	scf7180000773739:5644-5809 +		TATAATGTTG-------GTCA----------AATGTGTGCAACGCGAAGTGAAGGAAACATCTCGGACCCTATAAAGTATATATATCTTGATCA----G----------G----------G-----GATCCCGTCCTGAGTTAATATAAGCATGTCC-------GTCTGTCTGTCCGTCTGTCTG----TCCG---TCTGCCTGTCCGTCTGTCTGTCGTCTGTCTG
droBia1	scf7180000296997:4160-4282 -		TATG------------G----------------------TAATGA----------TCCGGACCATATAAAGTACATATATCTTGATCA----G----------G----------G-----CGT-ACTAGACAAGTGGATCTAGCCATGTCC-------GTCCGTCT--------GTCCG----CCCG---TCTGTCCGCCGTCTGTCTGTCGTCCGTCCG
droTak1	scf7180000415914:687150-687289 +		A---------------G----------------------CGCA-GTGAAGGAGAC-TTTCGGACCCTATAAAGTATATATATCTTGATCA----G----------G----------G-----CATCACTAGACGAGTCGATCTAGCCATGTCC-------GTCTGTCCGTCTGTCCGTCTG----TCCG---TCTGTCCGTCTGACGTCTGTCGTCCGTCTGTCCG
droEug1	scf7180000409474:2886815-2886972 -		TAGAGTA----------G----------------------AAAGGGTATAGTAAA-TTCGTTGAAAAGTTTGCGACCCTATAAAGTATATATATCTTGATCA----G----------G----------G-----GATCAATAGCGAAGTCGATTGAGCCATGTCC-------GTCTGTCTGTCCGTCCGTCCGTCCG----TCCG---TCCGTCCTCCGTCCGTCCGTCCGTCCGTCCG
dm3	chrX:13863700-13863853 -		TGTACAT----ATA----C--GCA----------GA--TGTAGAACCCC-T------AGA----------------------CATTTCTTAGACTC----G----------G---GGTTGCAGTACGAGTATCTATCAACAATGCG-----------TCTCGCCG----------TCTGACTTCAGT----CTGACTCCCCGTCTGGATGTCTGGCATTGGTTTAACTGTCTGTCCGTCGTCCGTCTGTCTG
droSim2	3l:23861274-23861349 +		ACTG------------G--G----------G----------G-----------------GACGAATCGATCTGGCCATGTCC-------GAGTGTTC--------GACTG----TCAG---TCTGTCCATCTGTTTGTCTGTCGTCGTCCG
droSec2	scaffold_8:2478859-2478953 +		CATGGT----------G--TGGAAATA----G----------G----------G-----GATCACTAGCCGAGCCGATATAGCCATGTCT-------GTCCGTTC--------GCCTG----TCCG---TTCGGCTGTGCCGTTCGCGTGTCGTTCGCCGTG
droYak3	Y2_chrUn_5991:484-612 -		AAGGG-----------G----------------------------TTCCGACCATATAAAGTATATATATCTTGATCA----G----------G----------G-----GATCAATAGCCGAGTCGATTGGGCCATGTCC-------GTCTGTCGTCCGTCCGTCTG----TCCG---TCTGTCCGTCTGTCCGTCTGTCCGTCTGTCCG
droEre2	scaffold_4929:12379742-12379882 -		GGGTATACTC-A-AC-TCGTTG----------AAAGTATGTAAC----------------------AAGAATAAATATCTTTATCA----G----------G----------A-----GATCAATAGCCAAATCGATCTGCCATGTCT-------GTCCGTCTGTCCGTCCGTTG----TCCG---TCCGTTTGTCCGTCCGTTGTGTCCGTCCGTTG

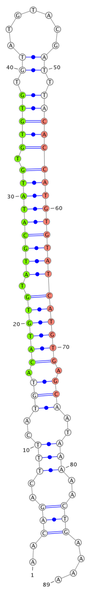
Generated: 09/08/2015 at 07:47 PM

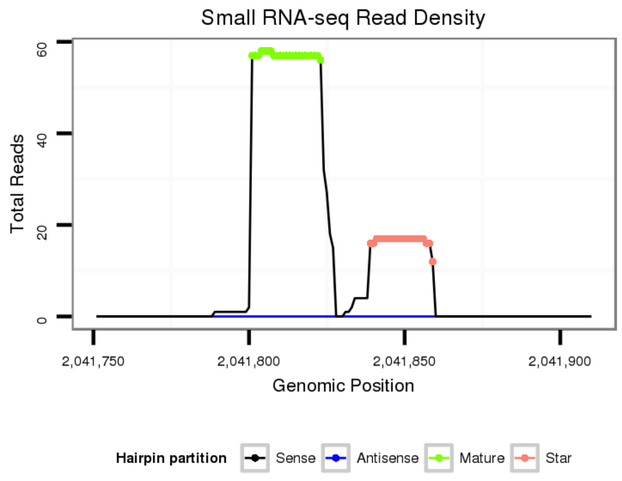
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

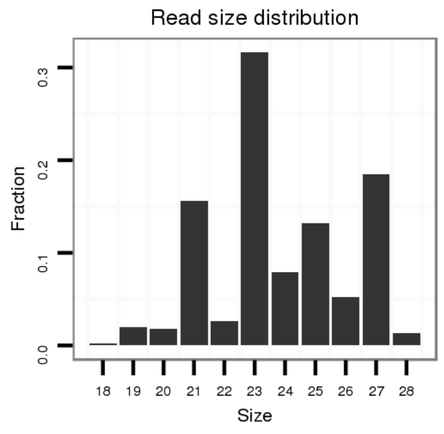
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_102	**scaffold_6496:2041801-2041860 +**	**confident**	**Canonical miRNA**	**5pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

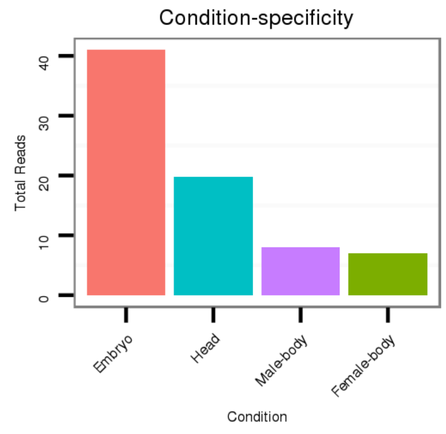
Legend: mature star mismatch in alignment mismatch in read

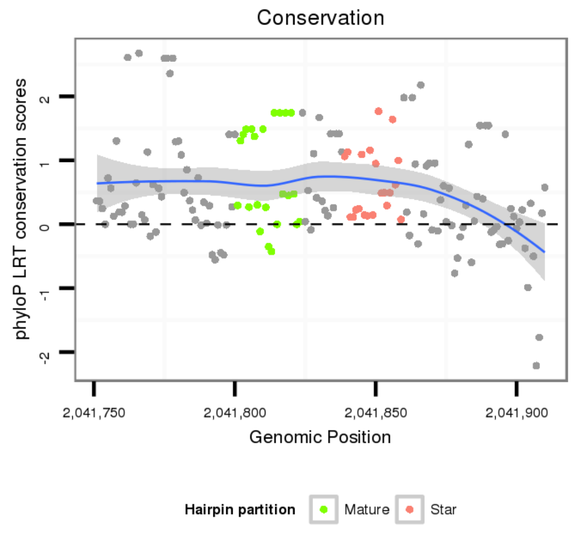
Predicted structure











Show Alternate Folds

Flybase annnotation

utr5 [utr5_plus_3623]

Repeatable elements

Name	Class	Family	Strand
(TATATG)n	Simple_repeat	Simple_repeat	+

mature	star
1. dmo_102 scaffold_6496:2041801-2041823 + 2. scaffold_6680:5750462-5750484 -	

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTGGTGGTGGTTTTTTTTCTAAGGAACTTTGCCTCAACAGACTTTCATGTACATGTGTATGCATATGTGTGTGTGTATGTACGATTTACACCATGTGTATCATGTGAGCAATAAAAACTGAAAAGAAAAAAGAATGAAAAAATAAAACGTGTTCATAAAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V041 embryo	M060 embryo	V056 head	V110 male body	V049 head	M046 female body
**********..(((..(((..(((.(((((((.((((((((((.(((((.((.......)).)))))))))))))))))).)))..)))..)))....**********											
.....ACATGTGTATGCATATGTGTGTG.....	23	0	2	23.00	46	15	3	13	0	11	4
.....ACATGTGTATGCATATGTGTGTGTGTA.....	27	0	1	14.00	14	9	2	0	2	1	0
.....CACCATGTGTATCATGTGAGC.....	21	0	1	11.00	11	5	6	0	0	0	0
.....ACATGTGTATGCATATGTGTGTGTG.....	25	0	1	9.00	9	3	0	4	2	0	0
.....ACATGTGTATGCATATGTGTGTGT.....	24	0	1	5.00	5	1	0	2	1	0	1
.....ACATGTGTATGCATATGTGTGTGTGT.....	26	0	1	3.00	3	0	0	0	2	0	1
.....ACATGTGTATGCATATGTGTGT.....	22	0	2	1.50	3	0	0	0	1	1	1
.....ATTTACACCATGTGTATCATGTG.....	23	0	1	1.00	1	0	0	0	0	0	1
.....ACATGTGTATGCATATGTGTGTGTA.....	26	1	1	1.00	1	0	0	0	1	0	0
.....ATTTACACCATGTGTATCATGTGAG.....	25	0	1	1.00	1	0	1	0	0	0	0
.....GATTTACACCATGTGTATCATGTGAG.....	26	0	1	1.00	1	0	1	0	0	0	0
.....AGACTTTCATGTACATGTG.....	19	0	1	1.00	1	0	1	0	0	0	0
.....CACCATGTGTATCATGTGAG.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TACATGTGTATGCATATGTGTGTG.....	24	0	1	1.00	1	1	0	0	0	0	0
.....CCATGTGTATCATGTGAGC.....	19	0	1	1.00	1	0	1	0	0	0	0
.....ACGATTTACACCATGTGTATCATGTGAG.....	28	0	1	1.00	1	0	1	0	0	0	0
.....TGTGTATGCATATGTGTGTGTGTA.....	24	0	1	1.00	1	0	1	0	0	0	0
.....ACATGTGTATGCATATGTG.....	19	0	2	0.50	1	0	0	0	0	0	1
.....ACATGTGTATGCATATGTGTGTT.....	23	1	2	0.50	1	0	0	0	0	1	0
.....ACATGTGTATGCATATGTGTG.....	21	0	2	0.50	1	0	0	0	0	0	1
.....TGTGTATGCATATGTGTGTGTG.....	22	0	4	0.50	2	0	0	0	2	0	0
.....CATGTGTATGCATATGTGTGT.....	21	0	3	0.33	1	0	0	1	0	0	0
.....CATGTGTATGCATATGTGTG.....	20	0	3	0.33	1	0	0	0	0	0	1
.....ATGTGTATGCATATGTGT.....	18	0	6	0.17	1	0	0	0	0	0	1

Anti-sense strand reads

AACCACCACCAAAAAAAAGATTCCTTGAAACGGAGTTGTCTGAAAGTACATGTACACATACGTATACACACACACATACATGCTAAATGTGGTACACATAGTACACTCGTTATTTTTGACTTTTCTTTTTTCTTACTTTTTTATTTTGCACAAGTATTTT	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body
**********..(((..(((..(((.(((((((.(((((((((.(((((.((.......)).)))))))))))))))).)))..)))..)))....**********							
.....CATAAATG--------AA--GAACA----------ACTAAAGAAA--G--------------CTGAC---AATT----------AAA	23	0	2	0.50	1	0	1
.....CATAAATG--------AA--GAACA----------ACTAAAGAAA--G--------------CAGAC---AATTAAATT----------CACA	23	0	2	0.50	1	0	1
.....CAAAAATTATAA-AT----------AATAATGT-TGAAAA---GA-ATACCATTCAAGTCATTATTAGA	24	0	3	0.33	1	0	1
.....CATATAATG--------AA--AAACA----------ACTAAAGAAA--A--------------CAGGC---AATTTAATTCA---AAAAA	21	0	3	0.33	1	0	1
.....CATAAATG--------AA--AAACA----------ACTAAAGAAA--A--------------CAGGC---AATT----------AAA	20	0	3	0.33	1	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6496:2041751-2041910 +	dmo_102	TTGGTGG--TGGTTTTTTT-TCTAAGGAACTTTGCCTCAACAGA----CT-TT--CATGTACATGTGT--ATGCATATGTGTGTGTGTATGTA------CGATTTACACCAT--------GTGTA---------TCATGTGAGCAA--TAAAAACTGAAAAGAAAAAAGA-AT----------GAAAAAAT-AAAACGT-----G---------TTCA---TAAAA
droVir3	scaffold_10324:224318-224467 +	dvi_24639	TTGGTGG--TGGTT--TTT-TCTAGTGAACTTTGCCTGAAACGACAGACACTA--CATGTACATGTGT--ATGCATATGTGTGTGTGT--GTA------CGATTTACACCAT--------GTGTA---------TCATGTGAGCAA--TAAGAACTGAAGAAAAA-----AAAAA--------AAAACG--------TGTAC--A---------------CAA
droGri2	scaffold_15245:15402574-15402719 -		TTGGTGG--TGGTT--TTT-TCTAATGAACTTTGCCAGAAGAAT----A-CGAAGACTATTCATGTGT--ATGCATATGTGTGTGTGT--GTA------CGATTTACACCAT------GATGTGTA---------TCATGTGAGCAATATAAAA----------------ACTGAGG-GGGC---AAAAACG--------T-----A---------GTA---TAAAA
droWil2	scf2_1100000004515:703338-703445 +		TTGGAGTTTCAGTT--TTC-TCAAGCAACTCTGTG-ACGGCGC-AGTT-TTTGGTATGTACATGTGT--GTGTGTGTGTGTGTGTGTGTGTGCGT----------------------------------GTGTGTGTAG--TAAGAA--CT	
dp5	3:15882317-15882399 +		TTGGTGG--TGGTT--TTCCCCAGTGAACTTTGCCTG--GAAC--AATAAATCATGTGA----------GAAAGCCAGAAA-AT----------AAAACGCC-GGAACG-----A---------GAA
droPer2	scaffold_4:879553-879635 -		TTGGTGG--TGGTT--TTCCCCAGTGAACTTTGCCTG--GAAC--AATAAATCATGTGA----------GAAAGCCAGAAA-AT----------AAAACGCC-GGAACG-----A---------CAA
droAna3	scaffold_13137:502256-502384 -		AATTTT---ACC----TC--TCCATAAACTTCTA---------TGTACATATGTATATTATTGTATATACATACATATGTATTTAT-ATTTACATTGAATGGGGT----------CGCAATT----------TAATCTTAAAGCAAA-----GCCGAAAGGA--T---------C-A-----TGAAA-A---------TAA
droBip1	scf7180000396733:471045-471082 -		AGCCTTT--TGTGT--GTG-----------------------TGTGA--GTGCCTATGTATGTGTGT---
droKik1	scf7180000302476:828224-828315 +		TTGGTGG--TGGTT--TTCCTCCAGTGAACTTTGCCTG--GAAC--TATAAATC---------AT--TAACA---------AAACTCGA---AT-AAAAAAA--TCG---------TAAAGCGA-----A---------TCGA---ACAAA
droFic1	scf7180000454073:1224171-1224222 +		CAAA---------------------------AAAAGC--C-----------GA-----------AAAAAACCAAAA-AC----------AAAAATAT-TAACGA---TA-A---------TTTT---TAAAA
droEle1	scf7180000491107:1673932-1673962 -		TTGGTGG--TGGTT--TTC-CTGGTGAACTTTGCCT---
droRho1	scf7180000777217:325867-325897 +		TTGGTGG--TGGTT--TTC-CTAGTGAACTTTGCCT---
droBia1	scf7180000301506:1281826-1281857 -		TTGGTGG--TGGTT--TTC-CCAGTGAACTTTGCCT---
droTak1	scf7180000415401:499432-499501 +		TTGGTGG--TGGTT--TTC-CCAGTGAACTTTGCCTGCAGAGC--CATAAATC---------AA--GAACA----------ACTAA-GAAA--C---------------CAGA-A---------CAG
droEug1	scf7180000409209:724217-724290 -		TTGGTGG--TGGTT--TTC-CCAGTGAACTTTGCCAGCAGAGC--CATAAATC---------AA--AAACA----------CA-ACTAAAAAAA--A---------CCAGA-A---------CAA
dm3	chr2R:5440550-5440625 +		TTGGTGG--TGGTT--TTC-CCAGTGAACTTTGCCTGCAGAGC--CATAAATC---------AA--GAACA----------ACTAAAGAAA--G---------CTGAC---AATT----------AAA
droSim2	2r:6225633-6225714 +		TTGGTGG--TGGTT--TTC-CCAGTGAACTTTGCCTGCAGAGC--CATAAATC---------AA--GAACA----------ACTAAAGAAA--G---------CAGAC---AATTAAATT----------CACA
droSec2	scaffold_6:246270-246395 +		AATATACA--TATAT--ATA----------TATATGTGTGAATAT--GTG------TAACTT-----AATAGGAAAATGAATTTAATAGAGAAACAACAGA-----------CAAAAATTATAA-AT----------AATAATGT-TGAAAA---GA-ATACCATTCAAGTCATTATTAGA
droYak3	2L:18071586-18071670 +		TTGGTGG--TGGTT--TTC-CCAGTGAACTTTGCCTGCAGAGC--CATTATATC---------AA--AAACA----------ACTAAAGAAA--A---------CAGGC---AATTTAATTCA---AAAAA
droEre2	scaffold_4929:8916625-8916700 -		TTGGTGG--TGGTT--TTC-CCAGTGAACTTTGCCTGCAGAGC--CATAAATC---------AA--AAACA----------ACTAAAGAAA--A---------CAGGC---AATT----------AAA

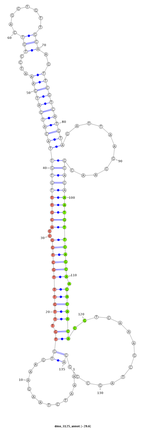
Generated: 09/08/2015 at 07:49 PM

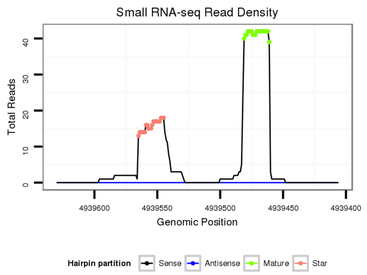
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

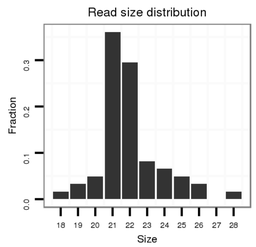
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_3125	**scaffold_6540:4939456-4939580 -**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

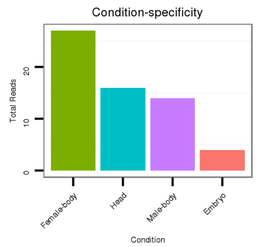
Legend: mature star mismatch in alignment mismatch in read

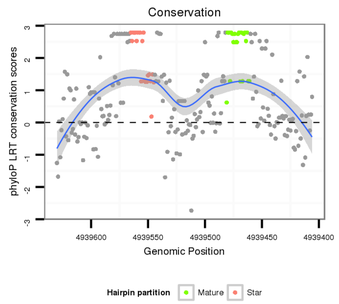
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dmoj\GI23585-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GATTTGTGATCTGCATTTCAGTGGCTATCGATGAGAGACTGCAACGAGACAAATCTAAGAAAGTGTGTTTGTTTGCTGGCCACGTTTGTGTTACATGATGAAATCCTGTCAGCTGTTGCAAGTTCGTCATGTAGATTAAGCAACGCACAAATGTTCAGCAAGACAACACGTCAAAGCTAGCCGCAAATAATCGAATTTATATACACCGATATATATATATATATA	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	V056 head	M060 embryo	V049 head	V041 embryo
**********.....((((.((((((((((..((((((((((((((((((((((.(((.....)))..)))))))))).....))))))))))))))))).))))))).....))**********.....												
.....AATGTTCAGCAAGACAACACG.....	21	0	1	16.00	16	6	3	4	1	2	0
.....AAATGTTCAGCAAGACAACACG.....	22	0	1	15.00	15	4	5	5	0	1	0
.....TGTTTGTTTGCTGGCCACGTT.....	21	0	1	4.00	4	3	0	0	0	1	0
.....TGTTTGTTTGCTGGCCACGTTTGTG.....	25	0	1	2.00	2	1	0	1	0	0	0
.....CAAATGTTCAGCAAGACAACACG.....	23	0	1	2.00	2	1	1	0	0	0	0
.....TGTTTGTTTGCTGGCCACGTTTGT.....	24	0	1	2.00	2	1	1	0	0	0	0
.....TTTGCTGGCCACGTTTGTGT.....	20	0	1	2.00	2	2	0	2	0	0	0
.....TGTTTGTTTGCTGGCCACGTTT.....	22	0	1	2.00	2	2	0	0	0	0	0
.....AAATGTTCAGCAAGACAACAC.....	21	0	1	2.00	2	2	0	0	0	0	0
.....AATGTTCAGCAAGACAACACGT.....	22	0	1	1.00	1	0	0	0	1	0	0
.....AATGTTCAGCAAGACAACACGTT.....	23	1	1	1.00	1	0	0	0	0	0	1
.....TGTTTGTTTGCTGGCCACGTTTG.....	22	1	1	1.00	1	0	0	0	0	0	0
.....GTTCAGCAAGACAACACG.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TACACCGATATATATATATATAT.	23	0	3	0.33	1	1	0	0	0	0	0

Anti-sense strand reads

CTAAACACTAGACGTAAAGTCACCGATAGCTACTCTCTGACGTTGCTCTGTTTAGATTCTTTCACACAAACAAACGACCGGTGCAAACACAATGTACTACTTTAGGACAGTCGACAACGTTCAAGCAGTACATCTAATTCGTTGCGTGTTTACAAGTCGTTCTGTTGTGCAGTTTCGATCGGCGTTTATTAGCTTAAATATATGTGGCTATATATATATATAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head
**********.....((((.((((((((((..((((((((((((((((((((((...((((.....)))).)))))))))).....))))))))))))))))).))))))).....))**********						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:4939406-4939630 -	dmo_3125	GATTTGT---------G--ATCTGCATTTCAGTGGCTATC---------GATGAGAGAC---T-GCAACGAGACAAATCTAAG-AAAGTGTGTTTGTTTGCTGG-CCACGTTTGTGTTACATGA----T---------GAAATCCTGTCAGC-----TGTTGC--AA---------GTTCGTCATGTAGATTA-AGCAACGCACAAATGTTCAGCAAGACAACACGTCAAAGCTAGCCGCAAATA-A---------TCGAA---------TTTATATACACCGATATAT---ATATATATATA
droVir3	scaffold_13047:936621-936812 -	dvi_24611	AATAAT---------G---[redacted]C-TC---------GATA-T-C---GG-T-GCGA-G-AAATCTCAG-AAAGTGTGTTTGTTTGCTAGCTAGGTTGTGTTACATG----T---------GAA-T-TG-A-GC-----G-GCTGC-G---------AGTCGTCATGTAGATTA-AGTACGCACAAATGTTCAGCAAGACAACACGTCAAGCAAGCCGCAAATA-A---------TCGA---------[redacted]GATC---GCG-TATATA
droGri2	scaffold_14906:5355642-5355862 +	dgr_460	GATTGT---------G---ATT---------GGTGC---------TCTC-GCAACGAAGAAGTCTGCAG-AAAGTGTGTTTGTTTGCTGG-CCACGTTTGTGTTACATGT----T---------GAA-T-TAG-C-CAGC-----A-T-TGC--TG---CTGCTGCTCCTGCTGCGGGTGCGTTCGTCATGTAGCTTA-AGCAACGCACAAATGTTCAGCAAGACAACACGTCAAAGCAAGCCGCAACGCA---------TCGGC---------TTTATAT---TGTG----ATA-----ATAGATA
droWil2	scaf2_11000000004902:913444-914537 -	dwi_5413	CAATAT---------G---[redacted]---------AA---------[redacted]---T-TCTTAAGAAAGTCTAAG-AAAGTGTGTTTGTTTGCTGGTCTAGGTTGTGTTACATGATTCAATGTT---------[redacted]---TTCTATTGGC---[redacted]---TCTGTAGGCTTATTTTTCACAAATGTTCAGCAAGACAACACGTCAAAGCAAGCCGCAATAATCGATTATCTCTCTTTT---TTTTATAA---------AACAAAA---------CAATATCTCTCTTTT---TTTTATAA
dp5	2:7251471-7251674 -	dps_3824	GATAAT---------G---[redacted]GTCTGTGTG---------[redacted]---TCT-T-T-T-A-GAAGTCTCAG-AAAGTGTGTTTGTTTGCTGGCTAGGTTGTGTTACATGA----T---------GCC-C---------TTTATGGACTCAAGTGTATCTGTCTATACATCCAAAAGGCCCTCATGTAGGCTA-ATAACACAATGTTCAGCAAGACAACACGTCAAAGCAAGCCGCAATAATCGATTATCTCTCTTTT---TTTTATAA---------TG---------[redacted]---------[redacted]---TTTTATAA
droPer2	scaffold_0:1112067-1112276 -	dpe_2478	GATAAT---------G---[redacted]GTCGTCTGTCGTCGTG---------[redacted]---TCT-T-T-T-A-GAAGTCTCAG-AAAGTGTGTTTGTTTGCTGGCTAGGTTGTGTTACATGA----T---------GCC-C---------TTTATGGACTCAAGTGTATCTGTCTATACATCCAAAAGGCCCTCATGTAGGCTA-ATAACACAATGTTCAGCAAGACAACACGTCAAAGCAAGCCGCAATAATCGATTATCTCTCTTTT---TTTTATAA---------TG---------[redacted]---------[redacted]---TTTTATAA
droAna3	scaffold_13340:938943-939149 +	dan_4036	GATATG---------CA-T---TCTCG---------A-ACTCTGAAT---------TGGA-GCAAATGAAAGTCTAG-AAAGTGTGTTTGTTTGCTGG-CTAGGTTGTGTTACATGA----AGGTC---------[redacted]---TCTTCGGGGGT---------[redacted]---TCTGTAGGCTTATGAGCAAAGCAACACGTCAAAGCAAGCCGCAATAATCGATTATCTCTCTTTT---TTTTATAA---------TG---------[redacted]---------[redacted]---TTTTATAA
droBip1	scf7180000394085:58642-58786 -		GATAAT---------G---[redacted]---------G---------TGGA-TTCTATGAAGAAGTCTGCAG-AAAGTGTGTTTGTTTGCTGGCTAGGTTGTGTTACATGA----T---------GCC-C---------[redacted]---TCTGTAGGCTTATGAGCAAAGCAACACGTCAAAGCAAGCCGCAATAATCGATTATCTCTCTTTT---TTTTATAA---------TG---------[redacted]---------[redacted]---TTTTATAA
droKik1	scf7180000302475:1404912-1405080 +		AAAA---------TTCAATGGC---[redacted]---------AAAC-TCAAAATGATCACTACTGCA-TGCGCTTGAAGAAGTCTGCAG-AAAGTGTGTTTGTTTGCTGGCTAGGTTGTGTTACATGA----T---------GCC-C---------[redacted]---TCATGTAGGCTTATGAGCAAAGCAACACGTCAAAGCAAGCCGCAATAATCGATTATCTCTCTTTT---TTTTATAA---------TG---------[redacted]---------[redacted]---TTTTATAA
droFic1	scf7180000453800:2293576-2293744 +		ATTTACAGCTTACAGC---[redacted]---------TCAAAAAACGAATGGAAAACTTTAT---------TGGA-GCAAATGAAAGTCTAG-AAAGTGTGTTTGTTTGCTGGCTAGGTTGTGTTACATGA----T---------GCC-C---------[redacted]---TCCAAATTGGAT---------[redacted]---TCTGTAGGCTTATGAGCAAAGCAACACGTCAAAGCAAGCCGCAATAATCGATTATCTCTCTTTT---TTTTATAA---------TG---------[redacted]---------[redacted]---TTTTATAA
droEle1	scf7180000490995:524425-524593 -		ATTTACAGCTCAAGCCCAATGG---[redacted]---------AAAC-TCTAC---------TGGA-GCAAATGAAAGTCTAG-AAAGTGTGTTTGTTTGCTGGCTAGGTTGTGTTACATGA----T---------GCC-C---------[redacted]---TCCGAATTGGAT---------[redacted]---TCTGTAGGCTTATGAGCAAAGCAACACGTCAAAGCAAGCCGCAATAATCGATTATCTCTCTTTT---TTTTATAA---------TG---------[redacted]---------[redacted]---TTTTATAA
droRho1	scf7180000077158:35349-35505 -		ACTTACAGCCCAAACCCAATGG---[redacted]---------AAAC-TCTAC---------TGG-T---------GCAAATGAAAGTCTAG-AAAGTGTGTTTGTTTGCTGGCTAGGTTGTGTTACATGA----T---------GCC-C---------[redacted]---TCCGAATTGGAT---------[redacted]---TCTGTAGGCTTATGAGCAAAGCAACACGTCAAAGCAAGCCGCAATAATCGATTATCTCTCTTTT---TTTTATAA---------TG---------[redacted]---------[redacted]---TTTTATAA
droBia1	scf7180000302402:8304870-8305117 +		GTAT---------GGC---[redacted]---------AAACGCCTATGAAGAAGTCTGCAG-AAAGTGTGTTTGTTTGCTGGCTAGGTTGTGTTACATGA----T---------GCC-C---------[redacted]---ACC-AATGGGCT---------[redacted]---TCTGTAGGCTTATGAGCAAAGCAACACGTCAAAGCAAGCCGCAATAATCGATTATCTCTCTTTT---TTTTATAA---------TG---------[redacted]---------[redacted]---TTTTATAA
droTak1	scf7180000415380:1425482-1425632 -		GTTCAA---------CATCCCATGGC---[redacted]---------AAAC-TTTAT---------TGAA-GCAAATGAAAGTCTAG-AAAGTGTGTTTGTTTGCTGGCTAGGTTGTGTTACATGA----T---------GCC-C---------[redacted]---TCCGAATTGGAT---------[redacted]---TCTGTAGGCTTATGAGCAAAGCAACACGTCAAAGCAAGCCGCAATAATCGATTATCTCTCTTTT---TTTTATAA---------TG---------[redacted]---------[redacted]---TTTTATAA
droEug1	scf7180000409692:688204-688377 +		ACATTAAGG---AAACCAATGG---[redacted]---------AAAC-TCTAT---------TGGA-GCAAATGAAAGTCTAG-AAAGTGTGTTTGTTTGCTGGCTAGGTTGTGTTACATGC----A---------GCC-C---------[redacted]---TCCGGATTGGAT---------[redacted]---TCTGTAGATTTATGCAAACGCACAACACGTCAAAGCAAGCCGCAATAATCGATTATCTCTCTTTT---TTTTATAA---------TG---------[redacted]---------[redacted]---TTTTATAA
dm3	chr3R:6217169-6217309 +		GATAT---------GGAATGG---TCC---------[redacted]---------CATAT---------TGGA-GCAAATGAAAGTCTAG-AAAGTGTGTTTGTTTGCTGGCTAGGTTGTGTTACATGA----T---------GCC-C---------[redacted]---TCCGAATTGGAT---------[redacted]---TCTGTAGGCTTATGAGCAAAGCAACACGTCAAAGCAAGCCGCAATAATCGATTATCTCTCTTTT---TTTTATAA---------TG---------[redacted]---------[redacted]---TTTTATAA
droSim2	2r:14862107-14862251 +		GCAAT---------TCCAATGGC---[redacted]---------ACGC-CATAT---------TGGA-GCAAATGAAAGTCTAG-AAAGTGTGTTTGTTTGCTAGCTAGGTTGTGTTACATGA----T---------GCC-C---------[redacted]---TCCGAATTGGAT---------[redacted]---TCTGTAGGCTTATGAGCAAAGCAACACGTCAAAGCAAGCCGCAATAATCGATTATCTCTCTTTT---TTTTATAA---------TG---------[redacted]---------[redacted]---TTTTATAA
droSec2	scaffold_0:15728125-15728295 -	dse_143	GCAAT---------TCCAATGGC---[redacted]---------ACGC-CATAT---------TGGA-GCAAATGAAAGTCTAG-AAAGTGTGTTTGTTTGCTAGCTAGGTTGTGTTACATGA----T---------GCC-C---------[redacted]---TCCGAATTGGAT---------[redacted]---TCTGTAGGCTTATGAGCAAAGCAACACGTCAAAGCAAGCCGCAATAATCGATTATCTCTCTTTT---TTTTATAA---------TG---------[redacted]---------[redacted]---TTTTATAA
droYak3	X:2130480-2130680 -		GTGAA---------[redacted]---------[redacted]---------[redacted]---------[redacted]---------[redacted]---TGTTTGTTTGTGAAGTTTCCCGATTAAA-TATGA----T---TGGTATTGGGCTTCAATTGCCAACTTATAAAGCGACGATTTCTGTTCAAGTTTCCGTTTTAGATAATGAGC--------ATTTTGGATTATCCTTCCATTTTGCTTTAAATTTTAGCGCCCCTTAT---TAATAGTAATA---------[redacted]---------[redacted]---TTTTATAATATATA
droEre2	scaffold_4770:15403130-15403286 -		GTAT---------CCCATTGGAC---[redacted]---------CA---------TGGAT---------TGGA-GCCCACGATCTCTGTAG-AAAGTGTGTTTGTTTGCTGGCTAGGTTGTGTTCAGCT---T---------GCC-C---------[redacted]---TTC-AAATGGAT---------[redacted]---TCTGTAGGCTTATGAGCAAAGCAACACGTCAAAGCAAGCCGCAATAATCGATTATCTCTCTTTT---TTTTATAA---------TG---------[redacted]---------[redacted]---TTTTATAA

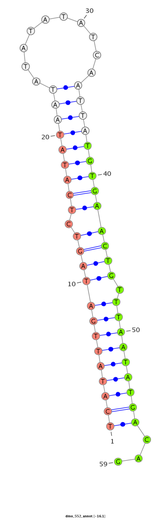
Generated: 09/08/2015 at 07:48 PM

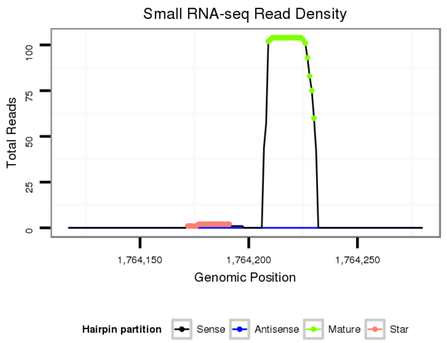
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.top2	1
crit.top3	1
crit.tpop3	1
crit.uri	0
crit.hack	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	0
rescue.candidate	5

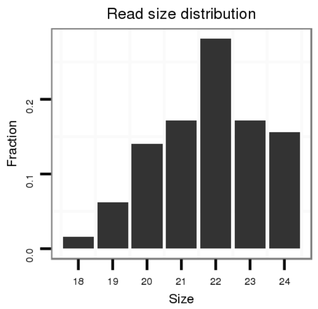
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_552	**scaffold_6359:1764167-1764230 +**	**confident-exception**	**5p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

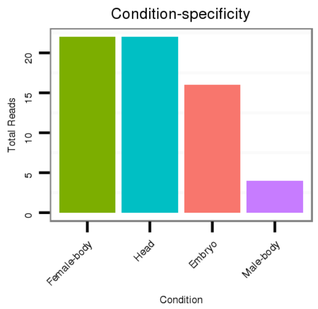
Legend: mature star mismatch in alignment mismatch in read

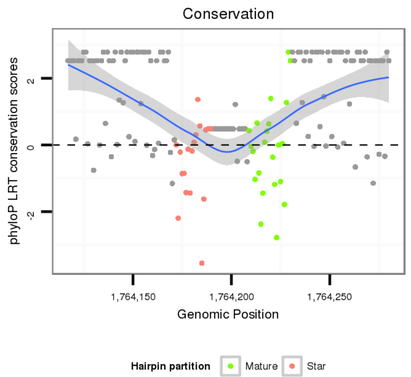
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI21691-in]; CDS [DmojGI21691-cds]; CDS [DmojGI21691-cds]; utr3 {utr3_plus_8319]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GGCGTCGCAACGGCGGACAGACACAGCTACACAAATACTATACACGCAAGGTGGGTCATATTGATAGTCTCATATAATATATATCAATTATGTGAACTGTTTAATATGACAGTGCAAGGAGCTGTATAATTGCATCAAGGAGGCCATGGAACGCGGCGGCAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V056 head	V041 embryo	V049 head	V110 male body
**********(((((((((((((.(((((((((.....)))))))))))))).)))))))...**********											
..TGTGAACTGTTTAATATGACAGT	23	0	1	38.00	38	26	3	0	7	0	2
..TGTGAACTGTTTAATATGACAGC	23	1	1	12.00	12	12	0	0	0	0	0
..TATGTGAACTGTTTAATATGACAG	24	0	1	10.00	10	3	3	3	0	1	0
..TATGTGAACTGTTTAATATGAC	22	0	1	8.00	8	2	1	2	0	3	0
..TATGTGAACTGTTTAATATGA	21	0	1	8.00	8	0	4	3	1	0	0
..TATGTGAACTGTTTAATATG	20	0	1	7.00	7	0	1	2	0	1	3
..TATGTGAACTGTTTAATATGACA	23	0	1	7.00	7	1	2	1	2	1	0
..ATGTGAACTGTTTAATATGACA	22	0	1	6.00	6	1	2	0	1	2	0
..TGTGAACTGTTTAATATGACAG	22	0	1	4.00	4	1	1	1	1	0	0
..ATGTGAACTGTTTAATATGACAG	23	0	1	4.00	4	2	2	0	0	0	0
..TGTGAACTGTTTAATATGACA	21	0	1	2.00	2	0	2	0	0	0	0
..TATGTGAACTGTTTAATAT	19	0	1	2.00	2	0	1	1	0	0	0
..TATGTGAACTGTTTAATATGAC	23	1	1	1.00	1	0	1	0	0	0	0
..TGTGAACTGTTTAATATGACAG	23	1	1	1.00	1	1	0	0	0	0	0
..TGTGAACTGTTTAATATGACAGT	24	1	1	1.00	1	0	0	0	1	0	0
..ATGTGAACTGTTTAATATG	19	0	1	1.00	1	0	1	0	0	0	0
..TATGTGAACTGTTTAATA	18	0	1	1.00	1	1	0	0	0	0	0
..ATGTGAACTGTTTAATATGA	20	0	1	1.00	1	0	1	0	0	0	0
..TATGTGAACTGTTTAATATGACAGC	25	1	1	1.00	1	1	0	0	0	0	0
..TGAACTGTTTAATATGACAGT	21	0	1	1.00	1	1	0	0	0	0	0
..TTGATAGTCTCATATAATATA	21	0	1	1.00	1	0	0	1	0	0	0
..TGTGAACTGTTTAATATGA	19	0	1	1.00	1	0	0	0	0	0	1
..TCATATTGATAGTCTCATAT	20	0	1	1.00	1	0	1	0	0	0	0
..GTGAACTGTTTAATATGACAGT	22	0	1	1.00	1	1	0	0	0	0	0
..GTGAACTGTTTAATATGACAGA	22	1	1	1.00	1	0	1	0	0	0	0
..TATGTGAACTGTTTAATATGACAGT	25	0	1	1.00	1	1	0	0	0	0	0
..ATGTGAACTGTTTAATATGACAGT	24	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

CCGCAGCGTTGCCGCCTGTCTGTGTCGATGTGTTTATGATATGTGCGTTCCACCCAGTATAACTATCAGAGTATATTATATATATAGTTAATACACTTGACAAATTATACTGTCACGTTCCTCGACATATTAACGTAGTTCCTCCGGTACCTTGCGCCGCCGTG	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_6359:1764117-1764280 +	dmo_552	GGCGTCGCAACGGCGGACAGACACAGCTACACAAATACTATACACGCAAGGTGGGTCA----------T----------ATTGATAGT----------CT----------CATA---TAATATATATA----------T----------CAATTA----------TG----------T--GA--A----CTG--T----------TTAA--TATGACAGTGCAAGGAGCTGTATAATTGCATCAAGGAGGCCATGGAACGCGGCGGCAC
droVir3	scaffold_13042:1854070-1854259 +		GGCGACGCAATGGCGGCAAACGCAGCTGCAAAATACTACGCGGCAAGGTGAAAT----------C----------GCCG---A----CATATCTTT---ACACATACATATACATATAATATATATA----------T--CGCATAATGCTTATATCCAATTC----------T--GT--GTGTACAGTGCAAGGAGCTGTATAATTGCATTAAGGAGGCATGGACGTGGCGGCAC
droGri2	scaffold_14853:3229543-3229720 +		GGCGTCGCAATGGTGCCAGACCAATTCACAAATACTACGCACGAAAGGTATTCCA----------C----------GATGA-TGC----------AT----------TA----------ATCG----AATTG----------GATAA-TAAGCAT-TAACTAAAACTAATGTTT--C---A--TAT----------TTGT--ATCGACAGTGCAAGGAGCTATATAATTGCATTAAAGAGGCTATGGACGCAGTGGCAC
droWil2	scf2_1100000004590:2422647-2422818 -		GGCGTCGCAATGGCGGTCAGACCAATTCACAAATACTATACGAAAGGTACCACA----------A----------ACAAAGATGC----------CA----------A----------AAATAATGCAAA--AC------TGCGA-TGACTCAAGCAAAT--T------CAT--T----------CCA--AATTTCAGTGTAAGGAGCTATATAATTGCATTAAAGAGGCTATGGAACGTGGTGGAC
dp5	Unknown_group_716:13459-13613 +		GGCGACGCAACGGCGGCAGACCAGTTCAAACTACTACGAGAAAGGTGATGTGAAGTCCGACTCGGTGGATTTTAATCTGAA----------A----------A----------C----------T----------GTT--T----------TTT--GTCCCAGTGCAAGGAACTGTATCAACTGCATCAAAGAGCCATGGACGTGGTGGAC
droPer2	scaffold_28:378801-378954 -		GGCGACGCAACGGCGGCAGACCAGTTCAAACTACTACGAGAAAGGTGATGTTCGAACTCCGACTCGGTGGATTCGAATCTGAA----------A----------A----------C----------T----------G--TGT----------TTT--TCCTCAGTGCAAGGAACTGTATCAACTGCATCAAAGAGCCATGGACGTGGTGGAC
droAna3	scaffold_13117:1238192-1238353 +		GGCGACGCAATGGCGGTCAGACCAGTTCACAACTACTACGACAAAGGTATTAG----------A----------ACTCCCCAGCA-GGACCGGG----------A----------TATA----------AT----------C----------GTAAA----A---CCTCATATGT--C----------TTC--ATTTCAGTGCAAGAGCTGTATAATTGCATTAAGGAGGCATGGACGCGGTGGCAC
droBip1	scf1800003964425:876557-876714 -		GGCGACGCAATGGCGGTCAGACCAGTTCACAAGTACTACGACAAGCAAGGTATGAT----------A----------GCTCCGCACAATTTCTGGG----------A----------TAT--C----------A----------GTATA----A---CCTCATAAAT--C----------G-TC--ATTTCAGTGCAAGAGCTGTATAATTGCATTAAGGAGGCATGGACGCAGTGGCAC
droKik1	scf1800000299277:434041-434201 +		GGCGACGCAACGGCGGACAGACCAGTTCACAAGTACTACGACAAGCAAGGTGGGTCC----------T----------CCGCA----AGCA----------A----------GGATAC-TGAATAG-TCAATCA----A---T-CAAT--A----A---E----------TTCCTTGTCCAGTGCAAGGAACTGTATCAACTGCATCAAGGAGGCCATGGACGCGGCGGCAC
droFic1	scf1800000454038:201369-201533 +		GGCGACGCAATGGCGGTCAGACCAATTCACAAATACTATACGCGAAGGTAAGTT----------T----------A----------CCAGA---GGAGGGGAATGAGGTCTT----------A----------TT----------T--TGCTGTAAACCAT-C----TGT--C----------TTT--ATGTGCAGTGCAAGGAGCTGTACAATTGCATCAAGGAGGCCATGGACGCGGCGGCAC
droEle1	scf1800000491277:496857-497022 +		GGCGACGCAATGGCGGTCAGACCAGTTCACAAATACTATACGCGAAGGTAAAGT----------T----------CAAGG---GAGTTTCCATAGAGTTTC----------A----------TAGG----------A----------CGTTTAA----CCCTA--CACTAT----------TTT--GTGCCAGTGCAAGGAGCTATACAATTGCATCAAGGAGGCCATGGACGCGGCGGCAC
droRho1	scf1800000779914:5027-5208 -		GGCGACGCAATGGCGGTCAGACACAGTTCACAAATACTATACGCGAAGGTGGGTT----------T----------C--CG----A----GG--TTTT----------A----------TCTTTTGACCCCCAAGGTGCTTAAGGTGTCT----------A----------AC----TTT--A----------AAT----CCAC--GCTAT----------TTCC--ATGTACAGTGCAAGGAGCTGTACAATGCATCAAGGAGGCATGGACGCGGCGGCAC
droBia1	scf1800000299226:448493-448648 -		GGCGACGCAACGGCGGTCAGACCAATTCACAATACTACGACGAAAGGTGGGTCA----------C----------CTGG---G----GGGA----------A----------AA----AT----------AT--GA--TTCCA----C----C----C----GATGACCAACTATTT--CCATGCAGTGCAAGGAGCTGTACAATTGCATCAAGGAGGCCATGGACGCGGCGGCAC
droTak1	scf1800000414452:112935-113098 -		GGCGACGCAATGGTGGTCAGACCAATTCACAATACTACGACGAAAGGTGGGTTT----------T----------CCG---G----A----------A----------AACTG-AGATATGCTGGG----GAT--A----CGATT--C----C----ACC--TTTCCGAT----C----GTCCTTAGTGCAAGGAGCTGTACAACTGCATCAAGGAGGCCATGGACGCGGCGGCAC
droEug1	scf1800000409533:91941-92094 +		GGCGACGCAATGGCGGTCAGACCAATTCACAAATACTATACAGAAAGGTGGGTTT----------A----------ATAGG---G----T----------A----------AAGGTG----------AT--AC----TAT----------C----C----C----GATAACTTACCAATTT--ACGTACAGTGTAAGGAACTGTACAACTTGCATACAAGAGGCCATGGACGCGGTGGCAC
dm3	chrX:14996889-14997059 +		GGCGACGCAATGGCGGTCAGACCAATTCACAAATACTATACGACGAAAGGTGGGTGT----------T----------T--AATTG----------A----------AAGTGAAGTTAAGATAT--AGCCCAT-TA-AGCA----A-----CGAAT--A-----GC--T----------TTTC--CCGTACAGTGCAAGGAGCTGTACAATTGCATCAAGGAGGCCATGGACGCGGCGGCAC
droSim2	x:14160778-14160946 +		GGCGACGCAATGGCGGTCAGACCAATTCACAAATACTACGACGAAAGGTGAGTGT----------T----------T--AGTTG----------TC----------A----------AAGTAAGGATAT--AGCCCAT-CA-AGCA----A-----CCAAT--A-----GC--T----------TTTC--CCGTACAGTGCAAGGAGCTGTACAATTGCATCAAGGAGGCATGGACGCGGCGGCAC
droSec2	scaffold_32:443573-443741 +		GGCGACGCAATGGCGGTCAGACCAATTCACAAATACTACGACGAAAGGTGAGTGT----------T----------T--AGTTG----------TC----------A----------AAGTAAAGATAT--AGCCCAT-CA-AGCA----A-----CGAAT--A-----CTC--T----------TTTC--CCGTACAGTGCAAGGAGCTGTATAATTGCATCAAGGAGGCATGGACGCGGCGGCAC
droYak3	X:9188023-9188204 +		GGCGACGCAATGGCGGTCAACCAATTCACAAATACTATACGACGAAAGGTGGGTGT----------ATTTTATTATTATT--AGTTG----------CA----------A----------TACTTAATTTAT--AGCACAT-CA-AACA----A-----GTTT--A-----GC--T----------TTTT--CCGTACAGTGCAAGGAGCTGTACAATTGCATCAAGGAGGCCATGGAACGAGGTGGCAC
droEre2	scaffold_4690:12015470-12015638 -		GGCGACGCAATGGCGGTCAGACCAATTCACAAATACTATACGACGAAAGGTGGGTGT----------T----------T--TGTTG----------TA----------A----------AACTAAAGATGT--ATCCCAT-CA-AGCA----A-----CGATT--A-----GC--T----------TTTC--CCGTACAGTGCAAGGAGCTGTACAATTGCATCAAGGAGGCCATGGAACGCGGCGGCAC

