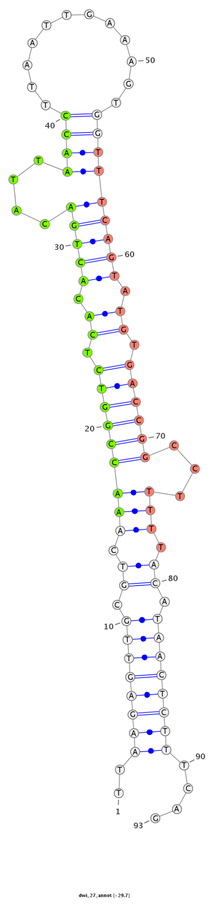
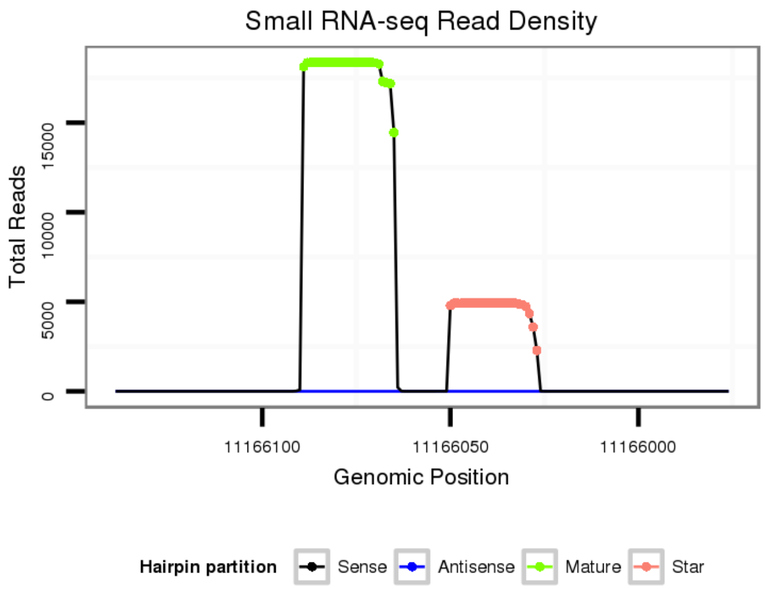
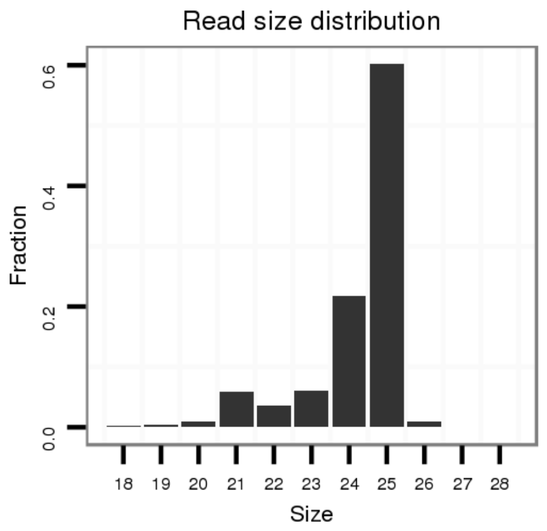
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_27	**scf2_1100000004902:11166026-11166089 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

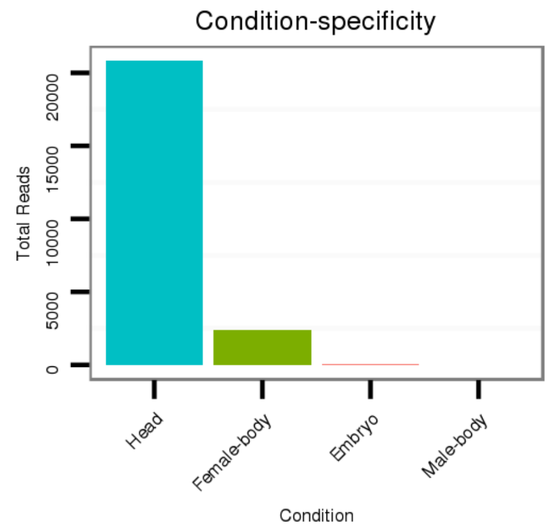
Legend: mature star **mismatch in alignment** mismatch in read

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

ATCTTAAATGCACTCATAATCGATTCGAATTATATTTAAGAGTTGCGTCAAACCGGTCTCACACTGACATTAACCTTAATTGAAAGTGGTTTCAGTATGTGACCGGCCTTTTTACATAACTCTTTCAGCATTAACTAACACTTAACAATTTAAATACCATCGAT **********************************..(((((((((.((.((((((((((.((.(((((....((((.....((((((((((.)).)))))))...)))).)).)))))))))....**********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	M045 female body	V119 head	V118 embryo	V117 male body
.....AACCGGTCTCACACTGACATTAACC.....	25	0	1	13981.00	13981	13883	82	15	1	0
.....AACCGGTCTCACACTGACATTAAC.....	24	0	1	2706.00	2706	2671	32	3	0	0
.....TTTCAGTATGTGACCGGCCTTTTT.....	24	0	1	2193.00	2193	1151	817	203	20	2
.....TTTCAGTATGTGACCGGCCTTTT.....	23	0	1	1259.00	1259	477	642	134	3	3
.....AACCGGTCTCACACTGACATT.....	21	0	1	941.00	941	656	159	102	22	2
.....TTTCAGTATGTGACCGGCCTTT.....	22	0	1	736.00	736	253	294	187	2	0
.....TTTCAGTATGTGACCGGCCTT.....	21	0	1	385.00	385	278	57	50	0	0
.....AACCGGTCTCACACTGACATTAACCT.....	26	0	1	204.00	204	204	0	0	0	0
.....ACCGGTCTCACACTGACATTAACC.....	24	0	1	166.00	166	160	6	0	0	0
.....TTTCAGTATGTGACCGGCCT.....	20	0	1	109.00	109	88	17	2	1	1
.....AACCGGTCTCACACTGACAT.....	20	0	1	69.00	69	51	8	9	1	0
.....TTCAGTATGTGACCGGCCTTTTT.....	23	0	1	65.00	65	1	63	1	0	0
.....TTTCAGTATGTGACCGGCCTTTTTT.....	25	1	1	60.00	60	55	5	0	0	0
.....AACCGGTCTCACACTGACATTA.....	22	0	1	59.00	59	21	29	9	0	0
.....AAACCGGTCTCACACTGACATTAACC.....	26	0	1	55.00	55	55	0	0	0	0
.....TTTCAGTATGTGACCGGC.....	18	0	1	49.00	49	38	2	8	1	0
.....TTCAGTATGTGACCGGCCTTTT.....	22	0	1	44.00	44	0	43	1	0	0
.....AACCGGTCTCACACTGACATTAA.....	23	0	1	42.00	42	29	12	1	0	0
.....TTTCAGTATGTGACCGGCC.....	19	0	1	38.00	38	37	1	0	0	0
.....AACCGGTCTCACACTGACA.....	19	0	1	29.00	29	27	1	1	0	0
.....ACCGGTCTCACACTGACATT.....	20	0	1	28.00	28	5	22	1	0	0
.....TTCAGTATGTGACCGGCCTTT.....	21	0	1	25.00	25	0	20	5	0	0
.....ACCGGTCTCACACTGACATTAAC.....	23	0	1	18.00	18	14	4	0	0	0
.....CAAACCGGTCTCACACTGACATTAACC.....	27	0	1	12.00	12	12	0	0	0	0
.....TTTCAGTATGTGACCGGCCTTTTC.....	24	1	1	11.00	11	9	2	0	0	0
.....TTTCAGTATGTGACCGGCCTTTTTC.....	25	1	1	10.00	10	8	1	1	0	0
.....AACCGGTCTCACACTGACATTAACCTT.....	27	0	1	9.00	9	7	1	1	0	0
.....TTTCAGTATGTGACCGGCCTTTTTA.....	25	0	1	8.00	8	2	3	3	0	0
.....AACCGGTCTCACACTGACATTAACA.....	25	1	1	8.00	8	8	0	0	0	0
.....AACCGGTCTCACACTGACATTAACT.....	25	1	1	8.00	8	7	1	0	0	0
.....CCGGTCTCACACTGACATTAACC.....	23	0	1	8.00	8	7	1	0	0	0
.....ACCGGTCTCACACTGACAT.....	19	0	1	7.00	7	0	7	0	0	0
.....TTCAGTATGTGACCGGCCTT.....	20	0	1	7.00	7	2	5	0	0	0
.....TTTCAGTATGTGACCGGCCC.....	20	1	1	7.00	7	7	0	0	0	0
.....TTTCAGTATGTGACCGGCCTTTTA.....	24	1	1	7.00	7	1	2	4	0	0
.....AAACCGGTCTCACACTGACATTAAC.....	25	0	1	6.00	6	6	0	0	0	0
.....TTTCAGTATGTGACCGGCCTC.....	21	1	1	6.00	6	6	0	0	0	0
.....ACCGGTCTCACACTGACATTAACCT.....	25	0	1	6.00	6	6	0	0	0	0
.....AACCGGTCTCACACTGACATTAACCC.....	26	1	1	6.00	6	6	0	0	0	0
.....TTTCAGTATGTGACCGGCCTTTA.....	23	1	1	5.00	5	1	0	4	0	0
.....CAAACCGGTCTCACACTGACATTAAC.....	26	0	1	5.00	5	5	0	0	0	0
.....TTTCAGTATGTGACCGGCCTTTTG.....	24	1	1	5.00	5	2	2	1	0	0
.....TTTCAGTATGTGACCGGCCTTTTG.....	25	1	1	5.00	5	3	1	1	0	0
.....TTTCAGTATGTGACCGGCCTTTTTG.....	25	1	1	5.00	5	3	1	1	0	0
.....ACCGGTCTCACACTGACATTA.....	21	0	1	4.00	4	0	4	0	0	0
.....CCGGTCTCACACTGACATTAAC.....	22	0	1	4.00	4	3	1	0	0	0
.....CGGTCTCACACTGACATTAACC.....	22	0	1	4.00	4	4	0	0	0	0
.....CAGTATGTGACCGGCCTTTTT.....	21	0	1	3.00	3	0	3	0	0	0
.....TCAGTATGTGACCGGCCTTTTT.....	22	0	1	3.00	3	0	3	0	0	0
.....CAAACCGGTCTCACACTGACATT.....	23	0	1	3.00	3	3	0	0	0	0
.....ACCGGTCTCACACTGACATTAA.....	22	0	1	3.00	3	0	3	0	0	0
.....CCGGTCTCACACTGACATT.....	19	0	1	3.00	3	0	3	0	0	0
.....AACCGGTCTCACACTGACATTAC.....	23	1	1	3.00	3	3	0	0	0	0
.....TTTCAGTATGTGACCGGCCTTTTTAC.....	26	0	1	3.00	3	3	0	0	0	0
.....TTTCAGTATGTGACCGGCCG.....	20	1	1	3.00	3	3	0	0	0	0
.....GTATGTGACCGGCCTTTTT.....	19	0	1	3.00	3	2	1	0	0	0
.....TATGTGACCGGCCTTTTT.....	18	0	1	3.00	3	1	2	0	0	0
.....GTTTCAGTATGTGACCGGCCTTTT.....	24	0	1	2.00	2	0	2	0	0	0
.....AACCGGTCTCACACTGAC.....	18	0	1	2.00	2	0	2	0	0	0
.....TTTCAGTATGTGACCGGCCTTTTCC.....	25	2	1	2.00	2	0	2	0	0	0
.....AACCGGTCTCACACTGACG.....	19	1	1	2.00	2	2	0	0	0	0
.....TCTCACACTGACATTAACC.....	19	0	1	2.00	2	2	0	0	0	0
.....AGTATGTGACCGGCCTTTTT.....	20	0	1	2.00	2	0	1	1	0	0
.....TTTCAGTATGTGACCGGCCTTTTTAA.....	26	1	1	2.00	2	0	1	1	0	0
.....AGTATGTGACCGGCCTTTT.....	19	0	1	2.00	2	0	2	0	0	0
.....GTTTCAGTATGTGACCGGCCT.....	21	0	1	2.00	2	2	0	0	0	0
.....ATTAACCTTAATTGAAAGTG.....	20	0	1	1.00	1	0	1	0	0	0
.....AAACCGGTCTCACACTGACATTAA.....	24	0	1	1.00	1	1	0	0	0	0
.....AACCGGTCTCACACTGACATTG.....	22	1	1	1.00	1	0	1	0	0	0
.....TTCAGTATGTGACCGGCCTTTTTT.....	24	1	1	1.00	1	0	1	0	0	0
.....AACCTTAATTGAAAGTGGTTTCAG.....	24	0	1	1.00	1	0	1	0	0	0
.....TTTCAGTATGTGACCGGCCTTC.....	22	1	1	1.00	1	1	0	0	0	0
.....TTTCAGTATGTGACCGGCCTTTTTTT.....	26	2	1	1.00	1	0	1	0	0	0
.....GTGGTTTCAGTATGTGACCGGCCTTTTT.....	28	0	1	1.00	1	0	1	0	0	0
.....TTCAGTATGTGACCGGCCTTTTTC.....	24	1	1	1.00	1	0	1	0	0	0
.....AACCGGTCTCACACTGACATTAAA.....	24	1	1	1.00	1	0	0	1	0	0
.....ACCGGTCTCACACTGACATTAACCTT.....	26	0	1	1.00	1	1	0	0	0	0
.....AACCGGTCTCACACTGACATTAACG.....	25	1	1	1.00	1	1	0	0	0	0
.....AACCGGTCTCACACTGACATC.....	21	1	1	1.00	1	1	0	0	0	0
.....AAACCGGTCTCACACTGACATT.....	22	0	1	1.00	1	1	0	0	0	0
.....ACCGGTCTCACACTGACATC.....	20	1	1	1.00	1	1	0	0	0	0
.....AACCGGTCTCACACTGACATTT.....	22	1	1	1.00	1	0	1	0	0	0
.....AGTATGTGACCGGCCTTT.....	18	0	1	1.00	1	0	1	0	0	0
.....CAGTATGTGACCGGCCTTTT.....	20	0	1	1.00	1	0	1	0	0	0
.....AACCGGTCTCACACTGACATTAACCA.....	26	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

TAGAATTTACGTGAGTATTAGCTAAGCTTAATATAAATTCTCAACGCAGTTTGGCCAGAGTGTGACTGTAATTGGAATTAACTTTCACCAAAGTCATACACTGGCCGGAAAAATGTATTGAGAAAGTCGTAATTGATTGTGAATTGTTAAATTTATGGTAGCTA **********************************..(((((((((.((.((((((((((.((.(((((....((((.....((((((((((.)).)))))))...)))).)).)))))))))....**********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	V119 head	V117 male body
.....CTGGCCGGAAAAATGTATTGA.....	21	0	1	1.00	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004902:11165976-11166139 -	dwi_27	ATCTTAAATGCACTCATAATCGATTCGAATTATATTTAAGAGTTGCGTCAAACCGGTCTCACACTGACATTAACCTTAATTGAAAGTGGTTTCAGTATGTGACCGGCCTTTTTACATAACTCTTTCAGCATTAACTAACACTTAACAATTTAAATACCATCGAT

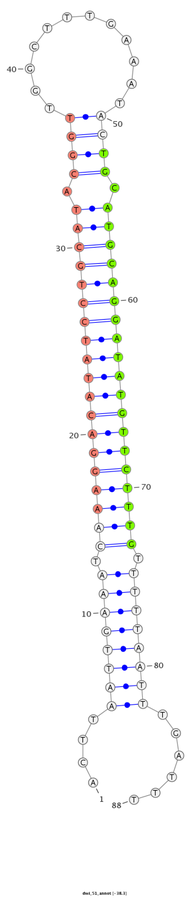
Generated: 09/08/2015 at 07:38 PM

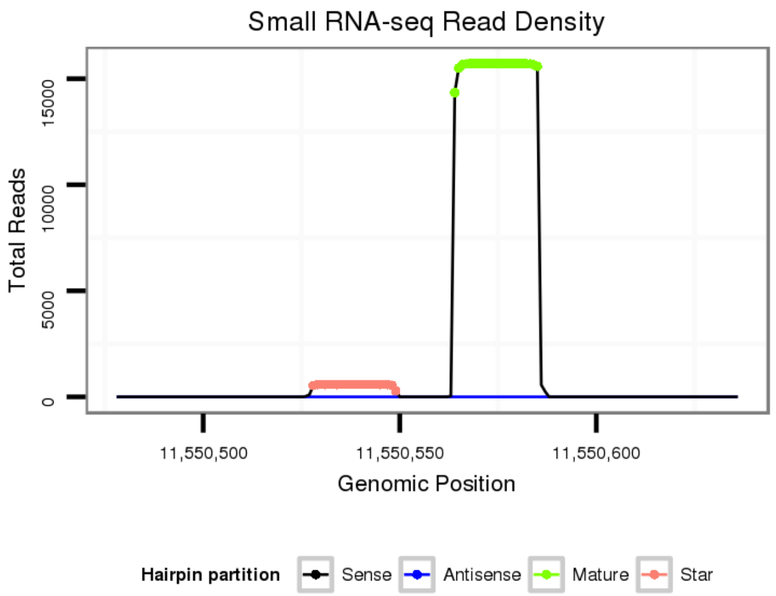
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