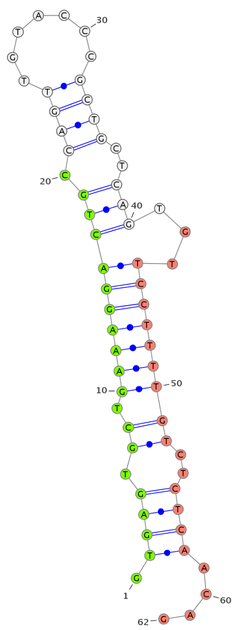
Generated: 09/08/2015 at 07:03 PM

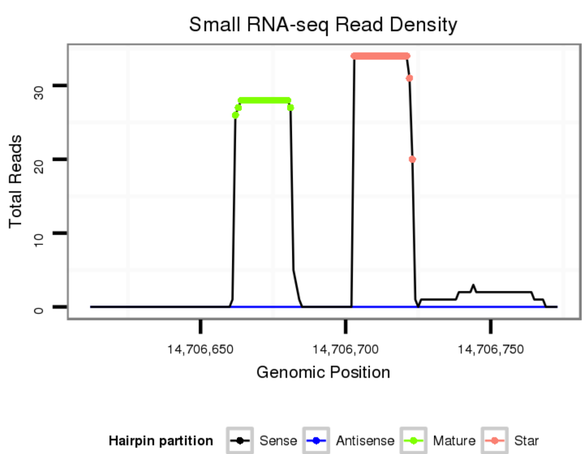
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

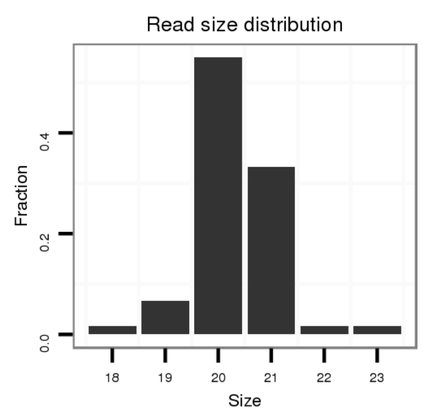
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1555	**scaffold_6500:14706662-14706723 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

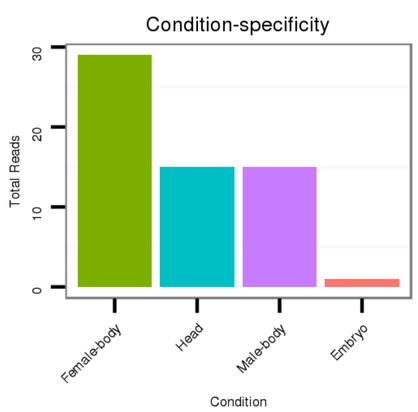
Legend: mature star mismatch in alignment mismatch in read

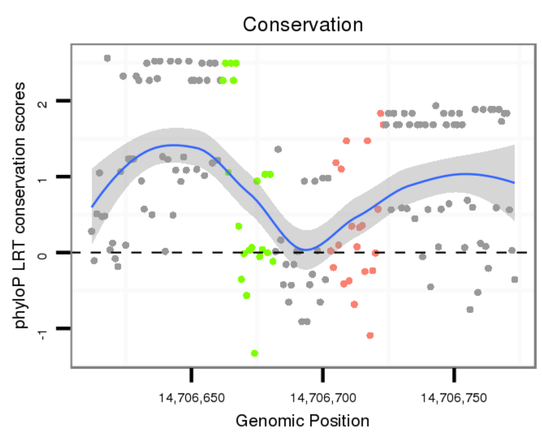
Predicted structure











dmo_1555_annot (-15.0)

Show Alternate Folds

Flybase annnotation

intron [DmojGI17576-in]; CDS [DmojGI17576-cds]; CDS [DmojGI17576-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AACGCCTGAGGGCGAATCCCTTGCTGTATTTGGTTAGTCCGCAAGTTAAGGTGAGTGCTGAAAGGACTGCCAGTTGTACCCGCTGCTCAGTGTTCCTTTTGTCTCTCAACAGGATTGGTTTGTGCGCCGCCAGCTGATGCTGCTCGTGCTCTTTGTCAATAT	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V056 head	V049 head	V110 male body	M060 embryo
**********.((((.((.((((((((((.((((.......)))).))).)))..)))))))))..)))).**********										
.....GTTCCTTTTGTCTCTCAACAGT.....	22	1	1	162.00	162	67	39	30	15	11
.....GTGAGTGCTGAAAGGACTGC.....	20	0	1	21.00	21	2	6	1	12	0
.....GTTCCTTTTGTCTCTCAACAG.....	21	0	1	19.00	19	15	3	0	0	1
.....GTTCCTTTTGTCTCTCAACA.....	20	0	1	11.00	11	8	0	3	0	0
.....GTTCCTTTTGTCTCTCAAC.....	19	0	1	3.00	3	1	1	1	0	0
.....TTCCTTTTGTCTCTCAACAGT.....	21	1	1	2.00	2	2	0	0	0	0
.....GTTCCTTTTGTCTCTCAACAGTT.....	23	2	1	2.00	2	2	0	0	0	0
.....GTTCCTTTTGTCTCTCAACAGA.....	22	1	1	2.00	2	1	0	1	0	0
.....TTGGTTTGTGCGCCGCCAG.....	19	0	1	1.00	1	1	0	0	0	0
.....GGTGAGTGCTGAAAGGACTGCCA.....	23	0	1	1.00	1	1	0	0	0	0
.....GTGAGTGCTGAAAGGACTG.....	19	0	1	1.00	1	0	0	0	1	0
.....GTGAGTGCTGAAAGGACTGCC.....	21	0	1	1.00	1	0	0	0	1	0
.....GTGAGTGCTGAAAGGACTGCCA.....	22	0	1	1.00	1	0	0	0	1	0
.....GTGAGTGCTGAAAGGACTGCCAG.....	23	0	1	1.00	1	1	0	0	0	0
.....TTCCTTTTGTCTCTCAACAGTT.....	22	2	1	1.00	1	1	0	0	0	0
.....GCTGATGCTGCTCGTGCTCTTTGTC.....	25	0	1	1.00	1	0	0	0	1	0
.....TGAGTGCTGAAAGGACTGCC.....	20	0	1	1.00	1	1	0	0	0	0
.....GTTCCTTTTGTCTCTCAACG.....	20	1	1	1.00	1	1	0	0	0	0
.....CGCCAGCTGATGCTGCTCGTGCTCTT.....	26	0	1	1.00	1	1	0	0	0	0
.....GAGTGCTGAAAGGACTGC.....	18	0	1	1.00	1	1	0	0	0	0
.....GTTCCTTTTGTCTCTCAACAGC.....	22	1	1	1.00	1	0	0	0	0	1
.....GTTCCTTTTGTCTCTCAACAGG.....	22	0	1	1.00	1	0	0	1	0	0

Anti-sense strand reads

TTGCGGACTCCCGCTTAGGGAACGACATAAACCAATCAGGCGTTCAATTCCACTCACGACTTTCCTGACGGTCAACATGGGCGACGAGTCACAAGGAAAACAGAGAGTTGTCCTAACCAAACACGCGGCGGTCGACTACGACGAGCACGAGAAACAGTTATA	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_6500:14706612-14706773 +	dmo_1555	AACGCCTGAGGGCGAATCCCTTGCTGTATTTGGTTAGTCCGCAAGTTAAGGTGAGTGCT-------G-AAAGGAC-TGCCAG-------------------TTGTACCCGCTGCTCAGTGT---TC-CTTTTGTC--TCTCAACAGGATTGGTTTGTGCGCCGCCAGCTGATGCTGCTCGTGCTCTTTGTCAATAT
droVir3	scaffold_12723:4017788-4017967 -		AACGCCTCCGGGCGAATCCCTTGCTGTATTTGGTTAGTCCGCAAGTGAAGGTGAGTGTTCCGTTCA-AGAGGG-G------CTTCAGCTCAGCCTAGCCTAGCCGCGGCACTAAATGCTACTTCGATTTATT--TCTGGACAGGATTGGCTGGTGCGACGACAGCTGATGCTGCTCGTGCTTTTGTCAATAT
droGri2	scaffold_15252:3641218-3641273 +		AACGCCTCCGAGCGAATCCCTTGCTGTATTTGGTTAGTCCGCAAGTTAAGGTGAGT--
droWil2	scf2_1100000004521:12227515-12227677 +		AGCGTTTGAAAGCGAATCCCCTGCTGTACTTAGTTAGTCCACAGGTTAAGGTGAGTTTAGATTTCG-AA------------ATTGATTTCCATTCAGAATA-------------------ATATTTTGATCCA-TTTTGTTTCTAGGATTGGTTTGTCCGGCAACAATTGATGCTGTTGGTGTTGATTTTCAATGC
dp5	4_group3:627019-627179 +		AGCGCCTCAAAGCGAATCCCTTGCTGTACCTGGTCAGTCCACAGGTTAAGGTGAGTGTTC------CCGAA-CACTTGATAGTGGGCTGCAT---------------------TCTATTT-CGTCTGTTCTTCTTTCCAGGATTGGTTTGTGCGCCAGCAGCTGGTGCTGCTTGTACTGTTTTTCAATGC
droPer2	scaffold_1:2102837-2102997 +		AGCGCCTCAAAGCGAATCCCTTGCTGTACCTGGTCAGTCCACAGGTTAAGGTGAGTGTTC------CCGAG-CACTTGATAGTGGGCTGCAT---------------------TCTATTT-CGTCTGTTCTTCTTTCCAGGATTGGTTTGTGCGCCAGCAGCTGGTGCTGCTTGTACTGTTTTTCAATGC
droAna3	scaffold_12943:923471-923542 -		TGTCGATATATTTCCCCC---ACAGGATTGGTTTGTGCGCCAACAGCTGATGCTGATTGTCCTGTTTTTCAATGC
droBip1	scf7180000396728:2212778-2212841 +		AACGCCTTCGAGCGAATCCGTTGTTGTACTTGGTCAGTCCACAGGTTAGGGTAAGTATCT------G-AA--A
droKik1	scf7180000302472:1882880-1882936 -		AGCGCCTCAGGGCGAATCCCCTGCTGTATTTGGTCAGTCCACAGGTTAAGGTGAGTC---
droFic1	scf7180000454076:105809-105865 +		AGCGCCTCAAGGCCAATCCCTTGCTGTATTTGGTCAGTCCACAGGTTAAGGTGAGTGC---
droEle1	scf7180000491186:2536824-2536880 -		AGCGCCTCAAGGCGAATCCCTTGCTGTATTTGGTCAGTCCACAGGTTAAGGTGAGTC---
droRho1	scf7180000778085:413465-413527 +		AGCGCCTCAAGGCGAATCCCTTGCTGTATTTGGTCAGTCCACAGGTTAAGGTGAGTGCC-------A-GA------------------------------------A----------------------------
droBia1	scf7180000302408:3626710-3626779 +		TC---ATGTTGTTTCTTATCCAGGACTGGTTTGTGCGCCAGCAACTGATGCTGCTCGTCCTGATTTTCAACAT
droTak1	scf7180000415880:353294-353350 +		AGCGCCTCAAGGCGAATCCCTTGCTGTATTTGGTCAGTCCACAGGTTAAGGTGAGTC---
dm3	chr2L:9549616-9549687 -		TCA-------------------ATGTTGTTTATCCAT---CCAGGACTGGTTTGTGCGCCAGCAGCTGATGCTGCTCGTCCTGATTTTCAACGT
droSim2	2l:9233569-9233625 -		AGCGGCTCAAGGCAAATCCCTTGCTGTATTTGGTCAGTCCACAGGTTAAGGTGAGTC---
droSec2	scaffold_3:4997493-4997549 -		AGCGGCTCAAGGCAAATCCCTTGCTGTATTTGGTCAGTCCACAGGTTAAGGTGAGTC---
droYak3	2L:12231508-12231564 -		AGCGGCTCAAGGCAAATCCCTTGCTGTATTTGGTCAGTCCACAGGTTAAGGTGAGTC---
droEre2	scaffold_4929:10155694-10155799 -		AGCGGCTCAAGGCAAATCCCTTGCTGTATTTGGTCAGTCCACAGGTTAAGGTGAGTCAC-------A-GT-GCAC-CGATAG-------------------TCTAGTTCGCTGGCAAATGC---------------------------------------CTTTGATGTTTTTC-----

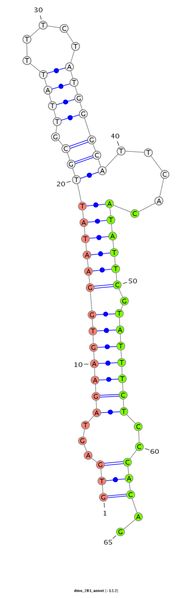
Generated: 09/08/2015 at 07:02 PM

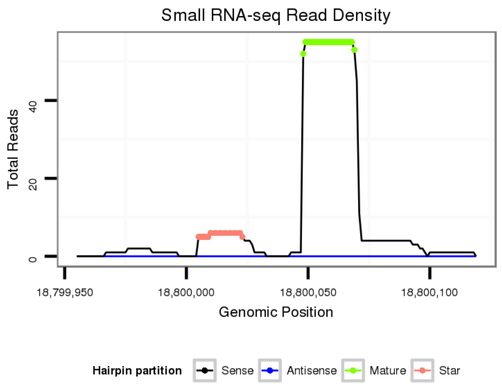
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptp3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

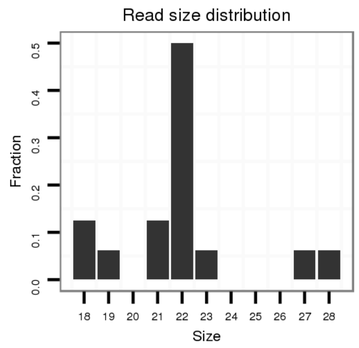
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_283	**scaffold_6540:18800005-18800069 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

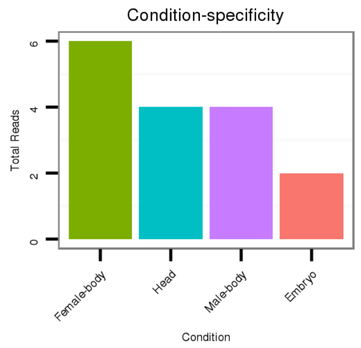
Legend: mature star mismatch in alignment mismatch in read

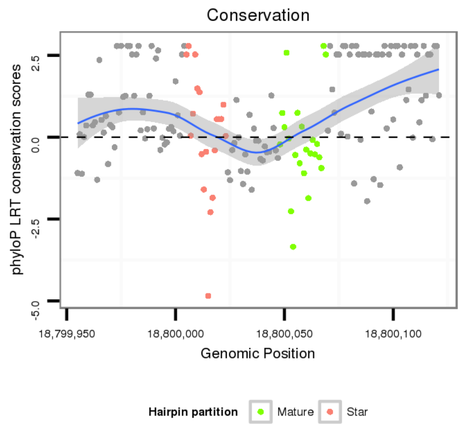
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI24844-in]; CDS [DmojGI24844-cds]; CDS [DmojGI24844-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACTGAGCCACATCTCTGCAATGCTTCCGACAGTAATGAGATTGCCGAAGAGTGAGTAGAAGTGGAATATTGCGTTATTTTCTATGGGCATTCACATATTCGTATTTCTCCCACAGTTATGCCTACGTCTGCGGGGAGCCGGAAGAGCA	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	M060 embryo	V056 head	V049 head	V041 embryo
**********(((...(((((((((((((((((.((((.....)))))))).....))))))).))))))).))))..**********												
..CATATTCGTATTTCTCCCACAGT	23	0	1	34.00	34	10	11	8	2	2	1
..CATATTCGTATTTCTCCCACAGTT	24	0	1	8.00	8	4	2	0	1	1	0
..CATATTCGTATTTCTCCCACAG	22	0	1	7.00	7	5	0	0	2	0	0
..ATATTCGTATTTCTCCCACAGT	22	0	1	3.00	3	2	0	1	0	0	0
..CATATTCGTATTTCTCCCACA	21	0	1	2.00	2	0	0	1	1	0	0
..ATTCACATATTCGTATTTCTCCCACAG	27	0	1	1.00	1	0	1	0	0	0	0
..TATTCAAATATGCGAAGGC	19	0	1	1.00	1	1	0	0	0	0	0
..GTGAGTAGAAGTGGAATAT	19	0	1	1.00	1	0	1	0	0	0	0
..GCTTCCGACAGTAATGAGATT	21	0	1	1.00	1	1	0	0	0	0	0
..TATGCCTACGTCTGCGGGGAGCCGGAAG	28	0	1	1.00	1	0	1	0	0	0	0
..CATATTCGTATTTCTCCCACAGC	23	1	1	1.00	1	0	0	1	0	0	0
..TAGAAGTGGAATATTGCG	18	0	1	1.00	1	1	0	0	0	0	0
..TATGCCTACGTCTGCGGGGAGCCGGAA	27	0	1	1.00	1	0	1	0	0	0	0
..TATGCCTACGTCTGCGGGGAGCCGG	25	0	1	1.00	1	1	0	0	0	0	0
..GTGAGTAGAAGTGGAATA	18	0	1	1.00	1	0	0	0	0	1	0
..GTGAGTAGAAGTGGAATATTGCGTTATT	28	0	1	1.00	1	0	1	0	0	0	0
..CTCTGCAATGCTTCCGACA	19	0	1	1.00	1	1	0	0	0	0	0
..GTGAGTAGAAGTGGAATATTGC	22	0	1	1.00	1	0	1	0	0	0	0
..ATGCCTACGTCTGCGGGGAGC	21	0	1	1.00	1	0	1	0	0	0	0
..GTGAGTAGAAGTGGAATATTGCG	23	0	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

TGACTCGGTGTAGAGACGTTACGAAGGCTGTCATTACTCTAACGGCTTCTCACTCATCTTCACCTTATAACGCAATAAAAGATACCCGTAAGTGTATAAGCATAAAGAGGGTGTCGAATACGGATGCAGACGCCCCTCGGCCTTCTATAAGTTTATACGCTTCCGT	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_6540:18799955-18800121 +	dmo_283	ACTGA-----GCCACA-----TCTCTGCAATGCTTCCGACAGTAATGAGATTGCCGAAGAGTGAGTAGAA--GTGGAATA----------TTGCG----------TT--------ATTTTCTATGGGCAT----------TCA----------CATATTCG---TA---TTT--CTCCCACAGTTATGCCTACGTCTGCGGGGAGCCGGAAGATATTCAAATATGCGAAGGCATC
droVir3	scaffold_13047:15322298-15322454 +		ACTGA-----GCCAA-----GGCGTTTAGTGCTTCCGACAATGATGATGACGCCGAAGAGTAAGTAGAA--ATT-----------------AGA----------TACT---GCCATT--------G--C---ACGCA----------CTATCAA---TG---ATT--CGCCCACAGTTACGGCTAAGTGTGTGGTGAACCAGAGGATATACAAATCTGTGAGGGCATC
droGri2	scaffold_14830:4665758-4665936 -		CTGATCCTCGGCCATA-----TCCTTATAATGTTCTGATGATGAC---AGTGCCGAAGAGTGAGTAACA--TTTAATATA----------TGTGAAT----------TTAT---GGAA----------C-AATTC--AAAAA----------TTA---ACTTC----------TCA--ATT---CT---TTC--TTTCCATAGTTTGTCCTAAGTCTGTGGCGAACCGGAGGATATTCAATTCTGTGAGGGCATC
droWil2	scf2_1100000004902:9935174-9935350 -		ATGGATCCCAGCACACGTTTCAATTCAATGTTCCGATTCAGATGATCAGTTGGAGGAGTAAGTAATCC-CAT-----------------------------------GTCATTTCCTGATG----------CCCAG---GCAAT----------CTATATGA-A-TTCTCATC--ATTCCACAGCTATGCCTAAGTGTGTGGTGAACCGGAGGATATTCAAATTTGTCACGGCATC
dp5	2:7848889-7849047 +		CCCTT------CAGAAGAGTTCAATTCAATGCTTCCGATAGCGCGATACC---GAGGAGTGAGTAACA--TTTTTT----------TCCCA----------TT--------GCTACTTACTTGTCT----------TCA----------ATTACAAT---CG---GT--TTGTGCAGCTATGCCTACGTCTGCGGTGAACCCGAGGACATTCAGATCTGCGACGGCAATC
droPer2	scaffold_0:1674238-1674396 +		CCCTT------CAGAAGAGTTCAATTCAATGCTTCCGATAGCGCGATGATACC---GAGGAGTGAGTAACA--TTTTTT----------CCCCA----------TT--------GCTACTTACTTGTCT----------TCA----------ATTACAAT---CG---GT--GTTGTGCAGCTATGCCTACGTCTGCGGTGAACCCGAGGACATTCAGATCTGCGACGGCAATC
droAna3	scaffold_13340:22360377-22360530 -		GCCCT------CAGAAGGGTTCGATTTTAATGCTTCCGATAGCGCGATGATGCCGAAGAGTAGGTTTCT--CAT-----------------------ACA----------TAGT---ATCTTC--------C--A---GTTTA----------TTTATAT---TG---CT--TCTTTACAGCTACGCCTAAGTATGTGGCGTCCGGAGGATATTCAGATCTGCGACGGCAATC
droBip1	scf7180000396721:794456-794609 +		GCCCT------CAGAAGGGTTCGAATACAATGCTTCCGATAGCGCGATGATGATGCCGAAGAGTAGGTTTCT--A-------------------------AG----------TCCAC---AGACTC--------ATCCT---GTTTA----------TTTAAAAT---TT---CC--TCTTTTTAGCTACGCCTACGTATGTGGCGTCCGGAGGATATTCAGATCTGCGACGGCAATC
droKik1	scf7180000302475:577675-577829 +		GCCCT------CAGAAGGACTTCGAACTCAATGCTTCCGACAGCGATGATGGTT---GCGGAGTAAGTTTAAATGGA-----------------------AAC----------A---TTTATA--------CTTTG---TTCCA----------GTAATTAATCTTC---TCC--ATTCCTAGCTATGCCTAAGTGTGCGGTGAACCGGAGCAGATCAGATCTGCGACGGCATC
droFic1	scf7180000454055:2190860-2191064 +		ACCCT------CAGAAGTTCAATTTACTGCTTCCGATAGCGCGATGATACC------GAGTAAGTTGAA--AAT-----A----------AGAGTTT----------A---TCGAACGGAAA-AGTTC--AAAAA---A-TCCCGAAACTAAATAGTTTCT-ATAACA----TATTTCTAAGGCATTAAATTTATTTGTTT--TTT--TTCCAAGCTATGCCTAAGTGTGCGGCGAATCCAGAAGACATGCAGATGTGCGACGGCAATC
droEle1	scf7180000491280:322812-323069 +		ATTCA-----GCCGGAGGACTTCGAGTTCAATGCTTCCGATAGCGCGATGATACC------GAGTGAGTTTCT--TTG-----------CTAGCTTACACTCC--AAACAAAAATATAACCAAAGTGTC----AGTTTAATTGTAGTCTAAGAC--CAAATTTTTAAACCACATATACTACCCAC--TCTTGCATGTTTTAAATGT----T--T---TATGGTATAATTATTGC--TTT--TTC--TTCTCCTAGCTATGCCTAAGTATGTGGCGGCGAGCCAGAAGACATTCACATATGCGACGGCATC
droRho1	scf7180000779718:14848-15078 -		ACCCT------CAGAAGTTCAATTCAATGCTTCCGATAGCGCGATGATACC------GAGTAAGTTTGT--GCT-----TAATTGCAGCTAGATTAAGCTGGAA----------------TT--------TCTACAATCTTTGTCCAATGGA-C-AATTT--AAGAA--ACATTTTAGGAGC--ATTAGTATATTTTTAAATA----T--T---TATAGTGTAATTATTGA---TT--CCCC--TTCCCCAGCTATGCCTACGTCTGCGGCGAGCCTGAAGACATCAGATCATATGCGACGGCATC
droBia1	scf7180000302113:2532637-2532793 +		GCCGC------AGAACTTCGAGTTCAATGCTTCCGATAGCGCGATGATACC------GAGTAGGTTATT--AGC-----------------------ATA----------A---GAA---TTATTTTA--------TAAAA---AATTT----------TTAAAA--TT---TTCG-CTTCCCTAGTTATGCCTAAGTCTGTGGGGAACCGGACGAACATCAGATCTGCGACGGCAATC
droTak1	scf7180000415712:190040-190197 +		TCGCC------AGAACTTCGAGTTCAATGCTTCCGACAGCGATGATACC------GAGTAGGTTATA--T-------------------------AG----------A---TAGGGGAT-ATATTT-G-------TAAGATCTGT---A----------TTA-AGA---TT---CCTAAATTCTCAGTTATGCCTAAGTCTGCGGGGAGCCGGAAGACATCAGATCTGCGACGGCAATC
droEug1	scf7180000409682:290986-291133 -		ACCCT------ACTTCGAGTTCAATGCTTCCGATAGCGCGATGATACC------GAGTAAGTTTTT--GTT-----------------------AAT----------A---TTAT---ATTTTC--------CACAG---TTTAT----------TTAATAAA---TT---CC--GTTTTAAGTTATGCTTAAGTCTGCGGCAGAGCCAGAAGACATTCACATCTGCGACGGCAATC
dm3	chr3R:22293773-22293919 +		ACCCT------CAGAAGTTCAATTCAATGCTTCCGAGATTAATGCTTCCGATAGCGCGATGATACC------GAGTAAGTTCAT--GCT-----------------------AAG----------A---AAT---GGTATG--------ACCAG---AGTTA----------CTAAATGA---TT---CC--TAT-ATTAGCTATGCTTAAGTTGTGCGGCAGAGCCGGAAGAATCCAGATTTGCGACGGCATA
droSim2	3r:21770114-21770260 +		ACCCT------CAGAAGTTCAGATCAATGCTTCCGATAGTGATGATACC------GAGTAAGTTCAT--ACT-----------------------AAG----------A---AATT---ATTATG--------ACCAG---AGTTA----------GTAAAGA---TT---CC--TTTGAATTAGCTATGCTTAAGTTGTGCGGCAGAGCCTGAAGAATCCAGATTTGCGACGGCATC
droSec2	scaffold_13:1085237-1085383 +		ACCCT------CAGAAGTTCAGGTCAATGCTTCCGATAGCGCGATGATACC------GAGTAAGTTCAT--GCT-----------------------AAG----------A---AATT---ATTATG--------ACCAG---AGTTA----------CTAAAGA---TT---CA--TTTGAATTAGCTATGCTTAAGTTGTGCGGCAGAGCCTGAAGAATCCAGATTTGCGACGGCATC
droYak3	3R:24194555-24194701 -		ACCCT------CAGAAGTTCAGATCAATGCTTCCGATAGCGCGATGATACC------GAGTAAGTTCAT--GGA-----------------------AAG----------A---CATT---GTTTTG--------AACAG---AGTTA----------CTAAATAA---TG---AC--TATTTTAGCTATGCTTAAGTTGTGCGGCAGAGCCGGAAGAATTCAGATTTGCGACGGCATC
droEre2	scaffold_4820:5751883-5752033 -		GCCCT------CAGAAGACCTCGAGATCAATGCTTCCGATAGCGCGATGATACC------GAGTAAGATCAT--AGC-----------------------AGC----------A---AATT---GTTATA--------AACAG---AGTTC----------CTAAATA---TT---TTC--CCAAATAGCTATGCTTAAGTTGTGCGGCGCGCCTGAAGAATTCAGATTTGCGACGGCATC

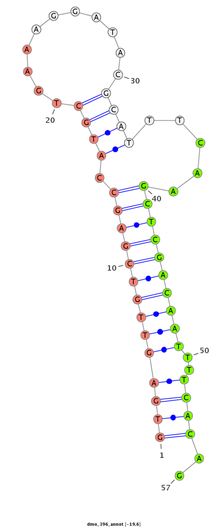
Generated: 08/18/2015 at 04:03 PM

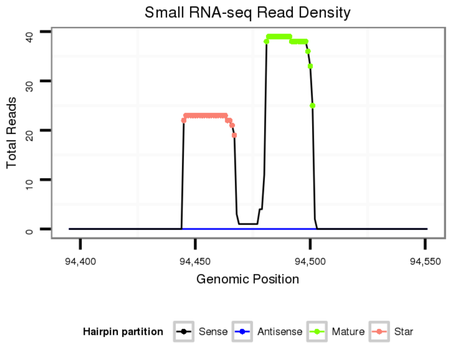
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

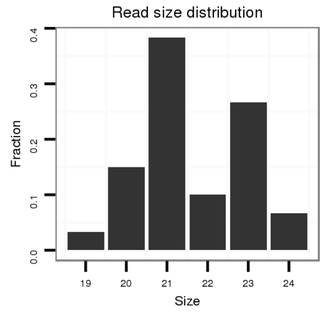
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_396	**scaffold_6308:94445-94501 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

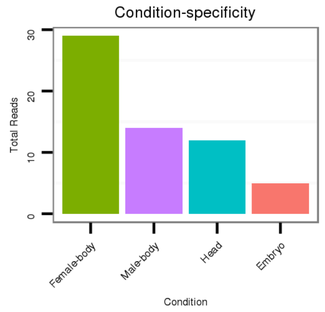
Legend: mature star mismatch in alignment mismatch in read

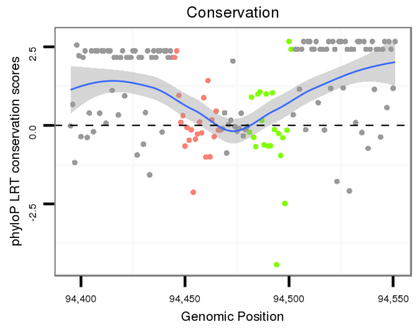
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI11066-in]; CDS [DmojGI11066-cds]; CDS [DmojGI11066-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTCACAGAGCTCATCATTATACCCGTGCGCATAGCCCTCGAGTACTACAGGTGAGTTGTCGAGCCATGCTGAAAGGATACGCATTTCAAGCTCGACAATTTTCACAGGCGCCTGAACGATGCACAGACCAAGACCCGCAAATCGGTGGCCGACAGCA					M046					
(((((((((((((((.((((.....)))).....)))))))))))..)))).	Read size	# Mismatch	Hit Count	Total Norm	Total	female body	M060 embryo	V056 head	V110 male body	V049 head	V041 embryo
..CAAGCTCGACAATTTTCACAGT..	22	1	1	107.00	107	34	30	18	10	13	2
..CAAGCTCGACAATTTTCACAGTT..	23	2	1	25.00	25	9	4	7	3	2	0
..CAAGCTCGACAATTTTCACAGA..	22	1	1	24.00	24	7	1	5	5	5	1
..CAAGCTCGACAATTTTCACAG..	21	0	1	18.00	18	12	1	3	1	1	0
..GTGAGTTGTCGAGCCATGCTGAA..	23	0	1	15.00	15	4	1	1	6	2	1
..AAGCTCGACAATTTTCACAGT..	21	1	1	6.00	6	5	1	0	0	0	0
..CAAGCTCGACAATTTTCACA..	20	0	1	6.00	6	6	0	0	0	0	0
..CAAGCTCGACAATTTTCACAGC..	22	1	1	5.00	5	0	3	1	0	1	0
..TCAAGCTCGACAATTTTCACAGT..	23	1	1	5.00	5	1	1	3	0	0	0
..CAAGCTCGACAATTTTCACAGAAA..	24	3	1	4.00	4	1	1	0	2	0	0
..GTGAGTTGTCGAGCCATGCTGAAA..	24	0	1	3.00	3	1	0	0	2	0	0
..TCAAGCTCGACAATTTTCACAG..	22	0	1	3.00	3	1	0	0	0	2	0
..CAAGCTCGACAATTTTCACAGAT..	23	2	1	3.00	3	3	0	0	0	0	0
..CAAGCTCGACAATTTTCACAGAA..	23	2	1	3.00	3	1	2	0	0	0	0
..TCAAGCTCGACAATTTTCAC..	20	0	1	2.00	2	1	0	0	1	0	0
..TCAAGCTCGACAATTTTCACA..	21	0	1	2.00	2	0	0	1	1	0	0
..CAAGCTCGACAATTTTCACAGG..	22	0	1	2.00	2	1	0	0	1	0	0
..GTGAGTTGTCGAGCCATGCTGA..	22	0	1	2.00	2	0	0	0	2	0	0
..TTTCAAGCTCGACAATTTTCA..	21	0	1	2.00	2	0	1	0	0	1	0
..GTGAGTTGTCGAGCCATGC..	19	0	1	1.00	1	1	0	0	0	0	0
..GTGAGTTGTCGAGCCATGCTG..	21	0	1	1.00	1	0	0	0	1	0	0
..CAAGCTCGACAATTTTCACAGTTA..	24	3	1	1.00	1	0	1	0	0	0	0
..TCAAGCTCGACAATTTTCACAGAA..	24	2	1	1.00	1	1	0	0	0	0	0
..TCAAGCTCGACAATTTTCACAGA..	23	1	1	1.00	1	1	0	0	0	0	0
..TTTCAAGCTCGACAATTTTCACAG..	24	0	1	1.00	1	1	0	0	0	0	0
..CAAGCTCGACAATTTTCAC..	19	0	1	1.00	1	0	0	1	0	0	0
..TGAGTTGTCGAGCCATGCTGAA..	22	0	1	1.00	1	1	0	0	0	0	0
..TCAAGCTCGACAATTTTCACAT..	22	1	1	1.00	1	1	0	0	0	0	0
..GGATACGCATTTCAAGCTCGACA..	23	0	1	1.00	1	0	1	0	0	0	0
..AAGCTCGACAATTTTCACAG..	20	0	1	1.00	1	1	0	0	0	0	0
..TCAAGCTCGACAATTTTCACAGC..	23	1	1	1.00	1	0	1	0	0	0	0
..CAAGCTCGACAATTTTCACAGTA..	23	2	1	1.00	1	1	0	0	0	0	0
..TCAAGCTCGACAATTTTCACC..	21	1	1	1.00	1	0	0	0	1	0	0
..CAAGCTCGACAATTTTCACATT..	22	2	2	0.50	1	0	1	0	0	0	0

Anti-sense strand reads

GAGTGTCTCGAGTAGTAATATGGGCACGCGTATCGGGAGCTCATGATGTCCACTCAACAGCTCGGTACGACTTTCCTATGCGTAAAGTTCGAGCTGTTAAAAGTGTCCGCGGACTTGCTACGTGTCTGGTTCTGGGCGTTTAGCCACCGGCTGTCGT					
(((((((((((((((.((((.....)))).....)))))))))))..)))).	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_6308:94395-94551 +	dmo_396	CTCACAGAGCTCATCATTATACCCGTGCGCATAGCCCTCGAGTACTACAGGTGAGTTGTCG----------AGCC----------ATGCTGAAAGG----------ATACGCA-------TTTCAAGCT-------CGACAA----------T----TTTCACAGGCGCCTGAACGATGCACAGACCAAGACCCGCAAATCGGTGGCCGACAGCA
droVir3	scaffold_12928:4695532-4695716 +		CTAACGAGCTCATTATCATACCCGTGCGCATGGACTCGAGTATACAGGTGAGTTCGGACTGGG----------G---CTGGGGTAGATCTTCTAGGAGT----------AGACTAG---TTAAAGCTTTTCTGTGACCAACGCAC----------G---GAACGCAGGCGCATCAACGATGCGCAGACAAAGACCGCAAATCGGTGGCAGACAGCA
droGri2	scaffold_14853:1590313-1590510 +		CTCACGAATTGATCATTATACCCGTGCGCATGGACTCGAGTATACAGGTGAGTTACAGCATTTCTGTTTGTTGCTGTACAGTCATCAGTCATATTGTCATCTCAAC----------TACTCACTCCTATTCTGA----------------------------------TGTC----------T-----TCTGT-----CTGGCGAGATCGCCTGAACGATGCGCAGACAAAGACCGCAAATCGTGGGCAGATAGCA
droWil2	scf2_1100000004401:788246-788416 -		TTAACAGAATTGATCATTATACCACTGTGCGCATGGACTCGAGTACTACAGGTGAGAGTGG----------AAATGAAAGA----GTGGGAGA----GA-------G----AGAAAG----------AG--AAGAATCAACGTTAT----------ACT-----GTTTC----------G----CTCTTAAGGCGCCTTAACGATGCTCAGACAAAGACCGAAATCTGTGGCAGATAGCA
dp5	XL_group3a:1773132-1773301 +		CTCACGAGCTCATCATCATACCATGTGCGCATGGCCCTCGAGTATACAGGTGAGGTGGCTCCGGC----------TGCCC----------GTCCGAATTGG----------ATAATCAA--TTAACTCCAAGCTGTGTTC----------CG----------T----CTCGTGAGACGCCTAAACGATGCCCAAACCAAGACCGCGAACTCGTTGCCGACAGTA
droPer2	scaffold_52:24206-24375 -		CTCACGAGCTCATCATCATACCATGTGCGCATGGCCCTCGAGTATACAGGTGAGGTGGCTCCGGC----------TGCCC----------GTCCGAATTGG----------ATAATCAA--TTAACTCCAAGCTGTGTTC----------CG----------T----ACCGTGAGACGCCTAAACGATGCCCAAACCAAGACCGCGAACTCGTTGCCGACAGTA
droAna3	scaffold_13117:3616007-3616067 -		AATAC----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----TTCAGACGCCTAACGATGCCAGACCAAGACCCGCAACTCGTGGCCGACAGCA
droBip1	scf7180000396499:56927-57091 -		CTCACGAACTGATCATCATACCCGTGCGCATAGCCCTCGAGTATACAGGTGAGTTTGG----------CT---ACTAGGCGT----------ATAC----------TTAATATTACGTATACTTATTATTGTAAACT----ATTTCAGACGCCTGAACGATGCCAGACCAAGACCCGCAACTCGGTGGCCGACAGCA
droKik1	scf7180000302621:7385-7584 +		CTGACGAACTCATCATTATTCCCGTGCGCATAGCTTCGAGTATACAGGTGAGAAAGGGGAGA----------TTCG----TATAAATTAT----------AGAAAATTAA---ATTAATTTAAATTTAATAAATA---ATAATATTT----------AT--TTTA----------A----TTGATTTACCT----------TTT----GTTCGTGAGACGCCTGAACGATGCCAGACAAAGACCCGCAAATCGTGGCCGACAGCA
droFic1	scf7180000454050:601412-601471 -		ACAA----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----TTCAGACGCCTGAACGACGCCAGACGAAGACCCGCAACTCGGTGGCCGACAGCA
droEle1	scf7180000490546:1224959-1225011 +		C----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----AGCGCCTGAACGATGCCAGACGAAGACCGCAAACTCGGTGGCCGACAGCA
droRho1	scf7180000779914:773425-773481 +		T----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----TCCAGCGCCTGAACGATGCCAGACGAAGACCGCAAACTCGGTGGCCGACAGCA
droBia1	scf7180000298389:299695-299754 -		CTCACGAACTCATCATCATACCCGTGCGCATGGCCCTGAGTACTACAGGTACGCATGC----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----------
droTak1	scf7180000415192:261409-261461 +		C----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----AGCGCCTGAACGATGCCAGACCAAGACCGCAAATCGGTGGCCGACAGCA
droEug1	scf7180000409110:1106987-1107205 -		CTCACGAACTCATCATCATACCCGTTGCGCATGGCTTCGAGTATACAGGTAATAAAGTCTC----------TCA----TATGCATTAT----------ATATCTTCAAGGAGGCATTTCCAATTCCATAAATCTAAGGAATCTTTCCATACTTTCATTATGTAA----------T----------A----TCCATTTCCTT----------TTTATACAAATCAGCGCCTGAACGATGCCAGACAAAGACCGCAAATCGGTGGCCGACAGCA
dm3	chrX:12687996-12688177 -		CTAACGAGCTCATCATCATACCCGTGCGCATGGCCCTGAGTACTACAGGTAC----------T----CTCGAGCCATGCTGAA----------TATTCATTTCTAATGCGAACTTGTGGC----AG----------A----ACACATTT----------TA--TTTAATT----------T----ATCTAATTAATTTTTGTGCCC----------C----ACTTCAGCGCCTGAACGATGCCAGACAAAGACCGCAAATCGGTGGCCGACAGCA
droSim2	x:12045657-12045831 -		CTAACGAGCTCATCATCATACCCGTGCGCATGGCCCTGAGTACTACAGGTAAC----------T----CTCGAGCCATGCTGAA----------TACTCATTTCTAATGCGAACTTGTGGC----AG----------A----ACATTT----------TG--TTAATTTTCGTATA----------AT-CTTA----------T----CAATCAGCGCCTGAACGATGCCAGACAAAGACCGCAAATCGGTGGCCGACAGCA
droSec2	scaffold_21:442391-442561 +		CTAACGAGCTCATCATCATACCCGTGCGCATGGCCCTGAGTACTACAGGTAAC----------T----CTCGAGCCATGCTGAA----------TACTCATTTCTAATG--CTTGTGGC----AG----------A----ACATGT----------TG--TTAATTTTCGTATA----------AT-CTTA----------T----CTCATCAGCGCCTGAACGATGCCAGACAAAGACCGCAAATCGGTGGCCGACAGCA
droYak3	X:6968526-6968577 -		CTCACGAGCTCATCATCATACCCGTGCGCATGCCCTCGAGTACTACAGGT----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----CTCGAGCCATGCTGAA----------T----------
droEre2	scaffold_4690:14159263-14159427 +		CTCACGAGCTCATCATCATACCCGTGCGCATGCCCTCGAGTACTACAGGTAGC----------T----CTCGAGCCATGCTGAA----------ACTCATTTTACTGCACACT----------T----CTCGAGCCATGCTGAA----------T----GGCCCCGTCCTACATATTCTCCTCCCTGTC--TT----GCTCAGCGCCTGAACGACGCCAGACGAAGACCGCAAACTCGGTGGCCGACAGCA

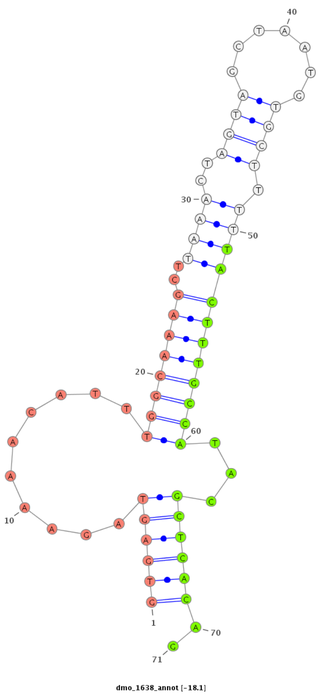
Generated: 09/08/2015 at 07:03 PM

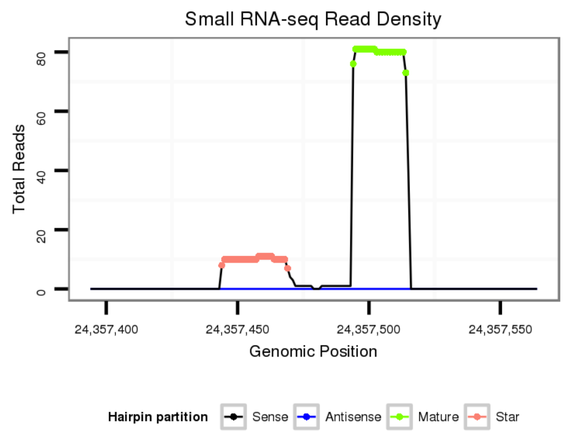
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

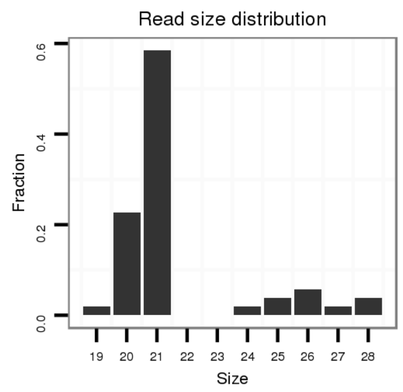
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1638	**scaffold_6500:24357444-24357514 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

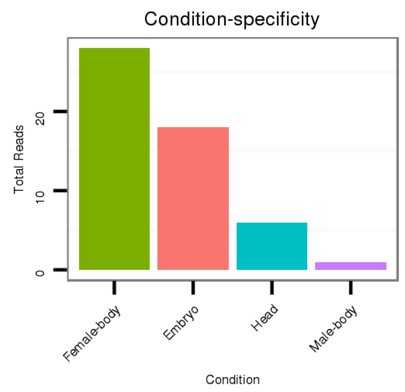
Legend: mature star mismatch in alignment mismatch in read

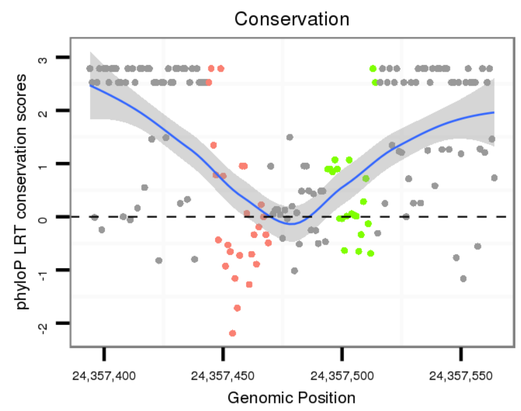
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI18037-in]; CDS [Dmoj\GI18037-cds]; CDS [Dmoj\GI18037-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACCGAAATGAATGCCGAGTCCTTTTTCGCGCGATGGAAGAATCTCAGCGGGTGAGTAGAAAACATTTGGCAAAGCTTAAACTAGTAGCTAATGTGCTTTTTACTTTGCCATACGCTCACAGCGAACAGCAGCGAGCGCAAAAGGTATTCAAAGCCGCGCAGCCGCTGGACT	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V056 head	V049 head	V041 embryo	V110 male body
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..TACTTTGCCATACGCTCACAGT.....	22	1	1	151.00	151	86	30	11	12	11	1
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..TACTTTGCCATACGCTCACAGC.....	22	0	1	39.00	39	38	1	0	0	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..TACTTTGCCATACGCTCACAG......	21	0	1	29.00	29	11	14	1	1	2	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..TACTTTGCCATACGCTCACAGA.....	22	1	1	28.00	28	16	10	1	0	1	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..TACTTTGCCATACGCTCACA.......	20	0	1	7.00	7	1	3	1	2	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..ACTTTGCCATACGCTCACAG......	20	0	1	5.00	5	0	5	0	0	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..ACTTTGCCATACGCTCACAGT.....	21	1	1	4.00	4	2	2	0	0	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..............................GTGAGTAGAAAACATTTGGCAAAGCT.....	26	0	1	3.00	3	3	0	0	0	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..............................GTGAGTAGAAAACATTTGGCAAAGC......	25	0	1	2.00	2	0	1	1	0	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..............................TACTTTGCCATACGCTCACAC......	21	1	1	2.00	2	2	0	0	0	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..............................GTGAGTAGAAAACATTTGGCAAAGCTTA....	28	0	1	2.00	2	0	1	0	0	0	1
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..............................TGAGTAGAAAACATTTGGC.....	19	0	1	1.00	1	0	1	0	0	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..............................TTTGCCATACGCTCACAGT.....	19	1	1	1.00	1	1	0	0	0	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..............................GTGAGTAGAAAACATTTGGCAAAGCTT....	27	0	1	1.00	1	1	0	0	0	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..............................ACTTTGCCATACGCTCACAGA.....	21	1	1	1.00	1	0	1	0	0	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..............................TACTTTGCCATACGCTCACAGTC....	23	2	1	1.00	1	0	1	0	0	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..............................TACTTTGCCATACGCTCACAA.....	21	1	1	1.00	1	1	0	0	0	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..........TAATGTGCTTTTTACTTTGCC.....	21	0	1	1.00	1	0	1	0	0	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..............................TGAGTAGAAAACATTTGGCAAAGC......	24	0	1	1.00	1	0	1	0	0	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..............................TACTTTGCCATACGCTCACAGTT....	23	2	1	1.00	1	1	0	0	0	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..............TTTGGCAAAGCTTAAACTAGT.....	21	0	1	1.00	1	0	1	0	0	0	0
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..............................TACTTTGCCATACGCTCACCAT.....	22	3	2	0.50	1	0	0	1	0	0	0

Anti-sense strand reads

TGGCTTTACTTACGGCTCAGGAAAAAGCGCGCTACCTTCTTAGAGTCGCCCACTCATCTTTTGTAAACCGTTTCGAATTTGATCATCGATTACACGAAAAATGAAACGGTATGCGAGTGTCGCTTGTCGTCGCTCGCGTTTTCCATAAGTTTCGGCGCGTCGGCGACCTGA	Read size	# Mismatch	Hit Count	Total Norm	Total	V041 embryo
....(((((((.........(((((((((..((((..((((.......)))).)))))))))))...)))))))..TACTTTGCCATACGCTCACAT.....	22	0	1	3.00	3	3

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6500:24357394-24357564 +	dmo_1638	ACCGAAATGAATGCCGAGTCCTTTTTCGCGCGATGGAAGAATCTCAGCGGGTGAGTAGA-A--AA----CATTTGGC--AAAGCTTAAACTAGTA---GCTAAT----------GTG----------CTTTTTACTTTGCC-A-TA-CGCTCACAGCGAACAGCAGCGAGCGCAAAAGGTATTCAAAGCCGCGCAGCCGCTGGACT
droVir3	scaffold_12963:18811681-18811858 -		ACCGAAATGAATGCCGAGTCATTTTTAGCACGATGGAAGAATCTCAGCGGGTGAGTAACCAAC-CAAACGGTTTGAT--CAAGTATCAAAAAGTA-TACCTAAT----------GCTTTTACTTTGCAATCA-CACCACACGCGAACAGCAGCGGTCGCACGAAGGTGTTCAAGGCCGCGCAGCCGCTGGATT
droGri2	scaffold_15252:6728174-6728347 -		ACCGAAATGAATGCCGAGTCCTTCTTTGCACGATGGAAAATCTCAGCGGGTGAGTAATTGCC---TC----A---------CAACAACTA-TAASA---------AAAT---CTTATCCTTGTTTCTTTGGTTGTGC------T---CC-A-CA-CACACACAGCGAACAGCAACGGTCGCAAAAGGTTTTAAGGCGGCACAGCCGCTGGATT
droWil2	scf2_1100000004585:2794801-2794974 +		ACTGAAATGAATGCTGAATCCTTTTTTGCGCGATGGAAAAATCTCAGCGGGTAGTAGCGC--TAGAACT----C---------TTTAAACG---ATCC-------CA-TACTAATCT----A---TATTATTG---C---TACTTCAAA-A-CCAACCAAAAAGAGAACACAAAGATCCAGAAGGTGTTCAAGGCTGCTCAGCCACTTGATT
dp5	4_group3:1224020-1224182 +		ACCGAAATGAATGCCGAGTCCTTCTTTGCCGATGGAAGAACCTAAGCGGGTAAATAGTG--CCGCTG--------CTCGA----------TGA--ATG---------AATGA----------ATAAAT-TAATGAAAC---ACTGT---CC----------T---C---------T---T---TTTAGGAACAACAACGATCACAGAAAGTGTTCAAGGCTGCCAGCCGCTGGATC
droPer2	scaffold_1:2694845-2695003 +		ACCGAAATGAATGCCGAATCCTTCTTTGCCGATGGAAGAACCTAAGCGGGTAAATAGTG--CCGCTG--------CTCGA----------TGA--ATG---------AATGA----------ATAAAT----------TAATGACTGT---CC----------T---C---------T---T---TTTAGGAACAACAACGATCACAGAAAGTGTTCAAGGCTGCCAGCCGCTGGATC
droAna3	scaffold_12943:4844247-4844407 +		ACCGAAATGAATGCAGAATCCTTCTTTGCCGATGGAAGAATCTCAGCGGGTATATTCA-G--AT----AATTCGA---------------------ATGTGTTTTATTCCTCA----------A---TTAC---------CA-TAATAATCT----------C---T---------T---T---CTTTAGGAGCAACAACGGCACAGAAAGTGTTCAAGGCTGGCCAGCCGCTGGATC
droBip1	scf7180000395654:190351-190510 -		ACCGACATGAATGCAGAATCCTTCTTTGCCGATGGAAGAATCTCAGCGGGTATATACA-A--GGATATT---CT---------------------TTATTTTGTTCTTGA----------G---TTAC---------TA-TATAATCT----C----------T---C---------T---T---TTTAGGAGCAACAACGGCACAGAAAGTGTTCAAGGCTGGCCAGCCGCTGGATT
droKik1	scf7180000302270:752039-752196 +		ACAGAGATGAATGCCGAGTCCTTCTTTGCCGATGGAAGAATCTAAGCGGGTAAATATA-T--ACAAAT-----T---------------------CCTTGAAAATGATTAGATTTAATCAGTT---A--T----TA----------C---T---------T---T---TTGCAGCGAACAACAACGGTCACAGAAAGTGTTCAAGGCGGCAGCCGTTGGATT
droFic1	scf7180000453904:679650-679806 -		ACTGAAATGAATGCCGAATCCTTCTTTGCGCGATGGAAGAATCTGAGCGGGTAACTGAA-A--GGGTTG-----T---TCAT----------T---------AGAGTGCTAA----------GTAC----------C-TACTAATTG---CT----------T---A---------T---T---ATTCAGAGAACAACAACGGTCACAGAAAGTGTTCAAGGCTGGTCAGCCACTGGATT
droEle1	scf7180000491026:427350-427510 +		ACCGAAATGAATGCCGAATCCTTCTTTGCCGCGATGGAAGAATCTAAGCGGGTAATTAGACA--GGGTTT-----CTTCTGGAATTTCGGCTTGTG---------------------AATT---------AA-TGTCAATT----------T---A---------T---T---TTTCAGGGAACAACAACGGTCACAGAAAGTGTTCAAGGCAGCCAGCCACTGGATT
droRho1	scf7180000779917:254791-254943 +		ACCGACATGAATGCCGAATCCTTCTTTGCGCGATGGAAGAATCTAAGCGGGTAATTAAATA--AGTTTT-----C---------------------TTTCAAAA-ATACTG----------AATTAATTT---GGT----------T---T---------T---T---CTTTAAGGAACAACAACGGTCCCAGAAAGTGTTCAAGGCAGCCAGCCCCTGGATT
droBia1	scf7180000302261:3431717-3431867 +		ACCGACATGAATGCCGAATCCTTCTTTGCACGATGGAAGAACCTCAGCGGGTAACTAAA-A--ACTTGC-----C---------------------TCCTAA---GCATTC----------GG-TATTAAGTG---TG----------T---A---------T---T---CTTTTAGGAACAACAACGTTGACAAAAAGTGTTCAAGGCCGCCAGCCGCTGGATT
droTak1	scf7180000413017:107758-107909 +		ACCGACATGAATGCCGAGTCCTTCTTTGCGCGATGGAAAAATCTAAGCGGGTAACTAGTT--GGACT---------------------TTCCAAAA-GTATTC----------GG-TATTAACTGT---TG----------G---T---------T---T---TTCGAGCGAACAACAACGGTCACAGAAAGTGTTCAAGGCTGCCAGCCACTGGATT
droEug1	scf7180000409554:1138558-1138709 -		ACAGAGATGAATGCCGAATCATTCTTTGCGCGATGGAAGAATCTAAGCGGGTAAGTAAA-A--GGTTC-----T---------------------TTACGGAA-ATGTTC----------AA-TATTAATTT---TA----------T---A---------T---T---TTGTAGGAGCAACAACGGTCACAGAAAGTGTTCAAGGCAGACAGCCACTGGATT
dm3	chr2L:409687-409839 -		ACCGAAATGAATGCGAATCATTCTTTGCACGATGGAAGAACCTAAGCGGGTATTAATA-A--AGGTGT-----C---------------------TTTTGATA-ATATTC----------AA-TATTAATTG---TG----------C---A---------T---T---TTGTAGTGAACAACAACGGTCACAGAAAGTGTTCAAGGCTGGCACAGCGACTGGATT
droSim2	2L:382441-382593 -		ACCGAAATGAATGCTGAATCATTCTTTGCACGATGGAAGAACCTAAGCGGGTATTAATA-A--AGGTGT-----C---------------------TTTTGATA-ATATTC----------AA-TATTAATTG---TG----------C---A---------T---T---TTGTAGTGAACAACAACGGTCACAGAAAGTGTTCAAGGCTGGCACAGCCACTGGATT
droSec2	scaffold_14:393508-393660 -		ACCGAAATGAATGCTGAATCATTCTTTGCACGATGGAAGAACCTAAGCGGGTATTAATA-A--AGGTGT-----C---------------------TTTTGATA-ATATTC----------AA-TATTAATTG---TG----------C---A---------T---T---TTGTAGTGAGCAACAACGGTCACAGAAAGTGTTCAAGGCTGGCACAGCCACTGGATT
droYak3	2L:393439-393592 -		ACCGAAATGAATGCTGAATCTTTCTTTGCACGATGGAAGAACCTAAGCGGGTATTAAA-A--CGGTGT-----C---------------------TTTTGATA-ATTTTC----------AATTATTAATTG---TG----------T---A---------T---T---TTGTAGTGAGCAACAACGGTCACAGAAAGTGTTCAAGGCTGGCCAGCCACTGGATT
droEre2	scaffold_4929:461122-461274 -		ACCGAAATGAATGCTGAATCATTCTTTGCACGCTGGAAGAACCTAAGCGGGTATTTAAA-A--AGGCGC-----C---------------------TTTCGATC-ATTTTC----------AA-TATTAATTG---TG----------T---A---------T---T---TTGTAGTGAGCAACAACGGTCACAGAAAGTGTTCAAGGCTGGCCAGCCCCTGGATT

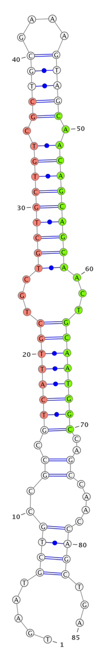
Generated: 09/08/2015 at 10:36 PM

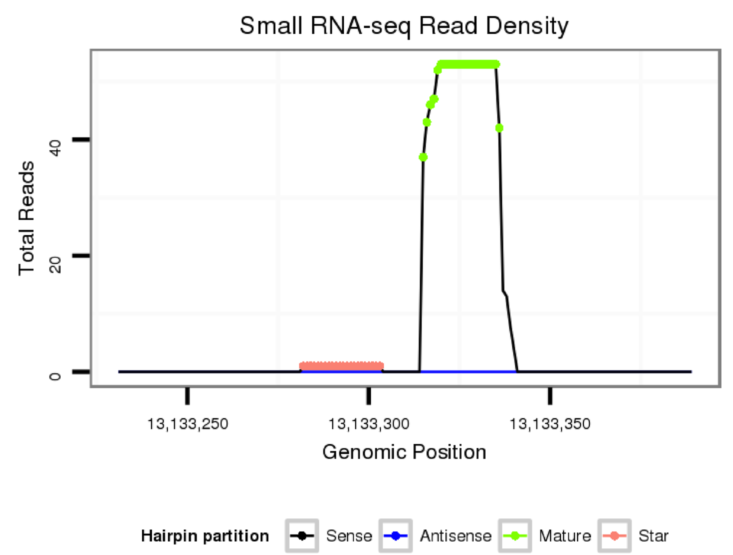
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

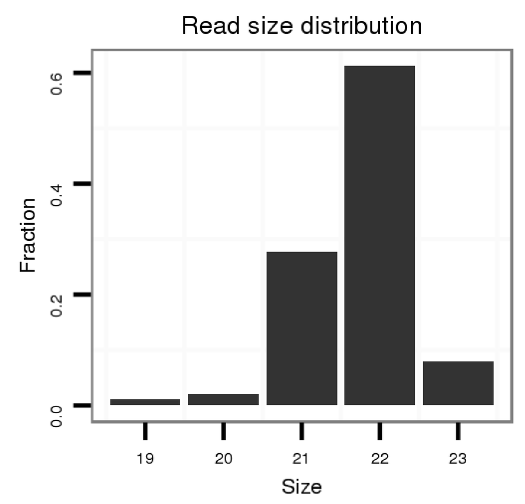
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_124	**scaffold_6473:13133281-13133339 +**	**confident-exception**	**Mirtron**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

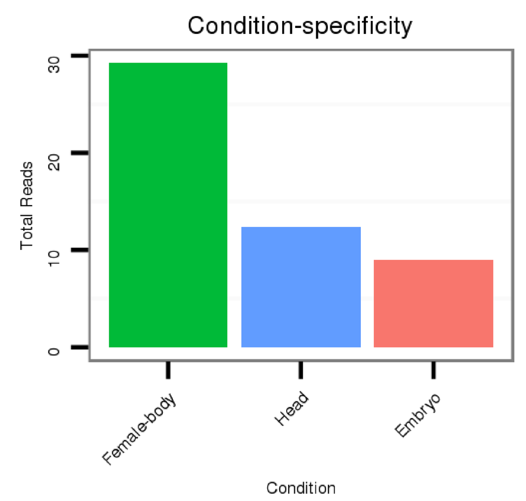
Legend: mature star mismatch in alignment mismatch in read

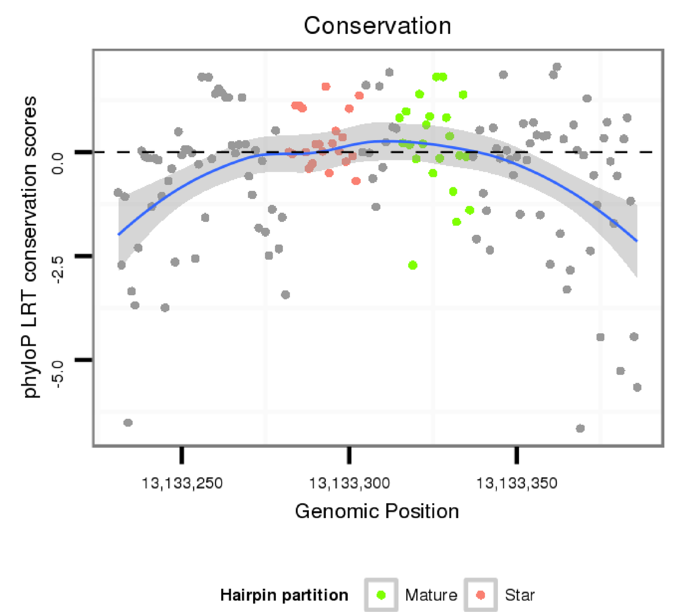
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
(CTG)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

ACTGCCAGCTGCGTTCGTTTAGTGAGTTTGAATGAATGAATGCTGCCGCCGTCATTGCTGCTGCTGCTGTCGCTGCGAAAGTAGCAACAGCAGCAACTGCAATGGCCAGCCAACCAGCTGATAACAATAATAATATTAATAACAAGAATCATAATAGTT ************************************.....((((..((.((((((((...(((((((((.(((((....))))).)))))))))...))))))))..))....))))...**************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V056 head	V049 head	M060 embryo	V110 male body	V041 embryo
....CAACAGCAGCAACTGCAATGGC...	22	0	1	26.00	26	14	4	3	5	0	0
....CAACAGCAGCAACTGCAATGG..	21	0	1	11.00	11	8	1	2	0	0	0
....AGCAGCAACTGCAATGGCCAGC...	22	0	1	4.00	4	2	1	1	0	0	0
....AGCAGCAACTGCAATGGCCAGT...	22	1	1	4.00	4	0	1	0	1	2	0
....CAGCAGCAACTGCAATGGCCAGT...	23	1	1	3.00	3	0	1	2	0	0	0
....AACAGCAGCAACTGCAATGGCCA..	23	0	1	3.00	3	2	0	0	1	0	0
....AACAGCAGCAACTGCAATGGC..	21	0	1	2.00	2	2	0	0	0	0	0
....ACAGCAGCAACTGCAATGGCCA..	22	0	1	2.00	2	0	0	0	1	0	1
....CAGCAGCAACTGCAATGGCCAG..	22	0	1	1.00	1	0	1	0	0	0	0
....AACAGCAGCAACTGCAATGGCC...	22	0	1	1.00	1	0	0	0	1	0	0
....GCAGCAACTGCAATGGCCAG..	20	0	1	1.00	1	1	0	0	0	0	0
....ACAGCAGCAACTGCAATGGCCAG..	23	0	1	1.00	1	1	0	0	0	0	0
....TCATTGCTGCTGCTGCTGTCGC..	22	0	1	1.00	1	0	1	0	0	0	0
....AGCAGCAACTGCAATGGCCAG..	21	0	1	1.00	1	1	0	0	0	0	0
....CAACAGCAGCAACTGCAATGGCA..	23	1	2	1.00	2	1	1	0	0	0	0
....CAACAGCAGCAACTGCAATGGT...	22	1	3	0.67	2	0	0	1	1	0	0
....CAACAGCAGCAACTGCAATGGCT..	23	1	2	0.50	1	0	1	0	0	0	0
....ATTGCTGCTGCTGCTGTCG..	19	0	3	0.33	1	0	0	1	0	0	0
....AGCAGCAACTGCAATGGCCAGAG..	23	2	3	0.33	1	0	1	0	0	0	0
....AACAGCAGCAACTGCAATGGCA..	22	1	3	0.33	1	0	0	1	0	0	0
....CAACAGCAGCAACTGCAAT..	19	0	4	0.25	1	1	0	0	0	0	0

Anti-sense strand reads

TGACGGTCGACGCAAGCAAATCACTCAAACTTACTTACTTACGACGGCGGCAGTAACGACGACGACGACAGCGACGCTTTCATCGTTGTCGTCGTTGACGTTACCGGTCGGTTGGTCGACTATTGTTATTATTATAATTATTGTTCTTAGTATTATCAA *************************************.....((((..((.((((((((...(((((((((.(((((....))))).)))))))))...))))))))..))....))))...**************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V056 head
....CGACGACGACGACAGCGACG...	20	0	20	0.05	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6473:13133232-13133387 +	dmo_124	CTG-----------------------CCAGCTGCGT-T------CG-TT-TAGTG-----AGTTT----------GAATG--AATGAATGCTGCCG---------------------------------------CCGTCATTGCTGCT-GC------------------------------------TGC---TGTCGCT---------GC--GAA------------------AG------TAGCAACAGC--AGCAACTGCAATGG-------------------CCAGC-CAACCAGCTGA---------------------T---A--ACAATAATAAT--ATTAA-T---AACAA-------GAATCATAA----TAG
droVir3	scaffold_12970:2289323-2289458 -		CTG-----------------------CCAGCTGCGT-T------TA-TCT-TGTG-----AGTTT----------------GAATGAAT-TG--C----C--------G---------CT--GCTGCTGCCGCTGCCAACAACAAC-----------------AA------------------C------------------ACAGCAGCAGCAGCAGCAGCAGCAG--CA----------TTTTCAA-------------------------------ACA-----------G---C--------ATAAT-A---AAAAA-------CAATTCCAA----AAA
droGri2	scaffold_15203:632680-632799 +		CTG-----------------------TCAGCTGCGT-T------GG-TTTTGTG-----AGTTT----------------GAATGAAT-TGCTTATGTTGCTGC--TGCCTAT---------G------------------------------------CAAAT--------------------G------ATAGAAACCAT-------------------------------CAAGC-CATCCAGCTAA---------------------T---A--CC--AACAA-C---AATTC-------GAATTATGA----TTT
droWil2	scf2_1100000004729:2158926-2159078 +		TTT-----------------------TTTTTTGTTA-T------AT-TTTTGTTTGTTGTTTTT-----TAATA---A-----------TTT----------GTTGTTGTGTGAAGTAGCAGCAGCA-------------GCAGCAGTCGCCGCCAAC---------------------------------AAACCGAC-----------------------------AACACCA-------------------GCAGCA----------------GCAGCAGCG---GTAGAATAAA--ACAACAAA--A--AA-T----AGC-------AAATCAAAA----TGG
dp5	2:16031730-16031850 +		CTT-----------------------CCGACTTGGG-GGCC----CCTTAAAC-----TGT-------------------TTGCATT---G--TTGTTG------------------------------------GTGGCGTTGCTCCA-GC---------------------------------TGCTCCTGT--TTGCTGTGG---GCTGC-TTGCCCG-CTGC------A-------------T---T--ACAATTAC--AA-T----A-------CAATTAGAA---AAGT
droPer2	scaffold_14:1642370-1642541 -		GTT-----------------------TGTGC------ATGGGTGA-GTGCAT----TGCGTGT------AA-----------------TTGCTGTGCTAACGGTAAAT-------------AAATGAAAAGCACCGCTAAATGT---------GCTGCTGCGAGAAACAACAA---CAAC----------AACAACAACAGCTGT---AAACATAGTG---TCATC-TCACTCG-GAAACA-CACA-------ACA-----------------AC---AACAA-C---AACAA-------AAA-ACCAA----ACA
droAna3	scaffold_13337:10613270-10613386 -		AAT-----------------------GA--------------------------------------GAATGGAC-------------------------------------TATCAAATGCCGCCG------------------------------------CCAGCATTGGCGCT---A-------------A------CAC------------------A------GCAGCAGCAACAGCAACAGCA------------------------------------C----GGCCTGC------A---------------ACATCAACAAA--ATCAA-CTGCAATTG------CTG-CACAA----TGT
droBip1	scf7180000395565:14530-14628 -		TG---CTGTTG------------------------------------CTGAGATTGCTGCT-GC------------------------------------TGCTGCTGT-T---------GC-------------------------------AGCACCT---GATTCTGCA---GATCCCACTGAA--A--AGCATGGTAAG--GTTCA-G---TACCA-------GGATCGGGA----AAG
droKik1	scf7180000302274:149216-149421 -		CAT-----------------------TTGGC------GCATG--T--------------------------------GAATGTGAATGCAGCAGCGGCAGTGGTGGCTGTGGCAGCC------AACAA-------CC----T--------GCA-----------------ACAGCAG--------------------------C----------------AGC--------------------------------------AGC--------------AACTTGCCACCGGCAACAA----------CAGCAA-----------------------------CAC-CAGTCCCGG-CAGC------AACA---------------------ATAACAACAACATACTCAATCACAACAATCTCAATATCATTATCAATAACCATAATAATAGTAA-C---AATAA-------TAATAACAA----CAA
droFic1	scf7180000454065:146265-146394 -		TGA---ATGTGAATGCGGCCGCCGCGGTGGTGGCAGTTGCAGCC------AACAA-------CC----T--------GC--------AAC---ATGCCAACAGCA--------------ACACCAGCACGGG-----------------AAA-CACCCCGG-CGGC------AACA---------------------ACAATAAT--AATAA-T---AACAA-------CAATAATAA----TAA
droEle1	scf7180000491193:3097467-3097635 -		CAT-----------------------CTGGC------GCATG--T--------------------------------AAATGTGAATGCAGCCGCTGCTGTGGTGGCAGTAGCAGCC------AACAA-------CC----T--------GCA--A-------------------------------------CAGCAACAGCAGCAGCAGC--AACATGCCAACAGCA--------------ACAACAGCACGGG-----------------CAA-CAGTCCAGG-CAGC------AATA---------------------ATAATAATAACATA---CTCAA-T---CACAA-------CAATCTCAA----T-A
droRho1	scf7180000777610:21366-21514 -		CTG-----------------------AAAACAGCGG-T------GA-CCTTAGCC-----AGTCTAAGCGAGATA---GC----C--------A---------CTGCACGCCAGCAGCAG--------------------------------C-----------------AGC---AG--------C----------------ACAGCAGCAGCAACAACAGCAGCAGCAG---CA----------ATTGCTG--------------------------GCGCTGCA------GCA---GCA-ACA--ACAACAGA---A--------ACTG-------C--CCACAAGGATAAT
droBia1	scf7180000302428:10378018-10378118 -		GCC-----------------------G--TCAA-------CG----T--------A---CAG-----------------------CAAG--TTTCGCT---------GC--AGC------------------AA------CAGCAACAGC---AGCAACAGCAGAT---------------------CTTC----------------T---TAACCA---------G----------------------------------CCAAATGCTGGTGG-G---AACAT-------CAACCACAA----TGA
droTak1	scf7180000414425:216417-216586 -		GTG-----------------------CAAAGAGAGA-G-----------------------AGAGATAGAA---G--TAC-----------------ACAACGTCAGCG----------------AT------AC---------A---GTCGAACTTCTTTCTGCCGCTTCA-CCGTTGACAAACCAGCCCAAGGGATTAAGACCCTCAT--TTACCAA------CTACAT--TGGCCAAA-CCACTTGTTG----------------GTATAG--CAAA---ATGGA-C---CAAAA-------AAAATAGGA----CAG
droEug1	scf7180000409524:820792-820946 +		CAT-----------------------TTGGC------TCATG--T--------------------------------GAATGTGAATGCAGCAGCGGCTGTGGTGGCTGTGGCAGCC------AACAG-------CC----T--------GCA--GC---AGC--------------AACATGCCAATGGCAACAGC----------AACGGAACGGG------------------CAA-CAGTGCCGG-CAGC------AACA---------------------ACAATAATAAT--AATAA-T---AATAA-------TAATAATAA----TAA
dm3	chrX:8260698-8260847 -		CCGCCTCAGCTGTAGGTTTACCGTTATTTTTTTTTT-GCATTCTCCA-CTT-----TGTTGTTTAT------AA-------------------------TTA---TTT---ATAATGCTAG------CTTTAC-------------CGT--TTGAATCCACTTTCTTGTGCCAGG-CAATCAGGGAA------------------G---AGAAA---AAAAA-A---AAAAC-------AAATAATAA----TAT
droSim2	x:7830586-7830750 -		CCGCCTCAGCTGTAGGTTAACCGTTA-TTTCTTTT-GCATTCTCCA-CTT-----TGTTGTTTAT------AA-------------------------TTA---TTT---TTAATGCCAG------CTTTAC-------------CGT--TTGAATCCACTTTCTTGTGCCAGG-CAATCAGGGAA-------------------T---AGGAAAATAAAAAT--ACTAATA---TATAGCCGCGATAAACAAAAC----AAA
droSec2	scaffold_10:1682835-1682971 +		CTG-----------------------AAAACAGCGG-T------GA-CCTTAGCC-----AGTCTAAGTGAGATA---GC----C--------A---------CAGCACGTCAGCAGCAG--------------------------C-------------------AGG---------------------AGCAGCAGCAGCAACAGCAGCAGCAG-----------------------------------CA----------ATTGCTG--------------------------GCGATGCA------ACA-----------------GCAAC--AG-C---AACAG-------CTA-ACCAA----ACT
droYak3	2L:3599084-3599211 -		CTG-----------------------CCAGCAGTTG-C------AG-T---CAGTTAT-----TAACGAGCGCTACTC--------CCAACAGCAACATCGC-TCAGCGGCAG-------------------C-----------------AG------------------------------------C------CAGCAACAGC--AGCAACAGCAACAG-------------------CAAC-------------A---GCAACA---------G---------C---AACAA-C---AGCAG-------CAACACAAG----TCA
droEre2	scaffold_4690:10685634-10685752 +		TTG-----------------------GT---------GCCTG--T-----------------------------AAATGTGTGA--GC----C--------ACAACAA-----------------------------CAAC----------AAC-----------------AG-------C-----------------------------------ACAGCAACAGCAACAGCA-------------------------------------GCAGCAGCCAGAG-------------------CCA------------C------A---ACCACA---------ACAACAACAAC---------------------------------ATTAGTT---AACAG-------CAGCAACAA----TTC

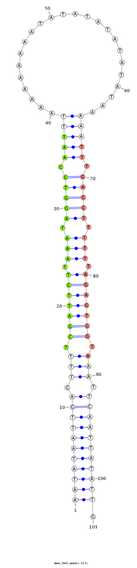
Generated: 09/08/2015 at 07:54 PM

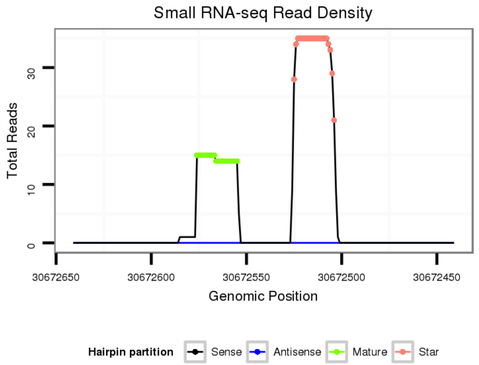
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

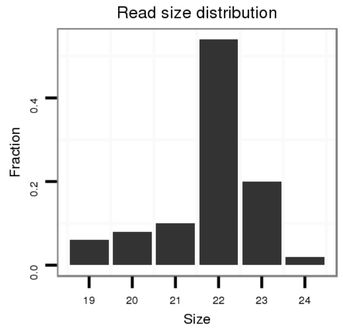
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2945	**scaffold_6500:30672491-30672591 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

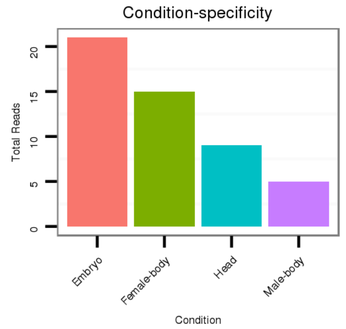
Legend: mature star mismatch in alignment mismatch in read

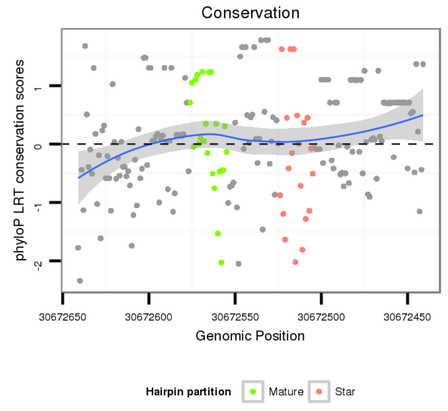
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
AT_rich	Low_complexity	Low_complexity	+
AT_rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACCAAAAGAATCCTGATTTGAAAGCAATAGCATATTATATATATATTTCAAATATAATTGACTTTTCGATTCTTAAATAGGTCCAATTTAAAAAAAAATATATATATATATAAAAATTTGACCTTTTTTAGAGTCGTAAATTCAATTATATTGCCTGCTTTTAAATTCGAATATTCGATGTCTATTTATTTGTCTGTGTAT	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	M060 embryo	V056 head	V110 male body	V049 head	V041 embryo
**********(((((((((((.(((.(((((((.(((.(((((.(((((.....................)))))..)))))..)))..)))))))..)))..)))))))))))).**********	**size**	**Mismatch**	**Count**	**Norm**	**Total**	**body**	**embryo**	**head**	**body**	**head**	**embryo**
.....TCGATTCTTAAATAGGTCCAAT.....	22	0	1	9.00	9	2	7	0	0	0	0
.....TTTGACCTTTTTTAGAGTCGTA.....	22	0	1	9.00	9	4	2	0	1	0	2
.....ATTTGACCTTTTTTAGAGTCGT.....	22	0	1	5.00	5	0	0	2	2	1	0
.....TCGATTCTTAAATAGGTCCAATTT.....	23	0	1	5.00	5	0	5	0	0	0	0
.....TTTGACCTTTTTTAGAGTCGTAA.....	23	0	1	4.00	4	1	1	0	1	1	0
.....TTGACCTTTTTTAGAGTCGTAA.....	22	0	1	4.00	4	0	1	2	0	1	0
.....ATTTGACCTTTTTTAGAGTCGTC.....	23	1	1	3.00	3	1	0	1	1	0	0
.....TTTGACCTTTTTTAGAGTCGT.....	21	0	1	2.00	2	1	0	1	0	0	0
.....TTTGACCTTTTTTAGAGTCG.....	20	0	1	2.00	2	1	0	0	1	0	0
.....TCGATTCTTAAATAGGTCCAAG.....	22	1	1	2.00	2	0	2	0	0	0	0
.....ATTTGACCTTTTTAGAGTCG.....	21	0	1	2.00	2	2	0	0	0	0	0
.....TGACCTTTTTAGAGTCGTA.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TTGACCTTTTTTAGAGTCGTA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....ATTTGACCTTTTTTAGAGTCGTA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TTTGACCTTTTTTAGAGTCGTAAA.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TTTGACCTTTTTTAGAGTC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TTGACCTTTTTTAGAGTCGT.....	20	0	1	1.00	1	0	0	0	0	1	0
.....ATTGACTTTTCGATTCTTA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....ATTTGACCTTTTTTAGAGT.....	19	0	1	1.00	1	0	0	0	0	0	1

Anti-sense strand reads

TGGTTTTCTTAGGACTAAACTTTCGTTATCGTATAATATATATATAAAGTTTATATTAACTGAAAAGCTAAGAATTTATCCAGGTTAAATTTTTTTTTATATATATATATATTTTTAAACTGGAAAAAATCTCAGCATTTAAGTTAATATAACGGACGAAAATTTAAGCTTATAAGCTACAGATAAATAAACAGACACATA	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head
**********(((((((((((.(((.(((((((.(((.(((((.(((((.....................)))))..)))))..)))..)))))))..)))..)))))))))))).**********	**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_6500:30672441-30672641 -	dmo_2945	ACCAAAAGAATCCT----------GATTTGAAAGCAATAGCATATTATATATATATTTCAAATATAATTGACTTTTCGA----------TTCTTAAATAG---------GTCCAATTTAAAAAAAAATATAT------ATATATAT----AAAAATTTGACCTTTTTTAGAGTCG----------TAAATTCAATTATATTGCCTGCTTTTAAATTCGAATATTCGATGTCTATTTATTTGTCTGTGTAT
droGri2	scaffold_15126:8013274-8013461 -		TTTCAAAA---CTA----------GAATACAATAATATTGTTCTTCATG----------TATATATTT---------AAATACGAAAGATTAATATTAT--TTAAATATTAT----AAATATATTATTTTTTTAAGTGACAAAAATAAAATATAAATTGGATATGCATATTAATAGTCAATTATAAAATCCATATGGATATCATTTAAAT----CTATAAGT
droWil2	scf2_1100000004762:4728425-4728619 -		TTTTAAAGTTATCC----------GATATA---------TATATATATATATCCCAAAATATTATAAACTTGTCATGTCT---------GC---TTTAAACAATAAAAAACAAACAAAAAATTAT------AGATGTAT----TCTTCTCACTCTATATTCTATGTCT----------ATGGCTAAATTGCATTTGCATTATTATACTGTTAGAATTTATGTCTGTTTATTTTT--GTATGT
droKik1	scf7180000298464:26183-26206 +		AAAAAA--------
droFic1	scf7180000453069:21180-21337 +		GCCCAACATATATAAATTTATAGAAAGCAGTTAAGGTAAGCCTAAAAA---------AACAAAATCATATAATTCGAAAGATTGGAAACC---CATGTCA---------------------------TACTTTAT----AAATTAAATATTTATATA---TAAA
droPse1	scf7180000762791:420-838 -		
droYak3	3L:11863192-11863391 -		TAATT----------------------TTTTTGGCAAGTTGTTCCTCTATTAGAATATCCATAACTCCCAAAGT-A---------------TTTTTATTGTTATATAATAGTGCATGAAGCGCAAATATATT------AAGTATAT----AAACATTTATTTTTTGTTATAGTTA
droEre2	scaffold_4770:443761-443915 -		TTAAAGGAAATACAAATTATTTAAACTACAAA---------TTTATT---------CTATTATTATTTTATTATTGTTATTATTATATTTAAAATATTATTTATTTATTTATTTATATTTATTATTATTA

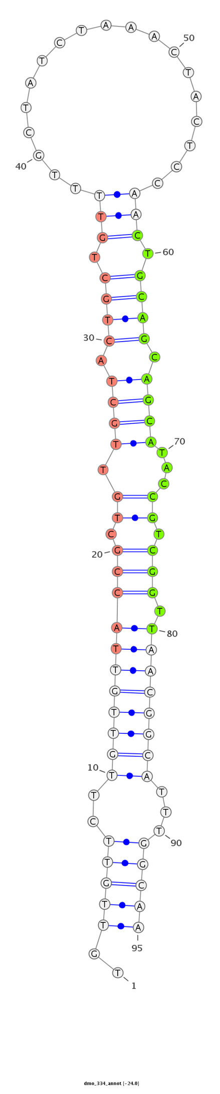
Generated: 09/08/2015 at 07:47 PM

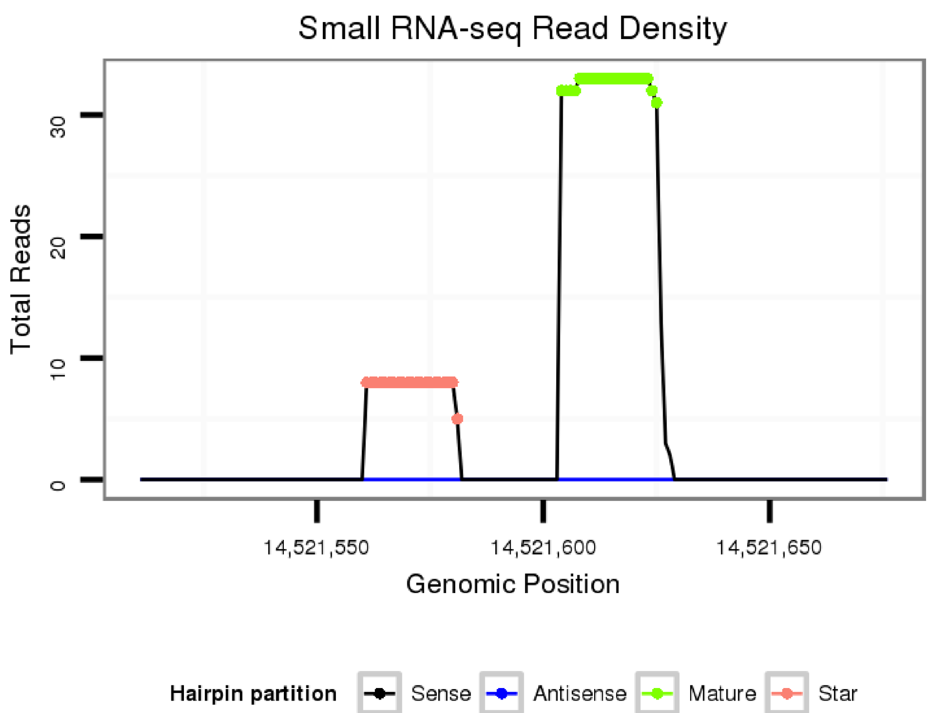
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

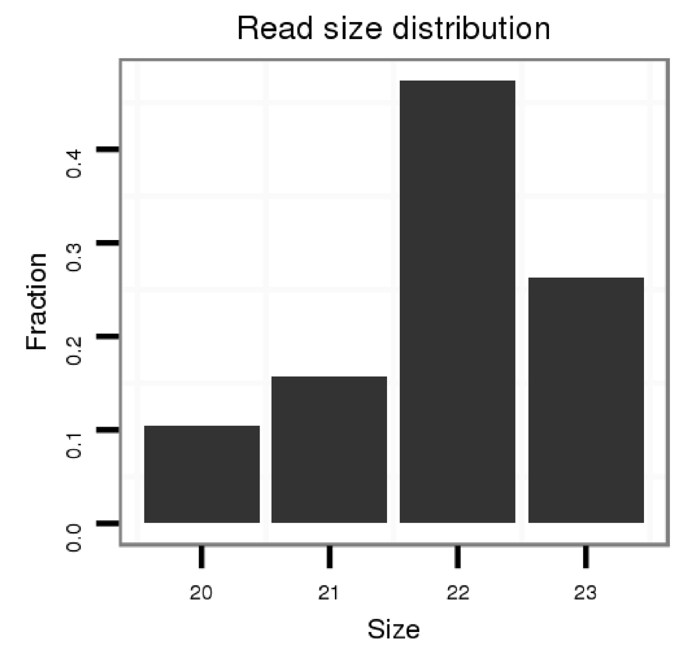
ID: dmo_334	Coordinate: scaffold_6540:14521561-14521626 +	Confidence: confident	Class: Canonical miRNA	Genomic Locale: intergenic	[View on UCSC Genome Browser {Cornell Mirror}]

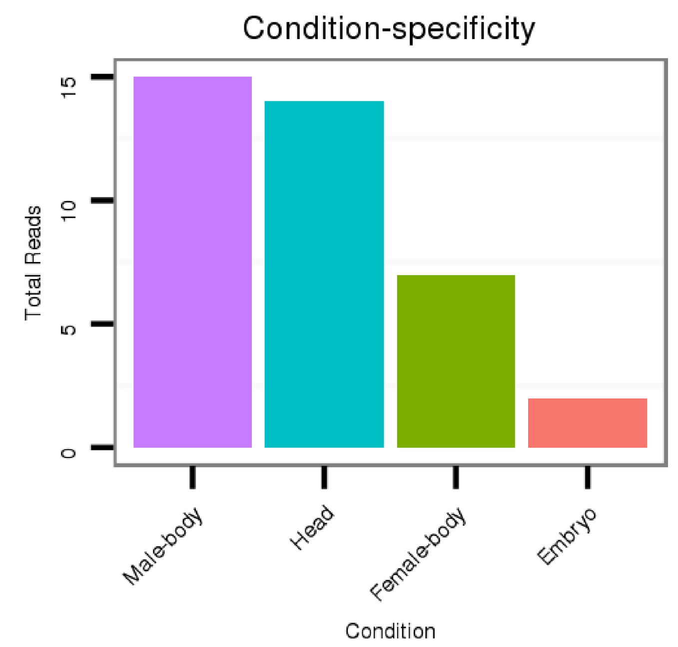
Legend: mature star mismatch in alignment mismatch in read

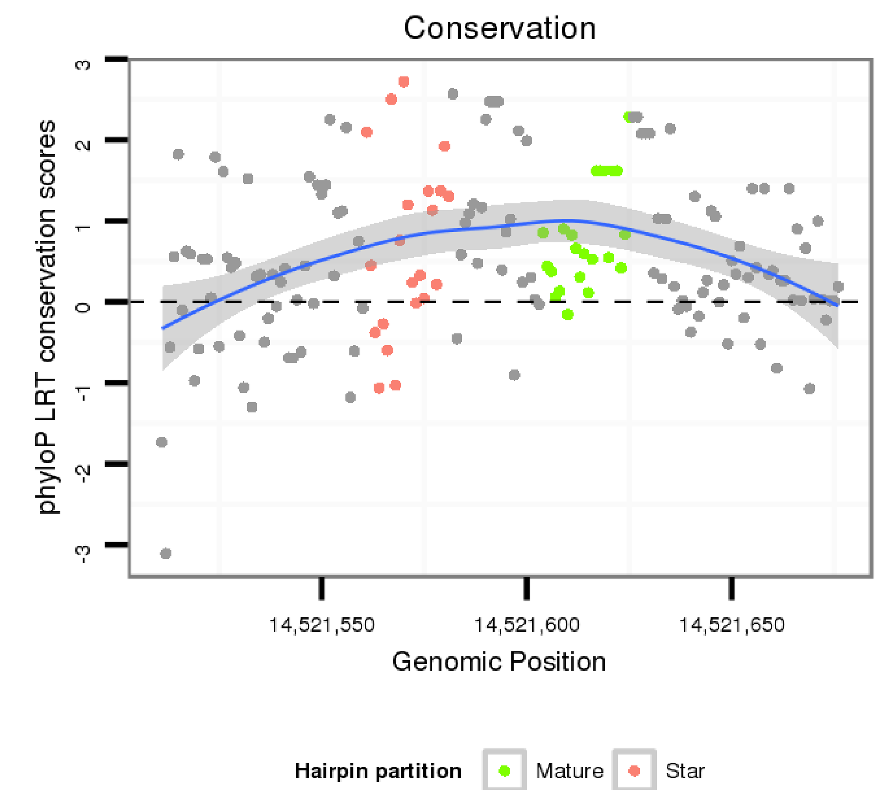
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTTTGCATGCCCATATACCAGCCACTACTGGCCAGTGTTGTTCTTGTTGTTACCGCTGTTGCTACTGCTGTTTTGCTATCTAAACTACTCCAACTGCAGCAGCATACCGTCGGTTAACGGCATTTGGCAACTCGACAGGCACGCAGAAAGTTCTCGTGGCCAGCCT ***********************************..(((((..((((((((((.((.((((.((((.(((..................))).)))).))))...)).))).))))))))...)))))***********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head	V110 male body	V049 head	M046 female body	M060 embryo	V041 embryo
....CTGCAGCAGCATACCGTCGGTT...	22	0	1	18.00	18	6	8	0	4	0	0
....CTGCAGCAGCATACCGTCGGTTA..	23	0	1	10.00	10	0	7	1	0	1	1
....CTGCAGCAGCATACCGTCGGTTT..	23	1	1	6.00	6	2	4	0	0	0	0
....TACCGCTGTTGCTACTGCTGT...	21	0	1	5.00	5	5	0	0	0	0	0
....TACCGCTGTTGCTACTGCTG..	20	0	1	3.00	3	1	0	0	2	0	0
....TGCAGCAGCATACCGTCGGTTT..	22	1	1	2.00	2	1	1	0	0	0	0
....CTGCAGCAGCATACCGTCGG...	20	0	1	1.00	1	1	0	0	0	0	0
....CTGCAGCAGCATACCGTCGGTTAA...	24	0	1	1.00	1	0	1	0	0	0	0
....CTGCAGCAGCATACCGTCGGT..	21	0	1	1.00	1	0	0	0	1	0	0
....CTGCAGCAGCATACCGTCGGTTAAC..	25	0	1	1.00	1	0	0	1	0	0	0
....CTGCAGCAGCATACCGTCGGTTC..	23	1	1	1.00	1	1	0	0	0	0	0
....AGCAGCATACCGTCGGTTAAC..	21	0	1	1.00	1	0	0	0	1	0	0
....TACCGCTGTTGCTACTGCTGTC..	22	1	1	1.00	1	0	0	0	0	1	0