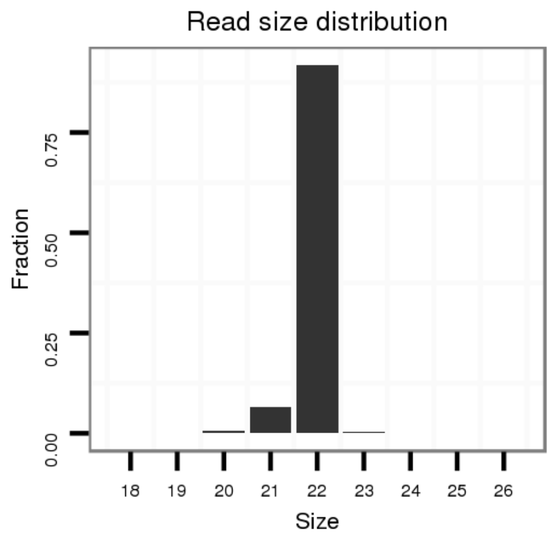
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_51	**scf2_1100000004521:11550528-11550586 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

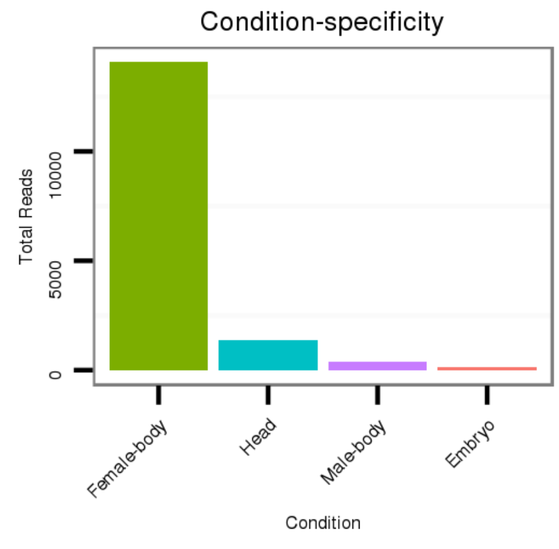
Legend: mature star **mismatch in alignment** mismatch in read

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

ATGAGAACCAATCTTTATTTGATATCATATTGATAACTTAATTGAAATCAAAGGACATATCCTGCATACGGTTGGCTTTGAAATACTGCATGCAGGATATGTTCTTTGTTTTTAATTTGATTTTTCCATCATTAATGCATTAATTTTAATTTTTGAGCT **********....(((((((.(((((((((((((((((((.((((...........)))).)))))))))))))))))))).)))))))......**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	V119 head	V117 male body	V118 embryo	M020 head
.....TGCATGCAGGATATGTTCTTTG.....	22	0	1	14139.00	14139	12369	1252	340	122	56
.....GCATGCAGGATATGTTCTTTG.....	21	0	1	780.00	780	770	9	1	0	0
.....GCATGCAGGATATGTTCTTTGT.....	22	0	1	253.00	253	220	15	16	2	0
.....AAGGACATATCCTGCATACGGT.....	22	0	1	251.00	251	221	12	3	3	12
.....AAGGACATATCCTGCATACGG.....	21	0	1	172.00	172	158	0	0	0	14
.....CATGCAGGATATGTTCTTTGTT.....	22	0	1	119.00	119	92	6	1	0	20
.....GCATGCAGGATATGTTCTTTGTT.....	23	0	1	117.00	117	114	0	0	0	3
.....AAAGGACATATCCTGCATACGG.....	22	0	1	74.00	74	73	0	0	0	1
.....TGCATGCAGGATATGTTCTTT.....	21	0	1	69.00	69	61	8	0	0	0
.....TGCATGCAGGATATGTTCTTTGT.....	23	0	1	47.00	47	43	2	2	0	0
.....TGCATGCAGGATATGTTCTT.....	20	0	1	35.00	35	35	0	0	0	0
.....CATGCAGGATATGTTCTTTG.....	20	0	1	32.00	32	32	0	0	0	0
.....CTGCATGCAGGATATGTTCTTTG.....	23	0	1	29.00	29	28	1	0	0	0
.....AGGACATATCCTGCATACGGT.....	21	0	1	24.00	24	24	0	0	0	0
.....TGCAGGATATGTTCTTTG.....	18	0	1	21.00	21	19	1	1	0	0
.....CAAAGGACATATCCTGCATACG.....	22	0	1	19.00	19	19	0	0	0	0
.....AGGACATATCCTGCATACGG.....	20	0	1	18.00	18	18	0	0	0	0
.....CATGCAGGATATGTTCTTTGT.....	21	0	1	17.00	17	16	0	1	0	0
.....TGCATGCAGGATATGTTCTTTGG.....	23	1	1	16.00	16	16	0	0	0	0
.....ATGCAGGATATGTTCTTTG.....	19	0	1	16.00	16	16	0	0	0	0
.....TGCATGCAGGATATGTTCTTTGA.....	23	1	1	16.00	16	10	0	1	0	5
.....TGCATGCAGGATATGTTCT.....	19	0	1	14.00	14	14	0	0	0	0
.....ATGCAGGATATGTTCTTTGTT.....	21	0	1	11.00	11	11	0	0	0	0
.....TGCATGCAGGATATGTTCTTTT.....	22	1	1	10.00	10	8	2	0	0	0
.....AAGGACATATCCTGCATACG.....	20	0	1	9.00	9	9	0	0	0	0
.....TGCATGCAGGATATGTTCTTG.....	21	1	1	8.00	8	5	1	1	1	0
.....CTGCATGCAGGATATGTTCTTT.....	22	0	1	8.00	8	8	0	0	0	0
.....TGCATGCAGGATATGTTCTTTA.....	22	1	1	7.00	7	4	3	0	0	0
.....AAGGACATATCCTGCATACGGTT.....	23	0	1	4.00	4	3	0	0	0	1
.....TGCATGCAGGATATGTTC.....	18	0	1	4.00	4	4	0	0	0	0
.....GCATGCAGGATATGTTCTTTGTA.....	23	1	1	4.00	4	4	0	0	0	0
.....AAAGGACATATCCTGCATACG.....	21	0	1	4.00	4	4	0	0	0	0
.....GCATGCAGGATATGTTCTTT.....	20	0	1	3.00	3	3	0	0	0	0
.....AAGGACATATCCTGCATACGGG.....	22	1	1	3.00	3	1	0	0	0	2
.....TGCATGCAGGATATGTTCTTTC.....	22	1	1	3.00	3	2	1	0	0	0
.....TGCATGCAGGATATGTTCTTTGC.....	23	1	1	3.00	3	3	0	0	0	0
.....GCATGCAGGATATGTTCTT.....	19	0	1	2.00	2	2	0	0	0	0
.....CAAAGGACATATCCTGCATAC.....	21	0	1	2.00	2	1	0	0	0	1
.....TGCATGCAGGATATGTTCTTTGTA.....	24	1	1	2.00	2	0	0	0	0	2
.....GGACATATCCTGCATACGGT.....	20	0	1	2.00	2	2	0	0	0	0
.....GGACATATCCTGCATACGG.....	19	0	1	2.00	2	2	0	0	0	0
.....AAGGACATATCCTGCATACGGA.....	22	1	1	1.00	1	1	0	0	0	0
.....TGCATGCAGGATATGTTCTTTTC.....	23	2	1	1.00	1	1	0	0	0	0
.....AAGGACATATCCTGCATACGGC.....	22	1	1	1.00	1	1	0	0	0	0
.....AGGACATATCCTGCATACGGC.....	21	1	1	1.00	1	1	0	0	0	0
.....AAGGACATATCCTGCATACGGTA.....	23	1	1	1.00	1	1	0	0	0	0
.....AAAGGACATATCCTGCATACGGC.....	23	1	1	1.00	1	1	0	0	0	0
.....ATACTGCATGCAGGATATGTTCTTTG.....	26	0	1	1.00	1	1	0	0	0	0
.....ATGCAGGATATGTTCTTTGT.....	20	0	1	1.00	1	0	0	1	0	0
.....TGCAGGATATGTTCTTTGTT.....	20	0	1	1.00	1	1	0	0	0	0
.....GCATGCAGGATATGTTCT.....	18	0	1	1.00	1	1	0	0	0	0
.....TGCATGCAGGATATGTTCTC.....	20	1	1	1.00	1	1	0	0	0	0
.....AGGACATATCCTGCATACG.....	19	0	1	1.00	1	1	0	0	0	0
.....AAGGACATATCCTGCATA.....	18	0	1	1.00	1	0	0	0	0	1
.....AGGACATATCCTGCATACGGTTT.....	23	1	1	1.00	1	1	0	0	0	0
.....GCATGCAGGATATGTTCTTTGG.....	22	1	1	1.00	1	1	0	0	0	0
.....AGGACATATCCTGCATACGGTTT.....	23	1	1	1.00	1	1	0	0	0	0
.....GCATGCAGGATATGTTCTTTG.....	22	1	1	1.00	1	1	0	0	0	0
.....CTGCATGCAGGATATGTT.....	18	0	1	1.00	1	1	0	0	0	0
.....CTGCATGCAGGATATGTTCTT.....	21	0	1	1.00	1	1	0	0	0	0
.....CAAAGGACATATCCTGCATACGG.....	23	0	1	1.00	1	1	0	0	0	0
.....GCATGCAGGATATGTTCTTTGTTT.....	24	0	1	1.00	1	1	0	0	0	0
.....AAGGACATATCCTGCATAC.....	19	0	1	1.00	1	1	0	0	0	0
.....CATGCAGGATATGTTCTTTA.....	20	1	1	1.00	1	1	0	0	0	0
.....TGCATGCAGGATATGTTCTTTGGC.....	24	2	1	1.00	1	1	0	0	0	0
.....GCATGCAGGATATGTTCTTG.....	20	1	1	1.00	1	1	0	0	0	0
.....TGCATGCAGGATATGTTT.....	18	1	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

TACTCTTGGTTAGAAATAAACTATAGTATAACTATTGAATTAACTTTAGTTTCCTGTATAGGACGTATGCCAACCGAAACTTTATGACGTACGTCCTATACAAGAAACAAAAATTAAACTAAAAAGGTAGTAATTACGTAATTAAAATTAAAAACTCGA **********....(((((((.(((((((((((((((((((.((((...........)))).)))))))))))))))))))).)))))))......**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	M045 female body	M020 head
.....AGGACATATCCTGCATACGGTTT.....	23	1	1	14139.00	14139	12369	1252	340	122	56
.....GCATGCAGGATATGTTCTTTG.....	21	0	1	780.00	780	770	9	1	0	0
.....GCATGCAGGATATGTTCTTTGT.....	22	0	1	253.00	253	220	15	16	2	0
.....AAGGACATATCCTGCATACGGT.....	22	0	1	251.00	251	221	12	3	3	12
.....AAGGACATATCCTGCATACGG.....	21	0	1	172.00	172	158	0	0	0	14
.....CATGCAGGATATGTTCTTTGTT.....	22	0	1	119.00	119	92	6	1	0	20
.....GCATGCAGGATATGTTCTTTGTT.....	23	0	1	117.00	117	114	0	0	0	3
.....AAAGGACATATCCTGCATACGG.....	22	0	1	74.00	74	73	0	0	0	1
.....TGCATGCAGGATATGTTCTTT.....	21	0	1	69.00	69	61	8	0	0	0
.....TGCATGCAGGATATGTTCTTTGT.....	23	0	1	47.00	47	43	2	2	0	0
.....TGCATGCAGGATATGTTCTT.....	20	0	1	35.00	35	35	0	0	0	0
.....CATGCAGGATATGTTCTTTG.....	20	0	1	32.00	32	32	0	0	0	0
.....CTGCATGCAGGATATGTTCTTTG.....	23	0	1	29.00	29	28	1	0	0	0
.....AGGACATATCCTGCATACGGT.....	21	0	1	24.00	24	24	0	0	0	0
.....TGCAGGATATGTTCTTTG.....	18	0	1	21.00	21	19	1	1	0	0
.....CAAAGGACATATCCTGCATACG.....	22	0	1	19.00	19	19	0	0	0	0
.....AGGACATATCCTGCATACGG.....	20	0	1	18.00	18	18	0	0	0	0
.....CATGCAGGATATGTTCTTTGT.....	21	0	1	17.00	17	16	0	1	0	0
.....TGCATGCAGGATATGTTCTTTGG.....	23	1	1	16.00	16	16	0	0	0	0
.....ATGCAGGATATGTTCTTTG.....	19	0	1	16.00	16	16	0	0	0	0
.....TGCATGCAGGATATGTTCTTTGA.....	23	1	1	16.00	16	10	0	1	0	5
.....TGCATGCAGGATATGTTCT.....	19	0	1	14.00	14	14	0	0	0	0
.....ATGCAGGATATGTTCTTTGTT.....	21	0	1	11.00	11	11	0	0	0	0
.....TGCATGCAGGATATGTTCTTTT.....	22	1	1	10.00	10	8	2	0	0	0
.....AAGGACATATCCTGCATACG.....	20	0	1	9.00	9	9	0	0	0	0
.....TGCATGCAGGATATGTTCTTG.....	21	1	1	8.00	8	5	1	1	1	0
.....CTGCATGCAGGATATGTTCTTT.....	22	0	1	8.00	8	8	0	0	0	0
.....TGCATGCAGGATATGTTCTTTA.....	22	1	1	7.00	7	4	3	0	0	0
.....AAGGACATATCCTGCATACGGTT.....	23	0	1	4.00	4	3	0	0	0	1
.....TGCATGCAGGATATGTTC.....	18	0	1	4.00	4	4	0	0	0	0
.....GCATGCAGGATATGTTCTTTGTA.....	23	1	1	4.00	4	4	0	0	0	0
.....AAAGGACATATCCTGCATACG.....	21	0	1	4.00	4	4	0	0	0	0
.....GCATGCAGGATATGTTCTTT.....	20	0	1	3.00	3	3	0	0	0	0
.....AAGGACATATCCTGCATACGGG.....	22	1	1	3.00	3	1	0	0	0	2
.....TGCATGCAGGATATGTTCTTTC.....	22	1	1	3.00	3	2	1	0	0	0
.....TGCATGCAGGATATGTTCTTTGC.....	23	1	1	3.00	3	3	0	0	0	0
.....GCATGCAGGATATGTTCTT.....	19	0	1	2.00	2	2	0	0	0	0
.....CAAAGGACATATCCTGCATAC.....	21	0	1	2.00	2	1	0	0	0	1
.....TGCATGCAGGATATGTTCTTTGTA.....	24	1	1	2.00	2	0	0	0	0	2
.....GGACATATCCTGCATACGGT.....	20	0	1	2.00	2	2	0	0	0	0
.....GGACATATCCTGCATACGG.....	19	0	1	2.00	2	2	0	0	0	0
.....AAGGACATATCCTGCATACGGA.....	22	1	1	1.00	1	1	0	0	0	0
.....TGCATGCAGGATATGTTCTTTTC.....	23	2	1	1.00	1	1	0	0	0	0
.....AAGGACATATCCTGCATACGGC.....	22	1	1	1.00	1	1	0	0	0	0
.....AGGACATATCCTGCATACGGC.....	21	1	1	1.00	1	1	0	0	0	0
.....AAGGACATATCCTGCATACGGTA.....	23	1	1	1.00	1	1	0	0	0	0
.....AAAGGACATATCCTGCATACGGC.....	23	1	1	1.00	1	1	0	0	0	0
.....ATACTGCATGCAGGATATGTTCTTTG.....	26	0	1	1.00	1	1	0	0	0	0
.....ATGCAGGATATGTTCTTTGT.....	20	0	1	1.00	1	0	0	1	0	0
.....TGCAGGATATGTTCTTTGTT.....	20	0	1	1.00	1	1	0	0	0	0
.....GCATGCAGGATATGTTCT.....	18	0	1	1.00	1	1	0	0	0	0
.....TGCATGCAGGATATGTTCTC.....	20	1	1	1.00	1	1	0	0	0	0
.....AGGACATATCCTGCATACG.....	19	0	1	1.00	1	1	0	0	0	0
.....AAGGACATATCCTGCATA.....	18	0	1	1.00	1	0	0	0	0	1
.....AGGACATATCCTGCATACGGTTT.....	23	1	1	1.00	1	1	0	0	0	0
.....GCATGCAGGATATGTTCTTTGG.....	22	1	1	1.00	1	1	0	0	0	0
.....AGGACATATCCTGCATACGGTTT.....	23	1	1	1.00	1	1	0	0	0	0
.....GCATGCAGGATATGTTCTTTG.....	22	1	1	1.00	1	1	0	0	0	0
.....CTGCATGCAGGATATGTT.....	18	0	1	1.00	1	1	0	0	0	0
.....CTGCATGCAGGATATGTTCTT.....	21	0	1	1.00	1	1	0	0	0	0
.....CAAAGGACATATCCTGCATACGG.....	23	0	1	1.00	1	1	0	0	0	0
.....GCATGCAGGATATGTTCTTTGTTT.....	24	0	1	1.00	1	1	0	0	0	0
.....AAGGACATATCCTGCATAC.....	19	0	1	1.00	1	1	0	0	0	0
.....CATGCAGGATATGTTCTTTA.....	20	1	1	1.00	1	1	0	0	0	0
.....TGCATGCAGGATATGTTCTTTGGC.....	24	2	1	1.00	1	1	0	0	0	0
.....GCATGCAGGATATGTTCTTG.....	20	1	1	1.00	1	1	0	0	0	0
.....TGCATGCAGGATATGTTT.....	18	1	1	1.00	1	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004521:11550478-11550636 +	dwi_51	ATGAGAACCAATCTTTATTTGATATCATATTGATAACTTAATTGAAATCAAAGGACATATCCTGCATACGGTTGGCTTTGAAATACTGCATGCAGGATATGTTCTTTGTTTTTAATTTGATTTTTCCATCATTAATGCATTAATTTTAATTTTTGAGCT