Anti-sense strand reads

GAAACGTACGGGTATATGGTCGGTGATGACCGGTCACAACAAGAACAACAATGGCGACAACGATGACGACAAAACGATAGATTTGATGAGGTTGACGTCGTCGTATGGCAGCCAATTGCCGTAAACCGTTGAGCTGTCCGTGCGTCTTTCAAGAGCACCGGTCGGA ***********************************..(((((..((((((((((.((.((((.((((.(((..................))).)))).))))...)).))).))))))))...)))))***********************************	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_6540:14521511-14521676 +	dmo_334	CTTTGCATGC--CCATATACCAGCCA---CTA---CTG------GC--------------CAGTGTTGTTCTT------GT------TGTT------ACC--GCTGTTGCTACTGC-------------------T-------GTTTTGCTATCTAAACT-------A--C-------TCCAAC-----TGCAGCAGCA------T--A--------------------------------CCGTCGGTTAACGGCATTTGG-CAACTCGACAGGCACGCAGAAAGTTCTCG-TGGCCAGCC---------------T
droVir3	scaffold_13047:17118114-17118291 -		CTTCGCATGC--CCATATACC-ACGA---CTG---CTGCT-G----------CTGCTGCTGCTGTTGTTGTT------GT-GGGCCCGTT------GTT--GCTATTGCTATTGC-------------------T-------GTTGTGCTCGCTAAACT-------A--C-------TCCAAC-----TGCAGAGC-------------------------------GC--AT------------CCGTCGGTTAACGGCATTTGG-TGACACGACCACCACGCAGAAAGTTCTTG-TGCTCAGCC---------------T
droGri2	scaffold_14906:12182429-12182590 -		CTTTGCATTC--CCATATACC-AC------------------A-A--------------------CTGT---TGTT------GC------TATT------G-----CTATTGCTATTGC-------------------T-------GTTTTGCTCTCTAAAAT-------T--CTCCA-----------ACTGCTGGAG-------------------------------CGT--TC------------CCGTCGGTTAACGGCATTTGG-CGACACGACAGCCACACAGAAAGTTCTCG-GGCCCAACCAGTT---GTGTTGTGT
droWil2	scf2_1100000004902:8577476-8577637 +		CTATGTATCACCCCCTTACCCTCCACCACCG---CATT-CTTGATGGTGA-------------------TGAT------GA------------------TGATTGTGTTGCTATTTC-------------------T-------GTTGTGCTCTCTAAACT-------G--CTCCTGCTCCTGCT-----AACAG-------------------------------------CCGTCGGTTAACGGTTCTTCT-TCGCAGG-----C---CAGTAAGGACTTGCT-GCCCAAA---------------G
dp5	2:23712084-23712286 -		GTT-GTATGG--TTATGTACC-GCTA---CGA---CTATG-A-------------------CTGC---TGTT------GC------TGTT------GCATCCCTATTGCTATTGC-------------------T-------GTTTTGCTCTCTAAGCCCTCTCCCT--CTCCCGCTCCCGCTCTAACTGCAGCAGCAATGGGGGCGGTCCAGGGCAGGGCCGG--GCACTGGAAACTAGCGCCGTCGGTTAACGGCACATTCGCCC-------GCCGC-A-GT-CG----AGCC---------TC------------T
droPer2	scaffold_3:6490097-6490299 -		GTT-GTATGG--TTATGTACC-GCTA---CGA---CTATG-A-------------------CTGC---TGTT------GC------TGTT------GCATCCCTATTGCTATTGC-------------------T-------GTTTTGCTCTCTAAGCCCTCTCCCT--CTCCCGCTCCCGCTCTAACTGCAGCAGCCATGGGGGCGGTCCAGGGCAGGGCCGG--GCACTGGAAACTAGCGCCGTCGGTTAACGGCACATTCGGCC-------GCCGC-A-GT-CG----AGCC---------TC------------T
droAna3	scaffold_13248:1388721-1388778 +		TGCTGCC---AAAAGATGTTGTT------GT------TGTT------GCT-----GCTGCTGCTGC-----------CGC------C-------GTTTGCCGCTCTAA---
droBip1	scf7180000396708:3041198-3041198 -		T--
droKik1	scf7180000302461:1036602-1036758 -		CATT--GCAGCTATATTGCTATTGC-------------------TGTGTG--TTGTGCTCTCTAAGCT-------CTTCCCCCGCCCCCAAT-----AAAAAAGGA------AGAAACATGCACAAAAAAAAAGG--ACCCGAAGCTTACGCCGTCGGTTAACGGCATT-CG-CCG-------AGCGA-A-CG-AA----AAAC---------GGC---CAGTGTTGT
droFic1	scf7180000451789:64502-64579 +		CTCTGCCTCA--CCATTTGGC---TT------GG------CGCTGCCATCAAAGCTCTGTTTTATTGTTGTTTTCGTTGCTGCTGCTGCT--GCT
droEle1	scf7180000491011:1681030-1681106 +		TT--GTTGTTGT------------------TGTT------GT------TGTT------GTT--GTTGTTGTCATTGT-------------------T-------GTTTCGTT-------------------GC---GTCGCAACAACTG--CAGCAAACTTT------------------------CGGT
droRho1	scf7180000758845:110-273 +		ACTT--GATGTTGT------------------TGTT------GCTGTTGCCGCT------GCAGCTATATTGCTATTGC-------------------TGTGTG--TTGTGCTCTCTAAACT-------T--CGCCCGCCCCCAAT-----TGAAAAAGGA------A--AACA---ACGA--AATAGTATAACCGAAGCCAAAACCGGCGCTTAACGGCACTTCC-CCC-------AA--A-A----AGG---AACT---------GCC-----------C
droBia1	scf7180000302402:8145049-8145175 +		CGCT--GCAGCTATATTGCCACGGC-------------------TGTGTG--TTGTGCTCTCTAAACT-------T--CGCCCGCCCCCAAT-----TGAAAAAGGA------A--AACA---TCGA--AATAGT--GACCGAAGCCA-----------CTAACGGCACTTCC-CCC-------AA--A-A----CG----AACT---------GCC-----------C
droTak1	scf7180000415811:123841-124002 -		ATAT--ACTGCTGC-----------------TGTTGTC------GTTGGTGCCGCT------GCAGCTATATTGCCATTGC-------------------TGTGTG--TTGTGCTCTCTAAACT-------T--CGCCCGCCCCCAAT-----TGAAAAAGGA------A--AACA---ACGA--AATAGT--AACCGAAGCCA-----------CTAACGGCACTTCC-CCC-------AA--A-A----CG----AACT---------GCC---CAGTATTGT
droEug1	scf7180000409562:810-950 +		CGTT--GCAGCTATATTGCCATTGT-------------------TGTATGTTGTTGTGCTCTCTAAACT-------T--CGCCCGCCCCCAAT-----TGAAAAAGGA------A--AACA---CCGA--AATCGT--AACCGAAGCCA-----------CTAACGGTACTTCC-CCC-------AA--A-A----CG----AACT---------GTCCGGCAGTATTGT
dm3	chr3L:14744647-14744731 +		ACTTGTCCGC--CCGTC-GCA-CGC---TCACTGTCATTGCTTGCTGCT---------------GTTGTTGTT------GT------TGTT------GCT-----GCTGCTGCTGC-----------TGC------T-------GCT-------------------------------GTT--GCT
droSim2	3r:7787964-7788098 -		CGCT--GCAGCTATATTGCCATTGC-------------------TGTGTG--TTGTGCTCTCTAAACT-------T--CGCCCGCCCCCAAT-----TGAAAAAGGA------A--AACA---ACGA--AATCGT--ATCCGAAGCTA-----------CTAACGGCACTTCC-CCC-------AA--A-A----CG----AACT---------GCC---CAGTATTGT
droSec2	scaffold_12:682323-682475 -		ACTT--GCTGTTGT-----------------TGTT------GT------CGCT------GCAGCTATATTGCCATTGC-------------------TGTGTG--TTGTGCTCTCTAAACT-------T--CGCCCGCCCCCAAT-----TGAAAAAGGA------A--AACA---ACGA--AATCGT--ATCCGAAGCTA-----------CTAACGGCACTTCC-CCC-------AA--A-A----CG----AACT---------GCC---CAGTATTGT
droYak3	X:6906592-6906676 +		TGTG--GCTGCTGCTGCTGCTGCTATTGTTGTTGTTATTAGTGT------------------TGCTAGTGTTGTTGT---------------------T-------------------------------TG--CTGCTGCTGCTGCTGTTACTGCT--GTT
droEre2	scaffold_4770:8152068-8152220 -		ACTT--GCTGTTGT-----------------TGTT------GC------CGCT------GCAGCTATATTGCCATTGC-------------------TGTGTG--TTGTGCTCTCTAAACT-------C--CGCCCGCCCCCAAT-----TGAAAAAGGA------A--AACA---ACGA--AATCGT--ATCCGAAGCTA-----------CTAACGGCACTTCC-CCC-------AA--A-A----CG----AACT---------GCC---CAGTATTGT

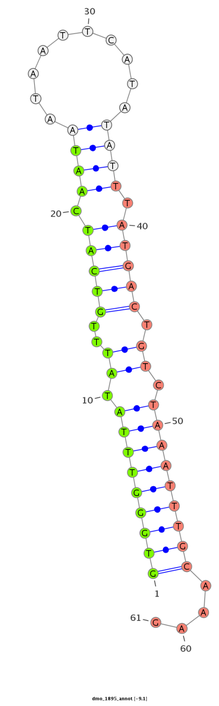
Generated: 09/08/2015 at 07:48 PM

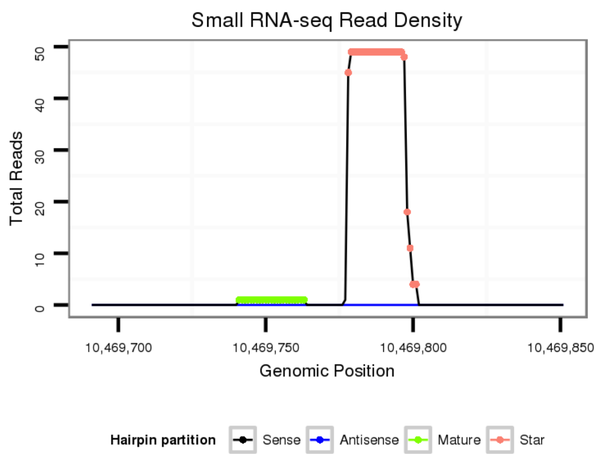
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

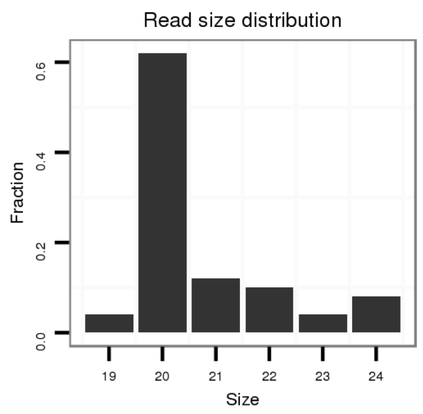
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1895	**scaffold_6540:10469741-10469801 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

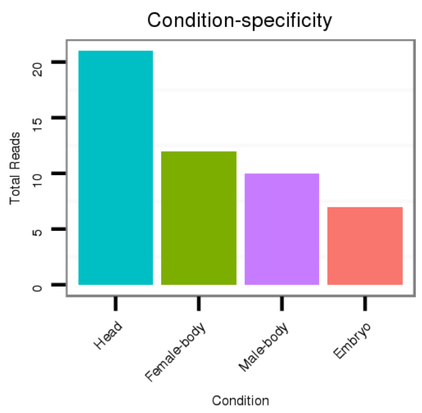
Legend: mature star mismatch in alignment mismatch in read

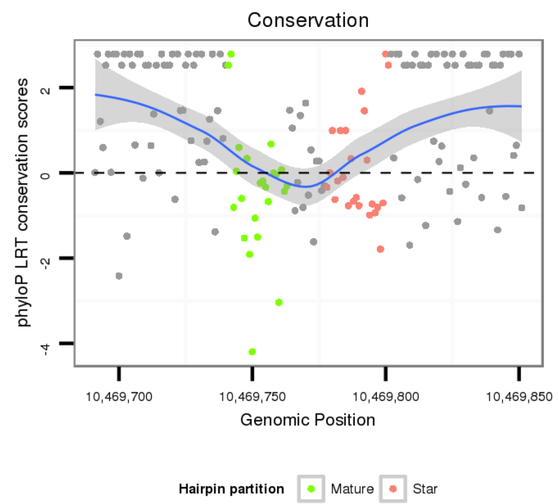
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI24351-in]; CDS [DmojGI24351-cds]; CDS [DmojGI24351-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CACCCACATCGACTCCATACGTTGCTGGCTGTTTCACCAGAGTGTGAATGGTGGGTTTATATTTGTCATCAATAATAATTCATATATTTATGACTGTCTAAATTTGCAAAGATATACCCGAACCGGTGTATTCCACACTACGTGGTATTGGCGAGATTCTG	Read size	# Mismatch	Hit Count	Total Norm	Total	V056 head	M046 female body	V049 head	V110 male body	M060 embryo	V041 embryo
**********(((((((((.((..(((((.((((.....)))).)))))).)).)))))))).....**********											
.....TTATGACTGTCTAAATTTGC.....	20	0	1	29.00	29	14	6	0	9	0	0
.....TTATGACTGTCTAAATTTGCAA.....	22	0	1	5.00	5	1	2	2	0	0	0
.....TTATGACTGTCTAAATTTGCA.....	21	0	1	5.00	5	2	1	1	0	1	0
.....TTATGACTGTCTAAATTTGCAAAG.....	24	0	1	4.00	4	0	0	0	0	3	1
.....TATGACTGTCTAAATTTGCA.....	20	0	1	2.00	2	0	1	0	1	0	0
.....TTATGACTGTCTAAATTTG.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TTATGACTGTCTAAATTTGCAAAGT.....	25	1	1	1.00	1	0	0	0	0	1	0
.....TATGACTGTCTAAATTTGC.....	19	0	1	1.00	1	0	0	1	0	0	0
.....GTGGGTTTATATTTGTCATCAAT.....	23	0	1	1.00	1	0	0	0	0	0	1
.....TATGACTGTCTAAATTTGCAA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TTTATGACTGTCTAAATTTGCAA.....	23	0	1	1.00	1	0	0	0	0	1	0
.....TTATGACTGTCTAAATTTT.....	19	1	2	0.50	1	0	0	1	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:10469691-10469851 +	dmo_1895	CACCCACATCGACTCCATACGTTGCTGGCTGTTTCACCAGAGTGTGAATGGTGGGT-TTAT--ATTT----------GTCA-TC---AA-------TAATAATTCATATA----------TTTATGACTG------TCT------AA-A---------T---TTGCAAAGATATACCCGAACCGGTGTATTCCACACTACGTGGTAT-TGGCGAGATT-CTG
droVir3	scaffold_13047:13231989-13232150 +		CACCCATATTGATTCCATACGCTGCTGGCTTTATCATCAGAACATTAATGGTAATGTTAAA--ATTA----------GACA-ATC---A-------CAATCAATAAAATAGATT----------|---------|-------|---|-----AA-ATATTGCC-A-TG---CCTTAAAGATATCCCGAACCGGTTTATTCCACATTACGTGGCAT-TGGTGAAATC-CTC
droGri2	scaffold_14906:4459377-4459529 -		CACCCACATTGATTCCATACGCTGCTGGCTTTATCACCAGAACGTTAATGGTAATGATCA-TTAG--CAGTT----------|---|--TTAAAATAT---|----------|----------ATCACATTTAAAATGGG---|-------C-A-TT---CCTTAAAGATATACCCGAACCGGTTTATTCCACATTACGTGGCAT-TGGTGAGATT-CTA
droWil2	scf2_1100000004902:1498169-1498324 +		CAACCACATTGACTCCATACGCAGTTGGCTATATCATCAGAGTGTGAATGGTGTAGA-TATA--GTTA----------GTCT-ATTTTAATTAT-----|----------|----------CCTTTTTTAAC---TTA---|---------TTTCATTCCGTTAGATATTCCGGACCGTGTTTTCTGTACATTACGTGGCAT-AGGTGAAATT-TTA
dp5	2:6301358-6301511 +		CACCCACATAGACTCCATTCGCAGCTGGCTCTATCATCAGAATGTGAATGGTAACG-AAAC--CAAA----------|---|--CA--AAAG---|----------|----------TCACCTATTTCGAGCTG---|-------CATTTCCTTCCATCAGATATACCGAACCAGTATTCTGTACGCTGCGTGGCAT-TGGCGAGATC-CTG
droPer2	scaffold_0:125389-125544 +		CACCCACATAGACTCCATTCGGAGCTGGCTCTATCATCAGAATGTGCATGGTAACG-CACA--CCGAA----------|---|--ACAA--AAAG---|----------|----------TCATCTATTTTGAGCTG---|-------CATTTCCTTCCATCAGATATACCGAACCAGTATTCTGTACGCTGCGCGGCAT-TGGCGAGATC-CTG
droAna3	scaffold_13340:12920177-12920330 -		CACCCATATCGACTCAATACGCAGCTGGCTCTATCATCAGAGTGTTAATGGTAAGCG-TATT--ACTTT-A----------GCTT-TC---TT--------TAACATTTATATGATTT----------|----------|-------|---|TA-A---------T---ATCGTAAGACATACCGAGCCTGTTTCTGCACCTACGTGGTAT-TGGCGAGATC-CTT
droBip1	scf7180000396691:1801396-1801549 -		TACCCATATTGATTCTATTCGCAGTTGGCTCTATCATCAAAGTGTTAATGGTGAGT-CAAT--TATTA----------|---|AACT-TTC--TT--------TAAGTATTGAATTATATTG----------|----------|-------|---|TA-A---------T---ATTTATAGACATACCGGACCCGTTTTCTCAACACTACGTGGTAT-TGGCGAGATC-CTG
droKik1	scf7180000302697:1087632-1087796 -		CACGCACATCGACTCCATTCGCAGCTGGCTTTACCATCAGAGTGTAAATGGTAATT-GATA--TTTT----------|---|--TTGGTACATTAA----------A--TCTGTATTATCTGCTAAGCACTC------CGT------AA-|---------CA---ATCGGCAGATATTCCCGAACCCGTTTTCTCCACCTTGCGTGGCAT-TGGCGAGATC-TTG
droFic1	scf7180000454055:287324-287480 +		TACCCATATTGACTCCATTCGCAGTTGGCTTATCATCAGAGTGTTAAGCGGTTAGT-GAAA--TTCAG----------|---|-TCT-AAATTAATACAGG---|----------|----------TTAATTT-TATTTG---|-------GATTT---TTTGGTAGATATTCCCGAACCGTTTACTGAACTCTACGTGGCAT-TGGCGAAATC-CTT
droEle1	scf7180000491017:225099-225252 -		CACCCATATAGACTCCATTCGCAGCTGGCTTTATCATCAGAGTGTCAATGGTGAGT-AAGA--ATGT----------|---|ATCT-ATATAAATATAAA---|------|TT-----AAATT--T---------|----------|-----AAAATC------|---|----------A---ACATATAGACATACCCGAACCTGTTTACTGCAACGCTACGTGGTAT-TGGCGAGATC-CTC
droRho1	scf7180000777285:86764-86934 +		CACCCACATAGATTCCATTCGCAGCTGGCTCTATCATCAAAGTGTGAATGGTGAGT-ATCT--ATCTGTA----------|---|--TGAATATATC---|--TC--TAA-----A--TGGGTATCTTCCGTAAACATTT------TA-------|---|-T------TTTA---TTTTATAGATATACCTGAACCCGTTTACTGTACACTACGTGGTAT-TGGCGAGATC-CTT
droBia1	scf7180000302402:5179707-5179889 +		CACCCATATCGACTCCATACGCAGCTGGCTCTATCATCAAAGTGTGAAGCGGTGAGA-AAAAATAATAATATAATATTATTATTCCAATCCTAAATTACCA--ATT-TA------ATCAATGA----------|----------|-------|---|TTGAA-T------AT-T---TCCTTTAGACATCCCGACCCGCTTTTCTGAACACTTCGTGGTAAT-TGGTGAAATC-CTT
droTak1	scf7180000415417:128217-128383 +		CACCCATATTAGATTCCATACGCAGCTGGCTCTATCATCAGAGTGTGAATGGTGGGT-CATC--TCTAGGATC---TCT----------|---|ATCT-TACATTATTACTAA---|------|CTATATTGTTT----------|----------|-------|---|TA-AA------AT-T---TTCCTTAGATATCCCTGAACCCGTTTTCTCAACACTCCGTGGCAT-TGGCGAGATC-CTT
droEug1	scf7180000409768:676230-676394 -		TACCCATATTAGATTCCATCCGCAGTTGGCTCTATCATCAGAGTGTTAATGGTGAGT-AATC--TTTAA----------|---|GCA-CTATTATTCT-----|---|ACAATAA----A--AAG---------|----------|----------A------|---|TATCCAA-ACTTTTT-A-CT---TTTTTTAGATATTCCCGAACCTGTTTTCTCAACTCTTCGAGGTAT-TGGCGAAATC-CTT
dm3	chr3R:18531423-18531583 -		AACCCATATCGACTCCATACGCAGCTGGCTCTATCATCAGAGTGTTAATGGTCAGT-AAAT--TATAACA----------|---|T-AGATAT--ATAT---|----------|----------TCATCAATAAGAATATACAA-C-------ATTT---CTTGGCAGATATTCCCGACCCTGTTTTTTCAACACTCCGTGGAAT-TGGTGAGATC-CTT
droSim2	3r:18056815-18056972 -		AACCCATATCGATTCCATACGCAGCTGGCTCTATCATCAGAGTGTTAATGGTCAGT-GAAT--TATAATA----------|---|T---A-AATTTAT---|----------|----------TCATCAATAAGAATATCCAA-T-------AT-T---CTTATAGATATTCCCGAACCGTTTTTTCAACACTCGGGAAT-TGGTGAGATC-CTT
droSec2	scaffold_0:18887850-18888011 -		AACCCATATCGACTCCATACGCAGCTGGCTCTATCATCAGAGTGTTAATGGTCAGT-AAAT--TATATTA----------|---|T---A-AAATATAT---|----------|----------TCATCAATAAAAATATCCAAT-------ATT---TCTTATAGATATTCCAGAACCTGTTTTTTCAACACTCCGTGGAATTTGGTGAGATCCCTT
droYak3	3R:19382488-19382648 -		AAGTCATATTGATTCCATACGCAGCTGGCTCTATCATCAGAGTGTTAATGGTCAGT-AAAG--TATATAA----------|---|T-AAATTT-ATAT---|----------|----------TCATGAATATGAATATGCAA-T-------ATTT---CCTTGCAGATATTCCAGACCCTGTTTTTTCAACACTTCGTGGAAT-TGGTGAAATC-CTT
droEre2	scaffold_4820:9541759-9541911 +		AACCCATATCGATTCCATACGCAGCTGGCTCTATCATCAGAGTGTTAATGGTCAGT-AAAC--TATA----------|---|--TAATATAT---|----------|----------GCATCAATAAGGCATATA---|-------CATTT---CTTGCAGATATTCCTGAACCTGTTTTTTCAACGCTTCGTGGAAT-TGGTGAAATC-CTT

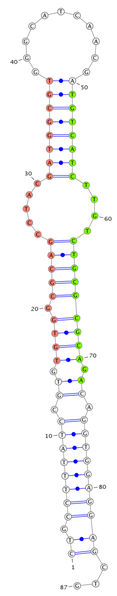
Generated: 09/08/2015 at 10:37 PM

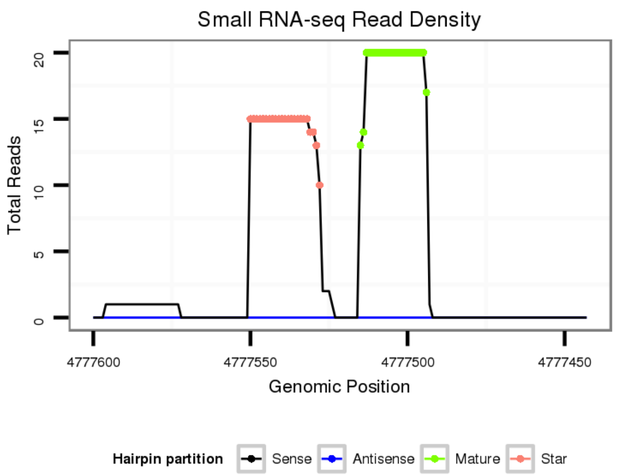
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

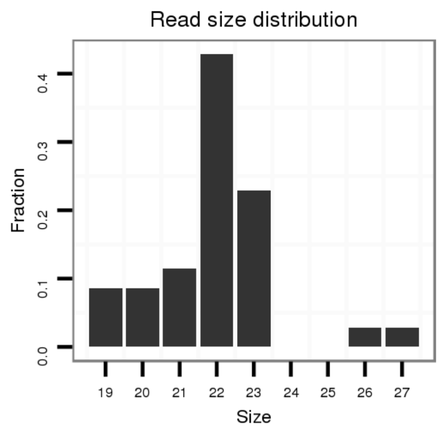
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_134	**scaffold_6540:4777493-4777550 -**	**confident**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

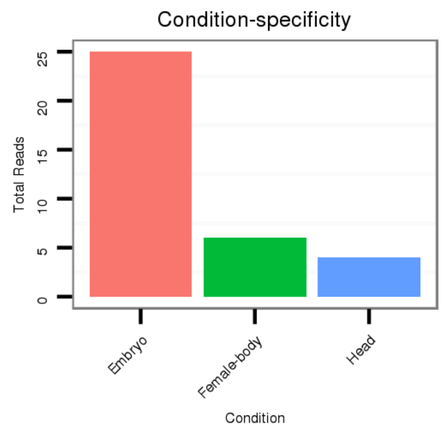
Legend: mature star mismatch in alignment mismatch in read

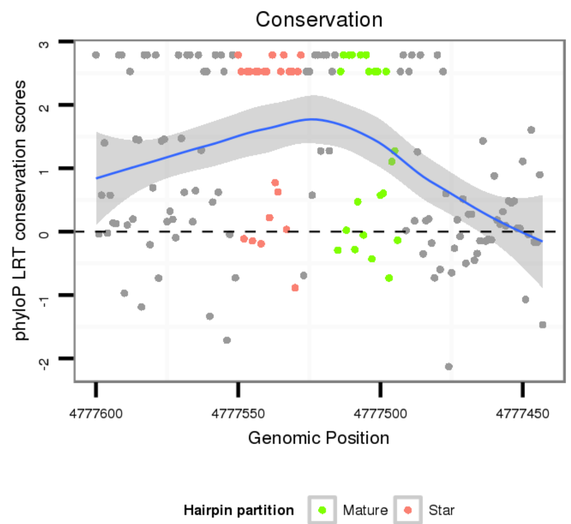
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dmoj\GI23588-cds]; utr3 [utr3_minus_8675]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGGAGAACATTAGGAAGTACATCAAGGACTACAAACTGCCTTTATCCGTGTGTGGCGCAGCCTACGATGGCGTGGGCATCAACGATGTCATCTTGTCTGCGCGCAGACAGGTGGAGGAGCTGCCATCGCCGTCGGAACCTTGAACTGAAATTCACATG **********(.(((((((((.((.((((.(((((.....(((((((((...........)))))))))....)))))))))).)).)))))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V041 embryo	M046 female body	V056 head	V110 male body
..........TGTCATCTTGTCTGCGCGCAGA..........	22	0	1	12.00	12	6	4	2	0	0
..........TGTGGCGCAGCCTACGATGGCGT..........	23	0	1	8.00	8	2	4	0	2	0
..........TGTGGCGCAGCCTACGATGGCG..........	22	0	1	3.00	3	1	0	1	1	0
..........TCATCTTGTCTGCGCGCAGA..........	20	0	1	3.00	3	2	1	0	0	0
..........TCATCTTGTCTGCGCGCAG..........	19	0	1	2.00	2	0	1	0	1	0
..........TGTGGCGCAGCCTACGATGGCGC..........	23	1	1	1.00	1	1	0	0	0	0
..........TGTGGCGCAGCCTACGATGGCGTGGG..........	26	0	1	1.00	1	0	0	1	0	0
..........TCATCTTGTCTGCGCGCAGAC..........	21	0	1	1.00	1	1	0	0	0	0
..........GTCATCTTGTCTGCGCGCAGA..........	21	0	1	1.00	1	1	0	0	0	0
..........TGTCATCTTGTCTGCGCGCAG..........	21	0	1	1.00	1	0	0	1	0	0
..........TGTGGCGCAGCCTACGATGGCGTGGGC..........	27	0	1	1.00	1	1	0	0	0	0
..........TGTGGCGCAGCCTACGATG..........	19	0	1	1.00	1	0	0	1	0	0
....GAACATTAGGAAGTACATCAAGGA..........	24	0	1	1.00	1	0	0	0	0	1
..........TGTCATCTTGTCTGCGCGCAGC..........	22	1	1	1.00	1	1	0	0	0	0
..........TGTGGCGCAGCCTACGATGGC..........	21	0	1	1.00	1	1	0	0	0	0
..........TGTCATCTTGTCTGCGCGCAGT..........	22	1	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

ACCTCTTGTAATCCTTCATGTAGTTCCTGATGTTTGACGGAAATAGGCACACACCGCGTCGGATGCTACCGCACCCGTAGTTGCTACAGTAGAACAGACGCGCGTCTGTCCACCTCCTCGACGGTAGCGGCAGCCTTGGAACTTGACTTTAAGTGTAC **********(.(((((((((.((.((((.(((((.....(((((((((...........)))))))))....)))))))))).)).)))))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V049 head
..........GAACATTAGGAAGTACATCAAGGA..........	24	0	1	1.00	1	0	1
..........TGTCATCTTGTCTGCGCGCAGC..........	22	1	1	1.00	1	1	0
..........TGTGGCGCAGCCTACGATGGC..........	21	0	1	1.00	1	1	0
..........TGTCATCTTGTCTGCGCGCAGT..........	22	1	1	1.00	1	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6540:4777443-4777600 -	dmo_134	TGGAGAACATTAGGAAGTACATCAAGGACTACAAACTGCCTTTATCCGTGTGTGGCGCAGCCTACGATGGCGTGGGCATCAACGATGTCATCTTGTCTGCGCGCAGACAGGTGGAGGAGCTGCCATCGCCGTCG----------G-AACCTTGAA---C-----TGAAAT----------T--CA-------CATG
droVir3	scaffold_13047:782851-783032 -		TGGAGAACATAAGGAGCTACATCAAAAACTACAAACTGCCCATTGTCGCTGTGCGGCGCAGCCTATGATGGGGTTGGCATCAACGACGTCATTATTGTCTGCCGGCAGACAGGTAAACAAGTTGCCGGTGGACCACGCCGCCGCCGGGTCATTGAGGCTAATCGCC---ATGAACTGAAAT----------E--E---TATATATA
droGri2	scaffold_14906:5527010-5527159 +		TGCAGCAGATTCGGGATTACATACGCAACTACAAGTTGCCCATTGTCGCTGTGTGGTGCTGCCTACGATGGCGTCGGCATCAACGATGTCATCGTCTCTGCCGCCGCCAGGTGGAGTTGCTCCGCATGCCACAAAC------G--------C--ACTGA---E---E------EAATT----------G--E--E-------EETT
droWil2	scf2_1100000004902:9615266-9615404 +		TTGCAAACATACGGAAATACATTAAGACCTATAAGCTGCCCATTGTCCTCTGTGGTGCTGCCTTTGACGGTGTTGGAATCAACGATGTCATCCTTTCGCCCGCCGACAAGTCGAGGCCCTACCCACGTCATTTC------C--------C--A-------E---E------E----------E--E-------E----
dp5	2:1749976-1750126 +		TGAAGAGGATCCGCAAGTATCTGAAGGACTACAAGCTGCCCTTGTCGCTGTGCGGTGCTGCCTTCGATGGCGTAGGCATCAACGATGTTATATTGTCGGCTCGTCGTCAGGTGGACGCCATACCGTAGTCCTAATT------G--------C--ATTC---CCCCG------E----------E--E-------EETTG
droPer2	scaffold_7:1903387-1903537 +		TGAAGAGGATCCGCAAGTATCTGAAGGACTACAAGCTGCCCTTGTCGCTGTGCGGTGCTGCCTTCGATGGCGTAGGCATCAACGATGTTATATTGTCGGCTCGTCGTCAGGTGGACGCCATACCGTAGTCCTAATT------G--------C--ATTC---CCCCG------E----------E--E-------EETTG
droAna3	scaffold_13340:4688515-4688682 +		TGGACAACATCAGAAAGTACCTAAAGACTTACAAACTGCCCACTTCCCTTTGCGGTGCCGCCTACGATGGCAGTAGGAATCAACGATGTCATTCTGTCTGCCGCCGCGTCAGGTGGAAGCACTGCAACTAGCCTAGTT------G--------AAAACCATTCC---C-----E------E----------CGAAACTATCCCCTGTTATA
droBip1	scf7180000396359:501598-501762 -		TGGACAATATCCGAAAGTACCTTAAGACTTATAAACTGCCGCTTTCCCCTTCCGGAGCCGCGTACGACGGCAGTAGGAATCAACGATGTCATTCTGTCTGCCGCCGACCGTCAGGTGGAAGCACTGCAGCTGGCCTAGTG------G--------A-AACCATTCC---C-----E------E----------TGAAACTATCCCC--TGTA
droKik1	scf7180000302388:1717165-1717340 +		TGGAGAGCATTAGAAACTATATCAAGTTCTTCAAGTTGCCTTTTGTCGCTGTCCGGAGCCGCCTACGACGGTGTGGGCATTAACGACGTCATCCTGTCCGCCACGACGTCAGGTGGAGGCAATGCCATATGGCGGAGCAG------G--------C--AGTG---T---E------E----CCTGGTTTGGTTTAAGCTTACTTAGCTGA--------CATG
droFic1	scf7180000454106:1826002-1826164 +		TGGAGACCATTCGGAACTACATCAAGACGTACAAGCTGCCGTTGTCATTGTGTGGAGCCGCCTACGATGGAGTGGGCATCAACGATGTTATTCTGTCCGCCAGGCGACAAGTAGAGTCGCTACCGCTGCTCCTAATT------T--------T--ACCATTCC---C-----E------E----------ATTAAGAATACCC--TCC
droEle1	scf7180000491194:541977-542133 -		TGGAGGGCATCCGGAACTATATCAAGACGTACAAGCTGCCGCTGTCGTTGTCCGGAGCCGCCTACGATGGCGTGGGCATCAACGATGTCATCCTGTCGGCCCGGCACCAGGTGGAAGCCATGCCGTCGTCCTAAAC------C--------A--ACCATTCC---C-----E------E----------AA-GGGCATA-----E---C
droRho1	scf7180000779488:584282-584437 -		TGGAGGCCATCCGGAATTACATCAAGACGTACAAGCTGCCGCTGTCGCTGTCCGGAGCCGCCTACGATGGCAGTGGGCATCAACGACGTCATCCTGTCAGCCCGGCGCCAGGTGGAGGCCATTCCGCTCCTCCTAGAT------C--------A--ACCATTCC---C-----E------E----------AA-E--ACAT-----E-ACC
droBia1	scf7180000302402:4265594-4265735 -		TCGAGGGCATCCGGAACTATATCAAGACTTACAAGCTGCCGCTGTCCCTTTGCGGTGCTGCCTACGATGGCGAGTGGGCATCAACGACGTCATCCTATCCGCCCGGCGACAGGTGGAGGCCTTGCCTTTGCCCTAAAT------C--------A--ATCA----E---E------E----------E--E-------E----
droTak1	scf7180000415310:654287-654434 +		TCGAAGGCATCCGGAACTACATCAAGACTTACAAGCTGCCCACTGTCGCTGTCGGAGCTGCCTACGATGGCGTGGGCATCAACGACGTCATCCTGTCCGCCCGGCGACAAGTGGAGGCCATGCCGCT--------E----------A--ACCATTCC---C-----E------E----------CCCGAGCACA-----E--CC
droEug1	scf7180000409881:210611-210760 -		TCGAGCCCATCCGGAATTACATCAAAAACTACAAGCTGCCCACTGTCCTCTTGCGGAGCTGCCTACGATGGCAGTCGGCATCAAGACGTCATTCTGTCCGCCCGTCGACAGGTGGAGGCCTTGCCTTTATCCCTAAAA------C--------A--ACCATTCC---C-----E------E----------CT-E--E-------E---G
dm3	chr3R:20485995-20486153 -		TTGAAGCCATTCGGAACTACATCAAGACCTACAAACTGCCCACTGTCGTGTCTGTGGAGCTGCCTACGATGGCGTGGGCATCAACGATGTTATCCTATCCGCCCGGCGACAAGTGGAAGCCATACCCTTGTCCTAAAT------C--------A--ACCATTCC---C-----E------E----------TTCTAGCACA-----E--CC
droSim2	x:5234640-5234781 +		TTGAGGCCATTCGGAACTACATCAAGACTACAAACTGCCCACTGTCGTGTCTGCGGAGCTGCCTACGATGGCGTGGGCATCAACGATGTTATCCTGTCCGCCCGGCGACAAGTGGAGGCCAATACCCTTGTCCTAAAT------C--------A--ACCA----E---E------E----------E--E-------E----
droSec2	scaffold_0:20820407-20820548 -		TTGAGGCCATTCGGAACTACATCAAGACTACAAACTTCCCACTGTCGTGTCTGCGGAGCAGCTACGATGGCGTGGGCATCAACGATGTTATCCTGTCCGCCCGGCGACAAGTGGAGGCCATACCCTTGTCCTAAAT------C--------A--ACCA----E---E------E----------E--E-------E----
droYak3	3R:26011375-26011524 +		TAGAGGCCATCCGGAACTACATCAAGACTTACAAACTGCCCACTGTCTGTCTGCGGAGCTGCCTACGACGGCGTGGGCATCAACGATGTCATCCTGTCCGCCCGCCGACAGGTGGAGGCCATACCCCTGTCCTAAAT------C--------A--ACCATTCC---C-----E------E----------TT-E--E-------E---C
droEre2	scaffold_4820:7572288-7572444 +		TTGAGGCCATTCGGAACTATATCAAGACTTACAAACTGCCCACTGTCCGTCTGCGGAGCTGCCTACGATGGCGTGGGCATCAACGATGTTATCCTGTCGCCCGCCGACAGGTGGAGGCCATACCCTTGTCTTAAAT------C--------A--ACCATTCC---C-----E------E----------TTCTAGC-E------E-ACA

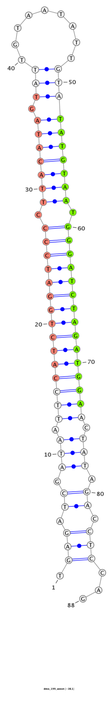
Generated: 09/08/2015 at 07:48 PM

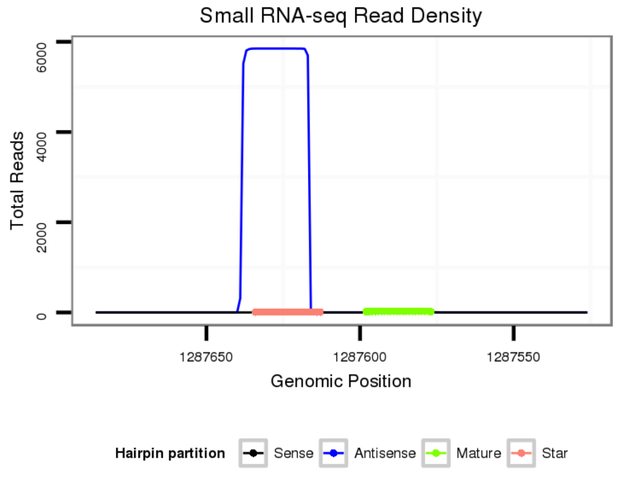
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

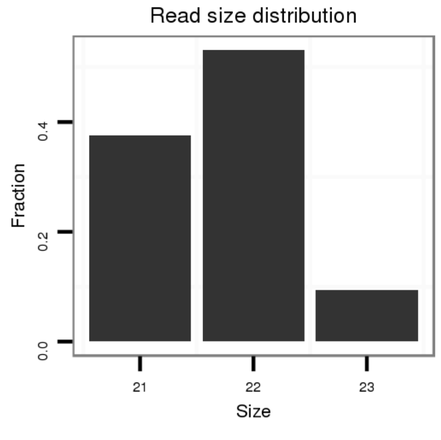
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_199	**scaffold_6308:1287576-1287636 -**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

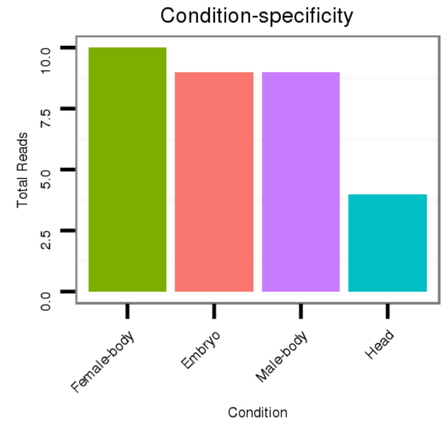
Legend: mature star mismatch in alignment mismatch in read

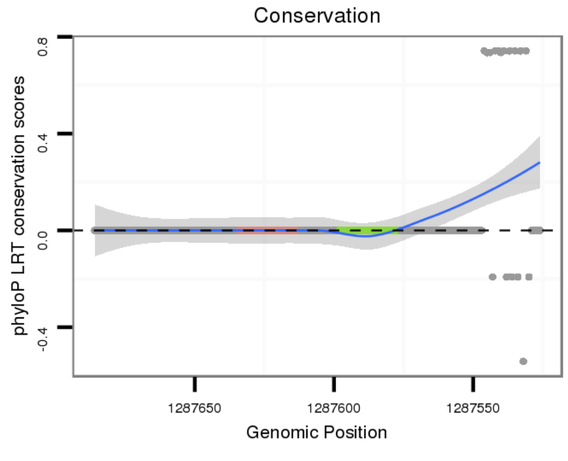
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI10984-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AACTATTTCACTGTGATCCATAGCAAACTCAGCTTCTTGAGATCGATAATTCCATCTGGATCCCCTTACATAGTATTGTAATATTGTATATGTAATGGGATCTAGATGGAACTATAGACCTCCAGCAGCAGACCCTGTTATGGGAACATATATAGATCGTC **********.(((.((.(((.((((((((((((((.(((((((.(((........)))))))))).))))))))))))))).))).))).)))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	M060 embryo	V056 head	V049 head	V041 embryo
..........TATGTAATGGGATCTAGATGGA..........	22	0	1	10.00	10	5	1	1	0	2	1
..........TATGTAATGGGATCTAGATGG..........	21	0	1	9.00	9	3	2	3	1	0	0
..........TATGTAATGGGATCTAGATGGT..........	22	1	1	9.00	9	8	1	0	0	0	0
..........CATCTGGATCCCCTTACATAGT..........	22	0	1	4.00	4	1	1	2	0	0	0
..........TGTAATGGGATCTAGATGGAAC..........	22	0	1	3.00	3	3	0	0	0	0	0
..........CATCTGGATCCCCTTACATAGTA..........	23	0	1	2.00	2	0	2	0	0	0	0
..........CATCTGGATCCCCTTACATAG..........	21	0	1	1.00	1	0	1	0	0	0	0
..........TGTAATGGGATCTAGATGGAACT..........	23	0	1	1.00	1	1	0	0	0	0	0
..........GGAACTATAGACCTCCAGCA..........	20	0	1	1.00	1	0	1	0	0	0	0
..........TCTGGATCCCCTTACATAGTA..........	21	0	1	1.00	1	0	1	0	0	0	0
..........TATGTAATGGGATCTAGATGGC..........	22	1	1	1.00	1	1	0	0	0	0	0
..........ATCTGGATCCCCTTACATAGTA..........	22	0	1	1.00	1	0	1	0	0	0	0
..........AATGGGATCTAGATGGAACT..........	20	0	1	1.00	1	1	0	0	0	0	0
..........ATATGTAATGGGATCTAGATGG..........	22	0	1	1.00	1	0	0	0	1	0	0
..........ATGTAATGGGATCTAGATGGA..........	21	0	1	1.00	1	0	1	0	0	0	0
..........TATGTAATGGGATCTAGATGGAA..........	23	0	1	1.00	1	0	0	1	0	0	0
..........TCCATCTGGATCCCCTTACATA..........	22	0	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

TTGATAAAGTGACACTAGGTATCGTTTGAGTCGAAGAACTCTAGCTATTAAGGTAGACCTAGGGGAATGTATCATAACATTATAACATATACATTACCCTAGATCTACCTTGATATCTGGAGGTCGTCGTCTGGGACAATACCCTTGTATATATCTAGCAG **********.(((.((.(((.((((((((((((((.(((((((.(((........)))))))))).))))))))))))))).))).))).)))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V110 male body	M046 female body	V056 head	V049 head	M060 embryo	V041 embryo
..........TAAGGTAGACCTAGGGGAATGT..........	22	0	1	5080.00	5080	5006	48	16	5	2	3
..........CTAAGGTAGACCTAGGGGAATGT..........	23	1	1	407.00	407	401	6	0	0	0	0
..........TTAAGGTAGACCTAGGGGAATGT..........	23	0	1	291.00	291	288	3	0	0	0	0
..........AAGGTAGACCTAGGGGAATGT..........	21	0	1	284.00	284	277	4	2	1	0	0
..........CAAGGTAGACCTAGGGGAATGT..........	22	1	1	163.00	163	162	0	0	1	0	0
..........TAAGGTAGACCTAGGGGAATG..........	21	0	1	122.00	122	118	4	0	0	0	0
..........AGGTAGACCTAGGGGAATGT..........	20	0	1	32.00	32	31	0	1	0	0	0
..........CTAAGGTAGACCTAGGGGAATG..........	22	1	1	30.00	30	29	1	0	0	0	0
..........CTTAAGGTAGACCTAGGGGAATGT..........	24	1	1	19.00	19	19	0	0	0	0	0
..........TTAAGGTAGACCTAGGGGAATG..........	22	0	1	18.00	18	18	0	0	0	0	0
..........GTAAGGTAGACCTAGGGGAATGT..........	23	1	1	15.00	15	14	1	0	0	0	0
..........ATAAGGTAGACCTAGGGGAATGT..........	23	1	1	13.00	13	13	0	0	0	0	0
..........AAAGGTAGACCTAGGGGAATGT..........	22	1	1	11.00	11	11	0	0	0	0	0
..........CAAGGTAGACCTAGGGGAATG..........	21	1	1	9.00	9	9	0	0	0	0	0
..........CTTAAGGTAGACCTAGGGGAAT..........	22	1	1	8.00	8	8	0	0	0	0	0
..........GGTAGACCTAGGGGAATGT..........	19	0	1	8.00	8	8	0	0	0	0	0
..........TTTAAGGTAGACCTAGGGGAATGT..........	24	1	1	7.00	7	7	0	0	0	0	0
..........TTTAAGGTAGACCTAGGGGAAT..........	22	1	1	7.00	7	7	0	0	0	0	0
..........GAAGGTAGACCTAGGGGAATGT..........	21	1	1	6.00	6	6	0	0	0	0	0
..........AAGGTAGACCTAGGGGAATG..........	20	0	1	5.00	5	5	0	0	0	0	0
..........GTTAAGGTAGACCTAGGGGAATGT..........	24	1	1	4.00	4	4	0	0	0	0	0
..........GAAGGTAGACCTAGGGGAATGT..........	22	1	1	3.00	3	3	0	0	0	0	0
..........ATAAGGTAGACCTAGGGGAATG..........	22	1	1	3.00	3	3	0	0	0	0	0
..........TATAAGGTAGACCTAGGGGAATGT..........	24	2	1	3.00	3	3	0	0	0	0	0
..........TAAGGTAGACCTAGGGGAAT..........	20	0	1	2.00	2	1	0	0	0	0	1
..........AAGGTAGACCTAGGGGAAT..........	19	0	1	2.00	2	2	0	0	0	0	0
..........ATTAAGGTAGACCTAGGGGAATGT..........	24	0	1	2.00	2	2	0	0	0	0	0
..........CTACATTACCCTAGATCTACCT..........	22	1	1	2.00	2	1	1	0	0	0	0
..........GTAAGGTAGACCTAGGGGAATG..........	22	1	1	2.00	2	2	0	0	0	0	0
..........TAAGGTAGACCTAGGGGA..........	18	0	1	1.00	1	1	0	0	0	0	0
..........TTAAGGTAGACCTAGGGGAAT..........	21	0	1	1.00	1	1	0	0	0	0	0
..........CTGGTAGACCTAGGGGAATGT..........	21	2	1	1.00	1	1	0	0	0	0	0
..........TTTAAGGTAGACCTAGGGGAATG..........	23	1	1	1.00	1	1	0	0	0	0	0
..........CTTTAAGGTAGACCTAGGGGAATGT..........	25	2	1	1.00	1	1	0	0	0	0	0
..........CGTAGACCTAGGGGAATGT..........	19	1	1	1.00	1	1	0	0	0	0	0
..........TGTAAGGTAGACCTAGGGGAAT..........	22	2	1	1.00	1	1	0	0	0	0	0
..........CAAGGTAGACCTAGGGGAA..........	19	1	1	1.00	1	1	0	0	0	0	0
..........TACATTACCCTAGATCTACCT..........	21	0	1	1.00	1	1	0	0	0	0	0
..........TCTAAGGTAGACCTAGGGGAATGT..........	24	2	1	1.00	1	1	0	0	0	0	0
..........CCAAGGTAGACCTAGGGGAATGT..........	23	2	1	1.00	1	1	0	0	0	0	0
..........AAAAGGTAGACCTAGGGGAATGT..........	23	2	1	1.00	1	1	0	0	0	0	0
..........CGGTAGACCTAGGGGAATGT..........	20	1	1	1.00	1	1	0	0	0	0	0
..........AGGTAGACCTAGGGGAATG..........	19	0	1	1.00	1	1	0	0	0	0	0
..........TACAAGGTAGACCTAGGGGAAT..........	22	3	1	1.00	1	1	0	0	0	0	0
..........ATACATTACCCTAGATCTACCT..........	22	0	1	1.00	1	0	1	0	0	0	0
..........GTAGACCTAGGGGAATGT..........	18	0	1	1.00	1	1	0	0	0	0	0
..........TAAGACCTAGGGGAATGT..........	18	2	5	0.20	1	1	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6308:1287526-1287686 -	dmo_199	AACTATTTCACTGTGATCCATAGCAAACTCAGCTTCTTGAGATCGATAATTCCATCTGGATCCCCTTACATAGTATTGTAATATTGTATATGTAATGGGATCTAGATGGAACTATAGACCTCCAGCAGCAGACCCTGTTATGGGAACATATATAGATCGTC
droKik1	scf7180000302798:195250-195266 +		----------TGGAAACACACACACAC---

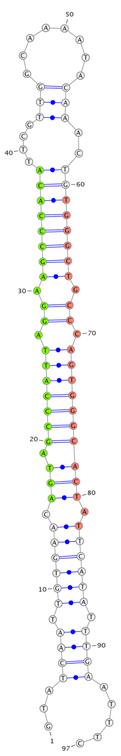
Generated: 09/08/2015 at 07:48 PM

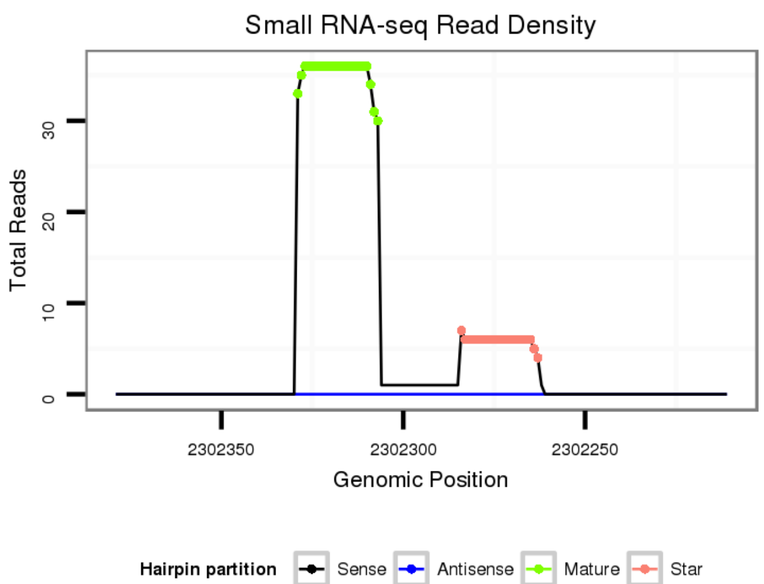
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

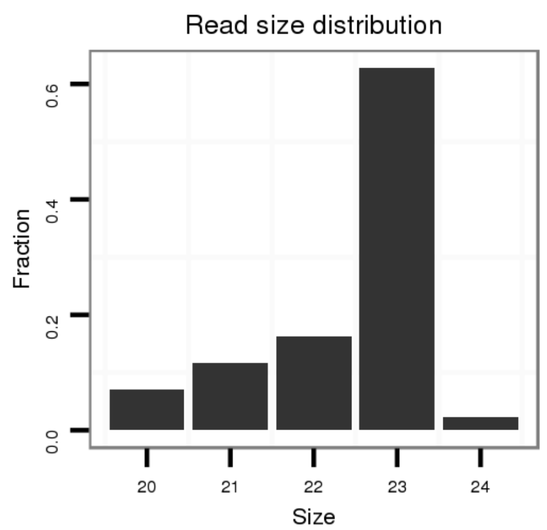
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_126	**scaffold_6328:2302261-2302329 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

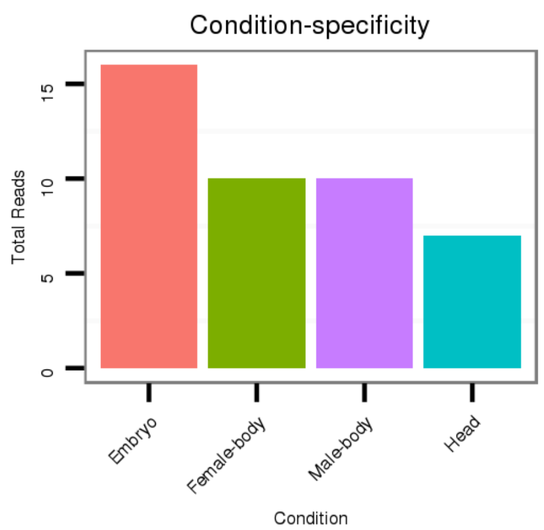
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CGCAGGTTTATAAAAGCCAATCAGGTGAACTATGTGTATCAATTGTGAACAGTAGCCCATTAGGAAGCCCACATTCGTTGGCAAAATACAAACTGTGGGCTGCCCAGTGGGCACTATTCATATTTGAATTTCCCGCCAACCAATTGACAATTAACTTGGACTTGATAAT **********...((((.((((((.(((.(((((((.((.(((((((((....(((........))))..))))))))).)).)))))))))).))))))..))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V110 male body	M046 female body	V056 head	V049 head	V041 embryo
.....AGTAGCCCATTAGGAAGCCCACA.....	23	0	1	26.00	26	11	7	3	1	3	1
.....TGGGCTGCCCAGTGGGCACTAT.....	22	0	1	3.00	3	1	0	1	1	0	0
.....AGTAGCCCATTAGGAAGCCCA.....	21	0	1	3.00	3	0	2	0	0	1	0
.....AGTAGCCCATTAGGAAGCCC.....	20	0	1	2.00	2	0	0	1	1	0	0
.....AGTAGCCCATTAGGAAGCCCAC.....	22	0	1	2.00	2	0	1	1	0	0	0
.....GTAGCCCATTAGGAAGCCCACA.....	22	0	1	2.00	2	1	0	1	0	0	0
.....TGGGCTGCCCAGTGGGCACTATAA.....	24	2	1	1.00	1	0	0	1	0	0	0
.....ATTCGTTGGCAAAATACAAACTGT.....	24	0	1	1.00	1	0	0	1	0	0	0
.....TGGGCTGCCCAGTGGGCACT.....	20	0	1	1.00	1	0	0	1	0	0	0
.....TGGGCTGCCCAGTGGGCACTA.....	21	0	1	1.00	1	0	0	1	0	0	0
.....TGGGCTGCCCAGTGGGCACTATT.....	23	0	1	1.00	1	0	0	0	0	0	1
.....AGTAGCCCATTAGGAAGCCCATC.....	23	2	1	1.00	1	0	1	0	0	0	0
.....TAGCCCATTAGGAAGCCCACA.....	21	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

GCGTCCAAATATTTTCGGTTAGTCCACTTGATACACATAGTTAACACTTGTCATCGGGTAATCCTTCGGGTGTAAGCAACCGTTTTATGTTTGACACCCGACGGGTCACCCGTGATAAGTATAAACTTAAAGGGCGGTTGGTTAACTGTTAATTGAACCTGAACTATTA **********...((((.((((((.(((.(((((((.((.(((((((((....(((........))))..))))))))).)).)))))))))).))))))..))))).....**********	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_6328:2302211-2302379 -	dmo_126	CGCAGGTTTATAAAAGCCAATCAGGTGAACTATGTGTATCAATTGTGAACAGTAGCCCATTAGGAAGCCCACATTCGTTGGCAAAATACAAACTGTGGGCTGCCCAGTGGGCACTATTCATATTTGAATTTCCCGCCAACCAATTGACAATTAACTTGGACTTGATAAT

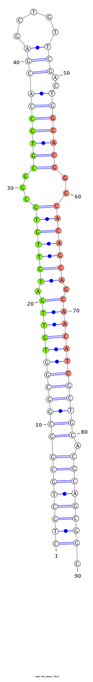
Generated: 09/08/2015 at 07:48 PM

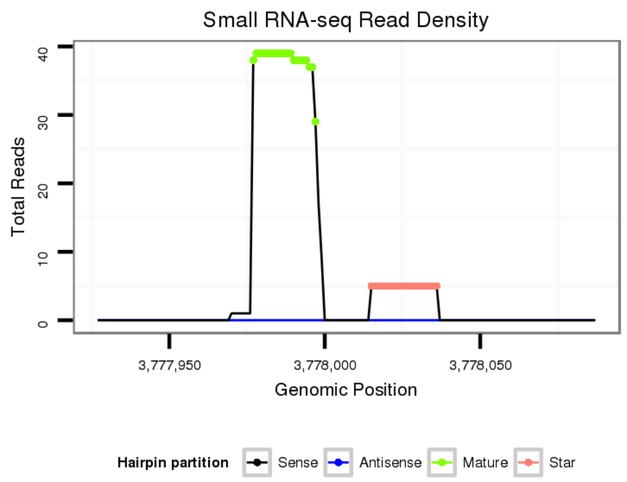
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

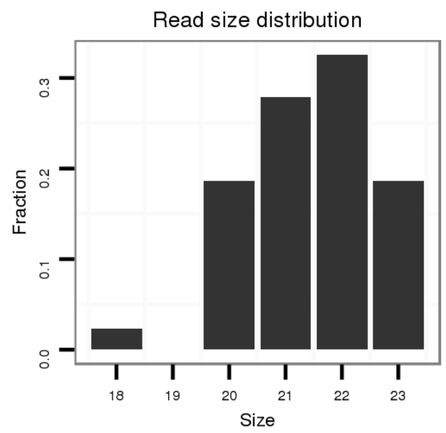
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_164	**scaffold_6359:3777977-3778037 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

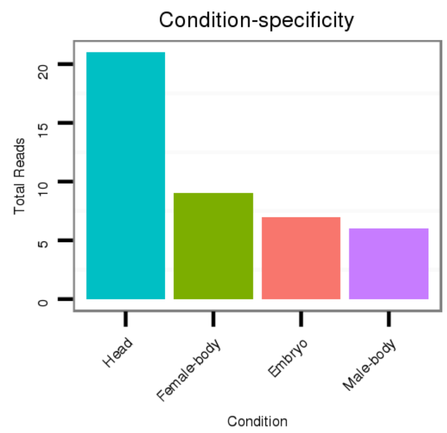
Legend: mature star mismatch in alignment mismatch in read

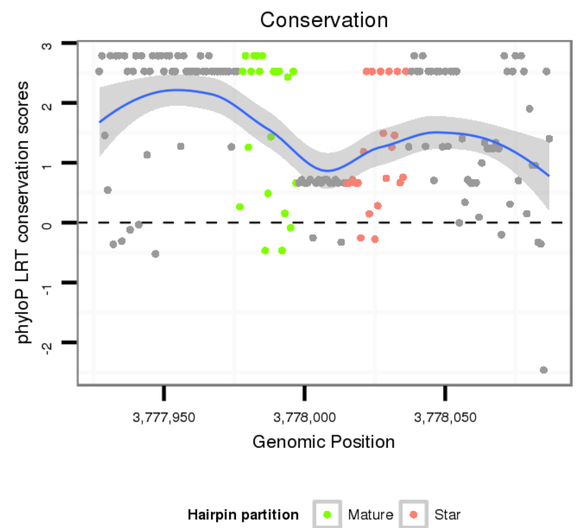
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI21783-in]; CDS [Dmoj\GI21783-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GATTTGTATTCTGTGACGGAATTGTAGGAGTGCGCCTGCTGCGGCGGCGGTGTTGATGTTGTGCGGCGTGCCACGAGCTGTTCGACTGGCACGGCCACAGCAGCAACATCGCTGCACGCAGCGGCGGCAGCAGCCTCAGCCAGCACACAGACACAAGCCCA **********(((((((((((((((((((.(((((((...((((((((((.....)))).))))))).))))))).)))))))))))).)))))))).********** **Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V049 head**	**V056 head**	**M046 female body**	**M060 embryo**	**V110 male body**	**V041 embryo**
.....TGTTGATGTTGTGCGGCGTGC.....	21	0	1	12.00	12	6	1	2	1	2	0
.....TGTTGATGTTGTGCGGCGTGCCA.....	23	0	1	8.00	8	0	2	2	0	3	1
.....TGTTGATGTTGTGCGGCGTGCC.....	22	0	1	8.00	8	1	2	3	0	1	1
.....TGTTGATGTTGTGCGGCGTG.....	20	0	1	8.00	8	4	3	1	0	0	0
.....GCACGGCCACAGCAGCAACATC.....	22	0	1	5.00	5	0	1	0	4	0	0
.....GCGGCGGTGTTGATGTTGTG.....	20	0	1	1.00	1	0	0	0	1	0	0
.....GTTGATGTTGTGCGGCGTGCCA.....	22	0	1	1.00	1	0	0	1	0	0	0
.....TGTTGATGTTGTGCGGCG.....	18	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

CTAAACATAAGACACTGCCTTAACATCCTCACGCGGACGACGCCGCCGCCACAACTACAACACGCCGCACGGTGCTCGACAAGCTGACCGTGCCGGTGTCGTCGTTGTAGCGACGTGCGTCGCCGCCGTCGTCGGAGTCGGTCGTGTGTCTGTGTTCGGGT **********(((((((((((((((((((.(((((((...((((((((((.....)))).))))))).))))))).)))))))))))).)))))))).********** **Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M060 embryo**
.....GTTGATGTTGTGCGGCGTGCCA.....	22	0	1	1.00	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6359:3777927-3778087 +	dmo_164	GATTTGTATTCTGTGACGGAATTGTAGGAGTGCGCCTGCTGCGGCGGCGGTGTTGATGTTGTGCGGCGTGCCACGAGCTGTTCGACTGGCACGGCCACAGCAGCAACATCGCTGCACGCAGCGGCGGCAGCAGCCTCAGCCAGCACACAGAC----------ACAA----------GCCCA
droVir3	scaffold_12928:5263551-5263708 +	dvi_130	GATTTGTATTCTGTGACGGAATTGTAGGAGTGCGCCTGCTGCGGCGGCGGCGTTGATGTGCGGCGT---GCCACGAACTGTTCGACGGGCACGAGGCAACATCAACGGCGCTGCACGCAGCGGCGGCGGCAGCCTCAGCCAGCACACAGAC----------ACAA----------ACTCA
droGri2	scaffold_14853:9936519-9936685 +		GATTTGTATTCCGTAACGGAGTTGTAGGAGTGCGCCTGCTGCGGCGGCGGCGTTGATGTTTGTGCGACGTGCCACGAACTGTTCGACCGGCACGACACACGATCACGCTGCTGCACGCAGCAGCGGCGGCAGCCTCAGCCAGTACACAGAC----------TCAAGCTC----AA----------GCTCA
droWil2	scf2_1100000004909:2563022-2563152 -		GATTTATATTCTGTTACCGAATTGTAGGAGTGCGCCTGCTGCGGCGGCGGTGGCGTTGATGTAGTGCGTAGCG----------GCACACAACAACGTCACTGCACGCAGCGGCGGCC------ACAGCCAGTACACAGAC----------ACAGA----------TGCC
dp5	XL_groupla:4975084-4975214 +		GACCTCTACTCCGTGACGGAGTTGTAGGAGTGCGCCTGCTGCGGCGGCGGCGTTGATGTTGTGCGAGGCG----------GCACATCATCAACGTCGCTGCACGCAGCGGCGGCGGCGT------AGCCAGCACACAGAC----------CCAGA----------CCCA
droPer2	scaffold_11:1564045-1564175 +		GACCTCTACTCCGTGACGGAGTTGTAGGAGTGCGCCTGCTGCGGCGGCGGCGTTGATGTTGTGCGAGGCG----------GCACATCATCAACGTCGCTGCACGCAGCGGCGGCGGCGT------AGCCAGCACTCAGAC----------CCAGA----------CCCA
droAna3	scaffold_12929:978060-978193 +		GATCTGTACTCCGTGACGGAGTTGTAGGAGTGCGCCTGCTGCGGCGGCGGTGTGGATGTGGTGCGTCGCG----------GCGCCTCATCCACATCGCTGCACGCAGCGGCGGC----------CACCCAAAC----------CCCAGCACAGAGTCAA----------GCCCA
droBip1	scf7180000394786:11037-11173 -		GATCTATATTCTGTAACGGAATTGTAGGAGTGCGCCTGCTGCGGCGGCGGTGTGGATGTGGTGCGTCGCG----------GCGCCTCATCCACATCGCTGCACGCAGCGGCGGC----------CACCCAAAC----------CCAAGGACA--GCCGG----------CGCCGGGACA
droKik1	scf7180000302469:59512-59654 -		GATCTTTATTCTGTGACGGAATTGTAGGAATGCGCCTGCTGCGGCGGCGGTGTGGATGTGGTGCGTCGCG----------GCGCCTCATCCACAACGCTGCATGCAGCGGCGGCGGC----------CACACAGACAACACAAACACAACAAAATCAGA----------CACA
droFic1	scf7180000454072:2002067-2002221 +		GATCTGTACTCCGTGACGGAATTGTAGGAGTGCGCCTGCTGCGGCGGCGGTGTGGATGTGGTGCGCAGAG----------GCGCCTCATCCACATCGCTGCACGCGGCGGCGGCGGC----------CACACAAAC----------TCAGAGCCACAACCAAAACCAAACACAGACGCAGACCCA
droEle1	scf7180000491043:339249-339376 +		GATCTGTATTCGGTGACGGAATTGTAGGAGTGCGCCTGCTGCGGCGGCGGTGTGGATGTGGTGCGCCGAG----------GCACTTCATCCACATCGCTGCACGCGGCGGCGGC----------CACACAAAC----------TCAGAG------CCAA----------AACCA
droRho1	scf7180000779976:81342-81493 +		GATCTGTACTCGGTGACGGAGTTGTAGGAGTGCGCCTGCTGCGGCGGCGGTGTGGATGTGGTGCGCCGAG----------GCGCCTCATCCACATCGCTGCACGCGGCGGTGGC----------CACACAAAC----------TCAGAGCCACAACCAAAACCAGACGCAGTCACAACCGCA
droBia1	scf7180000302069:825521-825654 -		GATCTGTACTCCGTGACGGAGTTGTAGGAGTGCGCCTGCTGCGGCGGCGGTGTGGATGTTGTGCGCCGAG----------GCGCCTCATCCACATCGCTGCACGCGGCGGCGGC----------CACACAAAC----------TCAGAGCCACACCCAA----------AACCA
droTak1	scf7180000413933:64340-64488 +		GATCTGTATTCGGTGACGGAGTTGTAGGAGTGCGCCTGCTGCGGCGGCGGTGTGGATGTGGTGCGAAGAG----------GCGCTTCATCCACATCGCTGCACGCAGCGGCGGC----------TACACAAAC----------TCAGAGCCACAACCAAAACCCGACG---ACGCAATCGCA
droEug1	scf7180000408973:234325-234458 +		GATTTATAGTCGGTGACGGAGTTGTAGGAGTGCGCCTGCTGCGGCGGCGGTGTGGATGTAGTGCGCCGAG----------GCGCCTCATCCACATCGCTGCACGCGGCGGCGGC----------CACACAAAC----------TCAAACCCACAACCAA----------AACCA
dm3	chrX:1113631-1113764 -		GATCTGTACTCGGTGACGGAGTTGTAGGAGTGCGCCTGCTGCGGCGGCGGTGTGGATGTGGTGCGCCGAG----------GCGCATCGTCCACATCGCTGCACGCGGCGGCGGC----------TACACAAAC----------TCAGACCCACACCCAA----------AACCA
droSim2	x:1003017-1003150 -		GATCTGTACTCGGTGACGGAGTTGTAGGAGTGCGCCTGCTGCGGCGGCGGTGTGGATGTGGTGCGCCGAG----------GCGCATCATCCACATCGCTGCACGCGGCGGCGGC----------TACACAAAC----------TCAGACCCATACCCAA----------AACCA
droSec2	scaffold_10:947883-948016 -		GATCTGTACTCGGTGACGGAGTTGTAGGAGTGCGCCTGCTGCGGCGGCGGTGTGGATGTGGTGCGCCGAG----------GCGCATCATCCACATCGCTGCACGCGGCGGCGGC----------TACACAAAC----------TCAGACAAATACCCAA----------AACCA
droYak3	X:1028374-1028507 -		GATCTGTACTCGGTGACGGAGTTGTAGGAGTGCGCCTGCTGCGGCGGCGGCGGTGGATGTGGTGCGCCGAG----------GCGCCTCATCCACATCGCTGCACGCGGCGGCGGC----------CACACAAAC----------TCAGACACACACCCAA----------AACCA
droEre2	scaffold_4644:1098901-1099034 -		GATCTGTACTCGGTAACGGAGTTGTAGGAGTGCGCCTGCTGCGGCGGCGGTGTGGATGTGGTGCGCCGAG----------GCGCCTCATCCACATCGCTGCACGCGGCGGCGGC----------TACCCAAAC----------TCAGACACACACCCAA----------AACCA

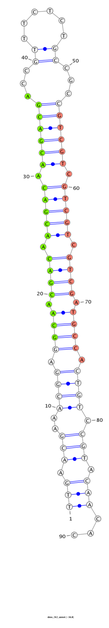
Generated: 09/08/2015 at 07:49 PM

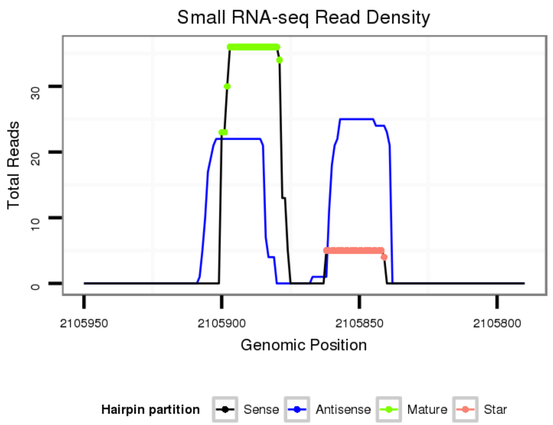
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

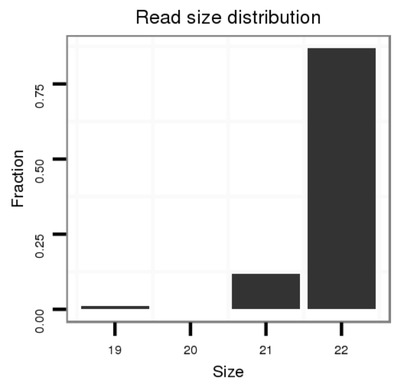
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_262	**scaffold_6359:2105840-2105900 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

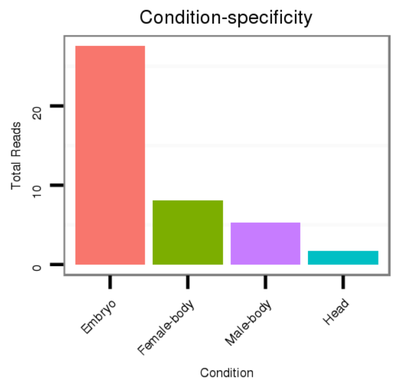
Legend: mature star mismatch in alignment mismatch in read

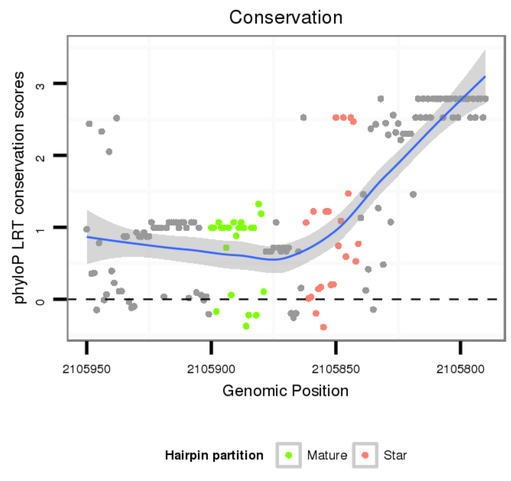
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dmo_262 scaffold_6359:2105879-2105900 - 2. scaffold_6473:8207900-8207921 - 3. scaffold_6680:14609463-14609484 -	

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTTGTTTTTGCCGTTGCTGTTGCTGCTGCGCTCAATTGAACGAAACGGAGGCAACGACAACGACAACGACGACCGTTTCTCTGCCGCCGTCGTCGTCGTCGATGCCACTGTCCGTACAACACACAAAAACAGTCAGTTTTCATTCTCATTTGACATCA **********(((.(((..((((.((((.((((.((((((.((((((...((.....))...))))))).))))).))))).))))).))).)))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V049 head	V056 head
.....GCAACGACAACGACAACGACGA.....	22	0	3	21.00	63	36	12	12	0	2	1
.....AACGACAACGACAACGACGACC.....	22	0	1	7.00	7	7	0	0	0	0	0
.....ACGACAACGACAACGACGACCG.....	22	0	1	5.00	5	2	2	0	1	0	0
.....GTCGTCGTCGTCGTCGATGCCA.....	22	0	1	4.00	4	3	1	0	0	0	0
.....GCAACGACAACGACAACGACG.....	21	0	4	2.75	11	2	2	5	2	0	0
.....ACGACAACGACAACGACGACC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GTCGTCGTCGTCGTCGATGCC.....	21	0	2	1.00	2	1	1	0	0	0	0
.....GTCGTCGTCGTCGTCGATG.....	19	0	8	0.50	4	0	1	0	0	1	2
.....CCGTCGTCGTCGTCGATG.....	21	0	3	0.33	1	0	0	0	0	1	0
.....GCAACGACAACGACAACGACGAA.....	23	1	5	0.20	1	0	0	1	0	0	0
.....CAACGACAACGACAACGACGAC.....	22	0	19	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

CAACAAAAACGGCAACGACAACGACGACGCGAGTTAACTTGCTTTGCCTCCGTTGCTGTTGCTGTTGCTGCTGGCAAAGAGACGGCGGCAGCAGCAGCAGCAGCTACGGTGACAGGCATGTTGTGTGTTTTTGTCAGTCAAAAGTAAGAGTAAACTGTAGT **********(((.(((..((((.((((.((((.((((((.((((((...((.....))...))))))).))))).))))).))))).))).)))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V041 embryo	V056 head	V110 male body	V049 head
.....AGCAGCAGCAGCAGCTACGGTGA.....	23	0	1	8.00	8	4	0	3	1	0	0
.....GCAGCAGCAGCAGCTACGGTGA.....	22	0	1	7.00	7	0	3	2	2	0	0
.....GCCTCCGTTGCTGTTGCTGTT.....	21	0	1	5.00	5	1	1	1	1	1	0
.....TGCCTCCGTTGCTGTTGCTGTT.....	22	0	1	5.00	5	5	0	0	0	0	0
.....GCAGCAGCAGCTACGGTGA.....	19	0	1	3.00	3	1	1	0	0	1	0
.....TTGCCTCCGTTGCTGTTGCTGTT.....	23	0	1	3.00	3	0	1	1	0	0	1
.....AGCAGCAGCAGCAGCTACGGTG.....	22	0	1	2.00	2	0	0	0	2	0	0
.....CTCCGTTGCTGTTGCTGTTGCTG.....	23	0	1	2.00	2	1	0	0	0	1	0
.....CAGCAGCAGCAGCTACGGTGA.....	21	0	1	2.00	2	0	1	0	1	0	0
.....GCCTCCGTTGCTGTTGCTGTTG.....	22	0	1	2.00	2	2	0	0	0	0	0
.....TCCGTTGCTGTTGCTGTTGCTG.....	22	0	2	1.50	3	0	0	2	0	1	0
.....TTTGCCTCCGTTGCTGTTGCTGTT.....	24	0	1	1.00	1	0	1	0	0	0	0
.....GGCGGCAGCAGCAGCAGCTA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....CTGCCTCCGTTGCTGTTGCTGTT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....CCTCCGTTGCTGTTGCTGTTGCTG.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TTGCCTCCGTTGCTGTTGCTGT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....CCTCCGTTGCTGTTGCTGTTG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....AGCAGCAGCAGCTACGGTGA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....CAGCAGCAGCAGCTACGGT.....	19	0	1	1.00	1	0	1	0	0	0	0
.....CCGTTGCTGTTGCTGTTGCTGC.....	22	0	3	0.67	2	1	0	1	0	0	0
.....CGCCTCCGTTGCTGTTGCTGTT.....	22	1	4	0.50	2	2	0	0	0	0	0
.....CGGCAGCAGCAGCAGCTA.....	21	0	3	0.33	1	0	0	0	0	0	1
.....TGGCAGCAGCAGCAGCTAC.....	22	1	6	0.17	1	0	0	1	0	0	0
.....GCAGCAGCAGCAGCTA.....	20	1	20	0.05	1	1	0	0	0	0	0
.....GGCAACGACAACGACGAC.....	18	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_6359:2105790-2105950 -	dmo_262	----------GTTGTT--TTTGCCGTT------GCTGTTGCTGCTGC---GCTCAATTGAACG----------AAACGGAGGCAACGACAA----------CGA---C-AACGACGA----------CCGTTTCTCTGCCG----------CCGTCGTCGTCGTCGTCG---ATGCCACTGTC---CGTACA--ACACACAAAA--------ACAGTCAGTTTTCATTCTCATTTGACATCA
droVir3	scaffold_13042:4327252-4327416 +	dvi_24645	----------GTTGTT--TTTGCTGCC-----**----------**TGC---GCTCAATTGAACG----------AAACACAGGCAACGACGACG----------**-GACGA-G**CACGACGA----------CCGTTTCTCTGTCGCCGTCGCTGCTGG-TCGCCGTCGCG**----------**GCCG---TTGCCTCTACCG--CAC--AACACAAAA--------ACAGTCAGTTTTCATTCTCATTTGACATCA
droGri2	scaffold_14853:7184297-7184494 +		----------GTTATT--T-TGTTGTTGTTGCTGCTGCTGCTGGCCGCTCAATTGAACG----------AAACAGAAGGCACGACGACGATGC----CGACTTGTCGA---CTGTCGTC-TCGCCTAGCGCCCGTTCCGTTTCTCTATTGCC----------G-----AG---GCGCCGTTGCCG---TTGCCTCTGTCGGCAGCACA---AC-ACAC----AAAAAACAGTCAGTTTTCATTCTCATTTGACATCA
droWil2	scf2_1100000004909:8778446-8778532 -		CG----TTG------GTCGTTGGTTCGTTGTC-----**----------**---**----------**----------**----------**----**----**-**--------**----------**----------**----------GTCGGTCG-----TC**----------**GTCG---TTGCGCGCTGCGGCAGCAG---**----------**------CAGCAGTCAGTTTTCATTCTCATTTGACATCA
dp5	XL_groupla:1470282-1470462 -		----------GTCGCC--TCTGCTGC-----**----------**TGC---GCGCAATTGAACTCACAGAGCAGCAGCAAGCAGCAGCGACG-CGACTTCGTCTCGACACATCGA---C-ATCGTCGTCG--TAG---------**----**T**---------**-----CC--------G----CCGTCGCCGTCGCTATCGTTGTCG---TTGCGTCTCT**---**GGCGCGCACACAAAACACAAAA------ACACAGTCAGTTTTCATTCTCATTTGACATCA
droPer2	scaffold_53:327882-328064 +		----------GT-----**----------**---GTCGCTCTGCTGCTGC---GCGCAATTGAAGTCACAGAGCAGCAGCAAGCAGCAGCGACG-CGACTTCGTCTCGACACATCGA---C-ATCGTCGTCG--TAG---------**----**T**---------**-----CC--------G----CCGTCGCCGTCGCTATCGTTGTCG---TTGCGTCTCT**---**GGCGCGCACACAAAACACAAAA------ACACAGTCAGTTTTCATTCTCATTTGACATCA
droAna3	scaffold_13117:3146030-3146137 -		CG----TCGCCCCAA-**----------**-----CGT-----**----------**---**----------**----------**----------**----**----**-**--------**----------**----------**----------GTCG----CCGACGCCGCGCATGTGAGGCTGTGCTGCCTCTGGC---AGCACA-AAAACACAAAA------ACACAGTCAGTTTTCATTCTCATTTGACATCA
droBip1	scf7180000395515:16096-16203 -		ACGACGTCGCCCCAA-**----------**-----CGT-----**----------**---**----------**----------**----------**----**----**-**--------**----------**----------**----------GTCG----CCGACGCCGCGCGGTTGAGGCTGTGCTGCCTCTGGC---AGCACA-AAAACACAAAA------ACACAGTCAGTTTTCATTCTCATTTGACATCA
droKik1	scf7180000302586:297324-297413 +		----------TTACGGC--T-----GC-----**----------**---**----------**----------**----------**----**----**-**--------**----------**----------**----------CACAGTCGCTGCTGC-----AG**----------**GTCG---CCGCCTCTGCTGCCGGCGCAGA-AAACACACAAAA--------ACAGTCAGTTTTCATTCTCATTTGACATCA
droFic1	scf7180000453926:215984-216075 +		----------GTCGCC--TTCGGTGCC-----**----------**---**----------**----------**----------**----**----**-**--------**----------**----------**----------G-----AG**----------**GTCG---CTGCCTCTGCTGCCGGCGCACA-AAACACAAAA**ACAGAAAAC**ACAGTCAGTTTTCATTCTCATTTGACATCA
droEle1	scf7180000491087:1168345-1168429 -		----------------**------**--TTGGTGCC-----**----------**---**----------**----------**----------**----**----**-**--------**----------**----------**----------G-----AG**----------**GTCG---CTGCTTCTGCCGGCAGCACA-AAACACAAAA**ACAGAAAAC**ACAGTCAGTTTTCATTCTCATTTGACATCA
droRho1	scf7180000779980:50820-50911 -		----------GTCGGC--TTTGCTGCC-----**----------**---**----------**----------**----------**----**----**-**--------**----------**----------**----------G-----AG**----------**GTCG---CTGCTTCTGGCCACAGCACA-AAACACAAAA**ACAGAAAAC**ACAGTCAGTTTTCATTCTCATTTGACATCA
droBia1	scf7180000302432:371571-371654 -		----------GTCGTC--TTTGCTGCC-----**----------**---**----------**----------**----------**----**----**-**--------**----------**----------**----------G-----AG**----------**GTCG---CTGCCTCTGCCGGCGCACA-AAAAC**------**--**AGAAAAC**ACAGTCAGTTTTCATTCTCATTTGACATCA
droTak1	scf7180000415769:193079-193174 -		CA----------TCGTCGTC--TGCGGTGCC-----**----------**---**----------**----------**----------**----**----**-**--------**----------**----------**----------G-----AG**----------**GTCG---CTGCCTCTAGCCGGCGCACA-AAACACAAAA**ACAGAAAAC**ACAGTCAGTTTTCATTCTCATTTGACATCA
droEug1	scf7180000408193:234800-234890 -		CA----------TCGTCGT--C----GCGCA-----**----------**---**----------**----------**----------**----**----**-**--------**----------**----------**----------G-----AG**----------**GTCG---CTGCCTCTGCCGGCGCACA-AAACACAAAA**ACAGAAAAC**ACAGTCAGTTTTCATTCTCATTTGACATCA
dm3	chrX:21239004-21239091 +		--------------TC--TCTGCTGCC-----**----------**---**----------**----------**----------**----**----**-**--------**----------**----------**----------A-----AG**----------**GTCG---CTGCCTCTGCCGGCGCACA-AAACACAAAA**ACAGAAAAC**ACAGTCAGTTTTCATTCTCATTTGACATCA
droSim2	x:19972277-19972368 +		----------GTCGTC--TTTGCTGCC-----**----------**---**----------**----------**----------**----**----**-**--------**----------**----------**----------G-----AG**----------**GTCG---CTGCCTCTGCCGGCGCACA-AAACACAAAA**ACAGAAAAC**ACAGTCAGTTTTCATTCTCATTTGACATCA
droSec2	scaffold_8:3546865-3546956 +		----------GTCGTC--TTTGCTGCC-----**----------**---**----------**----------**----------**----**----**-**--------**----------**----------**----------G-----AG**----------**GTCG---CTGCCTCTGCCGGCGCACA-AAACACAAAA**ACAGAAAAT**ACAGTCAGTTTTCATTCTCATTTGACATCA
droYak3	X:20418071-20418154 +		----------GTCGTC--TTTGCTGCC-----**----------**---**----------**----------**----------**----**----**-**--------**----------**----------**----------G-----AG**----------**GTCG---CTGCCTCTGCCGGCGCACA-AAAAC**------**--**AGAAAAC**ACAGTCAGTTTTCATTCTCATTTGACATCA
droEre2	scaffold_4690:17769587-17769690 +		CG----TCTCCACATCGTCGTC--TTTGCTGCC-----**----------**---**----------**----------**----------**----**----**-**--------**----------**----------**----------G-----AG**----------**GTG---CTGCTTCTGCCGGCGCACA-AAACACAAAA**ACAGAAAAC**ACAGTCAGTTTTCATTCTCATTTGACATCA

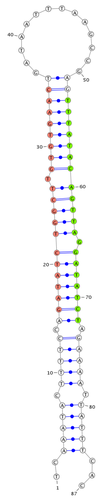
Generated: 09/08/2015 at 07:50 PM

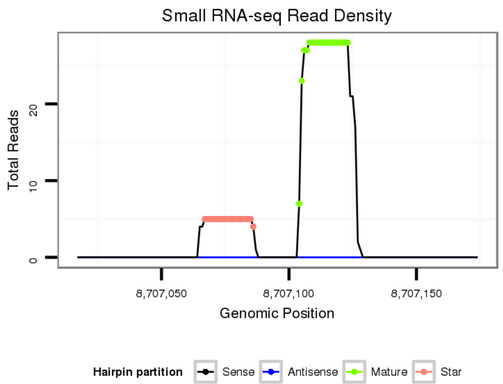
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

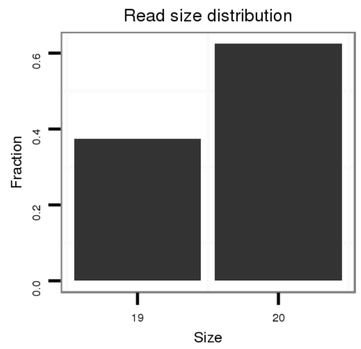
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_154	**scaffold_6496:8707067-8707124 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

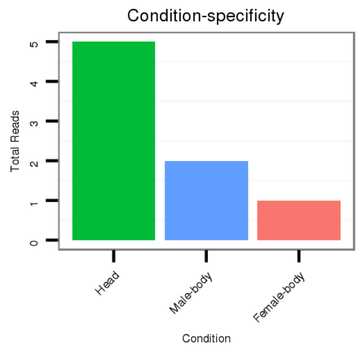
Legend: mature star mismatch in alignment mismatch in read

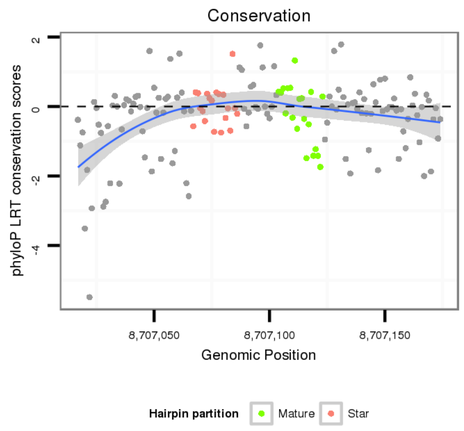
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTATTCTCTTCACTCATTGATATGTTTCAATTATATCAAATACTTTTCCAGATATCTGGCTTGTGTGAACTGATAATTTAAGCCGAGTTTATACAGTTAGGATATCTAGAAAATTATTTCACTATATTTGCTATATATTTTACTAAACGAAATTTATG	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	V056 head	M060 embryo	V049 head	V041 embryo
**********..(((((.(((((.(((((((((((((.(((((((((.....)))))))))))))).)))))))).)))))...**********												
.....TTATACAGTTAGGATATCTAGA.....	22	0	1	10.00	10	9	0	0	0	0	1
.....TTATACAGTTAGGATATCT.....	20	0	1	4.00	4	0	1	3	0	0	0
.....TTATACAGTTAGGATATCTAGA.....	23	0	1	3.00	3	3	0	0	0	0	0
.....TTATACAGTTAGGATATCTAG.....	21	0	1	3.00	3	3	0	0	0	0	0
.....TTATACAGTTAGGATATCT.....	19	0	1	3.00	3	1	0	0	0	2	0
.....CAGATATCTGGCTTGTGTGAAC.....	22	0	1	2.00	2	1	1	0	0	0	0
.....TATACAGTTAGGATATCTAGAAT.....	23	1	1	2.00	2	0	1	0	1	0	0
.....TATACAGTTAGGATATCTAGAA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TATACAGTTAGGATATCTAGA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TATACAGTTAGGATATCTAGG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TATACAGTTAGGATATCTAGAAA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....CAGATATCTGGCTTGTGTGAA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GATATCTGGCTTGTGTGAAC.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TATACAGTTAGGATATCTAG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TACAGTTAGGATATCTAGA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....CAGATATCTGGCTTGTGTGAACT.....	23	0	1	1.00	1	0	0	0	1	0	0