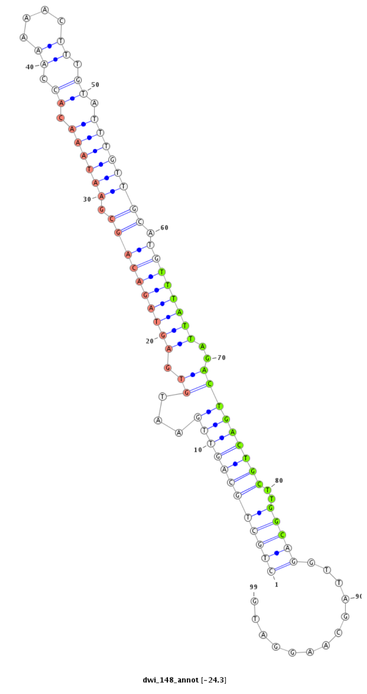
Generated: 09/08/2015 at 07:38 PM

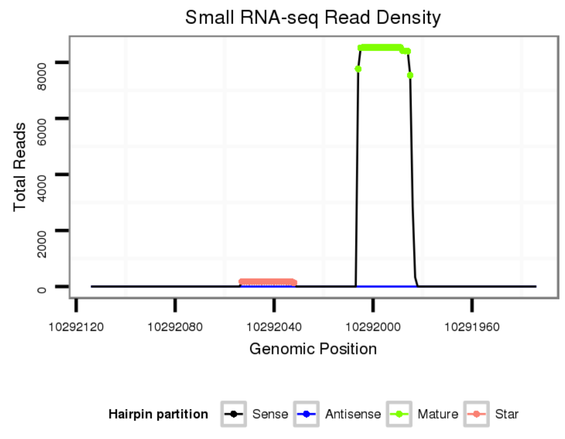
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

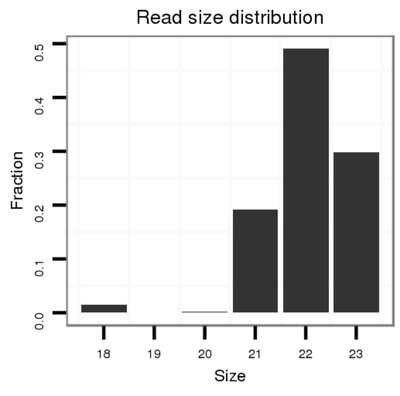
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_148	**scf2_1100000004943:10291984-10292064 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

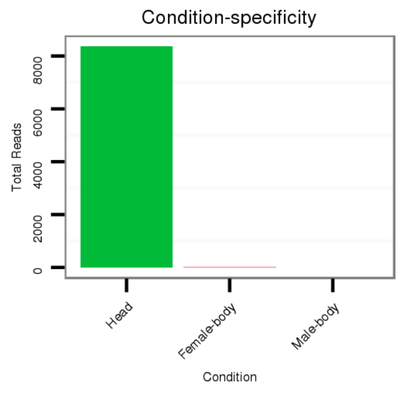
Legend: mature star mismatch in alignment mismatch in read

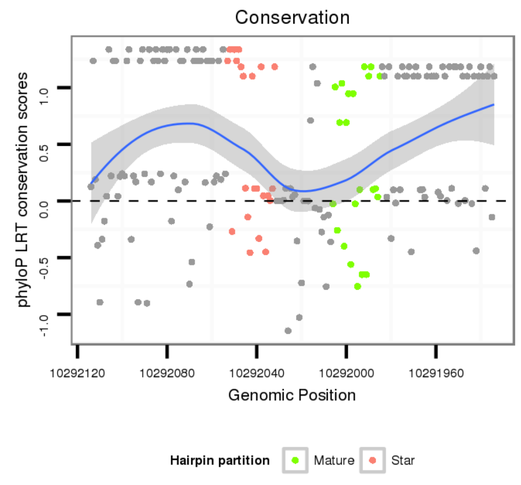
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CGAATCAGAAGCCGAACAATTTCAAGTTCTCTACAAATTGCGAACTCTGCTGCAGTTGAATGTGAGTAGACAGCGAATAAACACCAAAAACTTTGTATTTGTTGCATGTTTATTAGACTGACTGCTTGGCAGGTTAGCAAGGATGACTACCTGCCCAAGTATATCTGTGAGCCGTGTCTGG	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V119 head	M045 female body	V117 male body	V118 embryo
**********(((((((((((...((.((((((((((.((((((.((.((....)).)).)))))))).))))))))..)))))))..)))))..**********										
..........TTTATTAGACTGACTGCTTGGC..........	22	0	1	3956.00	3956	3716	236	4	0	0
..........TTTATTAGACTGACTGCTTGGCA.........	23	0	1	2503.00	2503	2408	92	2	1	0
..........TTTATTAGACTGACTGCTTGG...........	21	0	1	851.00	851	608	234	7	2	0
..........TTATTAGACTGACTGCTTGGC...........	21	0	1	719.00	719	667	52	0	0	0
..........TTTATTAGACTGACTGCTTGGCAG........	24	0	1	323.00	323	271	46	6	0	0
..........GTGAGTAGACAGCGAATAAACA..........	22	0	1	136.00	136	18	118	0	0	0
..........TTTATTAGACTGACTGCT..............	18	0	1	125.00	125	125	0	0	0	0
..........TTTATTAGACTGACTGCTTGGCG.........	23	1	1	93.00	93	93	0	0	0	0
..........TTTATTAGACTGACTGCTTGGCG.........	23	1	1	86.00	86	86	0	0	0	0
..........TTTATTAGACTGACTGCTTGGCAGT.......	25	1	1	70.00	70	55	14	1	0	0
..........TTTATTAGACTGACTGCTTGGT..........	22	1	1	46.00	46	27	19	0	0	0
..........GTGAGTAGACAGCGAATAAAC...........	21	0	1	33.00	33	15	18	0	0	0
..........TTTATTAGACTGACTGCTTGGTT.........	23	2	1	23.00	23	22	1	0	0	0
..........TTATTAGACTGACTGCTTGGCA..........	22	0	1	21.00	21	20	1	0	0	0
..........TTTATTAGACTGACTGCTTGGCT.........	23	1	1	18.00	18	17	1	0	0	0
..........TTTATTAGACTGACTGCTTGGCAA........	24	1	1	18.00	18	18	0	0	0	0
..........TTTATTAGACTGACTGCTTGGG..........	22	1	1	14.00	14	13	1	0	0	0
..........TTTATTAGACTGACTGCTTGGCAGA.......	25	1	1	12.00	12	10	2	0	0	0
..........TTATTAGACTGACTGCTTGG............	20	0	1	12.00	12	7	5	0	0	0
..........TTTATTAGACTGACTGCTTGGCAT........	24	1	1	11.00	11	10	1	0	0	0
..........TTATTAGACTGACTGCTTGGCAGT........	24	1	1	10.00	10	8	2	0	0	0
..........TTTATTAGACTGACTGCTTGGA..........	22	1	1	7.00	7	5	2	0	0	0
..........TATTAGACTGACTGCTTGGCA...........	21	0	1	7.00	7	6	1	0	0	0
..........TTTATTAGACTGACTGCTTGT...........	21	1	1	5.00	5	2	3	0	0	0
..........TTTATTAGACTGACTGCTTG............	20	0	1	4.00	4	2	2	0	0	0
..........TTTATTAGACTGACTGCTT.............	19	0	1	4.00	4	4	0	0	0	0
..........TTTATTAGACTGACTGCTTGGCAGG.......	25	0	1	4.00	4	4	0	0	0	0
..........GTGAGTAGACAGCGAATAAA............	20	0	1	4.00	4	0	4	0	0	0
..........TTTATTAGACTGACTGCC..............	18	1	2	4.00	8	8	0	0	0	0
..........GTGAGTAGACAGCGAATAA.............	19	0	1	3.00	3	0	2	1	0	0
..........TTTATTAGACTGACTGCG..............	18	1	1	2.00	2	2	0	0	0	0
..........TTATTAGACTGACTGCTTGGCG..........	22	1	1	2.00	2	2	0	0	0	0
..........TTTATTAGACTGACTGCTTGGCAGC.......	25	1	1	2.00	2	2	0	0	0	0
..........TTTATTAGACTGACTGCTTGGCAG........	24	1	1	2.00	2	2	0	0	0	0
..........TTATTAGACTGACTGCTTGGCAGA........	24	1	1	1.00	1	0	1	0	0	0
..........TTATTAGACTGACTGCTTGGA...........	21	1	1	1.00	1	0	1	0	0	0
..........TTATTAGACTGACTGCTTGGCAG.........	23	0	1	1.00	1	1	0	0	0	0
..........TGAGTAGACAGCGAATAAACAC..........	22	0	1	1.00	1	1	0	0	0	0
..........TTTATTAGACTGACTGCTTGGCTT........	24	1	1	1.00	1	0	1	0	0	0
..........TTATTAGACTGACTGCTTGGCT..........	22	1	1	1.00	1	1	0	0	0	0
..........ATTAGACTGACTGCTTGGCA............	20	0	1	1.00	1	1	0	0	0	0
..........TTTATTAGACTGACTGCTTGGCCT........	24	2	1	1.00	1	1	0	0	0	0
..........TTTATTAGACTGACTGCTTGGCTG........	23	2	1	1.00	1	1	0	0	0	0
..........TATTAGACTGACTGCTTGGCAGT.........	23	1	1	1.00	1	0	1	0	0	0
..........ATTAGACTGACTGCTTGG..............	18	0	1	1.00	1	0	0	1	0	0
..........TATTAGACTGACTGCTTGGC............	20	0	1	1.00	1	0	0	1	0	0
..........TTATTAGACTGACTGCTTGGCAGG........	24	0	1	1.00	1	1	0	0	0	0
..........TATTAGACTGACTGCTTGGA............	20	1	1	1.00	1	0	1	0	0	0
..........TTATTAGACTGACTGCTTGGG...........	21	1	1	1.00	1	1	0	0	0	0
..........TTATTAGACTGACTGCTTGGCG..........	22	1	1	1.00	1	1	0	0	0	0
..........TTGAGTAGACAGCGAATAAACAC.........	23	0	1	1.00	1	1	0	0	0	0
..........TTTATTAGACTGACTGCTTGGCTTC.......	24	2	1	1.00	1	0	1	0	0	0
..........TTATTAGACTGACTGCTTGGCT..........	22	1	1	1.00	1	1	0	0	0	0
..........TTTATTAGACTGACTGCTTGGTC.........	23	2	1	1.00	1	1	0	0	0	0
..........TATTAGACTGACTGCTTGGCAGG.........	23	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

GCTTAGTCTTCGGCTTGTTAAAGTTCAAGAGATGTTTAACGCTTGAGACGACGTCAACTTACACTCATCTGTCGCTTATTTGTGGTTTTTGAAACATAAACAACGTACAAATAATCTGACTGACGAACCGTCCAATCGTTCCTACTGATGGACGGGTTCATATAGACACTCGGCACAGACC	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body
**********(((((((((((...((.((((((((((.((((((.((.((....)).)).)))))))).))))))))..)))))))..)))))..**********						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004943:10291934-10292114 -	dwi_148	CGAATCAGAAGCCGAACAATTTCAAGTTCTCTACAAATTGCGAACTCTGCTGCAGTTGAATGTGAGTAG-ACAGCGAATAAACACCAAAAACTTTGTATTTG--------TTGC--------ATGTTTATTAGACTGACTGCTTGGCAGGTTAGCAAGGATGACTACCTGCCCAAGTATATCTGTGAGCCGTGTCTGG
droVir3	scaffold_13047:11544060-11544233 -		TGACCCGCAGGCGGAGCAGCGCCAACTGCTCTACAAGGTGCCCACGCTGCTGCAGCGAATGTGAGTAGGTGTGCGTAAGTGGA---TGGGTGTGC----T--------------GTGTTTATTGGCCT-----GCCATTACTTGACAGATAACCAAGGAGGACTATCTGCCCAACCACATATGCGAGCTGTGCCTGG
droMoj3	scaffold_6540:30215815-30215990 +		TGAGCGCAGGCGGAGCAGCGCCAATTGCTCTACAAGGTGCGCAGTCTGCTGCAGCGAATGTGAGTAGCTGAGTATATGAGTA---TGTGTGCAT---TTACATATATATATGTGTTTG--------T--------GGTGCTCAACAGATAACCAAGGAGGACTATGTGCCAAACACACATATGCGAGCTGTGCCTGG
droGri2	scaffold_14624:1595965-1596031 -		TGAGAAAGAGGCCGAGCAGCCAATTGCTCTACAAACGTGCGCACTCTGCTCCTGGCGAATGTTAGT---
dp5	2:464840-465021 +		CGCGGAGGAGGCCATGCAGCGGCAGCTGCTCCACAAGCTGCGCAGCCTGCTGCTGGCGCCACGTAAGTAG-TCTGCGGATCAACA---AGCGCGCCG----TATATCCGTATATC--------CGGCCTAATGAGCCCCACTGCTTGGCAGGTCGCCGAGGAGGACCTCCTGCCCCAGTAGATCTGTGACCGTGCCTGG
droPer2	scaffold_7:3247393-3247574 +		CGCGGAGGAGGCCATGCAGCGGCAGCTGCTCCACAAGCTGCGCAGCCTGCTGCTGGCGCCACGTAAGTAG-TCTGCGGATCAACA---AGCGCGCCG----TATATCCGTATATC--------CGGCCTAATGAGCCCCACTGCTTGGCAGGTCGCCGAGGAGGACCTCCTGCCCCAGTAGATCTGTGACCGTGCCTGG

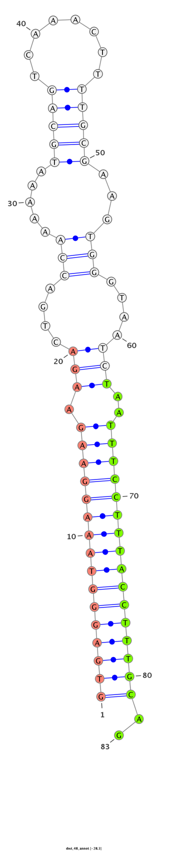
Generated: 09/08/2015 at 07:43 PM

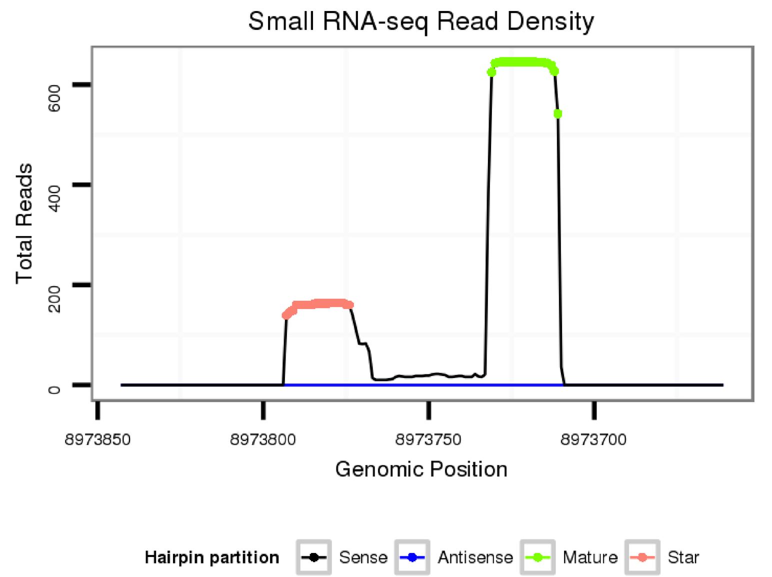
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

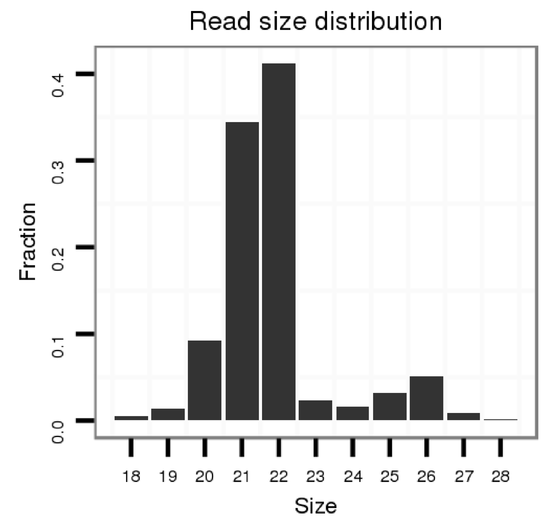
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_48	**scf2_1100000004521:8973711-8973793 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

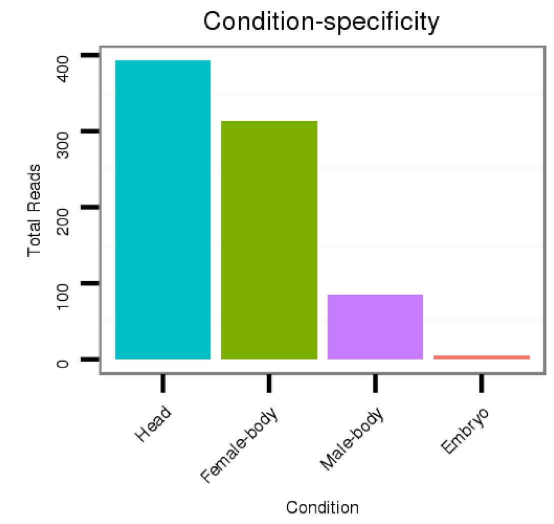
Legend: mature star mismatch in alignment mismatch in read

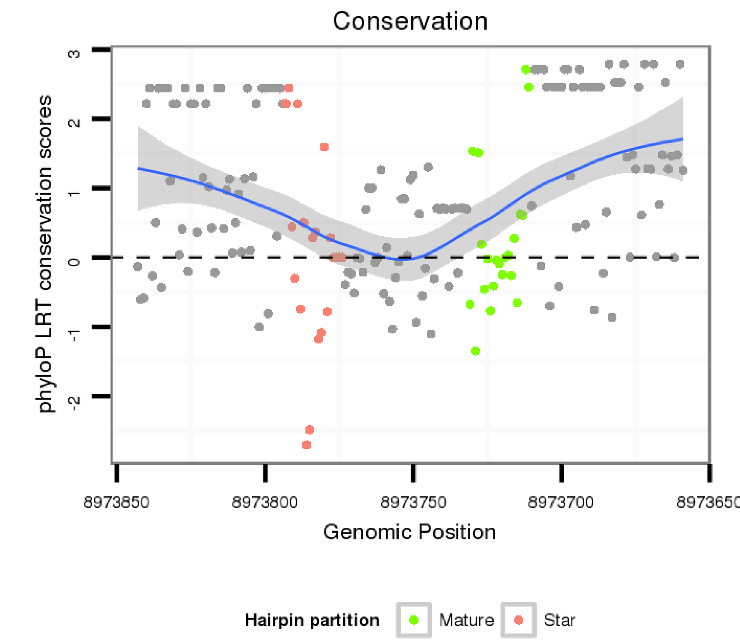
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK14675-in]; CDS [Dwil\GK14675-cds]; CDS [Dwil\GK14675-cds]; utr3 [utr3_minus_341]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TGCGAAATCTTTGCCATTCCCAAGGCAAAGCACTGCAATTCGATTATAAGGTGAGGGTAAAGGAAGAAGACTGACCAAAAAAATGCAGTCAAACTTTTGCGAAGTGGGTAATCTAATTTCCTTTACCTTTGCAGATATACTCCAGATCCCACACCGCCAGTGCCCAACTGGTTGCAATTGGTTA **((((((((((((((((.(((....(((.....(((((........)))))...)))....)))..))))))))))))))))..**	Read size	# Mismatch	Hit Count	Total Norm	Total	V119 head	M045 female body	V117 male body	M020 head	V118 embryo
TAATTTCCTTTACCTTTGCAGT	22	1	1	1874.00	1874	1272	193	347	55	7
CTAATTTCCTTTACCTTTGCAG	22	0	1	297.00	297	103	133	3	55	3
TAATTTCCTTTACCTTTGCAG	21	0	1	182.00	182	88	83	2	8	1
CTAATTTCCTTTACCTTTGCAGT	23	1	1	129.00	129	83	16	23	5	2
CTAATTTCCTTTACCTTTGCA	21	0	1	59.00	59	23	18	0	18	0
GTGAGGGTAAAGGAAGAAGACTGACC	26	0	1	38.00	38	0	11	22	5	0
TAATTTCCTTTACCTTTGCAGA	22	0	1	29.00	29	16	7	3	2	1
GTGAGGGTAAAGGAAGAAGAC	21	0	1	28.00	28	8	5	13	2	0
AATTTCCTTTACCTTTGCAGT	21	1	1	26.00	26	9	11	6	0	0
GTGAGGGTAAAGGAAGAAGACT	22	0	1	25.00	25	0	6	16	3	0
TAATTTCCTTTACCTTTGCA	20	0	1	24.00	24	8	9	1	6	0
GTGAGGGTAAAGGAAGAAGA	20	0	1	21.00	21	12	4	3	1	1
AATTTCCTTTACCTTTGCAG	20	0	1	17.00	17	3	13	0	1	0
GTGAGGGTAAAGGAAGAAGACTGAC	25	0	1	16.00	16	0	2	11	3	0
TAATTTCCTTTACCTTTGCATT	22	2	1	13.00	13	11	1	1	0	0
CTAATTTCCTTTACCTTTGCAT	22	1	1	11.00	11	3	1	0	7	0
AGGGTAAAGGAAGAAGACTGACC	23	0	1	10.00	10	0	1	0	9	0
TAATTTCCTTTACCTTTGCAGG	22	1	1	8.00	8	0	0	0	8	0
TAATTTCCTTTACCTTTGCAGC	22	1	1	8.00	8	3	1	1	3	0
CTAATTTCCTTTACCTTTGC	20	0	1	7.00	7	2	1	0	4	0
CTAATTTCCTTTACCTTTGCAC	22	1	1	6.00	6	1	1	0	4	0
ATTTCCTTTACCTTTGCAGT	20	1	1	6.00	6	3	3	0	0	0
CTAATTTCCTTTACCTTTGCAGA	23	0	1	6.00	6	2	0	2	2	0
ATTTCCTTTACCTTTGCAG	19	0	1	5.00	5	1	4	0	0	0
TAATCTAATTTCCTTTACCTTTG	23	0	1	4.00	4	0	3	0	1	0
TCTAATTTCCTTTACCTTTGCAGT	24	1	1	4.00	4	4	0	0	0	0
GTGAGGGTAAAGGAAGAAGACTGACCA	27	0	1	4.00	4	0	1	1	2	0
CTAATTTCCTTTACCTTTGCATT	23	2	1	3.00	3	3	0	0	0	0
GTGAGGGTAAAGGAAGAA	18	0	1	3.00	3	0	2	1	0	0
TTTCCTTTACCTTTGCAGT	19	1	1	3.00	3	3	0	0	0	0
TAATCTAATTTCCTTTACCTTTGC	24	0	1	3.00	3	1	0	0	2	0
CCAAAAAAATGCAGTCAAACTTTTGC	25	0	1	3.00	3	3	0	0	0	0
AATTTCCTTTACCTTTGCAC	20	1	1	3.00	3	0	0	0	3	0
TAATTTCCTTTACCTTTGCACT	22	2	1	3.00	3	1	0	0	2	0
TGAGGGTAAAGGAAGAAGACTGACC	25	0	1	3.00	3	0	0	0	3	0
GTGAGGGTAAAGGAAGAAGACTGA	24	0	1	3.00	3	1	0	2	0	0
AATCTAATTTCCTTTACCTTTGCAGT	26	1	1	3.00	3	2	1	0	0	0
TCTAATTTCCTTTACCTTTGCAG	23	0	1	3.00	3	2	0	0	1	0
AAACTTTTGCGAAGTGGGT	19	0	1	2.00	2	0	1	1	0	0
TCTAATTTCCTTTACCTTTGCA	22	0	1	2.00	2	1	1	0	0	0
GTCAAACTTTTGCGAAGTGGGT	22	0	1	2.00	2	0	0	2	0	0
TAATCTAATTTCCTTTACCTTTT	23	1	1	2.00	2	0	0	0	2	0
TAATTTCCTTTACCTTTGC	19	0	1	2.00	2	0	1	0	1	0
GCAGTCAAACTTTTGCGAAGT	21	0	1	2.00	2	0	1	0	1	0
TAATTTCCTTTACCTTTGCAT	21	1	1	2.00	2	1	0	0	1	0
GAGGGTAAAGGAAGAAGACTGACC	24	0	1	2.00	2	0	0	0	2	0
TTTGCGAAGTGGGTAATCTA	20	0	1	2.00	2	1	0	1	0	0
CTAATTTCCTTTACCTTTGCAA	22	1	1	2.00	2	1	1	0	0	0
TAATTTCCTTTACCTTTGCAGTA	23	2	1	2.00	2	2	0	0	0	0
TGAGGGTAAAGGAAGAAGACT	21	0	1	2.00	2	0	1	1	0	0
CTTTTGCGAAGTGGGTAATC	20	0	1	1.00	1	0	0	1	0	0
TTTCCTTTACCTTTGCAG	18	0	1	1.00	1	0	1	0	0	0
AAGAAGACTGACCAAAAAAATGCA	23	0	1	1.00	1	0	1	0	0	0
TAATTTCCTTTACCTTTGCAGTC	23	2	1	1.00	1	1	0	0	0	0
TAATCTAATTTCCTTTACCTTT	22	0	1	1.00	1	0	1	0	0	0
GTGAGGGTAAAGGAAGAAG	19	0	1	1.00	1	1	0	0	0	0
TAATCTAATTTCCTTTACCTTTGT	24	1	1	1.00	1	0	0	0	1	0
AGTGGGTAATCTAATTTCCTTTACC	25	0	1	1.00	1	0	1	0	0	0
ATGCAGTCAAACTTTTGCGAAGTGGG	26	0	1	1.00	1	0	1	0	0	0
CTAATTTCCTTTACCTTTGCAGG	23	1	1	1.00	1	0	0	0	1	0
AGGGTAAAGGAAGAAGACTGA	21	0	1	1.00	1	0	1	0	0	0
TTTCCTTTACCTTTGCAGC	19	1	1	1.00	1	0	0	0	1	0
AATTTCCTTTACCTTTGCAGA	21	0	1	1.00	1	1	0	0	0	0
GAGGGTAAAGGAAGAAGACT	20	0	1	1.00	1	1	0	0	0	0
TTGCGAAGTGGGTAATCTA	19	0	1	1.00	1	1	0	0	0	0
CAGTCAAACTTTTGCGAAGTGGGT	24	0	1	1.00	1	0	0	1	0	0
GCAGTCAAACTTTTGCGAAGTGGG	24	0	1	1.00	1	1	0	0	0	0
TGAGGGTAAAGGAAGAAGACTGAC	24	0	1	1.00	1	0	1	0	0	0
CCAAAAAAATGCAGTCAAACTTTTG	24	0	1	1.00	1	1	0	0	0	0
AATTTCCTTTACCTTTGCAGC	21	1	1	1.00	1	0	0	0	1	0
CAGTCAAACTTTTGCGAAGTGGGTAAT	27	0	1	1.00	1	1	0	0	0	0
AAAGGAAGAAGACTGACCAAAAAAATGCA	28	0	1	1.00	1	0	1	0	0	0
AATCTAATTTCCTTTACCTTTGCAG	25	0	1	1.00	1	0	1	0	0	0
CCAAAAAAATGCAGTCAAACTTTT	23	0	1	1.00	1	0	0	1	0	0
TGCAGTCAAACTTTTGCGAAGTGGGTA	27	0	1	1.00	1	1	0	0	0	0
CTAATTTCCTTTACCTTTGCAGC	23	1	1	1.00	1	0	0	1	0	0
GCAGTCAAACTTTTGCGAAGTGGGT	25	0	1	1.00	1	1	0	0	0	0
TGAGGGTAAAGGAAGAAGACTG	22	0	1	1.00	1	0	0	1	0	0
AAGGAAGAAGACTGACCAAAAAAATGCA	27	0	1	1.00	1	0	1	0	0	0
GTGGGTAATCTAATTTCCTTTACCTT	26	0	1	1.00	1	0	1	0	0	0
AAGGAAGAAGACTGACCAAAAAAATGC	26	0	1	1.00	1	0	0	1	0	0
CAAAAAAATGCAGTCAAACTTTTGC	24	0	1	1.00	1	0	1	0	0	0
TAATTTCCTTTACCTTTGCAAT	22	2	2	1.00	2	1	0	1	0	0
TTCCTTTACCTTTGCAGT	18	1	2	1.00	2	1	1	0	0	0
ATTTCCTTTACCTTTGCAA	19	1	2	0.50	1	0	1	0	0	0
TAATTTCCTTTACCTTTGCAAC	22	2	2	0.50	1	1	0	0	0	0

Anti-sense strand reads

ACGCTTTAGAAACGGTAAGGGTTCCGTTTCGTGACGTTAAGCTAATATTCCACTCCCATTTCCTTCTTCTGACTGGTTTTTTACGTCAGTTTGAAAACGCTTCACCCATTAGATTAAAGGAAATGGAAACGTCTATATGAGGTCTAGGGTGTGGCGGTCACGGGTTGACCAACGTTAACCAAT **((((((((((((((((.(((....(((.....(((((........)))))...)))....)))..))))))))))))))))..**	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	M020 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004521:8973659-8973843 -	dwi_48	--TGCGAAATCTTTGCCATTCCCAAGGCAAAGCACTGCAATTCGATTATAAGGTGAGGGTA--------AA-GGAA-------------------GAAGACTGACCAAAAAAATGCAGTC-------------AAACTTT--T----GCG-------------------------------------AAGTGGGTAATCTA---------------ATT------------TC--------CTTTACCTTTGCAGATATACTCCAGATCCCACACCGCCAGTGCCCAACTGGTTGCAATTGGTTATG
droVir3	scaffold_12963:15282872-15283030 +		--T--GAAATATTTGCCTTGCCCAGGGTAAAGCACTGCAACTCCATCATCAGGTGTGTATT--------------------------A---------------------------GGTTT-------CACCTCTGT--GTTT--AACTG----ATTTAAT---TG-----------GTT-------TGCTTTTTTGGCAGATACACGCCCGATCCGACACCGCCCGTGCCCAGTTGGCTGCAGTTGGTCATG
droMoj3	scaffold_6500:18259570-18259766 +		TCAGCGACATCTTTGCCGTGCCGAAGGCCAAACATTGCAACTCGATCATCAGGTGCGTAGCT------C----------CGCTATCTCT-----------------TTCTC------------------TCTCT--C----TC------TCT------------------------CTC-TCAGTGTGTGATCGACTG----ATT-AAT---TGTCTCTTGGTCTC--------TCTGTCTCTTGGCAGGTACACACCCGATCCGACACCGCCTGTGCCCAACTGGCTGCAGTTGGTCATG
droGri2	scaffold_15126:4129321-4129489 -		--ACTGACATCTTTGCCGTGCCCAAGGCCAAGCATTGTAACTCCATCATCAGGTGCGTAACCACATGGAAA-GAA-----------------------------TGTAATTGAATTAAA-------------AA---GACT---------------CAACTGA--------TTG------------ATT--------TTCATTCTGGCAGATATACGCCGGATCCGACACCACCGGTGCCCAATTGGCTGCAGGTGGTCATG
dp5	4_group3:5248027-5248190 +		-----GAGTTCTTTGCTGTGCCCAAGGTCAAGACAGCCAATACAATGATGAGGTAAGCAGC-----------------------------ATCTCTAAAAA-TATCCCT----------------------T--A----AC-----TT-----T---------------------TACT---------------TAA----CTCA--CTT-----------ATA--------TTTCTTTTTTCAGATATACACCCGATACGACGCCCCCAGTTCCCAATTGGCTGCAGTTGGTCATG
droPer2	scaffold_1:6739879-6740042 +		-----GAGTTCTTTGCTGTGCCCAAGGTCAAGACAGCCAATACAATGATGAGGTAAGCAGC-----------------------------ATCTCTAAAAA-TATCCCT----------------------T--A----AC-----TT-----T---------------------TACT---------------TAA----TTCA--CATT-----------ATT--------TTTCTTTTTTCAGATATACACCCGATACGACGCCCCCAGTTCCCAATTGGCTGCAGTTGGTCATG
droAna3	scaffold_12916:5546485-5546644 -		--ACGGAAATTTTTGCAGTTCCCAAGACCAAGCACTGCAACTCGATTATCAGGTGGTCTG------A------------------------GCCTTC---------------------AATCTTT--C----AC-----TT-------------T----------TCCCTT-------------AATA----ATAT------------------AATTTTATTTCACAGATACACGCCCGATCCCACGCCTCCAGTGCCCAACTGGCTGCAATTGGTAATG
droBip1	scf7180000396568:1291784-1291966 +		--ACGGAACTTTTTGCAGTTCCCAAGACCAAACACTGTCACTCGATTATCAGGTGGTCCC------AG---TAA-----------T------AT---------------------GGCCTTCAATCTTT--C----AC------TTT----------------------TTC-TT------------ACTA----ATATACGTTTT-----------ATTTTTCTCCCATTTATCCCACAGATACACGCCCGATCCCACGCCTCCAGTTCCCAACTGGCTGCAATTGGTAATG
droKik1	scf7180000302270:1142271-1142442 +		--ACTGAGATCTTTGCGGTGCCCAAGACCAAGCACAGTAATTCGATAATCAGGTGAGGAAA-----ATATTATT---------------------------------AAT-T-----------------------------ATATTTAATTTGTTTATTT-----------------TACTA----ACCAAAT---CC-----------AC--------CTGATTTTTTATAGATACACGCCCGATCCCACGCCGCCTATACCCAACTGGCTGCAGTTGGTCATG
droFic1	scf7180000453924:1485077-1485162 -		--CTAATTTCCCTTTGGT----------------------------TTT-----------------------ATCTTTATCCGATAGATATACACCCGATCCCACGCCCCCAGTTCCCAACTGGCTGCAGTTGGTTATG
droEle1	scf7180000490728:172531-172615 -		--CTAATTTTCCTTGATCTT--GTCTTGATCTGACAGATATACGCCCGATCCCACGCCTCCAGTTCCCAACTGGCTGCAGTTGGTCATG
droRho1	scf7180000779523:179802-179875 -		--TG--ATATA---ATCTCTATTTAACAGATATACGCCCGATCCCACGCCTCCAGTTCCCAACTGGCTGCAGTTGGTCATG
droBia1	scf7180000302261:1049501-1049585 -		--AGCGAGATCTTCGCGGTTCCAAAGACCAAGCACTGCAACTCTATAATCAGGTAGGAACT---ATACCCAAAAA-GTGTAGAAGAGCTTT
droTak1	scf7180000415438:405814-405881 +		--TC---CTTTTATTTGACAGATATACGCCTGATCCCACGCCTCCGTTCCCAACTGGCTGCAATTGGTCATG
droEug1	scf7180000409554:2589278-2589481 +		--AGTGAGATCTTCGCGGTGCCCAAGACCAAGCACTGCAACTCCATTATCAGGTGAGAACA-----GAGTACTTAATAGTAGCTTTGGTATTTCTGAA----------------------TGTTT-------A--CCTTTA--TTTGACAATCGATTTGCTAATTTCCCGCTATCCT--------------------------------------AACTCTACTTGACAGATATACGCCCGATCCCACTCCTCCAGTCCCCAACTGGCTGCAATTGGTTATG
dm3	chr2L:3499371-3499560 -		--AGCGAGATTTCGCGGTTCCCAAGACGAAGCACTGCAACTCGATCATCAGGTGAGCATCTATCGGAATA-CAAG--------------------AA---------------------GGACT------GTCCTCTCT--CCTGACCTTCCAATTGCTAATTTCGCCTTATATT--------------------------------------ATCGCTATCCCACAGATACACACCAGATCCCACGCCTCCAGTGCCCAACTGGCTGCAGTTGGTCATG
droSim2	2L:3359017-3359204 -		--AGCGAGATGTTCGCGGTGCCCAAGACGAAGCACTGCAACTCGATCATCAGGTGAGCATCTATCGGAATA-CAAG--------------------AA---------------------GGACT------CCTCTCT--CCTGACCTTCCAATTGCTAATTTCCCATTATCTC--------------------------------------ATCGCTATCCCACAGATACACACCCGATCCCACGCCTCCAGTGCCCAACTGGCTGCAGTTGGTCATG
droSec2	scaffold_5:1601652-1601841 -		--AGCGAGATATTCGCGGTGCCCAAGACAAAGCACTGCAACTCGATCATCAGGTGAGCATCCATCGGAATA-GAAG--------------------AA---------------------GGACT-----ATCCTCTCT--CCTGACCTTACAATTGCTAATTTCCCCTTATCTC--------------------------------------ATCGCTATCCCACAGATACACACCCGATCCCACGCCTCCAGTGCCCAACTGGCTGCAGTTGGTCATG
droYak3	2L:3487837-3488019 -		--AGCGAGATCTTCGCGGTGCCCAAGACGAAGCACTGCAACTCGATCATCAGGTGAGCACG------AA------------TACTTCTGAT-------------------------AG-----GTCTTTCT--CCTGACCTTCCCATTGCTAATTTCCACTTATCTC--------------------------------------ATCGCTATTCCACAGGTATACACCCGATCCCACGCCTCCAGTGCCCAACTGGCTACAGTTGGTCATG
droEre2	scaffold_4929:3534357-3534532 -		--AGCGAGATCTTCGCGGTGCCCAAGACGAAGCACTGCAACTCGATCATCAGGTGAGCATC----GGAGTAAGCAT-------------------AA--------------------G-------------CT--GCTGACCTTCCAGTTGATAATTTCCCCTTATCTC--------------------------------------CTGGCTCATCCACAGATATACACCCGATCCCACGCCGCCAGTGCCCAACTGGCTGCAGTTGGTCATG