Anti-sense strand reads

AATAAGAGAAGTGAGTAACTATACAAAGTTAATATAGTTTATGAAAAGGTCTATAGACCGAACACACTTGACTATTAAATTCGGCTCAAATATGTCAATCCTATAGATCTTTTAATAAAGTGATATAAACGATATATAAAATGATTTGCTTTAAATAC	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_6496:8707017-8707174 +	dmo_154	TTATTCT-----CTTCACTCA--T--TGAT--ATG-TTT----------CAATTATA-TCAAATACTTTTCCAGATATC-----TGGCTTGTGTGAACTGA--TAATTTAAGCCG------AGTTTATAC----------A-GT----------TAGGATATCTAGA---AAATTA---TTT--------C---A----------CTATATTTG----CTATATA----TTTTAC----------TAAACGAAATT----------TA----------TG
droVir3	scaffold_12875:15127242-15127392 -	dvi_113	TTGAATCTTCTTCTTCGGCTT--T--AA--ATG-CAT----------CAT---TAATCAAATACTTTTCTAGATATC-----TGGCTTGTGTGAACTGA--AACTTAAAGCTG------AGTTTATAC----------A-GT----------TAGGATATCTAGA---AAATTATTTTAGC--------T---A----------CTATA----------------AAAATTTAACAAGCTC----------TA----------AA
droGri2	scaffold_14822:681585-681742 -		ACATTTT----GTTATTC-A--T--TAAT--AA--------------ACAGTTGTCGATTT---------TTAAAAGGATA-----TGAAATAAAAAAATGA--ATATTAAA---GTTACGAGTTAAAT----AA-TATA---AA-ATCAA---AAG-TGAATTATTAAAATAAT----------TAAATAGGCATTCAATGAATTCCCAAACTTATTTCTTA
droWil2	scf2_1100000004909:5761352-5761410 -		TTATATA----TTTAAAAT-A-T--ATAT--ATA-T--ATATAA-----T---APATATA---TATGAA----------AAAACAAAATA----------CA----------AA
dp5	Unknown_group_318:4726-4780 +		ATACTTT----TTTTGATCA--T--AAGA--AAA-TTA----------CGAATAAG-G-GAATATATGTACAT---GT
droPer2	scaffold_1:4847916-4848052 -		TTATTCT----TTTTTTTAA--T--TGTT--AAT-T--------------------TTT-TTTATTCATTTTTTAATTGT-----TGATTTTTTTTAT-----TC--TA
droAna3	scaffold_12929:1871317-1871392 +		TATTTAT----TTAAAAT--AT--TAG-------------------------TCTTTTT---TA
droKik1	scf7180000302517:725520-725636 +		TTATTTT----TTTAAAT--AT--TTT-------------------------TATTTATA-TTACATTATTTTATT-ATTGA-----AAAATCTGAATAT-----TT------AGCTTTAAAAGTTAATATTTAATTAT---AG
droEle1	scf7180000490141:420935-420961 +		TATATAA----TATA-----A-I---TA
droRho1	scf7180000777097:230467-230612 -		TTATCTG----TTAAAAA--CTC--TCAAATA-TTT----------TAGTTTTATTAAATAATTTGAACACATATTATGAGAATTTCTACAAATTGTTTAATTTAAAGTA------AGTCTTTAA----------A-CT----------TAGGATATTTCGA--TAGCTA---TTATTATTA
droBia1	scf7180000298858:2366-2501 +		TTATATG----TATAAAT--ATA--TAT--ATA-T--ATATAA-----TATACA--TATTTCAATCAATTTATAAAAATAAATAAATT----TATTAATAAAATTTTTATAAAACAATTTAATA----AA-TTTA---AA-TTTTA----TTT---AATTAT----------TA----------TA
droTak1	scf7180000413572:3351-3492 -		GTAAGGA----TTTGTGT--CGAAA--A--ATT-AATTTCTTTTTTCTGTTCTATGCAGCTG----------A-TAACTTA-----CGCAAG--CAATAAGAATTT-TAGGATTTTTTTATAGGAAGTTT---TTTA----------A---A----------TATTTCTTAAGTAGTT---TGCTT--A--G----------GACAATATACT----------GT----------TG
droEug1	scf7180000407468:13643-13717 -		ACTGACG-----CTAT-----A-I---TA
droSim2	X:18022378-18023066 +		AATTGGC----TCCGGG--AA--T--TT--A----TCATTTTACATATATATATATATA--TACAAT---TTTC----------A-G----------CAGAAGAAATAT----------TA----------AA
droSec2	scaffold_52:69770-69778 -		AAAATTA----------A-I---TA
droYak3	X:12271099-12271132 -		TGTATGC----T-AA-----A-I---TA

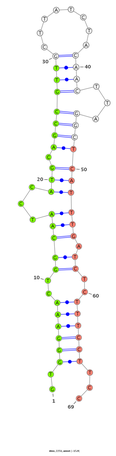
Generated: 09/08/2015 at 07:49 PM

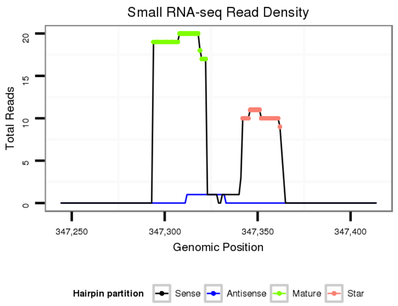
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	0

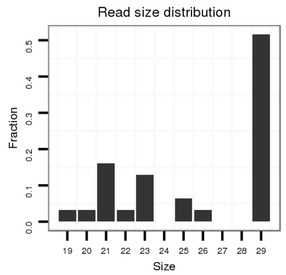
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2251	**scaffold_6654:347294-347364 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

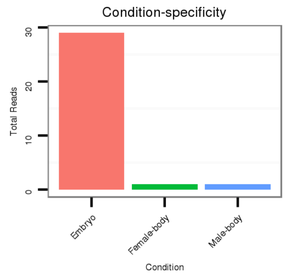
Legend: mature star mismatch in alignment mismatch in read

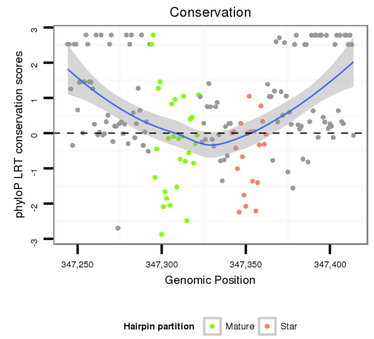
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI16710-in]; CDS [DmojGI16710-cds]; CDS [DmojGI16710-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GGCAGCCATCATGAAGGAGATGAAACATCCAAATCTCGTACAGCTAATCGGTGGGAAACTGGCAATCCATGCAGCCGTTGCTTATCTACAACTTAGGCTCATTTGATCTCTTTCCTTCCAGGTGTCTGCACTCGTGAGCCACCCTTCTACATCATCACAGAGTTTATGTCG	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V110 male body	M046 female body	V041 embryo	V049 head
**********..(((((((..(((((....(((..(((((((((.........))))...))))))))))..))..)))))))...**********										
.....GTGGGAAACTGGCAATCCATGCAGCCGTT.....	29	0	1	16.00	16	15	1	0	0	0
.....TCATTTGATCTCTTTCCTTCC.....	21	0	1	3.00	3	3	0	0	0	0
.....GTGGGAAACTGGCAATCCATGCAGC.....	25	0	1	2.00	2	1	0	1	0	0
.....TCATTTGATCTCTTTCCTTCCAG.....	23	0	1	2.00	2	2	0	0	0	0
.....TCATTTGATCTCTTTCCTTCCAGG.....	24	1	1	2.00	2	2	0	0	0	0
.....CTCATTTGATCTCTTTCCTTCCA.....	23	0	1	2.00	2	2	0	0	0	0
.....TCATTTGATCTCTTTCCTTCC.....	20	0	1	1.00	1	1	0	0	0	0
.....TCATTTGATCTCTTTCCTTCCA.....	22	0	1	1.00	1	1	0	0	0	0
.....ACAACTTAGGCTCATTTGATC.....	21	0	1	1.00	1	1	0	0	0	0
.....ATCCATGCAGCCGTTGCTTAT.....	21	0	1	1.00	1	1	0	0	0	0
.....TCATTTGATCTCTTTCCTTCT.....	21	1	1	1.00	1	1	0	0	0	0
.....TTGATCTCTTTCCTTCCAG.....	19	0	1	1.00	1	0	0	0	1	0
.....GTGGGAAACTGGCAATCCATGCAGCCGT.....	29	1	1	1.00	1	1	0	0	0	0
.....GTGGGAAACTGGCAATCCATGCAGCC.....	26	0	1	1.00	1	1	0	0	0	0
.....TCATTTGATCTCTTTCCTTCCAG.....	24	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

CCGTCGGTAGTACTTCCTCTACTTTGTAGGTTTAGAGCATGTCGATTAGCCACCCTTTGACCGTTAGGTACGTCGGCAACGAATAGATGTTGAATCCGAGTAAACTAGAGAAAGGAAGGTCCACAGACGTGAGCACTCGGTGGGAAGATGTAGTAGTGTCTCAAATACAGC	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body	V110 male body	V056 head	M060 embryo	V049 head
**********..(((((((..(((((....(((..(((((((((.........))))...))))))))))..))..)))))))...**********										
.....TACGTCGGCAACGAATAGATG.....	21	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_6654:347244-347414 +	dmo_2251	GGCAGCCATCATGAAGG---AGATGAAACATCCAAATCTCGTACA----------GCTAATCGGTGGGAACT----------G=--GCA-AT-------CC---A------TGC-------A----------GCCGTTGC---T-TATCTACAA--------CT----------T-------A----------GGCTCATTTGAT----------CT--CTTTCCTTCCAGGTGTCTGCACTCGTGAGCCACCCTTCTACATCATCACAGAGTTTATGTCG
droVir3	scaffold_12758:203068-203234 -	dvi_2138	GGCGCCATCATGAAGA---AGATGCGACACAATCGGCTGTGGGCACTCTACGCCGTCTGCTCGGCA----GTGT----------G----------C-TTTGACC----A----------AAGCAA----------AGCGGACTAA----------C--CGTTCCATTCA--TTATCGAGAGGAGCCCATTTATAATGCGCAGGAGTACATGTCG
droGri2	scaffold_3196:881-1049 +		GGCGCCATCATGAAGA---AGATGCGACACAATCGGCTGTGGGCCCTCTAGGCTGTCTGCGGCATTGAGTTACTGAACATTCTCCTCTCTATCAGTTTATTTAATA----G----------G----------G----------G----------GC-------GAAT----------GATGAT----------GTGATTTTT--GTTCTC----AGGAGGAGCCCATTCTAATATGCGCAGGAGTACATGTCG
droWil2	scf2_1100000004540:238870-239035 +		GGCGCCATCATGAAGG---AGATGAAACATCCGAATCTAGTGCA----------GCTAATCGTGGGAAAT----------T----------T----------T----------GCAA----------GTGAAG----------ACAGCTTTG----AA----------T----------T----------T----------T----------T----------T----GTTTGTCCAGGCGTCTCGACACGTGAGCCACCATTCTAATGATACACGAATTTATGTCG
dp5	XR_group8:8481282-8481451 -		GGCGCCATCATGAAGG---AGATGAACACCGAATCTAGTGCA----------GCTAATCGTCC-G----T----TC---G----C----CCCCT--C--------CCCGTACCCACACGCAGAGGTTCTTACATCTGC----------T----------T----------T----------T----------T----------T------TCCGCC----------CTGCCGTTGCAGGTGTTGCACGCGTGAGCCTCCTTCTACATCATCACGAATTTATGTCG
droPer2	scaffold_2:2728284-2728437 +		GGAGCCTGCTCCTGCCGCAATTGACATCCAAACATCGTGAA----------GCTGCATCGTCTGCGCCCTGGGCCGGCCTATGTGCCTGCTCTTCGAGTACATGCAC--C--C---------AGGAC----CT----------C----------T----------T----------T----------T----------T----AGCGAGTT----------T------CCTCGCGCCTGCTCACCCTTGCTCCACCCA----------C
droAna3	scaffold_13337:13973384-13973541 +		GGCGCCATCATGAAGG---AGATGAACACCGAATCTAGTGCA----------GCTCATCGTGGGGTGTCTTTAAACTAT----------G----------C----------C----------C-TTT----------T----------T----CATAA----AAAAGAATCTA----------T----------T----------T----------T----------T-------GTGTCC----------CTTCGTGAGCCACCGTTCTAATCATCACGAGTTTATGTCG
droBip1	scf1800000395832:914593-914751 +		GGCAGCCATCATGAAGG---AGATGAACACCGAATCTAGTGCA----------GCTCATCGTCATGTCCTAGGAAAGT----------GT----------C----------C----------C-TGT----------T----------T----TTATG----AAAATAATTGAA----------T----------T----------T----------T----------T-------ATG----------CTGTATCCTTGTAGGTGTTGCACGCGAGCCACCGTTCTACATCATCACGAAGTTTATGTCG
droKik1	scf1800000302577:989232-989389 -		GGCGCCATCATGAAGG---AGATGAACACCGAATCTAGTGCA----------AT-TAATACGTAAATCTATG----------T----------C----------C----------C----------C-TGT----------T----------T----GAGAAGAATGTCTTCAGG----------ATCTTAAC----------T----------T----------T----------T----------T----------T-------ATG----------CTGTCCTTGTTAGGTGTTGCACGCGTGAGCCACCGTTCTACATCATCACGAAGTTTATGTCG
droFic1	scf1800000453839:2008153-2008316 -		GGCGCCATCATGAAGG---AGATGAACACCGAATCTAGTGCA----------GCTCATCGTGGGGTTTATC----------T----------C----------C----------C----------C-TT----------T----------T----GGAGT--T----------T----------T----------T----------T----------T----CCTTTCGCACAGCAAACTGATTAAC----------T----------T----------T----------T----TGCTGTTTCCTAGGTGTTGCACGCGAGCCACCGTTCTACATCATCACGAGTTTATGTCG
droEle1	scf1800000491255:3048587-3048771 -		GGCGCCATCATGAAGG---AGATGAACACCGAATCTAGTGCA----------GCTCATCGTGGGTTTTACT----------T----------C----------C----------C----------C-A----A----TCAATTG--GAGAC----T----------T----------T----------T----------T----------T----------T----CTATCGCAG----------CTATGTTTCTGTTGAATGGAGAC----------T----------T----------T----------T----TCATCGATGAT----------TCCCCTTTTAGGTGTTGCACGCGAGCCACCGTTCTACATCATCACGAGTTTATGTCG
droRho1	scf1800000779409:48956-49168 +		GGCGCCATCATGAAGG---AGATGAACACCGAATCTAGTGCA----------GCTCATCGTGGGTTTTGT----------T----------C----------C----------C----A----TAAA----------T----------T----------T----------T----------T----------T----------T----AGTTCTTATTTCTGTAAGAGGAA----------ATCTCTTTATGGGAATAAC----------T----------T----------T----------T----TTCTGTTACTGTTGATCAGCAAAC----------T----------T----------T----------T----TCATCGATGAT----------TCCCCTTTTAGGTGTTGCACTCGAGCCACCATTCTAACATCATCACGAGTTTATGTCG
droBia1	scf1800000302428:1496360-1496537 +		GGCGCCATCATGAAGG---AGATGAACACCGAATCTAGTGCA----------GCTCATCGTGGGGTCTCTT----------A----------C----------C----------C----------C----------T----------T----------T----------T----------T----------T----------T----TCTAGTATAAACCCTTTTAAATGAAG--T----------T----------T----------T----CAAAATAGTAGAC----------T----------T----------T----------T----TAATCGGTTGATCCAAGGTGTTGCACGCAAGAACCGCCCTTCTACATCATCACGAGTTTATGTCG
droTak1	scf1800000415941:520465-520624 -		GGCGCGCATCATGAAGA---AGATGCGACACAATCGGCTGTGGGCCCTCTATGCGGTTTGCTCGGCA----GTGAGTGTACT----------G----------C----------C----------C----------C----------T----------T----------T----------T----------T----------T----------T----ACTGTAAT----------T----------T----------T----------T----------T----CCGTATATTAACCTAGATTTAAT--CTCTTT----------AGGAGGAGCCCATTCTACATCGTACAGAGGTACATGTCG
droEug1	scf1800000409711:722189-722403 +		GGCGCGCATCATGAAGG---AGATGAACACCAAATCTAGTGCA----------GCTCATCGTGGGGTTTAA----------T----------C----------C----------C----------C----------T----------T----------T----------T----------T----------A-ATTCGGTAATGATCTATGTTCCGTAAGTAGAA----------CGATCTTAATATGTA----------T----------T----------T----------T----T-----CTAAAACAT----------T----------T----------T----------T----TTATGTTAAGTATTGCGCTATCCATTGATGAT----------T----------T----------T----------T----TGTCCTTTTAGGTGTTGCACTCAGGACCGCCGTTCTACATCATCACAGAGTTTATGTCG
dm3	chr3L:16621139-16621323 -		GGCGCCATCATGAAGG---AGATGAACACCGAATCTAGTGCA----------GCTCATCGTGATGTAACGA----------T----------T----------T----------T----------T----------T----------T----AAAGT--TAAAATTTT-ACTAAGCAGAACGCAA----------T----------T----------T----------T----GAGGAA----------ATGCCATAA----------T----------T----------T----------T----AGTGT----------T----------T----------T----------T----TGCTTATTTTAGGTGTTGCACGCAAGAACCACCGTTCTACATCATCACGAGTTTATGTCG
droSim2	3L:16216453-16216637 +	dsi_6934	GGCGCCATCATGAAGG---AGATGAACACCGAATCTAGTGCA----------GCTCATCGTGATGTAACGA----------T----------C----------C----------C----------C----------T----------T----------T----------T----------T----------T----------T----AAAGT--TAAAATTTT-ACTAAGCAGAACGCAA----------T----------T----------T----------T----GAGGAA----------ATGCCATAA----------T----------T----------T----------T----AGTGT----------T----------T----------T----------T----TGCTTATTTTAGGTGTTGCACGCAAGAACCACCGTTCTACATCATCACGAGTTTATGTCG
droSec2	scaffold_0:8698993-8699177 -		GGCGCCATCATGAAGG---AGATGAACACCGAATCTAGTGCA----------GCTCATCGTGATGTAACGA----------T----------A----------C----------C----------C----------C----------T----------T----------T----------T----------T----------T----------T----AAAGT--TAAAATTTT-ACTAAGCATGAACGCAA----------T----------T----------T----------T----GAGGAA----------ATGCCATAA----------T----------T----------T----------T----AGTGT----------T----------T----------T----------T----TGCTTATTTTAGGTGTTGCACGCAAGAACCACCGTTCTACATCATCACGAGTTTATGTCG
droYak3	3L:17449620-17449795 +		GGCGCCATCATGAAGG---AGATGAACACCGAATCTAGTGCA----------GCTCATCGTGGGGTATT----------T----------C----------C----------C----ATAAATTTC----------T----------T----CACTC--AAAAGTTGT-ACTAAGC----------T----------T----------T----------T----GAGGAA----------ATGCCATTA----------T----------T----------T----------T----AC----------T----------T----------T----------T----TCCTCTTTTAGGTGTTGCACGCAAGAACCACCGTTCTACATCATCACGAGTTTATGTCG
droEre2	scaffold_4784:17207089-17207262 +		GGCGCCATCATGAAGG---AGATGAACACCGAATCTAGTGCA----------GCTCATCGTGGGGTATT----------T----------C----------C----AAAAATT----------T----------T----AATTT--GAAAATTCT-ACTAAGC----------T----------T----------T----------T----GAGGAA----------ATGTCATAA----------T----------T----------T----------T----AC----------T----------T----------T----------T----TCCGCTTTTAGGTGTTGCACGCAAGAACCGCCGTTCTACATCATCACGAGTTTATGTCG

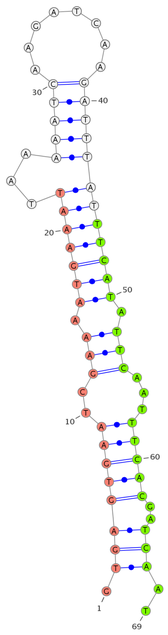
Generated: 08/18/2015 at 04:04 PM

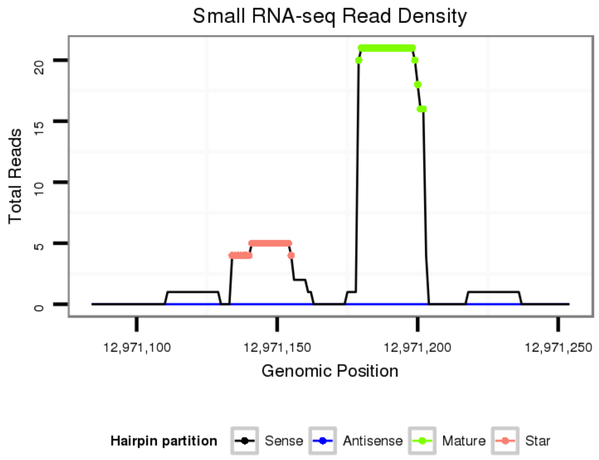
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	1
crit.total	1
crit.pairing	1
crit.plop2	1
crit.plop3	1
crit.uol	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	1
rescue.confident	1
rescue.candidate	0

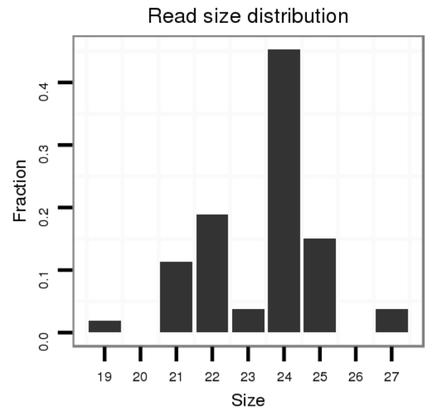
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1121	**scaffold_6496:12971134-12971204 +**	**confident**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

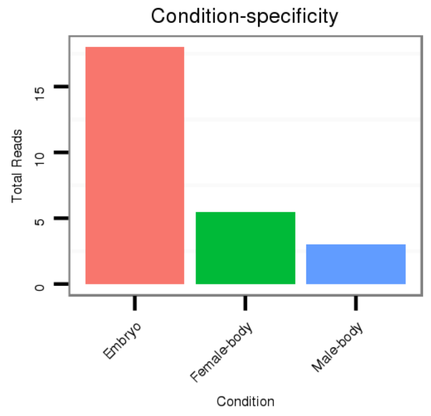
Legend: mature star **mismatch in alignment** mismatch in read

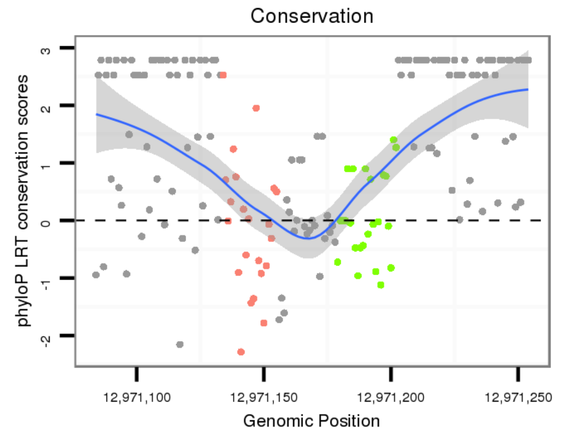
Predicted structure











dmo_1121_annot [–13.4]

Show Alternate Folds

Flybase annnotation

intron [DmojGI20554-in]; CDS [DmojGI20554-cds]; CDS [DmojGI20554-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GGACGATGTGCTAATGCCTGCCAAAATTACCTCGTTGGATCTGTCGAAGGGTGAGTGAATCGAAAATGAAATTAAAAATCAAGATCAAGATTTATTTCATATTCAATTTCACGATCAATAGATTGCAATTACCTGATATGTTCGGTGAGGGATGATACAATAAAACTATTA	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V041 embryo	V056 head	V049 head
**********.(((((((((..(((.(((((((...(((((........)))))))))))).)))...)))))..)))..**********											
.....TTCATATTCAATTTCACGATCAAT.....	24	0	1	11.00	11	9	1	0	1	0	0
.....TTCATATTCAATTTCACGATCAATA.....	25	0	1	4.00	4	4	0	0	0	0	0
.....TTCATATTCAATTTCACGATCAATT.....	25	1	1	3.00	3	3	0	0	0	0	0
.....TTCATATTCAATTTCACGATC.....	21	0	1	2.00	2	0	1	1	0	0	0
.....TTCATATTCAATTTCACGATCA.....	22	0	1	2.00	2	0	2	0	0	0	0
.....GTGAGTGAATCGAAAATGAAAT.....	22	0	1	2.00	2	1	0	0	1	0	0
.....TTATTTCATATTCAATTTCACGAT.....	24	0	1	1.00	1	1	0	0	0	0	0
.....GTGAGTGAATCGAAAATGAAATTAAAA.....	27	0	1	1.00	1	0	0	1	0	0	0
.....TTCATATTCAATTTCACGATT.....	21	1	1	1.00	1	0	0	0	0	0	1
.....TACCTCGTTGGATCTGTCG.....	19	0	1	1.00	1	0	0	0	0	1	0
.....GATATGTTCGGTGAGGGAT.....	19	0	1	1.00	1	0	0	1	0	0	0
.....TTCATATTCAATTTCACGATCAAC.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TCATATTCAATTTCACGATCAAT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TATTTCATATTCAATTTCACGAC.....	23	1	1	1.00	1	1	0	0	0	0	0
.....GTGAGTGAATCGAAAATGAAA.....	21	0	1	1.00	1	0	0	1	0	0	0
.....AATCGAAAATGAAATTAAAAAT.....	22	0	1	1.00	1	0	1	0	0	0	0
.....TTCATATTCAATTTCACGATCAATC.....	25	1	1	1.00	1	1	0	0	0	0	0
.....TCAATTTCACGATCAATAG.....	19	0	2	0.50	1	0	1	0	0	0	0

Anti-sense strand reads

CCTGCTACACGATTACGGACGGTTTTAATGGAGCAACCTAGACAGCTTCCCACTCACTTAGCTTTTACTTTAATTTTTAGTTCTAGTTCTAAATAAAGTATAAGTTAAAGTGCTAGTTATCTAACGTTAATGGACTATACAAGCCACTCCCTACTATGTTATTTTGATAAT	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_6496:12971084-12971254 +	dmo_1121	GGACGATGTGCTAATGCCTGCCAAAATTACCTCGTTGGATCTGTCGAAGGGTGAGTGAA---T------CG--A-AA----------AT----GAAATTAAAA--ATCAAGATC------AAGATTTA----------T-TTCATATTCAATTT----------C------ACG-ATC-AATAGATTGCAATTACCTGATATGTTCGGTGAGGGATGATACAATAAAACTATTA
droVir3	scaffold_12875:19278645-19278814 +	dvi_7947	TGACGATGTGCTATGCCTGCCAAAATCACCTCGCTGGACTTATCAAAGGGTGAGAGTAGCTC---AAACTA-----TGATG--AGAC----------TAAGAAAAGTCAT----TGTTAATC---TATAATCT----------T------TTT-TCC-AACAGATTGCAATTATCTGATATGCTCTGTGCGAGATGATACAATAAAACTATTA
droGri2	scaffold_15074:3773668-3773831 +		TGATGATGTGCTATGCCTGCCAAAATAACCTCACTGGATTATCAAAGGGTAAGAGTT---TTC-----A--AG----------AAAGCAAATTTAATA-------T-T----------------T----------TATTCAAATACGTCTTTATTTATTTGAACAGATTGCAATTACTGATATGTTCCGTTCGAGATGATACAATAAAACTATTA
droWil2	scf2_1100000004902:1963807-1963979 -		GGATGATGTTCTCATGCCAGCAAAATAACCTCGTTGGACTTGTCAAAGGGTGAGTAATGA-----------AA----TGACAAATTATTA-------T-T----TACATTATG-----TGTTAATA---TTTTGACT----------T------TCA-TTT-AACCAGATTGCAATTACCTCATATGTTCCGTAAGATGATGATACTATAAAACTTTTA
dp5	2:16496556-16496719 -		TGATGATGTCTTAATGCCTGCCAAAATCACGTCCCTAGACTTATCAAAGGGTGAGTAGT---CATTAAAAGAATAA----------------------ACAATATGCCAA-AAAAATACA-TTACA-----------AT----------C------GTA-TTC-TACAGATTGCAATTACCTCATATGTTCAGTGAGAGACGATACAATAAAGTTATTA
droPer2	scaffold_0:3899883-3900047 +		TGATGATGTCTTAATGCCGCCAAAATCACGTCCCTAGACTTATCAAAGGGTGAGTAGT---CATTAAAAGAATAA----------------------ACAATATGCCAAAAAAAATACA-TTACA-----------AT----------C------GTA-TTC-TACAGATTGCAATTACCTCATATGTTCAGTGAGAGACGATACAATAAAGTTATTA
droAna3	scaffold_13340:18757719-18757875 -		AGACGATGTCCTTATGCCAGCTAAAATCACCTCGCTGGACTTGTCAAAGGTCCGTATTA---------CAAGTA----------------------ATTAATCTTTGAA-GTATAAACT-T---------------------ATCAAGC------CTA-TTT-GACAGATTGCAATTACCTCATATGCTCTGTAAGAGATGATACTATTAAATTATTA
droBip1	scf7180000395652:415188-415343 +		AGACGATGTCCTTATGCCAGCTAAAATCACCTCGCTGGATTGTCAAAGGTGGATTAT---AT-----A---C-ACTCAGT-----AGC---TAAGAT----ATC-------A-C----------------------T-------------TTCTA-AATATAC------TTT-TTC-AACAGATTGCAATTACCTCATATGCTCTGTAAGAGATGATACTATTAAATTATTA
droKik1	scf7180000302388:707390-707544 +		AGACGATGTCCTGATGCCGCCAAAATAACGTGTTGGATTGTCAAAGGGTAGGTGCT---T------TG--A-A----------TTT----TAAATTAAAA--------C----------------AA---T-------------TTATTCAATAA-T------TTATTCGATACAGATTGCAATTACCTCATATGCTCTGTAAGAGATGATACCATTAAATTATTA
droFic1	scf7180000453826:942107-942259 +		AGATGATGTCTTGATGCCAGCCAAAATCACCTCCTTGGATTGTCAAAGGCGAGTGAT---TA------------------AGTTTCAC----ACTTTACCGGC---------------------------T-------------TCTT-ACTTAAT-------CTC-TTC-CACAGATTGTAATTACCTCATATGCTCTGTAAGAGACGATACTATTAAATTATTA
droEle1	scf7180000491280:1915054-1915210 -		TGATGATGTCCTAATGCCGCCAAAATCACCTCTTGGATTGTCAAAGGGCAAGTTAA---C------------TAATTTTTG----GCAATTCTAGTC-------A-C----------------------T-------------TTGTATAACATGT-------CAG-TTC-AACAGATTGCAATTACCTCATATGCTCTGTAAGAGACGATACTATTAAATTATTA
droRho1	scf7180000779916:269407-269561 +		TGATGATGTCCTAATGCCGCCAAAATCACCTCTTGGATTGTCAAAGGCAAGTGGA---A------TG--C---------ATTG----GTAATCCCAATT-------A-T----------------------T-------------TAATATAACATAC-------CAA-TTC-AACAGATTGCAATTACCTCATATGCTCTGTAAGAGACGATACTATTAAATTATTA
droBia1	scf7180000302113:1749468-1749624 +		GGACGAGGTCTTGATGCCGCCAAGATCACCTCCTTGGACTTGTCAAAGGTGAGTGCT---TGC-----CC--C---------ATCC----CCCGTTACGATC-------G--C----------------------T-------------AGCTACAATGAGT-------CAC-TTC-CACAGATTGCAATTACCTCATATGCTCTGTAAGAGATGATACTATTAAATTGTTA
droTak1	scf7180000415765:20717-20872 -		AGATGATGTCTTGATGCCGCCAAAATCACCTCTTGGATTGTCAAAGGCCAAGTTCTGCATAC-----------TA---------ACCATCCTGATC-------A-T----------------------T-------------AATTATAATGTAT-------TTTCATC-GACAGATTGCAATTACCTCATATGCTCTGTAAGAGATGATACTATTAAATTGTTA
droEug1	scf7180000409555:128529-128691 -		AGATGAGGTCTTGATGCCGCCAAGATCACCTCCTTGGACTTGTCAAAGGCGAGTTAAGG-CGTTAA----------GC-----ATTCGTGTACCATTTGAATC-------A-T----------------------T-------------AA--ATAACTTGT-------TAA-TTC-CACAGATTGCAATTACCTCATATGCTCTGTAAGAGACGATACTATTAAATTATTA
dm3	chr3R:25653830-25653997 -		GGACGAGGTCTTAATGCCGCCAAGATCACCTCTTGGATTGTCAAAGGCGAGTGCTGAATGC-----------T-AGT---TGATC--TGCCATGCCATACTAATC-------C-C----------------------T-------------TACTACAACATGT-------TAA-TTC-CACAGATTGCAATTACCTCATATGCTCTGTAAGAGACGATACTATTAAACTGTTA
droSim2	3r:25008605-25008772 -		GGACGAGGTCTTAATGCCGCCAAGATCACCTCCTGGATTGTCAAAGGCGAGTGCTGAGTGC-----------T-AGC---TGATC--TGGCATGCCATCCTAATC-------C-C----------------------T-------------TACTACAACATGT-------TAA-TTC-CACAGATTGCAATTACCTCATATGCTCTGTAAGAGACGATACTATTAAACTGTTA
droSec2	scaffold_4:4504288-4504454 -		GGATGAGGTCTTACTGCCGGGAAGATCACCTCCTGGATTGTCAAAGGCGAGTGCTGAGTGC-----------T-AGC---TGATC--TGGCATGCCATCCTAATC-------C-C----------------------T-------------TACTACAACATGT-------TAA-TTC-CACAGATTGCAATTACCTCATATGCTCTGTAAGAGACGATACTATTAAACTGTTA
droYak3	3R:20814009-20814170 +		GGACGAGGTCTTGATGCCGCCAAGATCACCTCGCTGGATTGTCAAAGGCGAGTGCT---TGC-----C---C-AGCCACC-----AGC---TGCCATCGTAATC-------C-C----------------------T-------------TACTACAACATGT-------TAA-TTC-CACAGATTGCAATTACCTCATATGCTCTGTAAGAGACGATACTATTAAACTGTTA
droEre2	scaffold_4820:2349611-2349772 +		GGACGAGGTCTTGATGCCGCCAAGATCACCTCCTGGATTGTCAAAGGCGAGTGCT---TGC-----C---C-AGCTGCC-----AGC---TGCCATCCTAATC-------C-C----------------------T-------------TACTACAACATGT-------TAA-TTC-CACAGATTGCAATTACCTCATATGCTCTGTAAGAGACGATACTATTAAATTGTTA

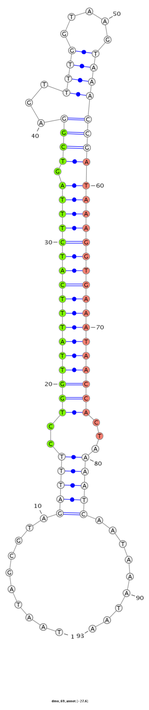
Generated: 08/18/2015 at 04:02 PM

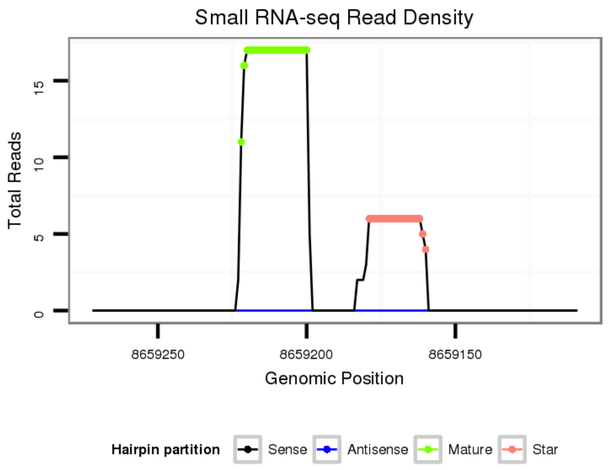
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

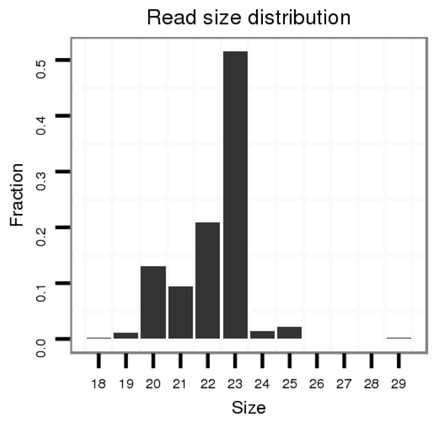
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_69	**scaffold_6473:8659159-8659222 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

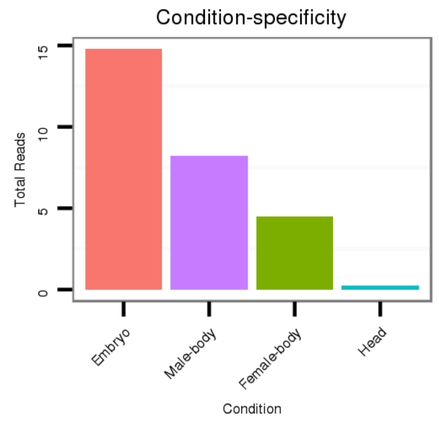
Legend: mature star mismatch in alignment mismatch in read

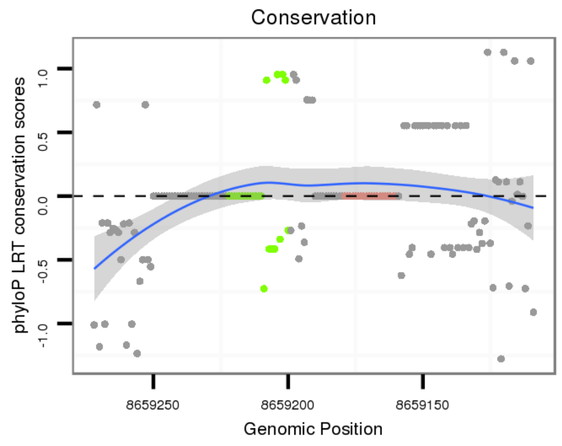
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

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

CACTGAGCTGCTGTGCCACTCATTCAACGGCTCTTTAATAGCGTAGATTTCCTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATAAATAATAGACTAGTGAGAGAGAGTGCTCCAGGCGAGACTGC **********.....(((((..(((((((((((((((((.((((...((((.....))))))))))))))))))))))))...)))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V110 male body	M046 female body	V041 embryo	V049 head	V056 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	1	0
.....CTGGTTATTTCATCTTTAGTCG.....	22	0	11	2.82	31	4	7	19	1	0	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
.....GATAAAGGTGAAATAACCACT.....	21	0	18	1.11	20	17	0	2	1	0	0
.....ACCGATAAAGGTGAAATAACCA.....	22	0	20	1.05	21	17	1	0	3	0	0
.....TCCTGGTTATTTCATCTTTAGTCGG.....	25	0	2	1.00	2	1	1	0	0	0	0
.....TGGTTATTTCATCTTTAGTCGG.....	22	0	20	1.00	20	14	0	6	0	0	0
.....ATAAAGGTGAAATAACCACC.....	20	1	19	0.95	18	18	0	0	0	0	0
.....CCTGGTTATTTCATCTTTAGT.....	21	0	2	0.50	1	1	0	0	0	0	0
.....TCCTGGTTATTTCATCTTTAGTC.....	23	0	2	0.50	1	1	0	0	0	0	0
.....CCTGGTTATTTCATCTTTAGTCGGA.....	25	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
.....TCCTGGTTATTTCATCTTTAGT.....	22	0	2	0.50	1	1	0	0	0	0	0
.....ACCGATAAAGGTGAAATAACC.....	21	0	20	0.45	9	9	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTTT.....	24	0	18	0.33	6	4	0	2	0	0	0
.....CGATAAAGGTGAAATAACCACT.....	22	0	18	0.28	5	5	0	0	0	0	0
.....GATAAAGGTGAAATAACCACTA.....	22	0	18	0.28	5	4	0	0	0	0	1
.....ATAAAGGTGAAATAACCAC.....	19	0	19	0.26	5	5	0	0	0	0	0
.....GATAAAGGTGAAATAACCACG.....	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
.....CTGGTTATTTCATCTTTAGTCGGT.....	24	1	11	0.18	2	1	0	1	0	0	0
.....CGATAAAGGTGAAATAACCACG.....	22	1	18	0.17	3	3	0	0	0	0	0
.....TGGTTATTTCATCTTTAGTCG.....	21	0	20	0.15	3	2	0	0	0	0	1
.....CCGATAAAGGTGAAATAACCA.....	21	0	20	0.15	3	2	0	1	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
.....TGGTTATTTCATCTTTAGTCGGA.....	23	0	20	0.10	2	0	0	1	1	0	0
.....AAACCGATAAAGGTGAAATAAC.....	22	0	20	0.10	2	2	0	0	0	0	0
.....TATTTCATCTTTAGTCGGAGTT.....	22	0	20	0.10	2	2	0	0	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGC.....	24	1	11	0.09	1	0	1	0	0	0	0
.....CTGGTTATTTCATCTTTAGTCAA.....	23	2	11	0.09	1	0	0	1	0	0	0
.....CTGGTTATTTCATCTTTAGTCGGAG.....	25	0	11	0.09	1	0	1	0	0	0	0
.....ACCGATAAAGGTGAAATAACCACT.....	24	0	15	0.07	1	1	0	0	0	0	0
.....ACCGATAAAGGTGAAATAACCACA.....	24	1	15	0.07	1	0	0	1	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
.....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
.....AAAGGTGAAATAACCACT.....	18	0	19	0.05	1	1	0	0	0	0	0
.....ATAAAGGTGAAATAACCACTTT.....	22	2	19	0.05	1	1	0	0	0	0	0
.....ATAAAGGTGAAATAACCACTGT.....	22	2	19	0.05	1	0	1	0	0	0	0
.....GGTTATTTCATCTTTAGTCGG.....	21	0	20	0.05	1	0	0	0	0	1	0
.....TTATTTCATCTTTAGTCGGA.....	20	0	20	0.05	1	1	0	0	0	0	0
.....TTATTTCATCTTTAGTCGGAGTT.....	23	0	20	0.05	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCG.....	19	0	20	0.05	1	0	0	1	0	0	0
.....GGTTATTTCATCTTTAGTCG.....	20	0	20	0.05	1	0	0	1	0	0	0
.....GTTATTTCATCTTTAGTCGGC.....	21	1	20	0.05	1	1	0	0	0	0	0
.....GTTATTTCATCTTTAGTCGGAA.....	22	1	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

GTGACTCGACGACACGGTGAGTAAGTTGCCGAGAAATTATCGCATCTAAAGGACCAATAAAGTAGAAATCAGCCTCAAAACCATTCATTTGGCTATTTCCACTTTATTGGTGATTTTAGTTATTTATTATCTGATCACTCTCTCTCACGAGGTCCGCTCTGACG **********.....((((((..((((((((((((((((((.((((...((((.....))))))))))))))))))))))))...)))))).....**********	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_6473:8659109-8659272 -	dmo_69	CACTGAGCTGCTGTGCCACTCATTCAACGGCTCTTTAATAGCGTAGATTTCCTGGTTATTTCATCTTTAGTCGGAGTTTTGGTAAGTAAACCGATAAAGGTGAAATAACCACTAAAATCAATAAATAATAGACTAGTGAG-AGAGAGTGCTCCAGGCGAGACTGC
droVir3	scaffold_12875:4611024-4611083 -		AAATTAATAAACATTTGCATAT----------GCCCAATCAAAGA----------AGTAGGTATTGTAGTCGGGCGTGA
droGri2	scaffold_15081:4118495-4118566 -		TAGCAGGTAGACCCACAAATA----------CAAATAATAAAAAATAAATAAAGTAAGAAGCTGCAGTCGAGAGAGC
droFic1	scf7180000453775:59517-59554 -		A----------TCTTTAATCGGAGTAGTGG----------TAGATAAGGAAAAGG

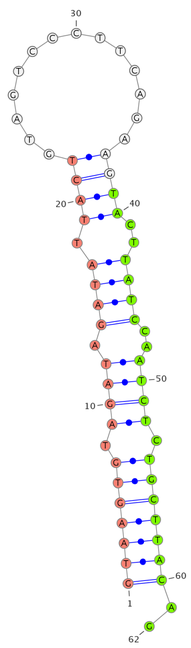
Generated: 09/08/2015 at 07:52 PM

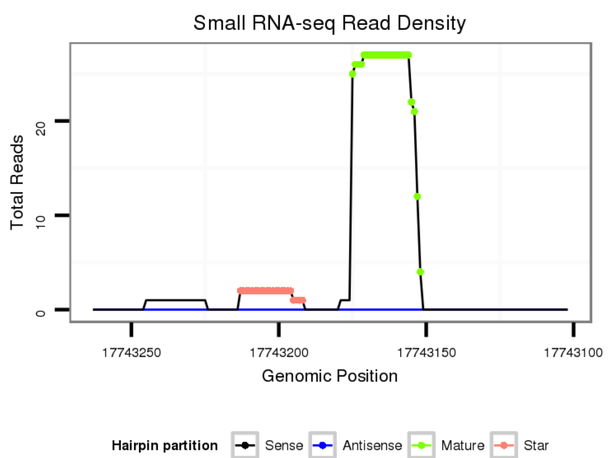
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

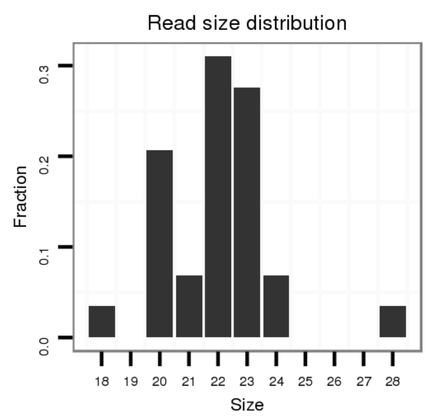
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1985	**scaffold_6540:17743152-17743213 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

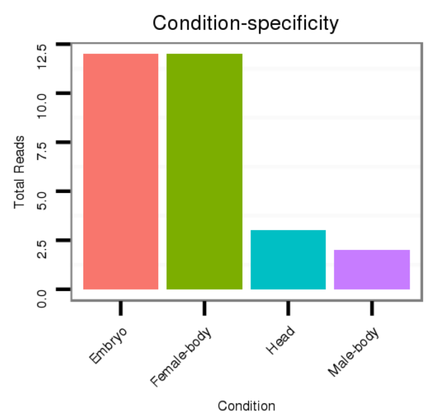
Legend: mature star mismatch in alignment mismatch in read