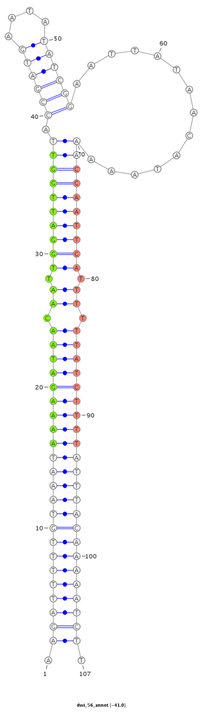
Generated: 09/08/2015 at 10:34 PM

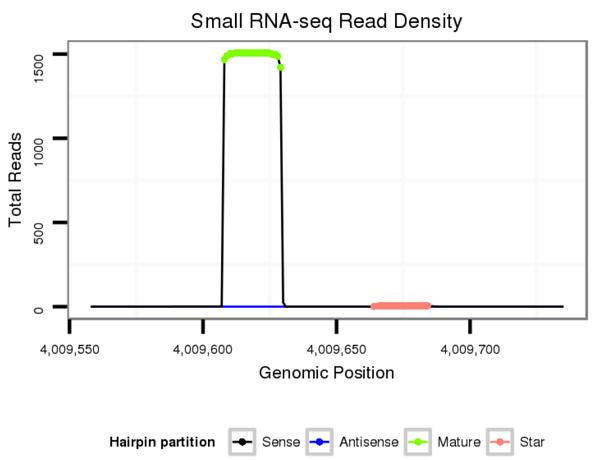
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

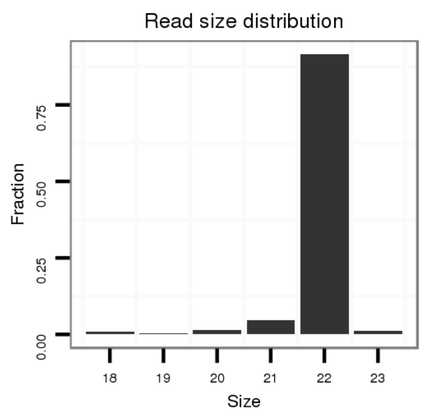
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_56	**scf2_1100000004585:4009608-4009685 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

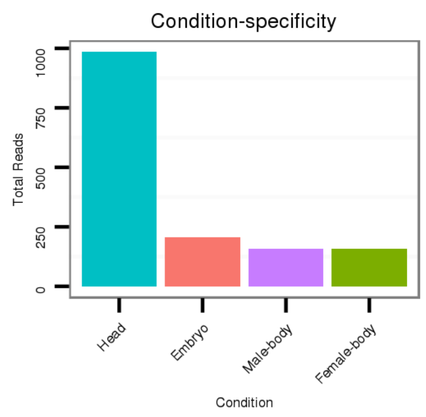
Legend: mature star mismatch in alignment mismatch in read

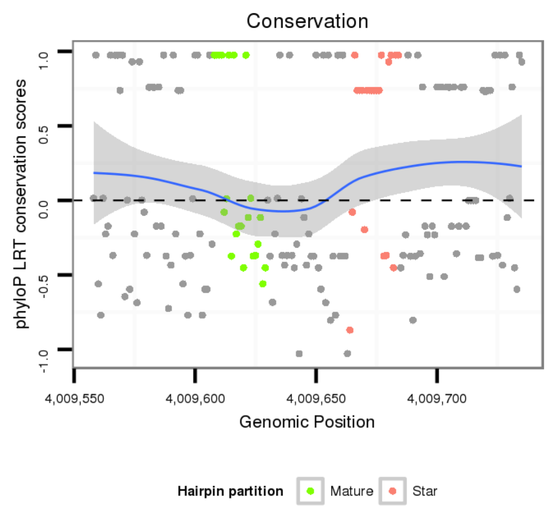
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTGTGGCATATATATAGCTCTGACAGCTCAACGTCAAGATTTTTGTAAATAAAAGATAACAATTGGATTGGTTACCGATGAATATATCGGAATTATAACATAAAAACCAATTCATTTTTTATCTTTTATTTACAAAAATCTTAAACTCGAGCCTGCAAATAACTTAAAAGTGGATAAG	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V119 head	V118 embryo	M045 female body	V117 male body
**********.((((((((((((((((((((((((.((.((((((((((.((((((....))))))..............))))))))))).)).)))))))))))))))))))).**********										
..........AAAAGATAACAATTGGATTGGT..........	22	0	1	1370.00	1370	647	287	192	95	149
..........AAAAGATAACAATTGGATTGG...........	21	0	1	57.00	57	13	3	6	35	0
..........AAAAGATAACAATTGGATTGGC..........	22	1	1	44.00	44	41	2	0	0	1
..........AAAAGATAACAATTGGATTGGG..........	22	1	1	43.00	43	41	0	2	0	0
..........AAAAGATAACAATTGGATTGGTT.........	23	0	1	17.00	17	3	6	0	6	2
..........AAAGATAACAATTGGATTGGT...........	21	0	1	12.00	12	1	2	2	6	1
..........AAAAGATAACAATTGGATTGGTC.........	23	1	1	12.00	12	9	3	0	0	0
..........AAAAGATAACAATTGGATTG............	20	0	1	10.00	10	4	3	0	3	0
..........AAAAGATAACAATTGGAT.............	18	0	1	10.00	10	10	0	0	0	0
..........AAGATAACAATTGGATTGGT............	20	0	1	8.00	8	0	1	0	3	4
..........AAAGATAACAATTGGATTGGTT..........	22	0	1	8.00	8	3	0	1	3	1
..........AAAAGATAACAATTGGATTGGTA.........	23	1	1	6.00	6	0	1	5	0	0
..........TAAAAGATAACAATTGGATTGG..........	22	0	1	4.00	4	0	1	0	3	0
..........GATAACAATTGGATTGGT..............	18	0	1	4.00	4	1	0	3	0	0
..........AAGATAACAATTGGATTGG.............	19	0	1	3.00	3	0	0	0	3	0
..........AAAAGATAACAATTGGATTGGTTT........	24	1	1	2.00	2	1	0	0	0	1
..........AATTCATTTTTATCTTTAT.............	21	0	1	2.00	2	0	0	0	2	0
..........AAAGATAACAATTGGATTGG............	20	0	1	2.00	2	0	0	0	2	0
..........CCAATTCATTTTTTATCTTTT...........	21	0	1	2.00	2	1	0	0	1	0
..........AGATAACAATTGGATTGGT.............	19	0	1	2.00	2	0	0	1	0	1
..........AAAGATAACAATTGGATTGGTTT.........	23	1	1	1.00	1	0	0	1	0	0
..........AAAAGATAACAATTGGATTGGTAT........	24	2	1	1.00	1	0	0	1	0	0
..........CGTCAAGATTTTTGTAAAT.............	19	0	1	1.00	1	0	0	1	0	0
..........CAATTCATTTTTTATCTTTAT...........	22	0	1	1.00	1	0	0	0	1	0
..........AGATAACAATTGGATTGGTA............	20	1	1	1.00	1	0	0	0	1	0

Anti-sense strand reads

CACACCGTATATATATCGAGACTGTCGAGTTGCAGTTCTAAAAACATTTATTTTCTATTGTTAACCTAACCAATGGCTACTTATATAGCCTTAATATTGTATTTTTGGTTAAGTAAAAAATAGAAAATAAATGTTTTTAGAATTTGAGCTCGGACGTTTATTGAATTTTCACCTATTC	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo
**********.((((((((((((((((((((((((.((.((((((((((.((((((....))))))..............))))))))))).)).)))))))))))))))))))).**********						
..........AGATAACAATTGGATTGGTA............	20	1	1	1.00	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004585:4009558-4009735 +	dwi_56	GTGTGGCATATATATA-------GCTCTGACAGCTCAACGTCAA----GATTTTTGTAAATAAAAGAT----AACAATTGGATTGG----------TT-ACCGATGAATATATCGGAATTATAACATAAAAAC------CAATTCATTTTTTATCTTTTATTTACAAAAATCTTAAACTCGAGCCTGCAAATAACTTAAAAGTGGATAAG
droFic1	scf7180000453246:14914-15074 +		AT-TAAA-ATATATTAAGAAATAAGTGCATA------ACGTTAACGGATGATCTTAAAAATAAAATGT----GAT--ATGAGTTGT----------AAAGATAATGAATTTCCCGAGGTAATCAGGAAGAGCTTTTTTTAAATTTATTTTTTGTCTATTTT-TGGGA----------GCACTTCAAAGTGA-AAAG
droEre2	scaffold_4426:6020-6206 -		ATGCAGTAAAT-TCACATGATAAGCTCATTCAGTTTAAGTTG------GACACTTGCCCACAAAATGTTTTTAACGGTTAAAACAGTTAACATTTAAAAGAAATAGATA-A-ACAAATTAAACGCTTGAATTCTAAAACAAAAGG------AA----------TAACTTTTAAATAAAACAGAGCAAAGTCAATTCTA----------AATATTAATCAG

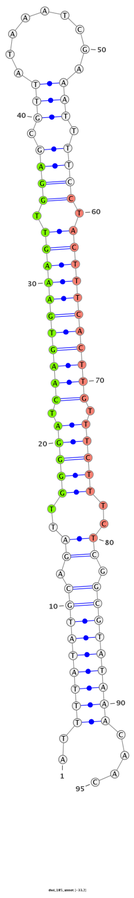
Generated: 09/08/2015 at 07:38 PM

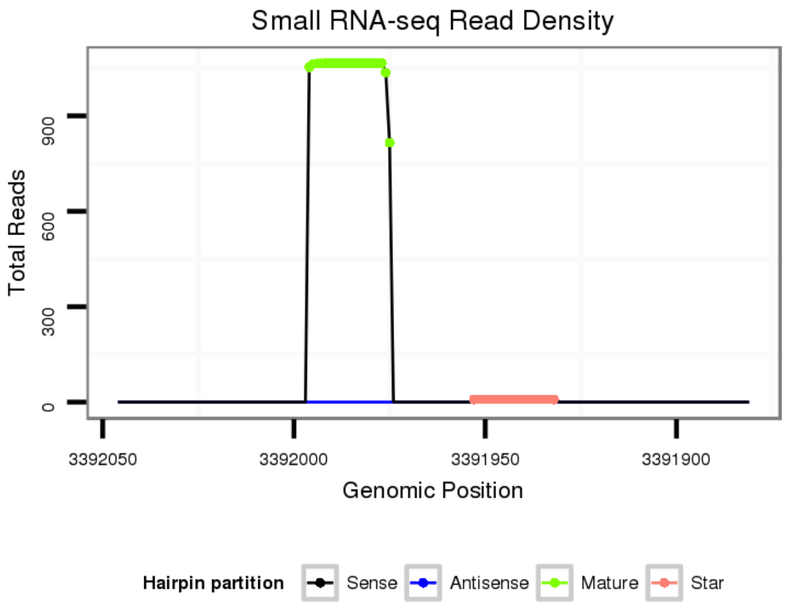
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

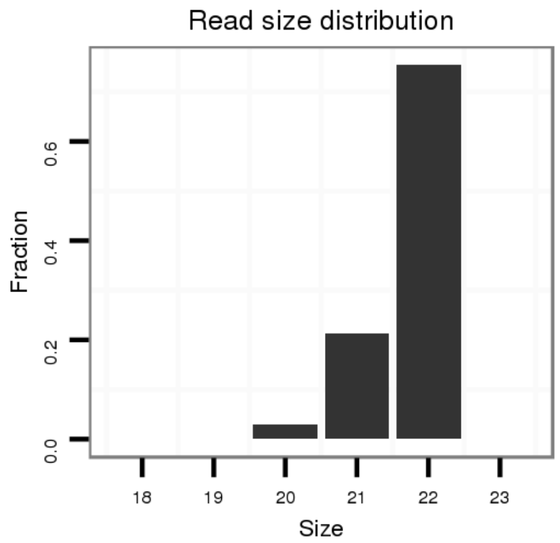
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_185	**scf2_1100000004511:3391931-3391996 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

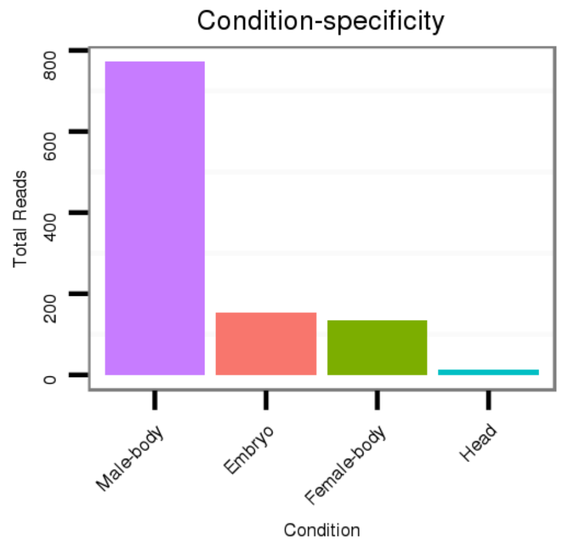
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAACTTTTTGATCGTCGGAGCATCATAAAAATTATATTTTATATGCAGATTGGGGATCAAGTGAAAGTTGGAGCGTTATAAATCGAAATTTTCCTACTTTCACTTGTTTCTTTCTCGGCGTATAAACAACTCTCTCTGGAAAAAAAAAACAAATCATAATTTTTTA ********************************..(((((((((.((..(((((.((((((((((.((((.(((.........))).))))).)))))))))))).)))))..)).)))))))))....********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	V118 embryo	M045 female body	V119 head
.....TGGGGATCAAGTGAAAGTTGGA.....	22	0	1	805.00	805	587	139	66	13
.....TGGGGATCAAGTGAAAGTTGG.....	21	0	1	217.00	217	165	10	41	1
.....TGGGGATCAAGTGAAAGTTGGAA.....	23	1	1	63.00	63	51	5	6	1
.....TGGGGATCAAGTGAAAGTTGGAT.....	23	1	1	31.00	31	31	0	0	0
.....TGGGGATCAAGTGAAAGTTG.....	20	0	1	30.00	30	17	4	9	0
.....TGGGGATCAAGTGAAAGTTGGT.....	22	1	1	10.00	10	10	0	0	0
.....TGGGGATCAAGTGAAAGTTGGAAA.....	24	2	1	9.00	9	7	2	0	0
.....GGGGATCAAGTGAAAGTTGGA.....	21	0	1	9.00	9	1	0	8	0
.....CTACTTTCACTTGTTTCTTTCT.....	22	0	1	6.00	6	0	0	6	0
.....TGGGGATCAAGTGAAAGTTGGG.....	22	1	1	2.00	2	1	0	0	1
.....GGGGATCAAGTGAAAGTTGG.....	20	0	1	2.00	2	0	0	2	0
.....TGGGGATCAAGTGAAAGTTGGAAT.....	24	2	1	2.00	2	2	0	0	0
.....TGGGGATCAAGTGAAAGTTGA.....	21	1	1	2.00	2	1	0	1	0
.....TGGGGATCAAGTGAAAGTTGGATA.....	24	2	1	2.00	2	2	0	0	0
.....CTACTTTCACTTGTTTCTTTCTC.....	23	0	1	1.00	1	0	0	1	0
.....TGGGGATCAAGTGAAAGTTGGATT.....	24	2	1	1.00	1	1	0	0	0
.....GGGATCAAGTGAAAGTTGG.....	19	0	1	1.00	1	0	0	1	0
.....TGGGGATCAAGTGAAAGTTGGAAAA.....	25	3	1	1.00	1	1	0	0	0
.....TGGGGATCAAGTGAAAGTTGGAG.....	23	0	1	1.00	1	1	0	0	0
.....CTACTTTCACTTGTTTCTTTC.....	21	0	1	1.00	1	0	0	1	0
.....GATCAAGTGAAAGTTGGA.....	18	0	1	1.00	1	1	0	0	0
.....TACTTTCACTTGTTTCTTTCT.....	21	0	1	1.00	1	0	0	1	0

Anti-sense strand reads

TTTGAAAAACTAGCAGCCTCGTAGTATTTTTAATATAAAATATACGTCTAACCCCTAGTTCACTTTCAACCTCGCAATATTTAGCTTTAAAAGGATGAAAGTGAACAAAGAAAGAGCCGCATATTTGTTGAGAGAGACCTTTTTTTTTTGTTTAGTATTAAAAAAT ********************************..(((((((((.((..(((((.((((((((((.((((.(((.........))).))))).)))))))))))).)))))..)).)))))))))....********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	V118 embryo	V117 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3391881-3392046 -	dwi_185	AAACTTTTTGATCGTCGGAGCATCATAAAAATTATATTTTATATGCAGATTGGGGATCAAGTGAAAGTTGGAGCGTTATAAATCGAAATTTTCCTACTTTCACTTGTTTCTTTCTCGGCGTATAAACAACTCTCTCTGGAAAAAAAAAACAAATCATAATTTTTTA

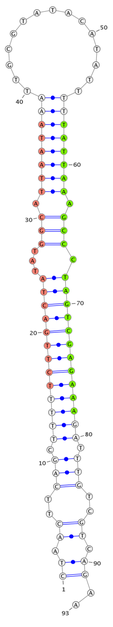
Generated: 09/08/2015 at 07:52 PM

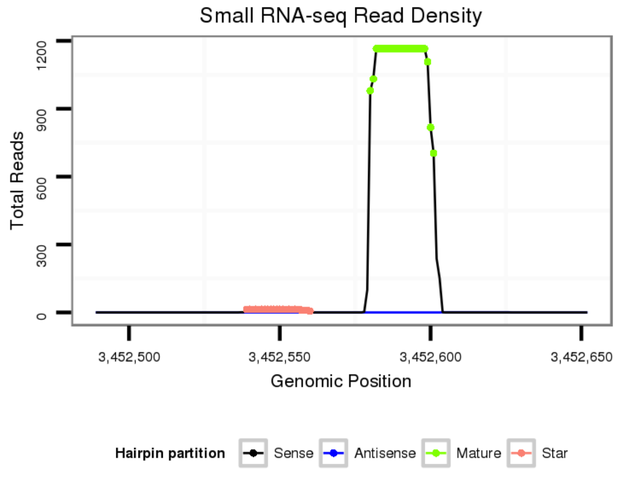
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

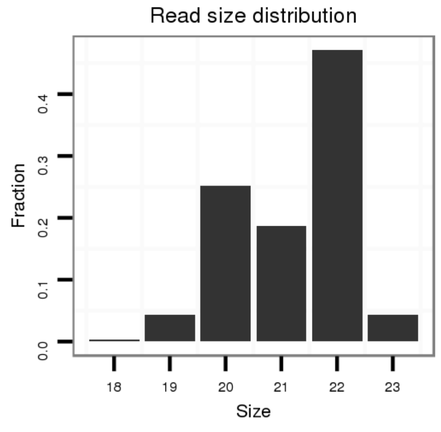
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_57	**scf2_1100000004513:3452539-3452602 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

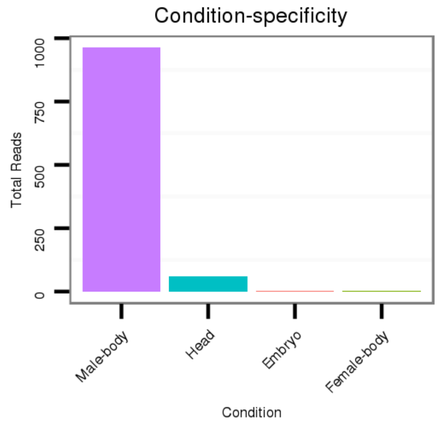
Legend: mature star mismatch in alignment mismatch in read

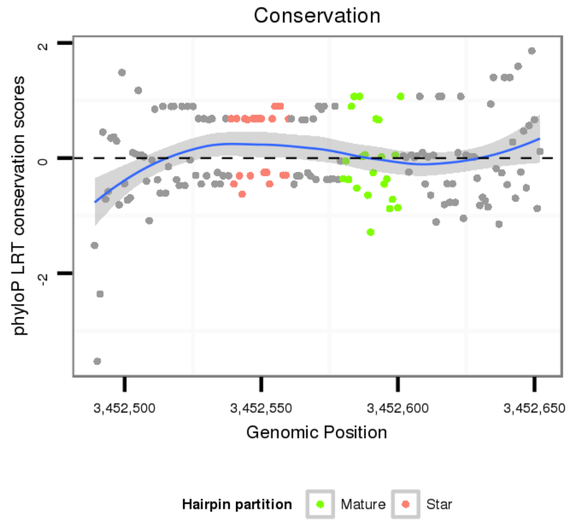
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AGCAGAAAATAACAACAATTAACAAAACTAATTTACTAACTTCAGCTTTTTCTTGACTATATGGCATTAATAAATTGCGTATACATATTTTTATTAAAGCCCTAGTCGAGAAAGATTTGTCGTCAGAAGTGTGTAAAATTAAGTGAAACGACACAACAGAAATA **********(((.(((..(((.((((((((((((...(((.(((((((((.....)))))))))...)))..)))))))))))))).)))..))..))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	M020 head	V119 head	V118 embryo	M045 female body
..TATTAAAGCCCTAGTCGAGAAA..	22	0	1	444.00	444	424	5	12	2	1
..TATTAAAGCCCTAGTCGAGA..	20	0	1	231.00	231	228	1	2	0	0
..TATTAAAGCCCTAGTCGAGAA..	21	0	1	97.00	97	94	1	1	0	1
..TTAAAGCCCTAGTCGAGAAAGA..	22	0	1	89.00	89	83	1	3	2	0
..TTATTAAAGCCCTAGTCGAGA..	21	0	1	55.00	55	51	1	2	1	0
..TATTAAAGCCCTAGTCGAGAAAA..	23	1	1	44.00	44	42	0	2	0	0
..TATTAAAGCCCTAGTCGAG..	19	0	1	41.00	41	39	1	1	0	0
..TATTAAAGCCCTAGTCGAGAAAG..	23	0	1	36.00	36	29	7	0	0	0
..TTAAAGCCCTAGTCGAGAAAG..	21	0	1	34.00	34	25	9	0	0	0
..TATTAAAGCCCTAGTCGAGAAAGA..	24	0	1	31.00	31	25	1	3	1	1
..ATTAAAGCCCTAGTCGAGAAAGA..	23	0	1	29.00	29	27	0	0	2	0
..ATTAAAGCCCTAGTCGAGAAAG..	22	0	1	18.00	18	16	2	0	0	0
..TTATTAAAGCCCTAGTCGAGAA..	22	0	1	16.00	16	16	0	0	0	0
..TTATTAAAGCCCTAGTCGAG..	20	0	1	16.00	16	15	0	0	1	0
..TTAAAGCCCTAGTCGAGAAA..	20	0	1	11.00	11	8	0	2	0	1
..TTATTAAAGCCCTAGTCGAGAAA..	23	0	1	9.00	9	9	0	0	0	0
..TTAAAGCCCTAGTCGAGAAAGAA..	23	1	1	6.00	6	6	0	0	0	0
..TATTAAAGCCCTAGTCGAGAAAGAA..	25	1	1	6.00	6	6	0	0	0	0
..TCTTGACTATATGGCATTAATA..	22	0	1	5.00	5	0	5	0	0	0
..TATTAAAGCCCTAGTCGAGAAC..	22	1	1	4.00	4	4	0	0	0	0
..TCTTGACTATATGGCATTAAT..	21	0	1	4.00	4	1	3	0	0	0
..TTATTAAAGCCCTAGTCGAGAAAA..	24	1	1	3.00	3	2	0	1	0	0
..TCTTGACTATATGGCATT..	18	0	1	3.00	3	0	3	0	0	0
..TCTTGACTATATGGCATA..	18	1	1	2.00	2	0	2	0	0	0
..TATTAAAGCCCTAGTCGAGAAAAC..	23	1	1	2.00	2	2	0	0	0	0
..TATTAAAGCCCTAGTCGAGAAAGT..	24	1	1	2.00	2	1	1	0	0	0
..ATTAAAGCCCTAGTCGAGAAAGAA..	24	1	1	2.00	2	2	0	0	0	0
..TTTATTAAAGCCCTAGTCGAGA..	22	0	1	2.00	2	2	0	0	0	0
..ATTAAAGCCCTAGTCGAGAAA..	21	0	1	2.00	2	2	0	0	0	0
..TATTAAAGCCCTAGTCGAGAAT..	22	1	1	2.00	2	2	0	0	0	0
..TTAAAGCCCTAGTCGAGAAAGT..	22	1	1	2.00	2	2	0	0	0	0
..ATTAAAGCCCTAGTCGAGAAAGT..	23	1	1	2.00	2	2	0	0	0	0
..ATTAAAGCCCTAGTCGAGA..	19	0	1	2.00	2	2	0	0	0	0
..TTAAAGCCCTAGTCGAGAAAGC..	22	1	1	1.00	1	1	0	0	0	0
..TTTCTTGACTATATGGCATTAATA..	24	0	1	1.00	1	0	1	0	0	0
..TATTAAAGCCCTAGTCGAGAAAT..	23	1	1	1.00	1	1	0	0	0	0
..TCTTGACTATATGGCATTA..	19	0	1	1.00	1	0	1	0	0	0
..TATTAAAGCCCTAGTCGAGAAAGAT..	25	0	1	1.00	1	1	0	0	0	0
..TATTAAAGCCCTAGTCGAG..	19	1	1	1.00	1	1	0	0	0	0
..TTTATTAAAGCCCTAGTCGAG..	21	0	1	1.00	1	1	0	0	0	0
..TTAAAGCCCTAGTCGAGAAAGAG..	23	1	1	1.00	1	1	0	0	0	0
..TATTAAAGCCCTAGTCGAGAAG..	22	1	1	1.00	1	1	0	0	0	0
..ATTAAAGCCCTAGTCGAGAA..	20	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

TCGTCTTTTATTGTTGTTAATTGTTTTGATTAAATGATTGAAGTCGAAAAAGAACTGATATACCGTAATTATTTAACGCATATGTATAAAAATAATTTCGGGATCAGCTCTTTCTAAACAGCAGTCTTCACACATTTTAATTCACTTTGCTGTGTTGTCTTTAT **********(((..(((..(((.((((((((((((...(((.(((((((((.....)))))))))...)))..)))))))))))))).)))..))..))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	M020 head
..AAACAGCAGTCTTCACACATTTT..	23	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004513:3452489-3452652 +	dwi_57	AGCAGAAAATAACAACAAT----------TAACAAAACTAAT--TTACTAACTTCAGCTTTTTCTTGACTATATGGCATTAATAAATTGCGTATACATATTTTTATTAAAGCCCTAGTCGAGAAAGAT----------TTGTCGTCAGAAGTGTGTAAAATT---AAGTGAAACGACACAACAGAAATA
droVir3	scaffold_12970:8501571-8501720 -		CATAA--ATCAAACACAAC----------CGCCAAAACTAAATATAATAATAAATACATTGATATATACACAATATAAAATTAAT---------TACATAATTAATTTAAAGCAA---TTTGCAAAAGA----------TCATTAAAATAAATAAAAAATAAAA-TTAAA---AAAAAAACAAAAGCAAAA
droMoj3	scaffold_6473:10865627-10865796 -		CTAGGCGAATACTTTAACTTAGAACAAAAATTCGGTCACTTATT--TTATTG----------ATATTTT---TTTTTTTAGAATATTTAAAAATTTGAAATAAAAAAATAAAATATAAAAACATATGAAAAGAAAAATGTTATTGGCAAATTTTAAATATTA--TCTATAAGCGATATCAATGAAATC
droGri2	scaffold_15245:11846698-11846798 +		GCA----------TTAGCAACAAGCAAAAACAATTTAATTATATAGCAGCAGCAGACAGAGAT----------TTGTTTTAAGAAGAGAGAACATTT---TGTCCAAATAATACCACAAAAAAA
dp5	Unknown_singleton_2584:781-792 +		ACA----------ACAAAAACG
droPer2	scaffold_13:1194458-1194476 +		AGCAGCAAAGACTAACAAT----------
droEle1	scf7180000488940:862-891 +		TATAAAA----------ATAAG---AGAAACACAAAAAAAACA
droBia1	scf7180000300750:1504-1512 +		ATA----------TAAATA
droEre2	scaffold_4784:21426267-21426282 +		CAAACCAGAGAC----------ACTA

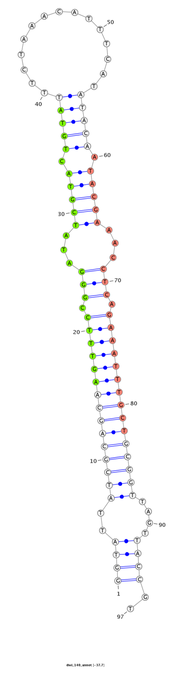
Generated: 09/08/2015 at 07:52 PM

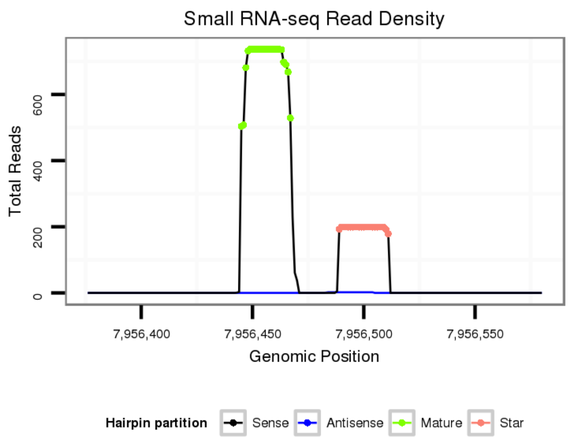
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

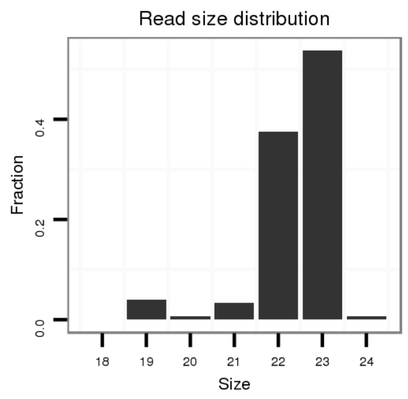
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_140	**scf2_1100000004909:7956426-7956530 +**	**Known Ortholog**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

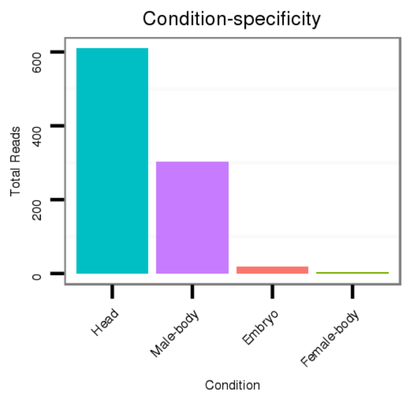
Legend: mature star mismatch in alignment mismatch in read