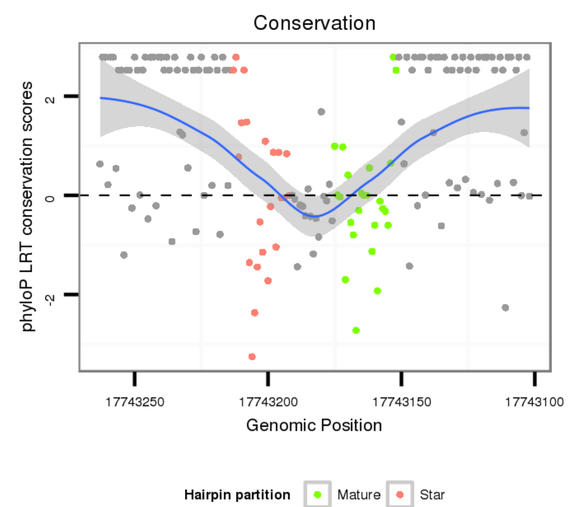
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI22827-in]; CDS [DmojGI22827-cds]; CDS [DmojGI22827-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CATCTATGCGGCCTGCGTCTATATGACCTGCCGCACCGAGGGCACGTCACGTAAGTGTAGATAGATATTACTGTAGTCCCTTCAGAAGTACTTATCCAATCTCTGCTTACAGATCTGCTCATCGACATCAGCGACGTACAACAGATTTGCTCCTACGAGCTG	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V041 embryo	V110 male body	V049 head	V056 head
**********(((((((.(((((.((((.(((((.............)))))..)))))..)))))..)))))).**********											
..........TACTTATCCAATCTCTGCTTACAGT..........	25	1	1	10.00	10	6	1	3	0	0	0
..........TACTTATCCAATCTCTGCTTACA..........	23	0	1	8.00	8	5	2	1	0	0	0
..........TACTTATCCAATCTCTGCTTAC..........	22	0	1	8.00	8	1	6	0	1	0	0
..........TACTTATCCAATCTCTGCTT..........	20	0	1	5.00	5	0	1	0	1	2	1
..........CTTATCCAATCTCTGCTTACAGC..........	23	1	1	5.00	5	5	0	0	0	0	0
..........CTTATCCAATCTCTGCTTACAGT..........	23	1	1	4.00	4	3	1	0	0	0	0
..........ACTTATCCAATCTCTGCTTACAGT..........	24	1	1	3.00	3	3	0	0	0	0	0
..........TACTTATCCAATCTCTGCTTACAGC..........	25	1	1	3.00	3	3	0	0	0	0	0
..........ACTTATCCAATCTCTGCTTACAGC..........	24	1	1	3.00	3	3	0	0	0	0	0
..........TACTTATCCAATCTCTGCTTACAG..........	24	0	1	2.00	2	1	0	1	0	0	0
..........TACTTATCCAATCTCTGCTTACAC..........	24	1	1	1.00	1	1	0	0	0	0	0
..........TACTTATCCAATCTCTGCTTA..........	21	0	1	1.00	1	0	1	0	0	0	0
..........GTAAGTGTAGATAGATAT..........	18	0	1	1.00	1	0	1	0	0	0	0
..........GAAGTACTTATCCAATCTCTGCTTACAG..........	28	0	1	1.00	1	1	0	0	0	0	0
..........ACTTATCCAATCTCTGCTTAC..........	21	0	1	1.00	1	0	1	0	0	0	0
..........CTATATGACCTGCCGCACCGA..........	21	0	1	1.00	1	0	1	0	0	0	0
..........TATCCAATCTCTGCTTACAG..........	20	0	1	1.00	1	1	0	0	0	0	0
..........GTAAGTGTAGATAGATATTACT..........	22	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

GTAGATACGCCGGACGCAGATATACTGGACGGCGTGGCTCCCGTGCAGTGCATTCACATCTATCTATAATGACATCAGGGAAGTCTTCATGAATAGGTTAGAGACGAATGTCTAGACGAGTAGCTGTAGTCGCTGCATGTTGTCTAAACGAGGATGCTCGAC	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_6540:17743102-17743263 -	dmo_1985	CATCTATGCGGCCTGCGTCTATATGACCTGCCGCACCGAGGGCACGTCACGTAAGTGTA--G-ATA----------GA--------TATTACTGTAGTCCCTTCAG---AAGTA-CTTA----------T-CC----------AATCTC-TGCTTACAGATCTGCTCATCGACATCAGCGACGTACAACAGATTTGCTCCTACGAGCTG
droVir3	scaffold_13047:14325838-14325998 -	dvi_16935	CATCTATGCTGCTTGCGTGTACATGACCTGCCGCACCGAGGGCACGTCACGTAAGTGGG---C--AGT----------GC-TTG-ACT-------GTGCACAACTAT---------G---GCA-------AC-TAAT---GAGTCTT---G-TTCTTGCAGATCTTCTTATCGACATAAGTGATGTACAGCAGATTTGCTCATACGAGCTT
droGri2	scaffold_14830:5640964-5641136 +		CATCTATGCGGCCTGCGTCTACATGACTTGCCGCACTGAGGGCACCTCACGTAAGTGAT--C-A-AAAT-CAGTTTGACTATT---------------------GACATAACAATT---------G---GTATGCTGTTGT-TTGT----CTGTGT--TG-TGTTTGCAGATTTACTTATCGACATTAGCGATGTACAACAGATCTGCTGCTATGAGCTG
droWil2	scf2_1100000004902:1816557-1816727 -		CATCTATGCGCGCCTGTGTCTATATGACCTGCCGCACCGAAGGAACTTCACGTGAGTGGCCAC-T--GGCCA----------ACGACCAAAG---T-------------TACCAGC---------G---GCATGTTGAAAC-TAAT--TTGATTAT---CTTTTAACAGATTTACTCATTGATATTAGCGATGTCCAACAGATTTGTTGTACGAATTG
dp5	2:9210189-9210357 +		CATCTACGCTGCTTGTTGTGTACATGACCTGCCGCACGAGGGCACCTCTCGTAAGTCCC--C-C--GTTTC----------CCCATGAAGC---T-------------GCTCAGACAGAGTGGTTTAA----------T-TGG-ATTTAC--TT---TCATTGTAGATCTCCTCATCGACATAAGCGATGTTCAGCAGATCTGTTGCTATGAGCTG
droPer2	scaffold_0:3017548-3017716 +		CATCTACGCTGCTTGTTGTGTACATGACATGCCGCACGGAGGGCACCTCTCGTAAGTCAC--C-C--GTTTC----------CCCATGAAGC---T-------------GGCCAGACGGAGTGGTTCAA----------T-TGG-ATTTAA--TT---TCATTGTAGATCTCCTCATCGACATAAGCGATGTTCAGCAGATTTGCTCGTATGAGCTG
droAna3	scaffold_13340:10427558-10427719 -		TATCTACGCAGCTTGCGTCTACATGACTTGCCGCACAGAGGGAACTTCCGTAAGTTAT--ATTAAAA----------------------------TATCGG-----TCCCTCGAGACG-----TATTCATTGTA------GT-GAA--------AA---TGTATTTCAGATCTGCTCATTGACATCAGCGATGTTCAGCAGATTTGCTGCTATGAACTG
droBip1	scf7180000396691:3121004-3121161 -		CATCTACGCAGCTTGCGTCTACATGACATGCCGCACAGAAGGCACTTCCGTAAGTCCT--T-TCA----------GA--------TCTCGG-----TCCCCTCGAG---A--TGGATACA----------T-TGC-----CTTCT---T-CCTTTTCAGATCTGCTCATTGACATCAGCGATGTTCAGCAGATTTGCTGCTATGAGCTA
droKik1	scf7180000302461:1317006-1317167 +		CATCTACGCTGCCTGTTGTCTACATGACCTGCAGGACAGAGGGCACCTCTCGTAAGTCCT--A-T--AGT----------TACATACATCT-------GTG----------GGTTAGGTTA----------C-TTAT--GCCTCTAT---AATCGGCACAGATCTTCTCATCGACATTAGTGACGTTCAGCAGATTTGCTCCTATGAACTG
droFic1	scf7180000453912:2263123-2263280 +		CATTTACGCGCGATGCGTGTATATGAGTTGCAGGACAGAAGGCACTTCTCGTAAGTCTT--A-T--CTT----------TGTTTTG-GTT-------TTT----------GT-AGTATATA----------T-CCCT---TTTTAATT---A-TCTCTTCCAGACCTTCTCATCGACATCAGTGACGTTCAGCAAATCTGCTGCTACGAACTG
droEle1	scf7180000491080:3066095-3066253 +		CATTTACGCGCCTGCGTGTACATGACCTGCAGGACAGAGGGCACTTCTCGTACGTACA--A-A--AAT----------AGTTTTG-CCT-------TAA----------GT-TAGTGTTA----------ATCCCT---GGCTCAC---T-CCTCCCCAGATCTCCTCATCGACATCAGCGACGTTCAGCAAATATGCTCCTATGAGCTA
droRho1	scf7180000778002:52319-52476 +		CATTTACGCGCCTGCGTGTATATGACCTGCAGGACAGAGGGCACCTGTCGTAAGTCCA--T-T--ACT----------AGTTTTC-CCT-------TTA----------GT-TTAGCTTA----------T-CCCT---GGCCCAT---T-CCTCCCCAGATCTCCTTATAGACATCAGCGACGTTCAGCAGATCTGCTGCTATGAGCTG
droBia1	scf7180000302075:4433773-4433931 -		CATCTACGCGCCTGCGTATACATGACCTGCAGAACGAAGGCACCTCTCGTAAGCTAC--A-C--GTT----------GTTATC-CCT-------AAG----------GT-AACTAGCTTA----------A-ACCT---CGCTCAT---T-ATCCTCCAGATCTTCTCATCGACATCAGCGACGTTCAGCAGATCTGCTCCTATGAGCTG
droTak1	scf7180000414001:868-1028 +		CATCTACGCGCGCCTGCGTTTACATGACCTGCAGGACGGAGGGCACCTCTCCCGTAAGTCTA--G-C--ATT----------TGTTTGTTCT-------ATG----------GT-GAGTATCTTA----------T-CCCT---GGCTCAT---TTGGCCCCAGATCTTCTCATCGACATCAGCGACGTTCAGCAGATCTGCTCCTATGAGCTG
droEug1	scf7180000409568:146745-146904 +		CATTTATGCGCCTGCGTGTATATGAGTTGTAGGACAGAGGGTACCTCTCGTAAGTTCC--G-C--ATT----------GTATTTG-CCA-------ATA----------GT-GAGACCGTTA----------G-CTT--AATTATGCAT---T-ATTTTCTAGATCTCCTTATTGACATAAGCGACGTTCAGCAAATCTGCTCATATGAGCTG
dm3	chr3R:13216273-13216431 -		CATCTACGCGCTTGCGTGTACATGACCTGCAGGACAGAGGGCACCTCTCCGTGAGTAGT--G-C--ATT----------CATTTTG-CCT-------AAA----------GT-GAGTAGCTTA----------T-TGAC---TGCTCAT---A-TCTTCACAGATCTCCTCATCGACATCAGCGACGTACAGCAAATCTGTTCCTATGAGCTT
droSim2	3r:8045279-8045438 +		CATTTACGCGGGTTGTTGTGTACATGACCTGCAGGACAGAGGGCACCTCTCCGTGAGTTGT--G-C--ATT----------CGTTTTG-CCT-------AAA----------GT-GAGTAGCTTA----------T-GG--ACTTATTGAC---A-TTTTCACAGATCTCCTCATCGACATCAGCGATGTACAGCAAATCTGTTCCTATGAGCTT
droSec2	scaffold_12:932079-932238 +		TTATTTACGCGCTTGTTGTGTACATGACCTGCAGGACAGAGGGCACTTCTCGTGAGTAGT--G-C--ATT----------CATTTTG-CCT-------AAG----------GT-GAGTAGCTTA----------T-GG--ACTTATTGAC---A-TTTTCACAGATCTCCTCATCGACATCAGCGATGTACAGCAAATCTGTTCCTATGAGCTT
droYak3	3R:17308076-17308234 -		CATTTACGCTGCCTGCGTGTACATGAGGTGCCAGGACAGAGGGCACCTCTCGTGAGTCGG--G-C--ATT----------CCTTTTG-CTT-------AAG----------GT-GAGTATGACA----------T-TAAC---TGCTCAT---A-TTTCTACAGATCTCCTCATCGACATCAGCGACGTACAACAGATCTGTTCTTATGAGCTT
droEre2	scaffold_4770:8413516-8413674 +		CATTTACGCGCCTGCGTGTACATGACCTGCAGGACAGAGGGCACCTCTCCGTGAGTCGG--G-C--ATT----------CCTTTTG-CCT-------AAG----------GT-GAATATGATA----------T-TGAC---TGCCCTT---T-TTTCTACAGATCTCCTTATCGACATCAGCGACGTACAACAGATCTGTTCCTATGAGCTT

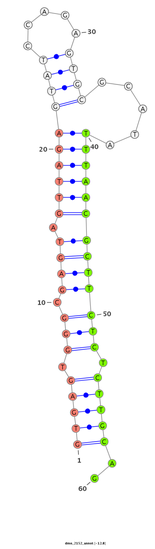
Generated: 09/08/2015 at 07:04 PM

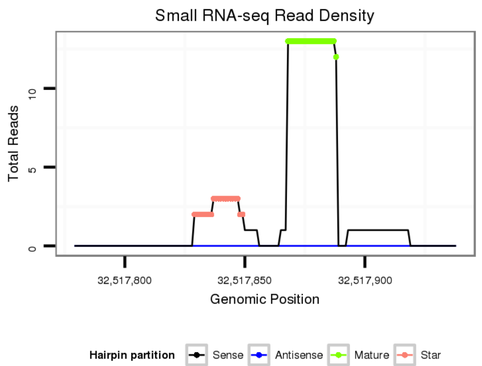
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

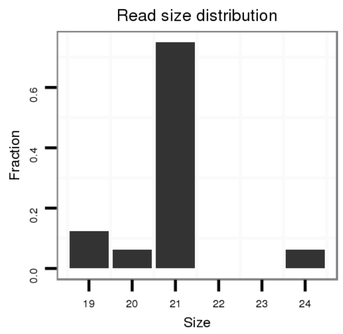
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_2152	**scaffold_6540:32517829-32517888 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Comell Mirror)]

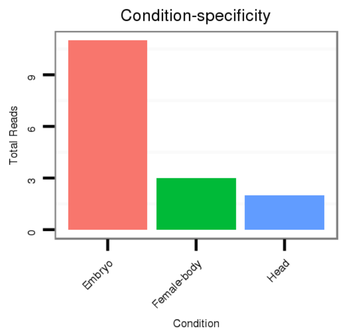
Legend: mature star mismatch in alignment mismatch in read

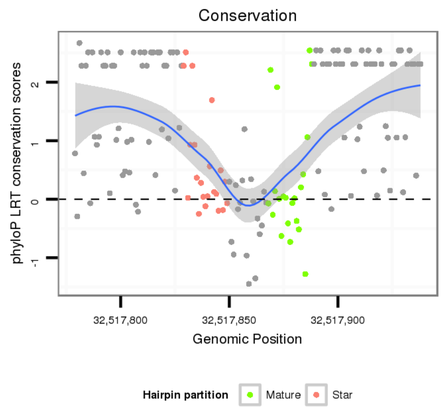
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DmojGI10751-in]; CDS [DmojGI10751-cds]; CDS [DmojGI10751-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGAGCCTGACGCTGGAGGGCATTGCCAACATGTCGAAGAAACGCAAGAAGGTGAGTGGGCGAGTAGTTAGAGTATCCAGAGTGCGCATATTTAACGCTTCTCTCTTGCAGGAGTGTCCCAGTCCAATTGCCTTGGAGCCCTGCAATGGCAATCGAGCCGC	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V041 embryo	V049 head	V056 head	V110 male body
....(((((.(((.(((((.((((((((((.....)))).....)))))))))))))).)))))..												
.....TTTAACGCTTCTCTCTTGCAG.....	21	0	1	11.00	11	7	2	2	0	0	0
.....TTTAACGCTTCTCTCTTGCAGT.....	22	1	1	10.00	10	8	0	2	0	0	0
.....TTTAACGCTTCTCTCTTGCAGG.....	22	1	1	5.00	5	5	0	0	0	0	0
.....ATATTTAACGCTTCTCTCTTGCAG.....	24	0	1	1.00	1	0	0	0	0	1	0
.....TTTAACGCTTCTCTCTTGCA.....	20	0	1	1.00	1	0	0	0	1	0	0
.....GTGAGTGGGCGAGTAGTTAGA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GCGAGTAGTTAGAGTATCC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....GTCCCAGTCCAATTGCCTTGGAGCCC.....	26	0	1	1.00	1	0	1	0	0	0	0
.....GTGAGTGGGCGAGTAGTTA.....	19	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

ACTCGGACTGCGACCTCCCGTAACGGTTGTACAGCTTCTTTGCGTTCTTCCACTCACCCGCTCATCAATCTCATAGGTCTCACGCGTATAAATTGCGAAGAGAGAACGTCCTCACAGGGTCAGGTTAACGGAACCTCGGGACGTTACCGTTAGCTCGGCG	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_6540:32517779-32517938 +	dmo_2152	TGAGCCTGACGCTGGAGGGCATTGCCAACATGTCGAAGAAACGCAAGAAGGTGAGTGGGCGAGTAG---TTAGAGTATCCAG----------A-GTGCGCA----------TATTT---A-AC----------GCT--TCTCTCTTGCAGGAGTGTCCCAGTCCAATTGCCTTGGAGCCCTGCAATGGCAATCGAGCCGC
droVir3	scaffold_12855:2209919-2210088 +	dvi_3518	TGAGCCTGACGCTGGAGGGCGTCAGCAACATGTCGAAGAAACGCAAAAAGGTGAGTAAG-----G---GCAAACACGAAG----------A-AAACG------------CTCTTGATAAGG----TTTCTTTAA---TGTTTCA--TTCTTCTGCAGGAGTGTCCCAGTCCGATTGCCGTGGAGCCCTGTAATGGCAATCGAGCCGC
droGri2	scaffold_15074:2210107-2210270 +		TGAGCCTGACGCTGGAAGGCATCAGCAACATGTCGAAGAAACGCAAGAAGGTGAGTGCAAGA----------AAT-GTGGGAAT----------AATG----------TTTC--AATG----TTTC-TTATCTATTTAATATATG-TTCCAGGAGTGTCCCAGTCCGATAGCGTTGGAGCCCTTGCAATGGCAATCGAGCCGC
droWil2	scf2_1100000004902:3662536-3662703 -		TAAGTCTAACCTGGAAGGCATCGTCAATTGTCCAAGAAACGCAAAAGGTAAGTCCAACT--T----------G--TG-AATGAAATC----------CA----------GG--CAAGTTTGATTCC-ATAAGCCTTTTTCA--TTCCTTGCAGGAATGTCCAAGTCCGATTGCGTTGGAGCCATGCAGTGGCAATCGAGCCGC
dp5	2:3774402-3774566 -		TGAGTCTAACGCTGGAGGGCATTGCCATATGTCCAAGAAACGCAAAAAGGTGGCCAAACG----------AGA-CTGCCTCA----------AA----------GG--GC--TTTATTTTC-TTAACCATATTTCGTTCATATTCTCAGGAATGTCCCAGTCCGATTGCGTTGGAGCCTTGCTGCGGCAATCGAGCGGC
droPer2	scaffold_7:574811-574975 +		TGAGTCTAACGCTGGAGGGCATTGCCATATGTCCAAGAAACGCAAAAAGGTGGCCAAACG----------AGA-CTGCCTCA----------AA----------GG--GC--TTTATTTTC-TTAACCATATTTCGTTCATGTCTCAGGAATGTCCCAGTCCGATTGCGTTGGAGCCTTGCTGCGGCAATCGAGCGGC
droAna3	scaffold_13340:19264536-19264759 +		TGAGCCTTATTGTGGAAGCGATTGCAACCTGTCCAAAAAACGCAAGAAGGTAGCCGG--CAATCA----ATCATATTATTGTC----------AGTTTGTGCTCCAAATTGGGTGCACAATAATGA----------ATATTCCTTA----AGCGGTACGACATTTTG----------ACATTCTGTACT--TTTTAT---------TTAT---TCCGTT--AATCTCTTGCAGGAATGTCCCAGTCCGATTGCGTTGGAGCCTTGTTAGCGGCAACGAGCCGC
droBip1	scf7180000396413:3101006-3101242 -		TGAGCCTTATTGTGGAAGCGATTGCGACACCTGTCCAAATAAGCGCAAGAAGGTAGCCGA--CAATCA----ATCATAGCTATTGAC----------AGGGCTGCTTCAAATTAGGGGCACAATA-TGAGAGCTTAAATTTGATATTCTTGA----AGCGGTATGACGCTTTG----------ACATTCTGTACT--TTTTAT---------TTAT---TGATTT--ATTTTTTTGTAGGAGTGTCCCAGTCCGATTGCGTTTAGAGCCTTGTTAGGCGGAAACGAGCTGC
droKik1	scf7180000302697:695398-695619 -		TTAGTCTGACGCTGGAGGGCATTGCCACTTGTCCAAGAAACGCAAAAAGGTGGCCAATCAATCA----ATAATATAATATA----TTTATAATTG----------T-TTTTCAGCTTTGTAAGACAGTTATAA----------CTAT----------ATTATATTAATTTTTG----------AAGCTAATTACT--TAATACATAAA----------GTT--AAATTTTCACAGGAATGCCCAGTCCGATTGCGTTTAGAGCCCTGCAGGGCAACAGAGCGC
droFic1	scf7180000453826:290412-290490 +		GGA----------T-TTTAATAATATTCTCAGGAATGCCCAGTCCGATTGCGTTGGAGCCTTGCAGTGGCAACGCGAGCCGC
droEle1	scf7180000491261:1918069-1918148 -		TGAGTCTGACGCTGGAGGGCATTGCCATCTGTCCAAGAAACGCAAAAAGGTGGCCAGTCAATCA----ATCAAATCTGTAG----------A--
droRho1	scf7180000767320:29702-29765 -		TGAGTCTGACGCTGGAGGGCATTGCCACCTGTCCAAGAAACGCAAAAAGGTGGCCAGTAAAT----------T--
droBia1	scf7180000302075:1501087-1501153 +		AT----------T--
droTak1	scf7180000413872:308526-308582 -		TGAGTCTGACGCTGGAGGGCATTGCCACTTGTCCAAAAAACGCAAAAAGGTGGCCG----------T--
droEug1	scf7180000409770:907853-908099 -		TGAGTCTGACGCTGGAGGGCATTGCCATCTGTCCAAAAAACGAAAAAGGTAGCCGAATAAATCAGTAAAT----------CAGTTCTAGAAAAATTGGTTTGGCT----AAGCTGGG--CTGTAAC----------CATATATAGTCGTAGAATCGATTTTGTTAT----AAACTAATTTCTTTAA----------ATATAGATAAATTGTATTTAATAAA----------GTT--TATTTCCTCAGGAATGTCCCAGTCCGATAGCGTTGGAGCCTTGCAGTGGCAATCGAGCCGC
dm3	chr3R:23425011-23425263 -		TGAGTCTGACGCTGGAGGGCATTGCCACCTGTCCAAAAAACGCAAAAAGGTAGCCGAATCAATCGG----TT----------CAGTGCTTAAAATTATGAGCCGACTTTTTAGCGG--GACGGAATC----------CATACAG----------AACAGATTATATAAAGCTAGGCCTA----ATTTGGACATTACAAGTTTGAGATTAAACTATGAAATA----------TTTTG----------CTT--ATTTGTACACAGGAATGCCCTAGTCCGATCGCGTTGGAGCCTTGCAGTGGCAACGCGAGCCGC
droSim2	3r:22849841-22850101 -	dsi_3594	TGAGTCTGACGCTGGAGGGCATTGCCACCTGTCCAAAAAACGCAAAAAGGTAGCCGAATCGATCG----TT----------CAGTGCTTAAAATTATGAGGCGACTTCTTAGCGG--GACGAAATC----------CATAAAGAAAAGTGGAACAGATTATATAAAGCTAGACCTA----ATTTGGGCATTACAAGTTTGAGATCAAACTCTAAAATA----------TTTTG----------CTT--ATTTGACACAGGAATGCCCTAGTCCGATCGCGTTGGAGCCTTGCAGTGGCAATCGAGCCGC
droSec2	scaffold_22:58732-58788 -		TGAGTCTGACGCTGGAGGGCATTGCCACCTGTCCAAAAAACGCAAAAAGGTAGCCG----------T--
droYak3	3R:23062987-23062949 +		TA----------T--
droEre2	scaffold_4820:4612917-4612979 +		TTA----------T--

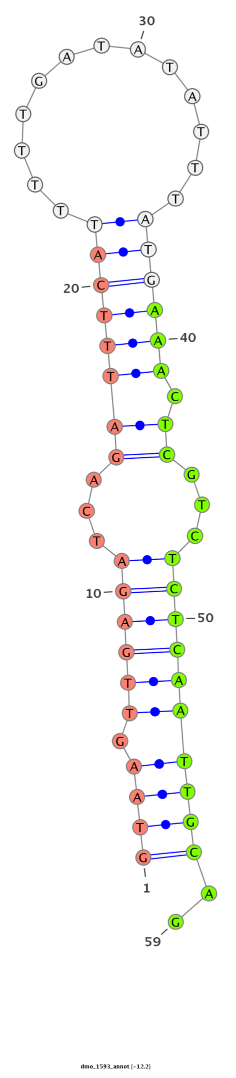
Generated: 09/08/2015 at 07:05 PM

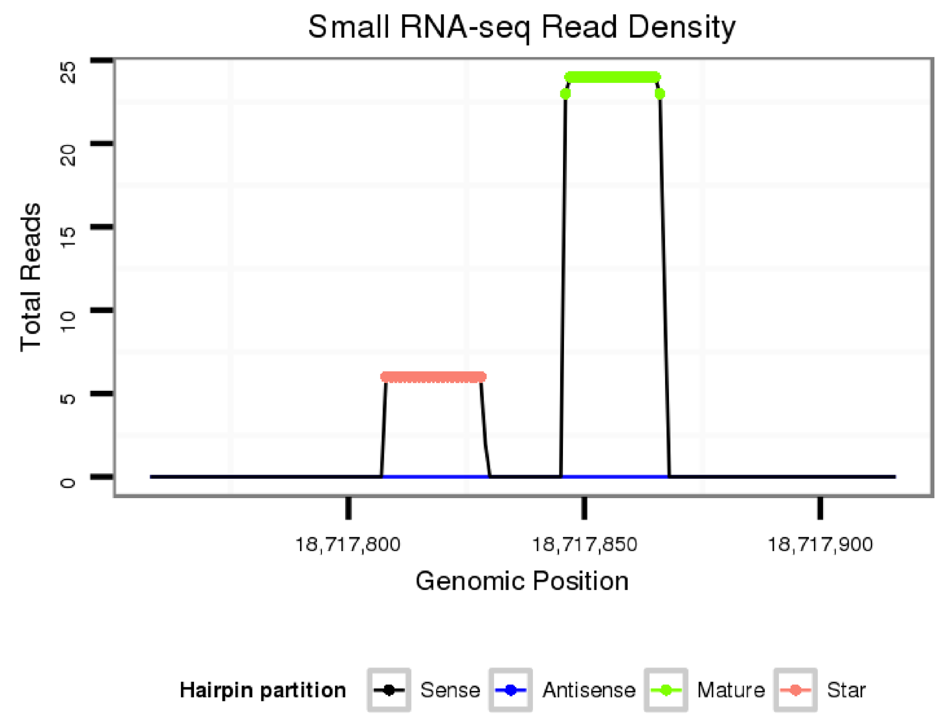
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

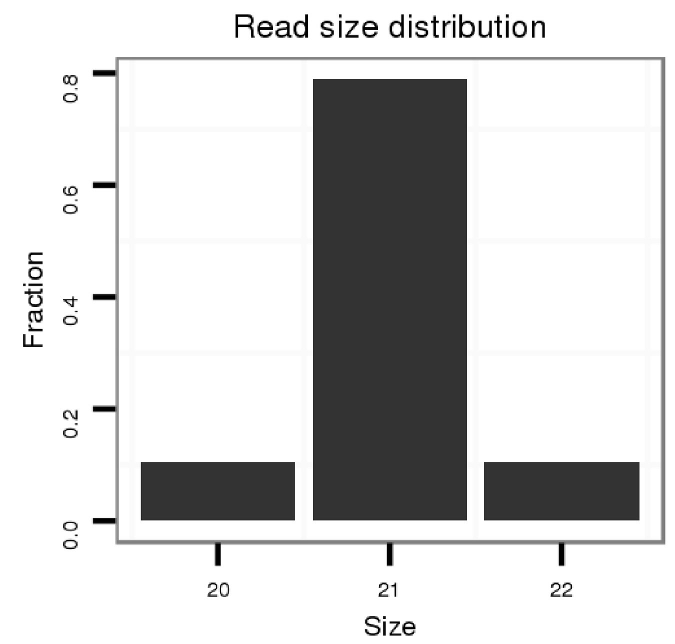
ID: dmo_1593	Coordinate: scaffold_6500:18717808-18717866 +	Confidence: confident	Class: Mirtron	Genomic Locale: intron	[View on UCSC Genome Browser {Cornell Mirror}]

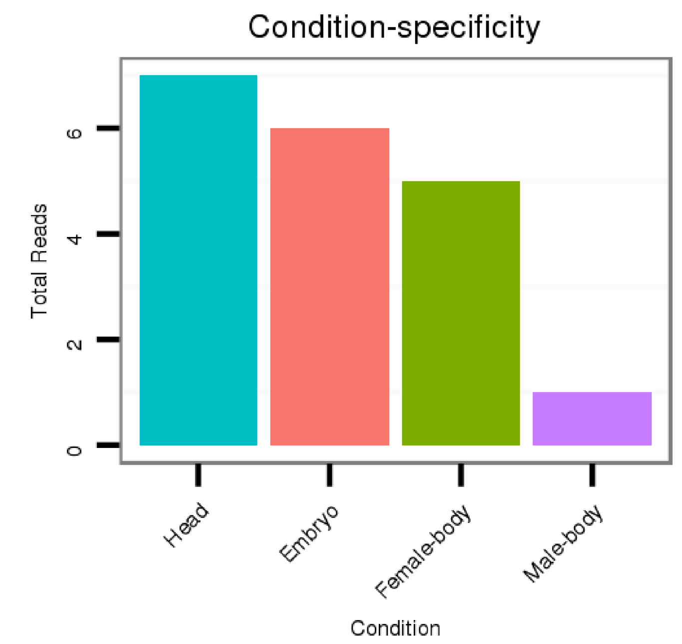
Legend: mature star mismatch in alignment mismatch in read

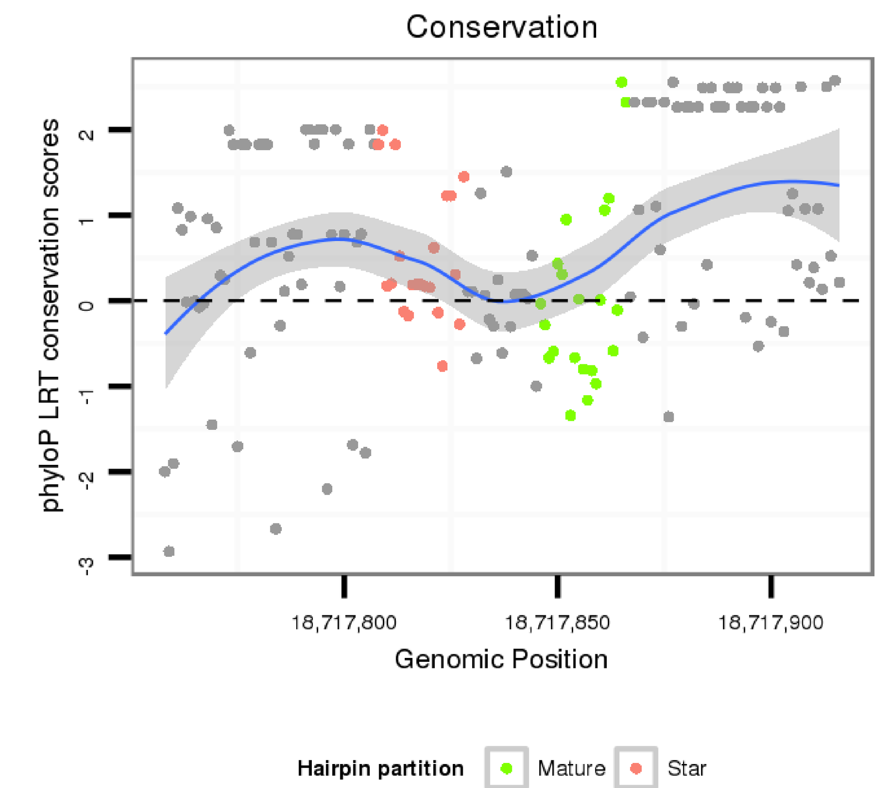
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI17800-in]; CDS [Dmoj\GI17800-cds]; CDS [Dmoj\GI17800-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AACTGGAGCGTTTACTCCCCGCCGCCGCCAAAGAAGATCTTCACCGATAGGTAAGTTGAGATCAGATTTCATTTTGATATATTTATGAAACTCGTCTCTCAATTGCAGCCGCGGCTCATCACCTGTGTGCCAATCGCCTTCGTCTGTGTGCCCCAGTC **((((.((((((...((((((((............)))))).))...))))))))))..**	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V041 embryo	V056 head	M046 female body	V049 head	V110 male body
....AAACTCGTCTCTCAATTGCAGT...	22	1	1	56.00	56	42	6	5	3	0	0
....AAACTCGTCTCTCAATTGCAG..	21	0	1	11.00	11	4	0	2	4	1	0
....AAACTCGTCTCTCAATTGCAGC...	22	0	1	11.00	11	11	0	0	0	0	0
....GTAAGTTGAGATCAGATTTCA...	21	0	1	4.00	4	0	0	2	0	1	1
....AACTCGTCTCTCAATTGCAGT...	21	1	1	3.00	3	1	1	0	1	0	0
....AAACTCGTCTCTCAATTGCAGA...	22	1	1	2.00	2	1	0	0	1	0	0
....GTAAGTTGAGATCAGATTTCAT..	22	0	1	2.00	2	0	2	0	0	0	0
....AAACTCGTCTCTCAATTGCAGTT..	23	2	1	1.00	1	1	0	0	0	0	0
....AACTCGTCTCTCAATTGCAG..	20	0	1	1.00	1	0	0	1	0	0	0
....AAACTCGTCTCTCAATTGCACT...	22	2	1	1.00	1	1	0	0	0	0	0
....ACTCGTCTCTCAATTGCAGT...	20	1	1	1.00	1	0	0	0	0	0	1
....AAACTCGTCTCTCAATTGCA...	20	0	1	1.00	1	0	0	0	1	0	0
....TCGTCTCTCAATTGCAGT...	18	1	2	0.50	1	0	1	0	0	0	0

Anti-sense strand reads

TTGACCTCGCAAATGAGGGGCGGCGGCGGTTTCTTCTAGAAGTGGCTATCCATTCAACTCTAGTCTAAAGTAAAAACTATATAAATACTTTGAGCAGAGAGTTAACGTCGGCGCCGAGTAGTGGACACACGGTTAGCGGAAGCAGACACACGGGGTCAG **((((.((((((...((((((((............)))))).))...))))))))))..**	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_6500:18717758-18717916 +	dmo_1593	AACTGGAGCGTTTACTCCCCGCCGCCGCCAAAGAAGATCTTCACCGATAGGTAAGTT-----------GAGAT------CAG-----------ATT--TCAT-TTTTGATAT-----ATTTATGA---------A---ACT---CGTCTCTCAATTGCAGCCGCGGCTCATCACCTGTGTGCCAATCGCCTTCGTCTGTGTGCCCCAGTC
droVir3	scaffold_12963:15721291-15721364 +		TTATGAAACTA--TTGCCTATTGCAGCCGTGGCTCATCACCTGTATGCCAATCGCCTTCATCCGTGTGTCCCAGTC
droGri2	scaffold_15126:4749019-4749289 -		AACTGGAGCGTCTACTCGCCACCGCC---AAAGAAGATCTTCACCGACAGGTAAGTAA------------TC-------GA----ATCTCGACTTTGAACGCTTTCGTTGTTGTTTATTCAAATTGATCAGAAGTGAGAAATAATTGTTAGTATAAATTTTCCATCAATGATAATTGAAGCAATCAAAACATTCGAGGCCAAAGTAAT-TATAATTCTCGTTAGTAACTCA---------A---CTT---TG---TCAAATTGCAGTCGCGGCTCGTCGCCCGTGTGCCAATCGCCGTCATCCGTGTGTCCTAGTC
droWil2	scf2_1100000004585:5591341-5591499 +		AACTGGAATGTCTATTCCCCACCGCCCCTAAAGAAGATCTTCACAGAGAGGTAAGTCCCCTGTTCCTCGAATT------CAATAGAATC---T-----------T---GTTACTAATCCTC-------------ATGGATTGCAGTCGTGGCTCTTCGCCTGTGTGCCAATCGCCCTCATCGATTTGTGCCAGTC
dp5	4_group2:835172-835339 -		AACTGGAGTGTCTACTCGCCGTCGCCCATCAAAAGATGTTTACAGAGAGGTACGTC-------------TAAATGCCGCCTAA-----------ATT--CCA----------------CTTACAGATCTTCCAATGATAATTTCT-CTCGCCTTAAATAGTCGCGGCTCTTCGCCCGTGTGCCAATCCCCCTCCTCTGTGTGTCCCAGTC
droPer2	scaffold_8:1623112-1623151 -		AGTTGCAGCATCCGC----------AGCAGTGAAAGATTCTCGCCTTTAG--
droAna3	scaffold_12943:3994262-3994400 +		AATTGGAGTGTGTACTCGCCGCCGCCGCTGAAAAAGATTTTCACGGAAAGGTAGGTTC-------------TT-------AA----T---TGAAGTAGTCACTTTGTTAGAAACCTT--TTAT-TTTTATACT-----ATTTATAG---------A---CTT---TG---TGTAATTAAAGCCAAGGCACGT---
droBip1	scf7180000395973:215298-215350 +		---CAGCCGGGGCTCCTCACCCGTTTGCCAATCGCCCTCGTCGGTGTGTCCCAGTC
droKik1	scf7180000302384:332732-332797 +		AACTGGAGTGTGTACTCCCCACCGCCCCTGAAGAAGATATTTACAGAAAGGTGAGATA-----------TATT------CAG---A
droFic1	scf7180000451508:80981-81082 -		CATA---TT--TCAAGCCTT--AA------------TAAATTTTTTAAAACTACCTT----TATTTCCTTTGCAGTCGCGGTACGTCACCGGTGTGCCAATCACCTTCGTCGGTGTGTCCCAGTC
droEle1	scf7180000491046:2857696-2857759 -		TC--TATCTTTCCAGTCGTGGCTCCTCACCGGTGTGCCAATCGCCCTCGTCGGTGTGTCCCAGTC
droRho1	scf7180000766081:15182-15280 +		AAGTTTTATTTCTGT--ACT-----------TAAGTTAATATTCCTCCT---T---CTATCTTTTAAGCCGCGGCTCTTCCCCGGTGTGCCAATCGCCCTCGTCGGTGTGTCCCAGTC
droBia1	scf7180000302422:8862736-8862802 -		TTG---GCTTTTCATTTCAGTCGCGGCTCCTCACCGGTGTGCCAATCCCCCTCATCGGTTTGCCCTAGTC
droTak1	scf7180000415604:421090-421160 +		AACTGGAGTGTTTACTCTCCTCCGCCCATCAAGAAGATATTCACGGAAAGGTGAGATA-------------TA-------AG----AT--CAGC--TT
droEug1	scf7180000409463:345980-346035 -		T---TACAGTCGCGGCTCCTCGCCGGTGTGCCAATCGCCCTCGTCGGTGTGTCCCAGTC
dm3	chr2L:7192001-7192067 -		TCC---CCTTCCCATTTCAGTCGCGGCTCCTCACCGGTGTGCCAATCGCCCTCGTCGGTGTGTCCCAGTC
droSim2	2L:6953272-6953344 -		AACTGGAGCGTGTACTCCCCTCCGCCTGTGAAGAAGATGTTCACGGAAAGGTAAGATA-------------TT---GAGTAATAGATTT
droSec2	scaffold_3:2715695-2715751 -		A--TTTCAGTCGCGGCTCCTCACCGGTGTGCCAATCGCCCTCGTCTGTGTGTCCCAGTC
droYak3	2L:5711113-5711168 +		T---TTTAGTCGCGGCTCCTCACCGGTGTGCCAATCGCCGTCGTCGGTGTGTCCCAGTC
droEre2	scaffold_4929:16109046-16109108 -		CT---TTCCATTTCAGTCGCGGCTCCTCACCGGTGTGCCAATCACCTTCGTCGGTGTGTCCCAGTC

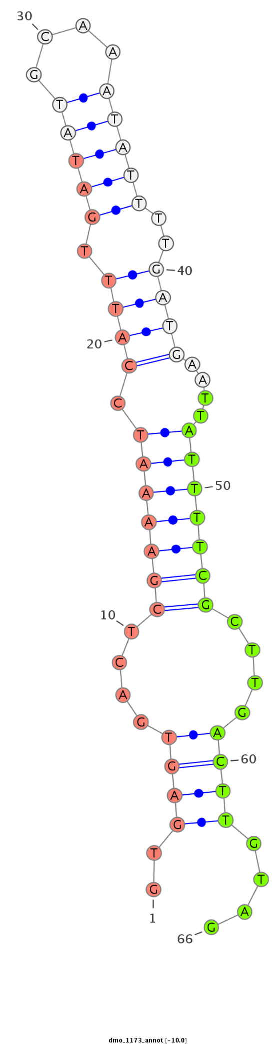
Generated: 09/08/2015 at 10:36 PM

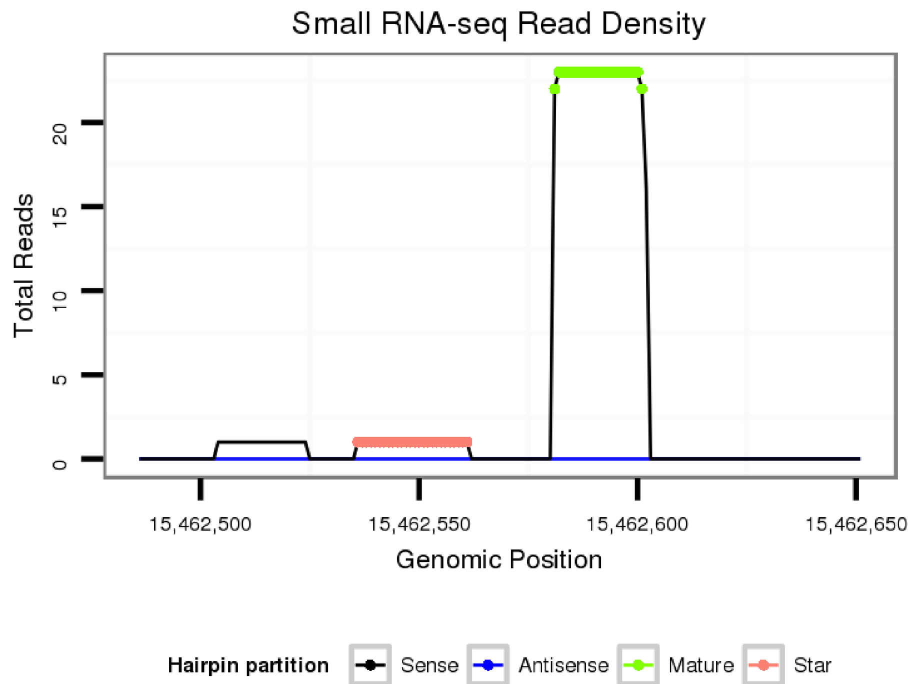
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

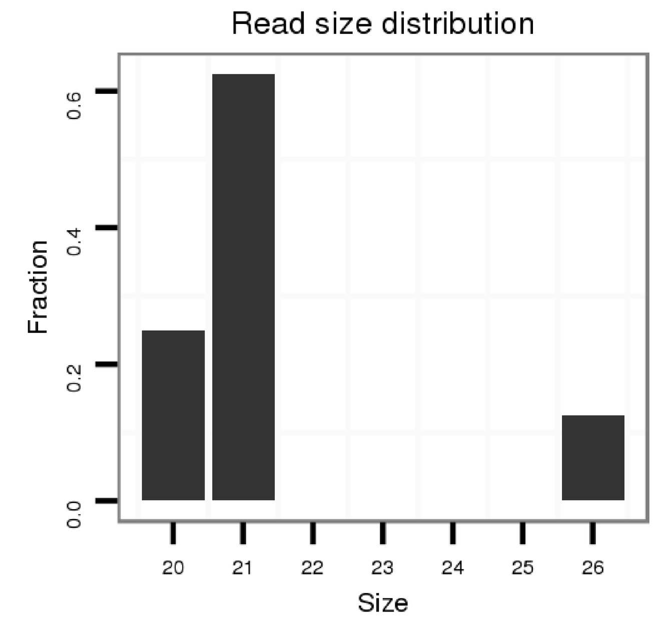
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1173	**scaffold_6496:15462536-15462601 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

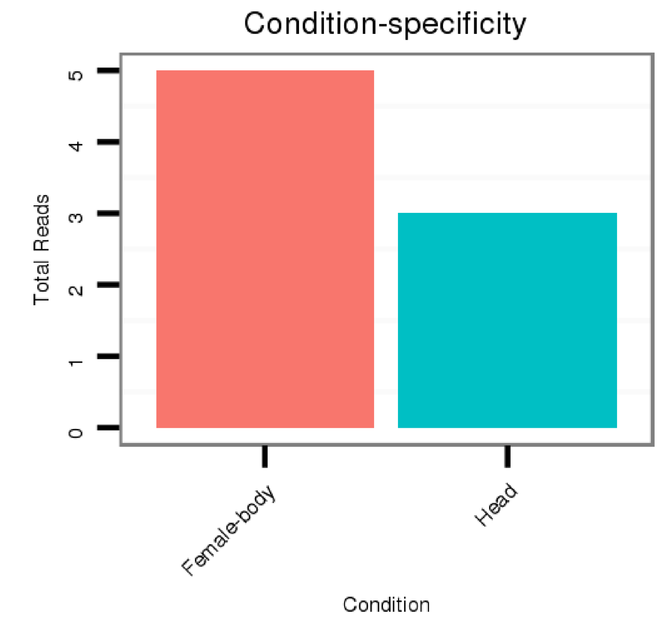
Legend: mature star mismatch in alignment mismatch in read