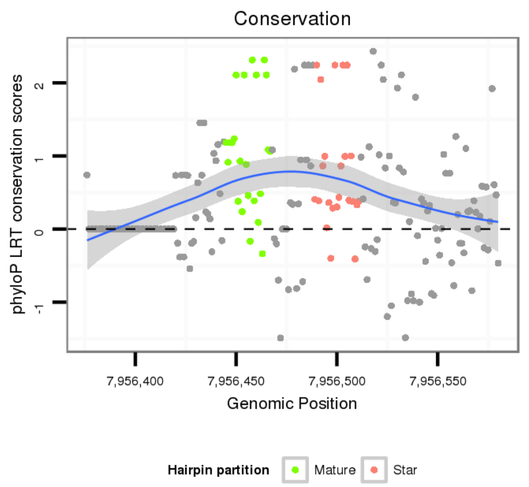
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTAGCTTAAATGCACAATTTATGCACTATGGAAATAATTAATTGGATATTGGTTGGTATTATCGCAGCAAGTTTCCGGGATATCGTACTGTATTTCTAAACATTTCATATACAATACGAAACCTCAGAAATTTGCTGCGGTTAGTTACCGTTAACAACTCATAAGAAAGGAGAGAATAAAAATGATCAATATACATGTGTGTGTG	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V117 male body	V119 head	V118 embryo	M045 female body
**********(((((..(((((((((((((((.(((...(((((.(((((.....)))))..)))))...)))).)))))))))))))))....)))))..**********										
.....AGTTTCCGGGATATCGTACTGTA.....	23	0	1	290.00	290	236	53	0	1	0
.....ATACGAAACCTCAGAAATTTGCT.....	23	0	1	173.00	173	10	81	66	15	1
.....TTTCCGGGATATCGTACTGTAT.....	22	0	1	161.00	161	123	34	2	0	2
.....AGTTTCCGGGATATCGTACTGT.....	22	0	1	139.00	139	49	89	1	0	0
.....AGTTTCCGGGATATCGTACTGTAA.....	24	1	1	124.00	124	103	21	0	0	0
.....AGTTTCCGGGATATCGTAC.....	19	0	1	38.00	38	38	0	0	0	0
.....TTCCGGGATATCGTACTGTATTT.....	23	0	1	33.00	33	30	3	0	0	0
.....AGTTTCCGGGATATCGTACTG.....	21	0	1	21.00	21	0	20	1	0	0
.....TTCCGGGATATCGTACTGTATT.....	22	0	1	16.00	16	13	3	0	0	0
.....ATACGAAACCTCAGAAATTTGC.....	22	0	1	13.00	13	3	3	4	2	1
.....TTTCCGGGATATCGTACTGTATT.....	23	0	1	7.00	7	5	2	0	0	0
.....AGTTTCCGGGATATCGTACTGTC.....	23	1	1	7.00	7	6	1	0	0	0
.....TACGAAACCTCAGAAATTTGCT.....	22	0	1	6.00	6	0	4	2	0	0
.....AGTTTCCGGGATATCGTACTGC.....	22	1	1	6.00	6	6	0	0	0	0
.....AGTTTCCGGGATATCGTACT.....	20	0	1	6.00	6	1	5	0	0	0
.....TTTCCGGGATATCGTACTGTAC.....	22	1	1	6.00	6	6	0	0	0	0
.....AGTTTCCGGGATATCGTACTGTAT.....	24	0	1	6.00	6	5	0	1	0	0
.....TTTCCGGGATATCGTACTGTA.....	21	0	1	5.00	5	4	1	0	0	0
.....AATACGAAACCTCAGAAATTTG.....	22	0	1	5.00	5	3	2	0	0	0
.....TCCGGGATATCGTACTGTATTT.....	22	0	1	5.00	5	5	0	0	0	0
.....GTTTCCGGGATATCGTACTGTA.....	22	0	1	4.00	4	3	1	0	0	0
.....AGTTTCCGGGATATCGTACTGC.....	22	1	1	4.00	4	4	0	0	0	0
.....AGTTTCCGGGATATCGTACTGTAC.....	24	1	1	3.00	3	3	0	0	0	0
.....ATACGAAACCTCAGAAATTTGCTT.....	24	1	1	3.00	3	0	2	1	0	0
.....AGTTTCCGGGATATCGTACTGTAAA.....	25	2	1	2.00	2	1	1	0	0	0
.....AGTTTCCGGGATATCGTACTGTT.....	23	1	1	2.00	2	0	2	0	0	0
.....ATACGAAACCTCAGAAATTTG.....	21	0	1	2.00	2	1	1	0	0	0
.....TTTCCGGGATATCGTACTGTATAA.....	24	2	1	2.00	2	2	0	0	0	0
.....ATACGAAACCTCAGAAATTTGCTA.....	24	1	1	2.00	2	0	1	1	0	0
.....ATACGAAACCTCAGAAATTTGCC.....	23	1	1	2.00	2	1	1	0	0	0
.....TTCCGGGATATCGTACTGTAT.....	21	0	1	2.00	2	2	0	0	0	0
.....TTTCCGGGATATCGTACTGTAA.....	22	1	1	1.00	1	1	0	0	0	0
.....CAAGTTTCCGGGATATCGTACT.....	22	0	1	1.00	1	1	0	0	0	0
.....AGTTTCCGGGATATCGTACTGTAG.....	24	1	1	1.00	1	1	0	0	0	0
.....AGTTTCCGGGATATCGTA.....	18	0	1	1.00	1	0	1	0	0	0
.....AATACGAAACCTCAGAAATTTGT.....	23	1	1	1.00	1	0	0	1	0	0
.....AGTTTCCGGGATATCGTACTGTCA.....	24	2	1	1.00	1	1	0	0	0	0
.....GTTTCCGGGATATCGTACTGTAAA.....	24	2	1	1.00	1	1	0	0	0	0
.....TTCCGGGATATCGTACTGTATTA.....	23	1	1	1.00	1	1	0	0	0	0
.....AAGTTTCCGGGATATCGTACTA.....	22	1	1	1.00	1	0	1	0	0	0
.....GTTTCCGGGATATCGTACTGTAA.....	23	1	1	1.00	1	1	0	0	0	0
.....AAGTTTCCGGGATATCGTACTG.....	22	0	1	1.00	1	0	1	0	0	0
.....AAGTTTCCGGGATATCGTACT.....	21	0	1	1.00	1	0	0	1	0	0
.....AGTTTCCGGGATATCGTACTGTCC.....	24	2	1	1.00	1	1	0	0	0	0
.....TTTCCGGGATATCGTACTGTATTAA.....	25	2	1	1.00	1	1	0	0	0	0
.....TTTCCGGGATATCGTACTGTAG.....	22	1	1	1.00	1	1	0	0	0	0
.....AGTTTCCGGGATATCGTACTGA.....	22	1	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

AATCGAATTTACGTGTTAAATACGTGATACCTTTATTAATTAACCTATAACCAACCATAATAGCGTCGTTCAAAGGCCCTATAGCATGACATAAAGATTTGTAAAGTATATGTTATGCTTTGGAGTCTTTAAACGACGCCAATCAATGGCAATTGTTGAGTATTCTTTCCTCTCTTATTTTTACTAGTTATATGTACACACACAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V118 embryo	M045 female body
**********(((((..(((((((((((((((.(((...(((((.(((((.....)))))..)))))...)))).)))))))))))))))....)))))..**********								
.....ATATGTTATGCTTTGGAGTCTT.....	22	0	1	1.00	1	0	1	0
.....TATGTTATGCTTTGGAGTCTT.....	21	0	1	1.00	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004909:7956376-7956580 +	dwi_140	TTAGCTTAAATGCACAATTTATGCACTATGGAAATAATTAATTGGATATTGGTTGGTATTATCGCAGCAAGTTTCCGGGATATCGTA----------CTGTATT--------TCTAAACATTTCATA-TACAATACGA--------AACCTCAGAAATTTGCTGCGGTTAGTTACCGTT-AACAACTCATAAGAAA-GGAGAGAA----------TAAAA-------ATGATCAATATACATGTGTGTGTG
droVir3	scaffold_13042:907857-907872 -		T----------GTGTGT----------|----------|-------|--------|----------|---------|--------|----------|----------|-------|----------|-----|-------|----------GTGTGTGTG
droMoj3	scaffold_6496:4195040-4195086 -		C----------AAAAAAAATGAGAAATACCT----------|----------|-------|--------|----------|---------|--------|----------ATACATA---------|----------|-------|----------|-----|-------|------CATATGCATGTGTGTGTG
droGri2	scaffold_15081:2044829-2044996 -	dgr_10	T----------GGTATTGCTGCAGCAATTTCCCGGTCTCGTA----------|----------TGTATTATCAAAATGGTAT---ACTCTGAACCACATACGA--------TTCCTCAGAAATTCGCTGGTGTAAGTTACCGTT-TTCAACCGTATAGCAACTGTGCCGATAAACCTATC-----CCAGTCTATCGA----TAGACA-ACGATTGTC
dp5	3:5184418-5184437 +		T----------CCAAGTCT----------|----------|-------|--------|----------|---------|--------|----------|----------|-------|----------|-----|-------|----------GTGTGTGTGTG
droAna3	scaffold_13417:2468029-2468191 -		T----------GGTATTATGGCAGCCAGTTTCCGGGATCTCGTA----------|----------CTGTATG--------AAGT---TTTCTATA-TACAATTCGA--------AAACTCAGAAACTTCCTGGCGTGAGTACCATTGATCAACGGCTGAGTATGCGACC-GGAAAGGGGACG-----CGAATGCGACGACTAAAGGATGGCGCGATGCGG
droBip1	scf7180000395874:40395-40520 -		G----------GGGAGTGCCTGGTATTATGGCAGCGAGTTTCCGGGATCTCGTA----------|----------GTGTATG--------AAGT---TTTATAAA-TACAATTCGA--------AAACTCAGAAACTTTCTGGCTTGAAGTACATTC-ATCAACGGCCGAGTA-|--------|----------|-----|-------|----------ATATA
droKik1	scf7180000302517:1183445-1183567 +		T----------GGTATAGCCGCAGAAAGTTTCCCAG-TTTCGTA----------|----------ATGTATG--------GTTA---TATTTGAAA-TACAGTACGA--------CAGATCAGAAATTTTCGGGAGTTAGTACCGTA-AACAACCAAAAATGGA-GCAAGGAG----------CA---|-------|----------|----------A
droFic1	scf7180000454073:1733616-1733722 +		T----------CGGTATTATCGCAGCAAGTTTCCGGGACTTCGTA----------|----------CTGTATG--------AAGA---ATTCTATA-TACAATACGA--------AACCTCAGAAATTTATTGCAATGAACCACGTTT-AAGTAATTGAT------|--------|----------|-----|-------|----------
droEle1	scf7180000490751:1118514-1118622 +		T----------TGGTATTATCGCAGCAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------AGAA---ATTCTATA-TACAATACGA--------AACCTTAGAAATTTTCTGAAGTTAGTACCATA-GAGTACCATAA----|--------|----------|-----|-------|----------
droRho1	scf7180000761121:190394-190496 -		T----------TGGTATTATCGCAGCAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------AGAA---ATTCTATA-TACAATACGA--------AACCTTAGAAATTTTCTGGAGTTATCTACGATT-AAGTAC----------|--------|----------|-----|-------|----------
droBia1	scf7180000302069:1151364-1151463 -		T----------TGGTATTATCGCAACACAAGTTTCCGGGATTTTGTA----------|----------TTGTATG--------ACTA---GATTCTATA-TACAATACGA--------AACCTCAGAAATTTTCTGGAGTTAGTACCATA-AA----------|--------|----------|-----|-------|----------
droTak1	scf7180000415169:845124-845246 -		T----------TGGTATTATCGCAACACAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------CTGA---ATTCTATA-TACAATACGA--------AAGCTCAGAAATTTTCTGGAGTTAGTACCATT-AAGTACTTACTTACGAA-GGATCGAT----------T----|-------|----------|----------A
droEug1	scf7180000409230:879979-880090 -		T----------TGGTATTATCGCAATAAGTTCCTGGGATTCGCA----------|----------CTGTATT--------ACGA---TTTTTACA-TACAATACGA--------AAGCTCAGAAACTAACTGGAATTAAGTACCGTA-AAGTACGGATCAGA---|--------|----------|-----|-------|----------A
dm3	chrX:19452595-19452757 +	dme-mir-4966-2	T----------TGGTATTATGGCAAAAGTTTCCAGGACATTGACAACCTATATATGTATGTACTTGTCGGCACTGGAGT--------AC---------TAAA-TATATTGCACATGTTCATGCATGTTCAACATATTTAGGAGCTCAAGTACCGAA-AA----------|--------|---ATGAACAACTAAAA-------GCGG---AGAATACGAAAGTG-C
droSim2	x:18341756-18341796 +		T----------TGGTATTATGGCAACAAGTTTCCAGGACATCGAG----------|----------CTGTGT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------
droSec2	scaffold_8:1734626-1734666 +		T----------TGGTATTATGGCAACAAGTTTCCAGGACATCGAG----------|----------CTGTGT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------
droYak3	X:11886139-11886241 -	dya_51	T----------TGGTATTATGGCAACAAGTTTCCGGGACTTCGTA----------|----------CTGTATG--------AGAG---ACTATATA-TACAATACGA--------AGCCTCTGAAATTTTCTGCGCTCAAGTACCAAA-AAGTAC----------|--------|----------|-----|-------|----------
droEre2	scaffold_4690:9688639-9688679 +		T----------TGGTATTAAGGCAACAAGTTTCAGGGACTTCGCA----------|----------CTGTAT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004909:7956376-7956580 +	dwi_140	TTAGCTTAAATGCACAATTTATGCACTATGGAAATAATTAATTGGATATTGGTTGGTATTATCGCAGCAAGTTTCCGGGATATCGTA----------CTGTATT--------TCTAAACATTTCATA-TACAATACGA--------AACCTCAGAAATTTGCTGCGGTTAGTTACCGTT-AACAACTCATAAGAAA-GGAGAGAA----------TAAAA-------ATGATCAATATACATGTGTGTGTG
droVir3	scaffold_13042:907857-907872 -		T----------GTGTGT----------|----------|-------|--------|----------|---------|--------|----------|----------|-------|----------|-----|-------|----------GTGTGTGTG
droMoj3	scaffold_6496:4195040-4195086 -		C----------AAAAAAAATGAGAAATACCT----------|----------|-------|--------|----------|---------|--------|----------ATACATA---------|----------|-------|----------|-----|-------|------CATATGCATGTGTGTGTG
droGri2	scaffold_15081:2044829-2044996 -	dgr_10	T----------GGTATTGCTGCAGCAATTTCCCGGTCTCGTA----------|----------TGTATTATCAAAATGGTAT---ACTCTGAACCACATACGA--------TTCCTCAGAAATTCGCTGGTGTAAGTTACCGTT-TTCAACCGTATAGCAACTGTGCCGATAAACCTATC-----CCAGTCTATCGA----TAGACA-ACGATTGTC
dp5	3:5184418-5184437 +		T----------CCAAGTCT----------|----------|-------|--------|----------|---------|--------|----------|----------|-------|----------|-----|-------|----------GTGTGTGTGTG
droAna3	scaffold_13417:2468029-2468191 -		T----------GGTATTATGGCAGCCAGTTTCCGGGATCTCGTA----------|----------CTGTATG--------AAGT---TTTCTATA-TACAATTCGA--------AAACTCAGAAACTTCCTGGCGTGAGTACCATTGATCAACGGCTGAGTATGCGACC-GGAAAGGGGACG-----CGAATGCGACGACTAAAGGATGGCGCGATGCGG
droBip1	scf7180000395874:40395-40520 -		G----------GGGAGTGCCTGGTATTATGGCAGCGAGTTTCCGGGATCTCGTA----------|----------GTGTATG--------AAGT---TTTATAAA-TACAATTCGA--------AAACTCAGAAACTTTCTGGCTTGAAGTACATTC-ATCAACGGCCGAGTA-|--------|----------|-----|-------|----------ATATA
droKik1	scf7180000302517:1183445-1183567 +		T----------GGTATAGCCGCAGAAAGTTTCCCAG-TTTCGTA----------|----------ATGTATG--------GTTA---TATTTGAAA-TACAGTACGA--------CAGATCAGAAATTTTCGGGAGTTAGTACCGTA-AACAACCAAAAATGGA-GCAAGGAG----------CA---|-------|----------|----------A
droFic1	scf7180000454073:1733616-1733722 +		T----------CGGTATTATCGCAGCAAGTTTCCGGGACTTCGTA----------|----------CTGTATG--------AAGA---ATTCTATA-TACAATACGA--------AACCTCAGAAATTTATTGCAATGAACCACGTTT-AAGTAATTGAT------|--------|----------|-----|-------|----------
droEle1	scf7180000490751:1118514-1118622 +		T----------TGGTATTATCGCAGCAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------AGAA---ATTCTATA-TACAATACGA--------AACCTTAGAAATTTTCTGAAGTTAGTACCATA-GAGTACCATAA----|--------|----------|-----|-------|----------
droRho1	scf7180000761121:190394-190496 -		T----------TGGTATTATCGCAGCAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------AGAA---ATTCTATA-TACAATACGA--------AACCTTAGAAATTTTCTGGAGTTATCTACGATT-AAGTAC----------|--------|----------|-----|-------|----------
droBia1	scf7180000302069:1151364-1151463 -		T----------TGGTATTATCGCAACACAAGTTTCCGGGATTTTGTA----------|----------TTGTATG--------ACTA---GATTCTATA-TACAATACGA--------AACCTCAGAAATTTTCTGGAGTTAGTACCATA-AA----------|--------|----------|-----|-------|----------
droTak1	scf7180000415169:845124-845246 -		T----------TGGTATTATCGCAACACAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------CTGA---ATTCTATA-TACAATACGA--------AAGCTCAGAAATTTTCTGGAGTTAGTACCATT-AAGTACTTACTTACGAA-GGATCGAT----------T----|-------|----------|----------A
droEug1	scf7180000409230:879979-880090 -		T----------TGGTATTATCGCAATAAGTTCCTGGGATTCGCA----------|----------CTGTATT--------ACGA---TTTTTACA-TACAATACGA--------AAGCTCAGAAACTAACTGGAATTAAGTACCGTA-AAGTACGGATCAGA---|--------|----------|-----|-------|----------A
dm3	chrX:19452595-19452757 +	dme-mir-4966-2	T----------TGGTATTATGGCAAAAGTTTCCAGGACATTGACAACCTATATATGTATGTACTTGTCGGCACTGGAGT--------AC---------TAAA-TATATTGCACATGTTCATGCATGTTCAACATATTTAGGAGCTCAAGTACCGAA-AA----------|--------|---ATGAACAACTAAAA-------GCGG---AGAATACGAAAGTG-C
~~droSim2~~	x:18341756-18341796 +		T----------TGGTATTATGGCAACAAGTTTCCAGGACATCGAG----------|----------CTGTGT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------
droSec2	scaffold_8:1734626-1734666 +		T----------TGGTATTATGGCAACAAGTTTCCAGGACATCGAG----------|----------CTGTGT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------
droYak3	X:11886139-11886241 -	dya_51	T----------TGGTATTATGGCAACAAGTTTCCGGGACTTCGTA----------|----------CTGTATG--------AGAG---ACTATATA-TACAATACGA--------AGCCTCTGAAATTTTCTGCGCTCAAGTACCAAA-AAGTAC----------|--------|----------|-----|-------|----------
droEre2	scaffold_4690:9688639-9688679 +		T----------TGGTATTAAGGCAACAAGTTTCAGGGACTTCGCA----------|----------CTGTAT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------