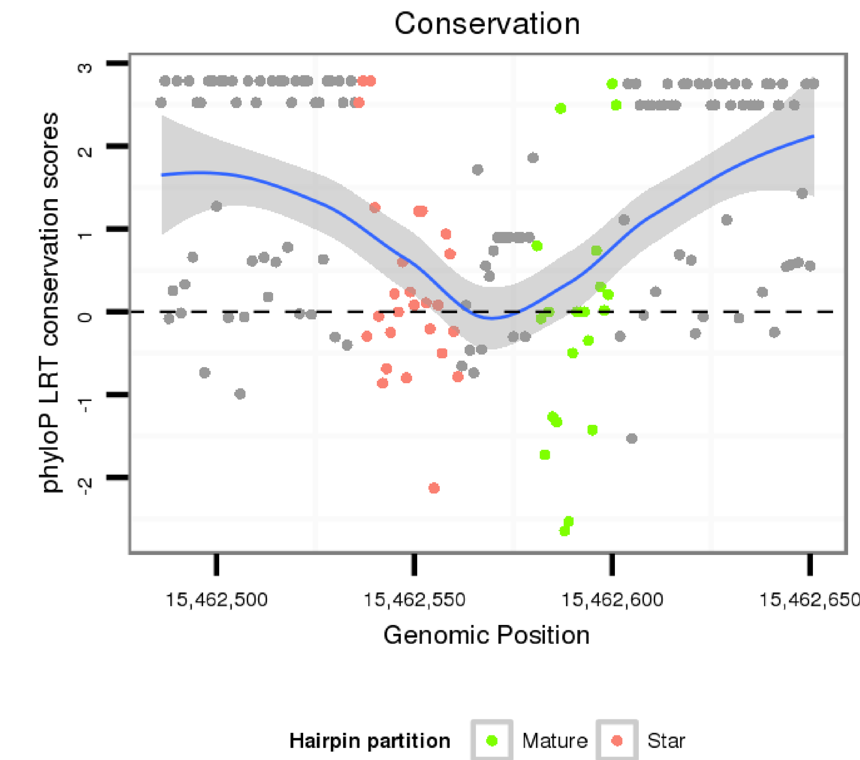
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI20769-in]; CDS [Dmoj\GI20769-cds]; CDS [Dmoj\GI20769-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CATCTTTTGCCCTTCTTCTGCTTGCAGTTGTTTGACTTTGCCATAACTACGTGAGTGACTCGAAAATCCATTTGATATGCAAATATTTTGATGAATTATTTTCGCTTGACTTGTAGTTTGACTGCTGCTGGTTACCTATGCTATCTGCAGGCCATTCACCGTTTCA **..((((....(((((((.((((.(((((....)))))..))))....)))))))....))))....**	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V049 head	V056 head	V041 embryo	V110 male body
....TTATTTTCGCTTGACTTGTAGT...	22	0	1	16.00	16	10	2	0	2	1	1
....TTATTTTCGCTTGACTTGTAG..	21	0	1	5.00	5	0	3	2	0	0	0
....TTATTTTCGCTTGACTTGTAGA...	22	1	1	5.00	5	5	0	0	0	0	0
....GTGAGTGACTCGAAAATCCATTTGAT..	26	0	1	1.00	1	0	1	0	0	0	0
....TTATTTTCGCTTGACTTGTA...	20	0	1	1.00	1	0	0	1	0	0	0
....TTATTTTCGCTTGACTTGTAGC...	22	1	1	1.00	1	1	0	0	0	0	0
....TTATTTTCGCTTGACTTGTAGTAA...	24	2	1	1.00	1	0	1	0	0	0	0
....TATTTTCGCTTGACTTGTAG..	20	0	1	1.00	1	0	1	0	0	0	0
..................TGCTTGCAGTTGTTTGACTTT...	21	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

GTAGAAAACGGGAAGAAGACGAACGTCAACAAACTGAAACGGTATTGATGCACTCACTGAGCTTTTAGGTAAACTATACGTTTATAAAACTACTTAATAAAAGCGAACTGAACATCAAACTGACGACGACCAATGGATACGATAGACGTCCGGTAAGTGGCAAAGT **..((((....(((((((.((((.(((((....)))))..))))....)))))))....))))....**	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_6496:15462486-15462651 +	dmo_1173	CATCTTTTGCCCTTCTTCTGCTTGCAGTTGTTTGACTTTGCCATAACTACGTGAGTG------AC----T-----------------CGAAAATCCATTTGA--------------TATG---CAAATA---------------------------------------TTTTGATGAATT---ATTT------TCGCTTGACTTGTAGTTTGACTGCTGCTGGTTACCTATGCTATCTGCAGGCCATTCACCGTTTCA
droVir3	scaffold_12875:11458149-11458315 -		CATCTGTTGCCCTTCTTCTGCTTGCAGCTGTTCGACTTTGCAATCACAACGTAAATG------TTAAAT----TTGATGTGATATAGTTTA--AC--------------------------------------TTTTAATAA---CTTGTTGCATGCT------TCGC---ATTTGTAGCTTGACCGCCGCTGGTTACTTGTGCTATCTACAGGCCATTCATCGTATCA
droGri2	scaffold_15245:6756185-6756347 +		CACTTGCTGCCGTTCTTCTGTCTGCAACTGTTTGACTTTGCCATCACCACGTGAGTGA-----CAATAA----TCGT----------TTTCGATTCCCGT-----------------------------TTG-----------------------------CATATA---TTATATTCTTC------TCTC---TTTTGTAGATTGACCGCCGCTGGTTACCTCTGCTATCTACAGGCCATTCATCGTATTA
droWil2	scf2_1100000004513:1712396-1712558 -		CATCTGTTGCCCTTCTTTTGTCTGCAGTTATTTGATTTTGCCATTACCACGTGAGTT------CT----TAGAAAGAGAGAAGAGAGTTAAAATCGTT--TTTTAATAAATG---AA---------TTT---CCTTACAGTTTGACAGCCGCTGGTTATTTATGCTATCTTCAGGCCATACATCGCATCA
dp5	3:13750413-13750572 -		CATCTGTTGCCCTTCTTCTGTCTGCAGCTGTTTGACTTCGCCATAACGACGTAAGAT------AA----T-----------------TTTAAATCGTTTTGTGGGCAACCTCCCCA----------GC----------T---CT---TT------CTTTCC---CGTTGCAGCCTCACCGCCGCTGGCTATCTGTGCTACCTACAGGCCATCCATCGCATCA
droPer2	scaffold_4:1570187-1570346 +		CATCTGTTGCCCTTCTTCTGTCTGCAGCTGTTTGACTTCGCCATAACGACGTAAGAT------CA----T-----------------TTTAAATCGCTTTGTGGGCAACCTCCCCA----------GC----------T---CT---TT------CTTTCC---CGTTGCAGCCTCACCGCCGCTGGCTATCTGTGCTACCTACAGGCGATCCATCGCATCA
droAna3	scaffold_13266:1414981-1415146 +		CACTTGCTACCGTTTTTCTGCCTCCAGCTCTTTGATTTTGCCATTACAACGTAAGTA------AA----CAGATCTAAAGTTGGAAAATA---A--TAT-------TATATA------TA---ACTTAAATATTT-----CTTCC-----TCCTTAGCCTAACTGCTGCTGGATATCTGTGCTACCTTCAGGCTATTCACCGCATGA
droBip1	scf7180000396730:2408210-2408373 +		CACTTGCTACCGTTTTTTTGTCTTCAGCTGTTTGATTTTGCCATTACAACGTAAGTG------TAGCA---------------------------------------ACATCTCAA------------------C---------------------CTAAGAA--TAT-------TATATT------AAGCCTTAATAA----------------ATC---TT---------G-----TTCCTTAGCCTCACTGCTGCTGGATACTTGTGCTACCTTCAGGCTATTCACCGCATGA
droKik1	scf7180000302481:556537-556771 +		CATCTTTTGCCCTTCTTCTGCCTGCAGTTGTTTGATTTCGCCATAACCACGTGAGGA------CTATAG----TTAGGGGG-------TG--------------------------ACTGCAGAAA--TCTCTAGGGATCTTGTCTGTAATC-----------------------------------TGGTCT-----------------------CCCTTAGGGGTTTCTGCGACCCTGTCAGTAG----------------CGATTAGTATATTAATACCGTGATTTAATTTGC---TACTACAGGCTGACTGCCGCTGGATATCTGTGCTACCTGCAGGCCATCCACAGCATCA
droFic1	scf7180000453851:1704599-1704861 +		CACCTATTGCCCTTCTTCTGCTTGCAGTTGTTCGATTTCGCCATTACCACGTGAGTACAAA--TTTTAA----TCCTGGGA-----------------------------------GTTACCGATA--TCTGTACAGATTCGAAGA---------------CA--AAAC-------------AT--TTTGCCTGCTTAAATAATAA---------ATACCTCAAGGCTTTTGAGGCTCCCTAAACCAGGAT-------TTTAAAGATTAATATACTAATTCAATGGTTTTTGTTTG---TATTGCAGTCTTACCGCCGCTGGATATTTGTGCTACCTGCAGGCCATCCACGGCATCA
droEle1	scf7180000491240:1472916-1473104 -		CACTTGTTGCCCTTCTTTTGTCTGCAGTTGTTTGACTTTGCCATTACCACGTGAGTG------TTATAA----TCGGGGGA-----------------------------------GTTCCATAAAGATCTCC------CTTG--TATTCTTTAAGATTTGTATAGTAATGCATCGA------T-CT---TATTACAGTCTCACCGCCGCTGGATATCTATGCTACCTGCAGGCCATCCACAGCATCA
droRho1	scf7180000779971:165526-165765 -		CACCTGTTGCCCTTCTTTTGTTTGCAGTTGTTTGATTTCGCCATTACCACGTGAGTT------TTATAA----GCGGGGGA-----------------------------------GTCACAGAAA--CCTCTACAGACTAAAAGA---------------AA--AGACTTTCGG------CT---GTTACCTTTTGTA----------------ATCCTTAGA---TCCGGGGACTGCCT---------------------GGTTTAATTTACTAATATAACGATCTATTTGCT---AATTACAGTCTCACCGCTGCTGGATATCTGTGCTACCTGCAGGCCATTCACAGCATCA
droBia1	scf7180000302291:2541008-2541208 -		CACCTGCTGCCATTCTTTTGCCTGCAGTTGTTTGACTTCGCCATTACCACGTGAGTATATCATTTATAA---AT---GGCGGTTTCTATTAATCCCTGAATAGGGAT---TATTCTTTAAGATTAATGTACTTATGGTTGAATTTTGTTGTT---TATGACAGTCTGACCGCCGCTGGATATCTGTGCTACCTGCAGGCCATCCACAGCATCA
droTak1	scf7180000415379:739625-739792 -		CACCTGTTGCCGTTCTTTTGCCTGCAGTTGTTTGACTTCGCCATTACCACGTAAGAT------TA--------------GG-----------------------------------GATACAGAAG--TTTGTACAGATTTAAAGC---------------TA--AAG-------------CATATATT--CTCT------TCCG---ATTGACAGTCTTACCGCCGCTGGATATCTGTGCTACCTGCAGGCCATCCACAGCATCA
droEug1	scf7180000409183:264155-264392 -		CACCTATTGCCCTTCTTCTGTCTGCAGTTGTTTGATTTCGCCATTACCACGTAAGGA------TTATAA----T-GGGGGA-----------------------------------TTAACAGAAA--TATCTACTGGTTTATAT--CTTTTTAA----------------ATCCGTAGATGTTCCTAGGATTCCCTTAAAG--AATTC-TATTCG-TAAGATTAATAAACTACAGCTATTG--TTATTATG---TATTACAGTCTTACCGCCGCTGGATATTTGTGCTACCTGCAGGCCATCCACAGCATCA
dm3	chr2R:4606945-4607200 -		CACCTGTTGCCGTTCTTCTGTTTGCAATTGTTTGATTTCGCTATTACAACGTAAGGA------TTATAA----TCGGTGGA-----------------------------------GTTACAGAGA--CCTCAAAAGATTTAAATCGCCACTTTACTTTAGTA--AAG-------------CTTAAATAGCCTTCTTAA----------------ATCCTTCGAGGTTTCTAGGACTCTTTTAATAGGG--------------AGATTAATGTACTTATGCATTGT------TCGT---TATCATAGTCTCACCGCCGCTGGATATCTGTGCTACCTGCAGGCCATTCACAGCATCA
droSim2	2r:5422260-5422502 -	dsi_13501	CACCTGTTGCCGTTCTTCTGTCTGCAGTTGTTTGATTTCGCCATTACAACGTAAGGA------TTACAA----TCGGTGGA-----------------------------------GTTACAGAGA--CCTCAACAGATTTAAACCGCTACC---------------G-------------CGAAAATAGCCTTCTTAA----------------ATCCCTAGAGGTTTCTGGGACTCCCTTAGAAGGG--------------AGATTAATGTACTTATGCATTGT------TCGT---TTTTATAGTCTTACCGCCGCTGGATATCTGTGCTACCTGCAGGCCATTCACAGCATCA
droSec2	scaffold_1:2251386-2251628		CACCTGTTGCCGTTCTTCTGTCTGCAGTTGTTTGATTTCGCCATTACAACGTAAGGA------TTACAA----TCGGTGGA-----------------------------------GTTACAGAGA--CCTCAACAGATTTAAACCGCTACC---------------G-------------CGAAAATAGCCTTCTGAA----------------ATCACTAGAGGTTTCTGGGACTCCCTTAGAAGGG--------------AGATTAATATACTTATGCATTGT------TCGT---TTTTATAGTCTTACCGCCGCTGGATATCTGTGCTACCTGCAGGCCATTCACAGCATCA
droYak3	ZL:17270579-17270840 -		CATCTGTTACCATTCTTCTGCCTGCAGTTGTTTGATTTTGCCATTACAACGTAAGGA------TTACAA----TCGGGGGA-----------------------------------AATTCAGAGA--GCTCAACAGATTTAAACCGCTACTTCATTC--------AG-------------CCAAATTAGCCTTCTTAA----------------ATCCGTAGAGGTTTCTGGGAATTCCTTAAAAGG--TTCATACTCTTTAAGCTTAATGTACTAATGCATTGT------TGAT---TGTTATAGTCTTACCGCCGCTGGATATCTGTGCTACCTGCAGGCTATTCACAGTATCA
droEre2	scaffold_4929:18034593-18034647 +		CATCTGTTGCCATTCTTCTGTCTGCAGTTGTTTGATTTCGCCATAACAACGTAAG---

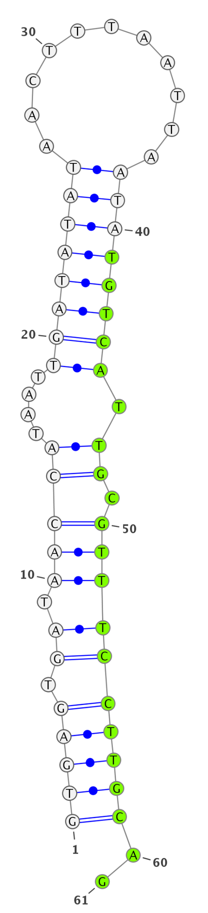
Generated: 09/08/2015 at 07:06 PM

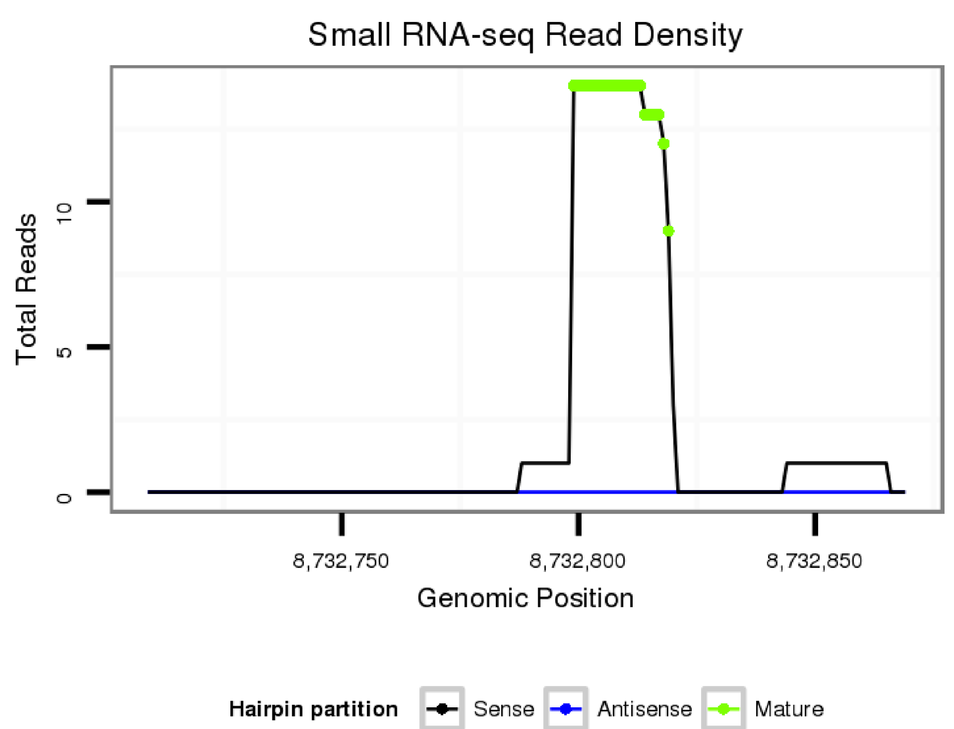
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	0
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

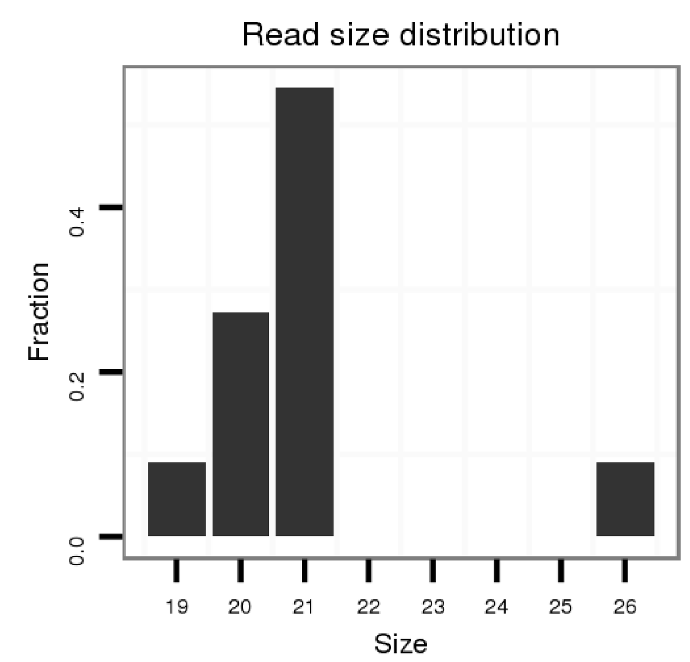
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1045	**scaffold_6496:8732759-8732819 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

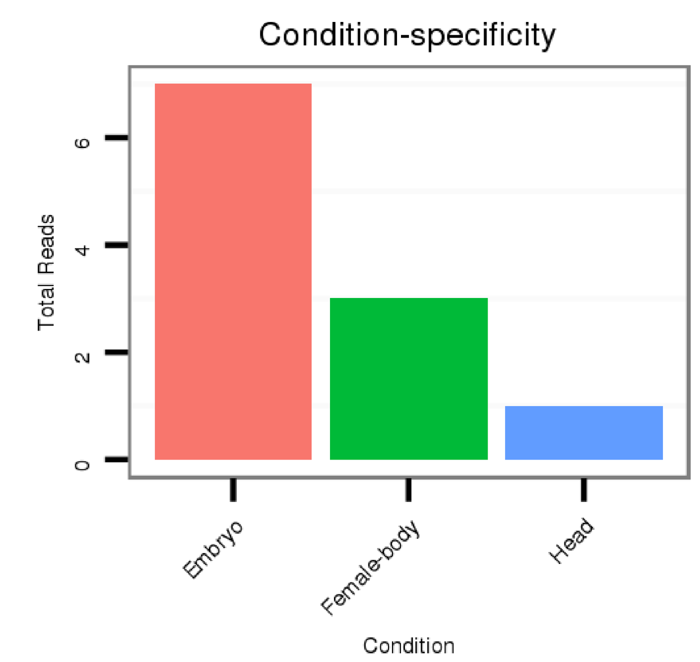
Legend: mature star mismatch in alignment mismatch in read

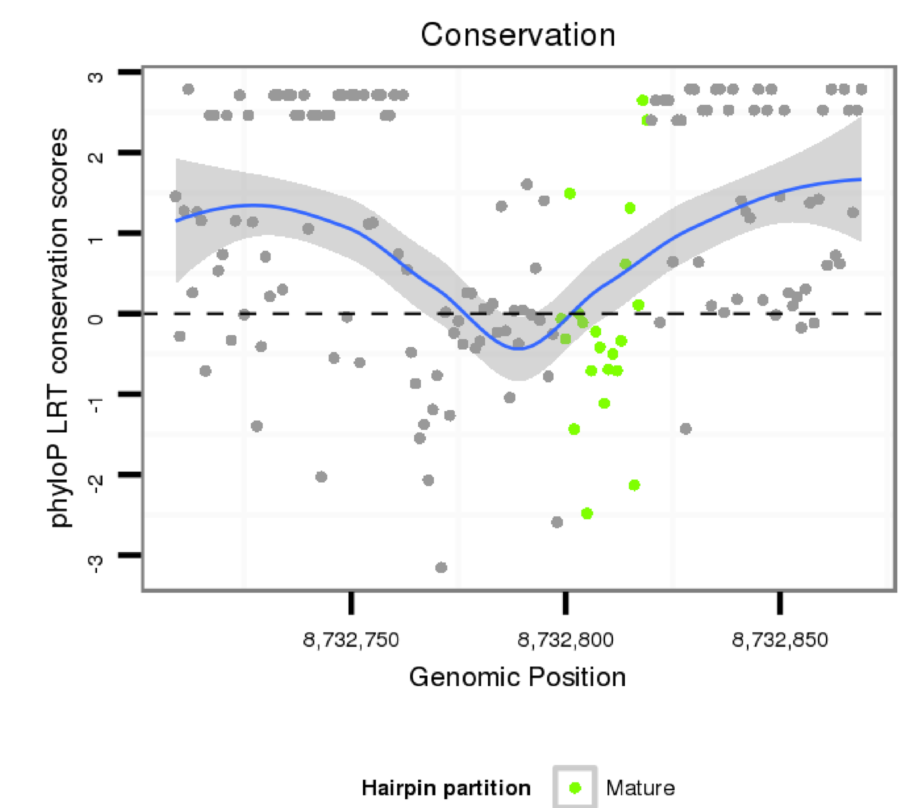
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dmoj\GI20249-in]; CDS [Dmoj\GI20249-cds]; CDS [Dmoj\GI20249-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads   show mid mismatch reads

TGGTGCCCGCAACGCTGGCGAACATTATGCAGGCGCCCAAGATAACGATGGTGAGTGATAACCATAATTGATATATAACTTTAATTAATATGTCATTGCGTTTCCTTGCAGCACAAACGCAAGCGCAAGCAAACCCACGACAGCGTCTACTCCTGCAGCGA **(((((.((.(((((....((((((((..........)))))))).)).))))))))))..***	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	V041 embryo	M046 female body	V110 male body	V049 head
....TGTCATTGCGTTTCCTTGCAGT...	22	1	1	14.00	14	11	3	0	0	0
....TGTCATTGCGTTTCCTTGCAG..	21	0	1	6.00	6	3	0	3	0	0
....TGTCATTGCGTTTCCTTGCA...	20	0	1	3.00	3	1	1	0	0	1
....TGTCATTGCGTTTCCTTGCAGC...	22	0	1	3.00	3	3	0	0	0	0
....TGTCATTGCGTTTCCTTGCAGA...	22	1	1	3.00	3	2	0	0	1	0
....GTCATTGCGTTTCCTTGCAGT...	21	1	1	2.00	2	2	0	0	0	0
....TGTCATTGCGTTTCCTTGC..	19	0	1	1.00	1	1	0	0	0	0
....ATGTCATTGCGTTTCCTTGCAGT...	23	1	1	1.00	1	0	0	1	0	0
....CACGACAGCGTCTACTCCTGCA....	22	0	1	1.00	1	0	0	0	1	0
....TGTCATTGCGTTTCCTTGCAAT...	22	2	1	1.00	1	1	0	0	0	0
....TTTAATTAATATGTCATTGCGTTTCC..	26	0	1	1.00	1	1	0	0	0	0
....TGTCATTGCGTTTCCTTGCAA..	21	1	1	1.00	1	1	0	0	0	0
....TCATTGCGTTTCCTTGCAGA...	20	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

ACCACGGGCGTTGCGACCGCTTGTAATACGTCCGCGGGTTCTATTGCTACCACTCACTATTGGTATTAACTATATATTGAAATTAATTATACAGTAACGCAAAGGAACGTCGTGTTTGCGTTCGCGTTCGTTTGGGTGCTGTCGCAGATGAGGACGTCGCT **(((((.((.(((((....((((((((..........)))))))).)).))))))))))..***	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6496:8732709-8732869 +	dmo_1045	TGGTGCCCGCAACGCTGGCGAACATTATGCAGGCGCCCAAGATAACGATGGTGAGTGA----TAACCATA--AT--------------------------------TG------ATATAT---AACTTTAAT-TAA-----T---------------------------------AT------------GTCAT----TGCGTTTCCTTGCAGCACAAACGCAAGCGCAAGCAAA---CCCACGACAGCGTCTACTCCTGCAGCGA
droVir3	scaffold_12875:15104028-15104201 -		TGGTGCCCGCAACGCTGGCGAACATTATGCAGGCGCCCAAGATAACCATGGTAAGCAA----CGGGTTA---GCT----------GTA----GTTACT------ACTGAGAGCTT--------ATTTCTATT-CAA-----T---------------------------------TTC--TTTTTGC-----------AA--TTCTCATGTAGCACAAACGCAAACGCAAGCAAA---CCCACGACAGCGTCTACTCCTGCAGTGA
droGri2	scaffold_15245:8217431-8217670 +		TGGTGCCAGCGACGCTGGCAAACATTATGCAGGCACCCAAAATCACCATGGTAAGTAGCCCTAACACAAAAGCATCTGTAAGTTCCACAAAAACTGACTTTTCGAGCCGA--GACCATGATTT---------------------------------------TGTCCATTCCATGCAAACTAATTAATAGCTTTCTCTGACTTGATTCAAA-----A-CT-TTTC-----------CA--ATCTTCGACAGCACAAGCGGAAGCGCAAGCAAA---CCCATGACAGCGTCTATTCCTGCAGCGA
droWil2	scf2_1100000004558:2560884-2561055 +		TAGTGCAAGCCTCGCTAGCCAACATTATGCAGGCCCCCAAAATTAGCATGGTAAGTCA----TCCCT--A--TCT----------TAG----GATTGAATTG------TGTCTTTTTATA---------AAT--------------CA---AT---CTTTTATTTTTGCTTACAGCATAAACGCAAGCGGAAACAACCAGCCCAGGATTGTAACAATTCATTTAGCGA
dp5	3:6446974-6447130 +		TAGTGCCTGCCACACTGGCACACATCATGCAGGCACCGAAGATCAGCATGGTAAGCTG----GA--ATGCGTTATTC---------------------------------------TAGCCATTCGAA-----TTTC-----------------------------------TTATTTT-----------CA--ATCTCTTGCAGCACAAGCGGAAGCGCAAGCAGA---TCCACGACAGCATGTACGCCTACAGCGA
droPer2	scaffold_2:6667980-6668136 +		TAGTGCCTGCCACACTGGCACACATCATGCAGGCACCGAAGATCAGCATGGTAAGCTG----GA--ATGCGTTATTC---------------------------------------TAGCCATTCGAA-----TTTC-----------------------------------TTATCTT-----------CA--ATCTCTTGCAGCACAAGCGGAAGCGCAAGCAGA---TCCACGACAGCATGTACGCCTACAGCGA
droAna3	scaffold_13266:10209335-10209496 -		TTGTGCCCGCCACTCTGGCCACCATTATGCAGGCTCCCAAGATCAGCATGGTAAGATG----AT-AGA-T--ACT----------CTG---GCTG-GG---A------------------------------TG-A-----ATTT-----------------------------------TAATCTTAAATCACTGA-----TACTTTTCCAGCATAAACGAAAACGAAAACAGA---CCCATGACAGTCAAGTGTCTTATAGCGA
droBip1	scf7180000396428:628595-628748 -		TGGTGCCCGCCACCCTGGCCACTATTATGCAGGCCCCCAAAATCAGCATGGTAAGATA----AC-AAA-T--GAT----------CCG---GG-TTGG---A------------------------------TG-G-----TCTT-----------------------------------TAATCT-----------TAG--ATCCTTTCCAGCATAAACGAAAACGAAAACAGA---CCCATGATAGTCAAGTGTCTTACAGCGA
droKik1	scf7180000302385:791531-791627 +		TGGTGCCCGCCACTCTAGGTCACATCATGCAGGCGCCCAAAATCAGCATGGTAAG--GAAGCGGAAGCAGA---CGCACGACAGCACCATGTCCTACAGCGA
droFic1	scf7180000453948:1447527-1447689 -		TGGTGCCCGCCACGCTGGCTAACATTATGCAGGCACCCAAGATTAGCATGGTAACTAT----TCAGTTTA--AT------TTAT--------CTT-AG----CGAATT------TAAATCT--A--ACGCGTCCT----------TT---------TCATCTTGTAGCATAAACGAAAGCGCAAGCAAA---CGCACGACAGTTCGATATCCTACAGCGA
droEle1	scf7180000491214:215848-216010 -		TGGTTCCCGCCACGCTGGCCCACATTATGCAGGCTCCCAAGATTAGCATGGTAATCCC----ACCACACAGTA-------------------------------------AC-------------------ATAAA----TAAACT------ATCAGCT--A--ACTAGTATT----------CTT----C----AATTTTGCAGCACAAACGAAAGCGCAAGCAGA---CGCACGATAGCTCCATATCCTACAGCGA
droRho1	scf7180000779949:117575-117730 -		TGGTGCCAGCCACGCTGGCCCACATTATGCAGGCACCTAAGATTAGCATGGTAAGATA----TTAAAA--TAAACT------ATAGAAT---AA-GCAT---TCTAACT----------TAT----CT--TTGATTTTCAGCACAAACGAAAGCGCAAGCAGA---CGCACGATAGCTCGATATCCTACAGCGA
droBia1	scf7180000301754:2549526-2549692 -		TTGTGCCCGCCACGCTGGCGCACATAATGCAGGCTCCCAAGATAAGCATGGTGAGATG----AGA-AA-C--ACA----------TTAATGGTTTGG-----GGTATT------ATAAACT--A--ACTTTCCCT----------TAT----C----ATTTTTTCAGCACAAACGCAAGCGCAAGCAGA---CGCACGACAGCTCGATATCCTACAGCGA
droTak1	scf7180000415795:346811-346903 +		TAATAA--GAACTT------ATAAACT--A--ATTGTAACT----------AAT----T----GTATTTCCAGCACAAACGCAAGCGCAAGCAAA---CGCACGACAGCTCGATATCCTACAGCGA
droEug1	scf7180000409672:1105001-1105162 -		TTGTGCCCGCCTCACTTGCCCATATTATGCAAGCACCTAAGATAAGCATGGTAAGATT----AAAGTTAA--AAT----------AAG----GCCTATTATA-----------------TT------------GAC--------------------------------------TTTCACT----------AACC--CAT--ACTCTTTTTAGCATAAACGAAAGCGCAAACAGA---CGCACGACAGCTCGATATCCTACAGCGA
dm3	chr2R:13987061-13987229 +		CTGTGCCTGCCACGCTAGCCAATATTATGCAAGCACCGAAGATAAGCATGGTAAGACT----TACACAAA--ACT----------CAG----ATATGTTAAA------TGAGCACTAAACCAT--------T--------------TA---AT---GTATCA--ATTTCTTGTAGCATAAACGTAAGCGCAAACAGA---CGCACGATAGCTCGATATCCTACAGCGA
droSim2	2r:14671406-14671574 +		CTGTGCCCGCCACGCTAGCTAATATTATGCAAGCACCGAAGATAAGCATGGTAAGACT----TACACAAA--ACT----------CAG----ATATGTAAAA------TGAGCACTAAACCAA--------T--------------TG---AT---GTATCA--ATTTCTTGTAGCATAAACGTAAGCGCAAACAGA---CGCACGATAGCTCGATATCCTACAGCGA
droSec2	scaffold_1:11480776-11480947 +		CTGTCCCCGCCACGCTAGCCTATATTATGCAAGCACCGAAGATAAGCATGGTAAGACT----TACACAAC--ACT----------CAG----ATTTGTAAAA------TGAGCACAAAACCAA--------T----------GTA-TA---AT---GTATAA--ATTTCTTGTAGCATAAACGTAAGCGCAAACAGA---CGCACGATAGCTCGATATCCTACAGCGA
droYak3	2R:15196014-15196182 -		CTGTGCCTGCCACGTTAGCCAACATTATGCAAGCGCCAAAGATCAGCATGGTAAGACT----TACACAAT--ACT----------CAG----CTTTGCACCA------TTAACAACAAACTTA--------A--------------TA---TT---TGACAT--CTTTATTGTAGCATAAACGAAAGCGCAAGCAGA---CGCACGATAGCTCGATATCCTACAGCGA
droEre2	scaffold_4845:8209303-8209466 +		CTGTGCCTGCCACGTTAGCCACCATTATGCAAGCACCTAAGATAAGCATGGTAAGACT----TACATACA--ACT----------CTG----CTTTGCAAAA------TTAACAACAAACCAA---ATACAA--CTTTATTTTAGCATAAACGTAAGCGCAAGCAGA---CGCACGATAGCTCGATATCCTACAGCGA

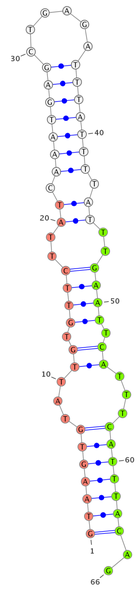
Generated: 09/08/2015 at 07:06 PM

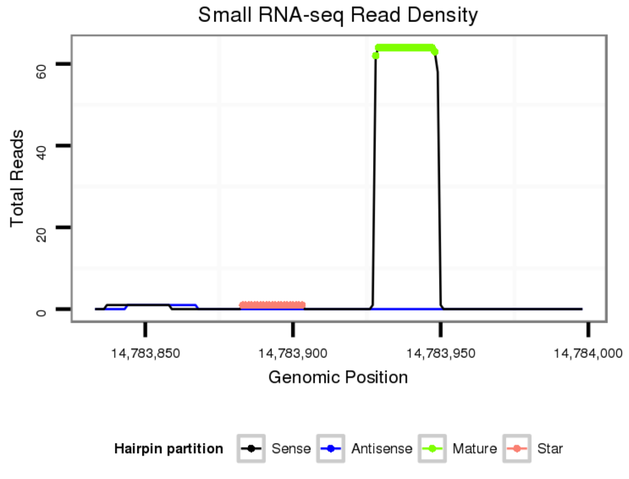
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

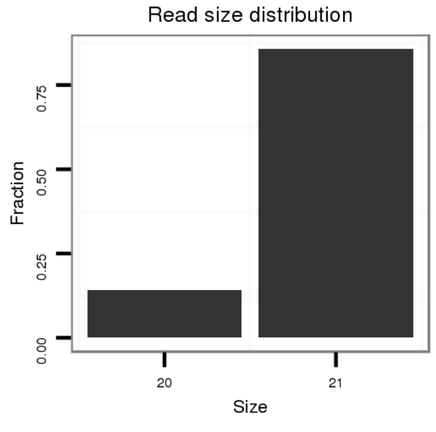
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dmo_1155	**scaffold_6496:14783883-14783948 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

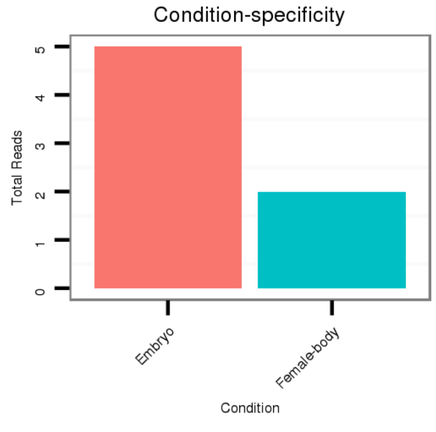
Legend: mature star mismatch in alignment mismatch in read

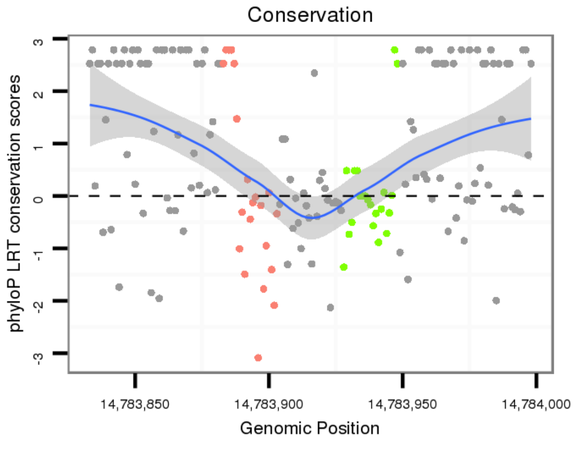
Predicted structure











dmo_1155_mirtron | 1132

Show Alternate Folds

Flybase annnotation

intron [DmojGI20691-in]; CDS [DmojGI20691-cds]; CDS [DmojGI20691-cds]; intron [DmojGI20691-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GATGGTTCCACTGATGATTCGGGCATCTTTCTACAGTATACGGAAAAACCGTAAGTGTATTGTGTTCTTATCAAATGAGCTGAGATTTATTTTATTTGAATTCATTTCATTTACAGTCTCACAAAATTGGCTGGTACCTTGCTGTTAGGTACCGACGGCGTTATTC	Read size	# Mismatch	Hit Count	Total Norm	Total	M060 embryo	M046 female body	V110 male body	V056 head
**********(((((((...((.((((..((.(((((((.....)))))))..))..))))..))...)))))))..**********									
.....TTGAATTCATTTCATTTACAGT.....	22	0	1	54.00	54	45	6	3	0
.....TTGAATTCATTTCATTTACAGC.....	22	1	2	9.50	19	18	1	0	0
.....TTGAATTCATTTCATTTACAGA.....	22	1	1	7.00	7	7	0	0	0
.....TTGAATTCATTTCATTTACAG.....	21	0	1	5.00	5	4	1	0	0
.....TGAATTCATTTCATTTACAGT.....	21	0	1	2.00	2	1	1	0	0
.....TTGAATTCATTTCATTTACAGTT.....	23	1	1	2.00	2	2	0	0	0
.....TTGAATTCATTTCATTTACAGTA.....	23	1	1	1.00	1	1	0	0	0
.....TTGAATTCATTTCATTTACA.....	20	0	1	1.00	1	0	1	0	0
.....TTTGAATTCATTTCATTTACAGT.....	23	0	1	1.00	1	1	0	0	0
....GTTCCACTGATGATTCGGGCAT.....	22	0	1	1.00	1	0	0	0	1
.....TTTGAATTCATTTCATTTACAGC.....	23	1	1	1.00	1	1	0	0	0
.....TTGAATTCATTTCATTTACAGTAA.....	24	2	1	1.00	1	0	1	0	0
.....TTGAATTCATTTCATTTACAGTC.....	23	0	1	1.00	1	1	0	0	0
.....GTAAGTGTATTGTGTTCTTAT.....	21	0	1	1.00	1	1	0	0	0
.....TTGAATTCATTTCATTTACAGTAAA.....	25	3	2	0.50	1	1	0	0	0

Anti-sense strand reads

CTACCAAGGTGACTACTAAGCCCGTAGAAAGATGTCATATGCCTTTTTGGCATTCACATAACACAAGAATAGTTTACTCGACTCTAAATAAAATAAACTTAAGTAAAGTAAATGTCAGAGTGTTTTAACCGACCATGGAACGACAATCCATGGCTGCCGCAATAAG	Read size	# Mismatch	Hit Count	Total Norm	Total	M046 female body
**********(((((((...((.((((..((.(((((((.....)))))))..))..))))..))...)))))))..**********						
...........ACTACTAAGCCCGTAGAAAGATGT.....	24	0	1	1.00	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droMoj3	scaffold_6496:14783833-14783998 +	dmo_1155	GATGGTTCCACTGATGATTCGGGCATCTTTCTACAGTATACGGAAAAACCGTAAGTGTATTGT--GTTCT------T--ATCAAATGAG-----CTGAGATTT-------ATTTTATT-----TGAATTCATTTCATTTACAGTCTCACAAAATTGGCTGGTACCTTGCTGTTAGGTACCGACGGCGTTATTC
droVir3	scaffold_12875:12060009-12060168 +		GACGGATCTACCGATGATTCTGGTATATTTTTGCAGTATACTGAAAAACCGTAAGTTTTTT---AGTTCT-----AA--A----TCTGT---ATTTA------------ATCTTATTCTGTGTTGAT---TTATTTTACAGACTTACAAAGCTAGCGGTACCTTACTTTTGGGTACTGACGGAGTAATTC
droGri2	scaffold_15245:11841132-11841284 +		GACGGATCTACCGATGATTCTGGCATCTTTTTGCATTACACTGAAAAACCGTAAGTAATG---ATTATT-----TT--T----ATGATTATATTTAGA-----------TTT-AATC-----------TTTTTTTCAGACTAAAAAAATTAGCTGGTACCCTACTATTGGGTACTGATGGCGTTATTC
droWil2	scf2_1100000004382:1007105-1007262 +		GACGGAACCACTGACGACTCGGGGGTATTTTATTGAGTACACAGAGAAACCGTAAGTTTGTTTA-AGACAA-----TTAAT----TTAAC---ATTCT-AATTA------ATA-AATA-----------CCTTTACAATAGACTAAAGAAATTAGCTGGAACTTTGTTACTCGGCACTGGTGGATCCATAC
dp5	3:7555077-7555235 -		GATGGTTCCACCGATGACTCTGGGGTGTTCCTGGACTACACAGAAAAGCCGTAAGTCTGCTCT--TTCATTT----T--T---AAGCGATTGCATTAGGG--T-------CTTACACA-----------CTTTCTCACACAGCCTTCAAAAGTTAGCTGGCACACTATTATTGGGCACAGACGGAATAATTC
droPer2	scaffold_2:7750474-7750632 -		GATGGTTCCACCGATGACTCTGGGGTGTTCCTGGACTACACAGAAAAGCCGTAAGTCTGCTCT--TTCATTT----T--T---AAGCGATTGCATTAGGG--T-------CTTACACA-----------CTTTCTCACACAGCCTTCAAAAGTTAGCTGGCACACTATTATTGGGCACAGACGGAATAATTC
droAna3	scaffold_13266:5743679-5743835 -		GATGGTTCTAGCGATGACTCTGGGGTGTTTTTGGATTACACAGAAACCCCGTAAGTAAATGTTGACTTTT--TATCG--C----GTAAT---CTCTAAAAT-A-------AAC-----------CCCCACTTTTAGTGCGCAAAAGTTGGCTGGCACCTTGTTGCTGGGCACAGACGGAATAATTC
droBip1	scf7180000396372:357029-357184 -		GATGGTTCCACCGATGACTCTGGGGAGTCTTTTTATGATTACACAGAAACCCCGTAAGTAAATTTT--GACATTTT-TCG--C----GTAAT---CTCTAAAAC-A-------AAA-----------CCCCCCTTTTAGTGCTAAAAAGTTGGCTGGCACCTTCTTGCTGGGCACTGATGGAATGATTC
droKik1	scf7180000302355:461821-461977 -		GACGGATCAACTGATGACTCTGGGGTGTTTCTGGACTACACGAGGAGCCGTAAGCCCCTT--AAATTA-----TT--T----ATTTTT--CTCTATTATAA-------ACAAACTT-----------CTCCTTGGCAGCCGCAAGAAGTTGGCCGGAACACTGTTGCTGGGCACCGATGGTGCGATCC
droFic1	scf7180000453858:1609535-1609690 -		GATGGTTCAACGGATGACTCTAGGAGTTTCTTGGATTATACAGAGGAGCCGTAAGTCCCTA---ACACAA-----AT--A----ATATT---TTTTGATTATTA-------GTCAAACT-----------GTTCCTGACAGTGCAGAAAAAGTTGGCTGGAACCCTATTGATGGGCACGGACGGAATGATTC
droEle1	scf7180000491214:5207941-5208097 +		GATGGTTCTACCGATGACTCTGGGGTGTTTTTTGGAGTACACAGAAGAGCCGTAAGTCTTGG--GCTTATT----AA--A----ATATA---TCTTAATAGTA-------ATTATACA-----------TTTCCCTGACAGTCTTAAAAAGTTGGCTGGCACTCTTCTGCTGGGCACAGACGGAATGATTC
droRho1	scf7180000767536:51367-51522 +		GATGGTTCCACTGATGACTCTGGGGTATTCTTGGATTATACAGAAGAGCCGTAAGTTCTG--GCTTAT-----AA--A----ATATG---TTTTAACACTA-------ATTTTACT-----------TTTCCCTAATAGACGTAAAAAGTTGGGAGGTACTCTATTGCTGGGCACTGACGGAATGATTC
droBia1	scf7180000302143:404880-405041 -		GATGGCTCCACTGACGATTCAGGAGTGTTCTTGGACTACACAGAAGAGCCGTAAGTTCGCA---AATCTT-----TC--C----GTATT---CCCTAACAC-AGCACCTTAACCAACT-----------CCGCATCCACAGCGCGTAAGAAGTTGGCTGGCACACTGCTGCTGGGCACAGACGGTCAGATTC
droTak1	scf7180000415878:998475-998630 -		GATGGATCCACCGATGATTCAGGGCTGTTCTTGGATTATCTCAGAAGAGCCGTAAGTCTTTA---AGTTTT-----AA--T----TCCTA---ACGCAGCACTT-------ATAAACT-----------CTTTTATTATAGTGCTAAAAAGCTAGCTGGCACTCTGTTGCTGGGCACAGATGGACAGATTC
droEug1	scf7180000409464:246301-246456 -		GATGGTTCCACCGATGACTCTGGAGTATTCTTAGATTACACAGAGGAGCCGTAAGTTTCTC---GCCAAT-----AT--T----GTACG---ATTTGTTATTA-------ATTATTCT-----------TTTCGCTGGCAGCCGCAAAAAGTTAGCTGGCACTCTTACTACTGGGAACAGACGGAATGATTC
dm3	chr2R:19873575-19873732 -		GATGGCTCCACTGATGATTCTGGTGTGTTTTGGATTACAGAGAAGAGCCGTAAGTTCCTTTC-GTTTAA-----TATGC----GTGAT---TTTCAAAAT-A-------ATC-AGTA-----------CCATCCTGGCAGTGCGAAAAAGCTGGCTGGCACTCTGCTGCTGGGCACTGACGGACAGATTC
droSim2	2r:20374433-20374586 -		GATGGCTCCACTGATGATTCTGGGGTGTTCTTGGATTACAGAGAAGAGCCGTAAGTCCCTT---GATAAA-----TA--C----GTGAT---TTCCAAAAT-A-------ACC-ATTA-----------CCATCCTGGCAGTGCGTAAAAAGCTGGCTGGCACTCTGCTGCTGGGTACAGACGGTCAGATTC
~~droSec2~~ droYak3	~~scaffold_9:3157576-3157729 -~~ 2R:19851519-19851673 -		~~GATGGCTCCACTGATGATTCTGGGGTGTTCTTGGATTACAGAAGAGCCGTAAGTCCCTT---GATAAA-----TA--C----GTGAT---TTCCAAAAT-A-------ACC-ATTA-----------CCATCCTGGCAGTGCGTAAAAAGCTGGCTGGCACTCTGCTGCTGGGCACAGACGGACAGATTC~~ GATGGCTCCACTGATGATTCTGGGGTGTTCCTGGATTACACAGAAGAACCGTAAGTTCCTTT---GTTACA-----AA--A----GTGAT---TCATAAAAT-A-------ATT-AACC-----------CTATCCGGCAGTGCGTAAAAAGCTGGCTGGCAACTGCTGCTGGGCACGGACGGACAGATTC
droEre2	scaffold_4845:21246680-21246838 -		GATGGCTCCACTGATGATTCTGGAGTGTTCCTGGATTACTCAGAAGAGCCGTAAGTTCCTTT---GTTACA-----TG--TGTAAATGATT---TCTTAAAATAA-------ACC-AGTC-----------CCCTCCTGGCAGTGCGTAAAAAGCTGGCTGGAACTCTGCTGCTGGGCACAGACGGACAGATTC

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

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