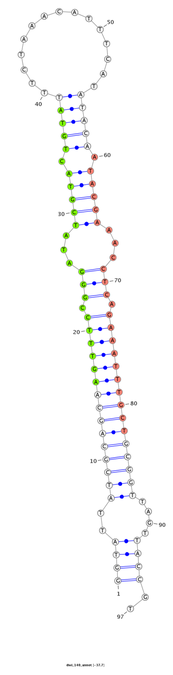
Generated: 09/08/2015 at 07:54 PM

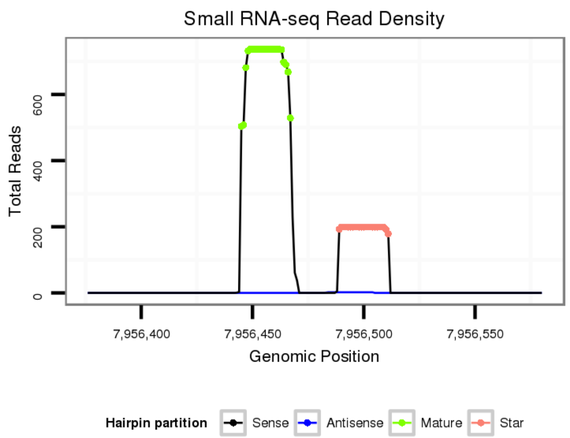
	PASS/FAIL		
crit.star	1	1	1
crit.loop	0	0	0
crit.mor	0	0	0
crit.half	0	0	0
crit.total	1	1	1
crit.pairing	1	1	1
crit.top3	1	1	1
crit.tptop3	1	1	1
crit.uri	0	0	0
crit.back	1	1	1
rescue.total	0	0	0
rescue.dominant	0	0	0
rescue.known	1	1	1
rescue.confident	5	5	6
rescue.candidate	0	0	0

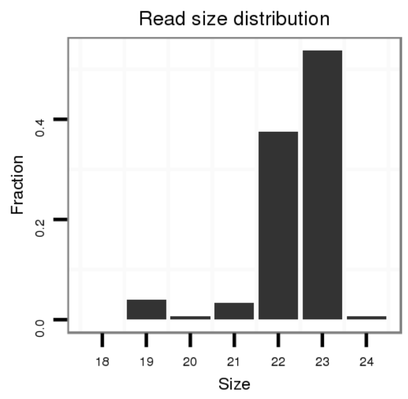
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_140	**scf2_1100000004909:7956426-7956530 +**	**Known Ortholog**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

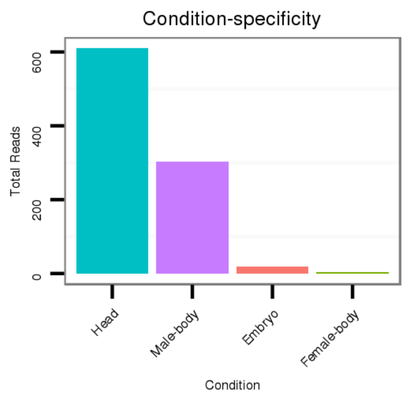
Legend: mature star mismatch in alignment mismatch in read

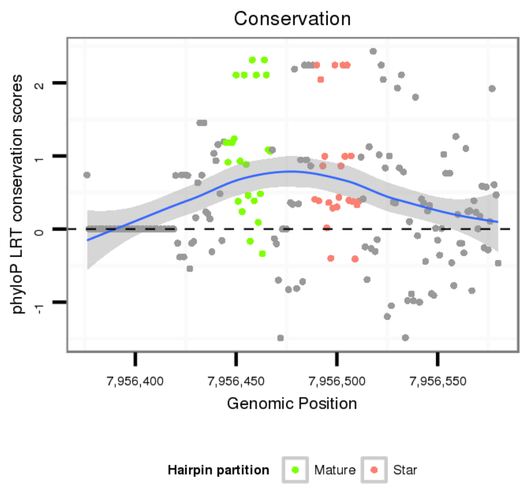
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTAGCTTAAATGCACAATTTATGCACTATGGAAATAATTAATTGGATATTGGTTGGTATTATCGCAGCAAGTTTCCGGGATATCGTACTGTATTTCTAAACATTTCATATACAATACGAAACCTCAGAAATTTGCTGCGGTTAGTTACCGTTAACAACTCATAAGAAAGGAGAGAATAAAAATGATCAATATACATGTGTGTGTG	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V117 male body	V119 head	V118 embryo	M045 female body
**********(((((..(((((((((((((((.(((...(((((.(((((.....)))))..)))))...)))).)))))))))))))))....)))))..**********										
.....AGTTTCCGGGATATCGTACTGTA.....	23	0	1	290.00	290	236	53	0	1	0
.....ATACGAAACCTCAGAAATTTGCT.....	23	0	1	173.00	173	10	81	66	15	1
.....TTTCCGGGATATCGTACTGTAT.....	22	0	1	161.00	161	123	34	2	0	2
.....AGTTTCCGGGATATCGTACTGT.....	22	0	1	139.00	139	49	89	1	0	0
.....AGTTTCCGGGATATCGTACTGTAA.....	24	1	1	124.00	124	103	21	0	0	0
.....AGTTTCCGGGATATCGTAC.....	19	0	1	38.00	38	38	0	0	0	0
.....TTCCGGGATATCGTACTGTATTT.....	23	0	1	33.00	33	30	3	0	0	0
.....AGTTTCCGGGATATCGTACTG.....	21	0	1	21.00	21	0	20	1	0	0
.....TTCCGGGATATCGTACTGTATT.....	22	0	1	16.00	16	13	3	0	0	0
.....ATACGAAACCTCAGAAATTTGC.....	22	0	1	13.00	13	3	3	4	2	1
.....TTTCCGGGATATCGTACTGTATT.....	23	0	1	7.00	7	5	2	0	0	0
.....AGTTTCCGGGATATCGTACTGTC.....	23	1	1	7.00	7	6	1	0	0	0
.....TACGAAACCTCAGAAATTTGCT.....	22	0	1	6.00	6	0	4	2	0	0
.....AGTTTCCGGGATATCGTACTGC.....	22	1	1	6.00	6	6	0	0	0	0
.....AGTTTCCGGGATATCGTACT.....	20	0	1	6.00	6	1	5	0	0	0
.....TTTCCGGGATATCGTACTGTAC.....	22	1	1	6.00	6	6	0	0	0	0
.....AGTTTCCGGGATATCGTACTGTAT.....	24	0	1	6.00	6	5	0	1	0	0
.....TTTCCGGGATATCGTACTGTA.....	21	0	1	5.00	5	4	1	0	0	0
.....AATACGAAACCTCAGAAATTTG.....	22	0	1	5.00	5	3	2	0	0	0
.....TCCGGGATATCGTACTGTATTT.....	22	0	1	5.00	5	5	0	0	0	0
.....GTTTCCGGGATATCGTACTGTA.....	22	0	1	4.00	4	3	1	0	0	0
.....AGTTTCCGGGATATCGTACTGC.....	22	1	1	4.00	4	4	0	0	0	0
.....AGTTTCCGGGATATCGTACTGTAC.....	24	1	1	3.00	3	3	0	0	0	0
.....ATACGAAACCTCAGAAATTTGCTT.....	24	1	1	3.00	3	0	2	1	0	0
.....AGTTTCCGGGATATCGTACTGTAAA.....	25	2	1	2.00	2	1	1	0	0	0
.....AGTTTCCGGGATATCGTACTGTT.....	23	1	1	2.00	2	0	2	0	0	0
.....ATACGAAACCTCAGAAATTTG.....	21	0	1	2.00	2	1	1	0	0	0
.....TTTCCGGGATATCGTACTGTATAA.....	24	2	1	2.00	2	2	0	0	0	0
.....ATACGAAACCTCAGAAATTTGCTA.....	24	1	1	2.00	2	0	1	1	0	0
.....ATACGAAACCTCAGAAATTTGCC.....	23	1	1	2.00	2	1	1	0	0	0
.....TTCCGGGATATCGTACTGTAT.....	21	0	1	2.00	2	2	0	0	0	0
.....TTTCCGGGATATCGTACTGTAA.....	22	1	1	1.00	1	1	0	0	0	0
.....CAAGTTTCCGGGATATCGTACT.....	22	0	1	1.00	1	1	0	0	0	0
.....AGTTTCCGGGATATCGTACTGTAG.....	24	1	1	1.00	1	1	0	0	0	0
.....AGTTTCCGGGATATCGTA.....	18	0	1	1.00	1	0	1	0	0	0
.....AATACGAAACCTCAGAAATTTGT.....	23	1	1	1.00	1	0	0	1	0	0
.....AGTTTCCGGGATATCGTACTGTCA.....	24	2	1	1.00	1	1	0	0	0	0
.....GTTTCCGGGATATCGTACTGTAAA.....	24	2	1	1.00	1	1	0	0	0	0
.....TTCCGGGATATCGTACTGTATTA.....	23	1	1	1.00	1	1	0	0	0	0
.....AAGTTTCCGGGATATCGTACTA.....	22	1	1	1.00	1	0	1	0	0	0
.....GTTTCCGGGATATCGTACTGTAA.....	23	1	1	1.00	1	1	0	0	0	0
.....AAGTTTCCGGGATATCGTACTG.....	22	0	1	1.00	1	0	1	0	0	0
.....AAGTTTCCGGGATATCGTACT.....	21	0	1	1.00	1	0	0	1	0	0
.....AGTTTCCGGGATATCGTACTGTCC.....	24	2	1	1.00	1	1	0	0	0	0
.....TTTCCGGGATATCGTACTGTATTAA.....	25	2	1	1.00	1	1	0	0	0	0
.....TTTCCGGGATATCGTACTGTAG.....	22	1	1	1.00	1	1	0	0	0	0
.....AGTTTCCGGGATATCGTACTGA.....	22	1	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

AATCGAATTTACGTGTTAAATACGTGATACCTTTATTAATTAACCTATAACCAACCATAATAGCGTCGTTCAAAGGCCCTATAGCATGACATAAAGATTTGTAAAGTATATGTTATGCTTTGGAGTCTTTAAACGACGCCAATCAATGGCAATTGTTGAGTATTCTTTCCTCTCTTATTTTTACTAGTTATATGTACACACACAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V118 embryo	M045 female body
**********(((((..(((((((((((((((.(((...(((((.(((((.....)))))..)))))...)))).)))))))))))))))....)))))..**********								
.....ATATGTTATGCTTTGGAGTCTT.....	22	0	1	1.00	1	0	1	0
.....TATGTTATGCTTTGGAGTCTT.....	21	0	1	1.00	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004909:7956376-7956580 +	dwi_140	TTAGCTTAAATGCACAATTTATGCACTATGGAAATAATTAATTGGATATTGGTTGGTATTATCGCAGCAAGTTTCCGGGATATCGTA----------CTGTATT--------TCTAAACATTTCATA-TACAATACGA--------AACCTCAGAAATTTGCTGCGGTTAGTTACCGTT-AACAACTCATAAGAAA-GGAGAGAA----------TAAAA-------ATGATCAATATACATGTGTGTGTG
droVir3	scaffold_13042:907857-907872 -		T----------GTGTGT----------|----------|-------|--------|----------|---------|--------|----------|----------|-------|----------|-----|-------|----------GTGTGTGTG
droMoj3	scaffold_6496:4195040-4195086 -		C----------AAAAAAAATGAGAAATACCT----------|----------|-------|--------|----------|---------|--------|----------ATACATA---------|----------|-------|----------|-----|-------|------CATATGCATGTGTGTGTG
droGri2	scaffold_15081:2044829-2044996 -	dgr_10	T----------GGTATTGCTGCAGCAATTTCCCGGTCTCGTA----------|----------TGTATTATCAAAATGGTAT---ACTCTGAACCACATACGA--------TTCCTCAGAAATTCGCTGGTGTAAGTTACCGTT-TTCAACCGTATAGCAACTGTGCCGATAAACCTATC-----CCAGTCTATCGA----TAGACA-ACGATTGTC
dp5	3:5184418-5184437 +		T----------CCAAGTCT----------|----------|-------|--------|----------|---------|--------|----------|----------|-------|----------|-----|-------|----------GTGTGTGTGTG
droAna3	scaffold_13417:2468029-2468191 -		T----------GGTATTATGGCAGCCAGTTTCCGGGATCTCGTA----------|----------CTGTATG--------AAGT---TTTCTATA-TACAATTCGA--------AAACTCAGAAACTTCCTGGCGTGAGTACCATTGATCAACGGCTGAGTATGCGACC-GGAAAGGGGACG-----CGAATGCGACGACTAAAGGATGGCGCGATGCGG
droBip1	scf7180000395874:40395-40520 -		G----------GGGAGTGCCTGGTATTATGGCAGCGAGTTTCCGGGATCTCGTA----------|----------GTGTATG--------AAGT---TTTATAAA-TACAATTCGA--------AAACTCAGAAACTTTCTGGCTTGAAGTACATTC-ATCAACGGCCGAGTA-|--------|----------|-----|-------|----------ATATA
droKik1	scf7180000302517:1183445-1183567 +		T----------GGTATAGCCGCAGAAAGTTTCCCAG-TTTCGTA----------|----------ATGTATG--------GTTA---TATTTGAAA-TACAGTACGA--------CAGATCAGAAATTTTCGGGAGTTAGTACCGTA-AACAACCAAAAATGGA-GCAAGGAG----------CA---|-------|----------|----------A
droFic1	scf7180000454073:1733616-1733722 +		T----------CGGTATTATCGCAGCAAGTTTCCGGGACTTCGTA----------|----------CTGTATG--------AAGA---ATTCTATA-TACAATACGA--------AACCTCAGAAATTTATTGCAATGAACCACGTTT-AAGTAATTGAT------|--------|----------|-----|-------|----------
droEle1	scf7180000490751:1118514-1118622 +		T----------TGGTATTATCGCAGCAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------AGAA---ATTCTATA-TACAATACGA--------AACCTTAGAAATTTTCTGAAGTTAGTACCATA-GAGTACCATAA----|--------|----------|-----|-------|----------
droRho1	scf7180000761121:190394-190496 -		T----------TGGTATTATCGCAGCAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------AGAA---ATTCTATA-TACAATACGA--------AACCTTAGAAATTTTCTGGAGTTATCTACGATT-AAGTAC----------|--------|----------|-----|-------|----------
droBia1	scf7180000302069:1151364-1151463 -		T----------TGGTATTATCGCAACACAAGTTTCCGGGATTTTGTA----------|----------TTGTATG--------ACTA---GATTCTATA-TACAATACGA--------AACCTCAGAAATTTTCTGGAGTTAGTACCATA-AA----------|--------|----------|-----|-------|----------
droTak1	scf7180000415169:845124-845246 -		T----------TGGTATTATCGCAACACAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------CTGA---ATTCTATA-TACAATACGA--------AAGCTCAGAAATTTTCTGGAGTTAGTACCATT-AAGTACTTACTTACGAA-GGATCGAT----------T----|-------|----------|----------A
droEug1	scf7180000409230:879979-880090 -		T----------TGGTATTATCGCAATAAGTTCCTGGGATTCGCA----------|----------CTGTATT--------ACGA---TTTTTACA-TACAATACGA--------AAGCTCAGAAACTAACTGGAATTAAGTACCGTA-AAGTACGGATCAGA---|--------|----------|-----|-------|----------A
dm3	chrX:19452595-19452757 +	dme-mir-4966-2	T----------TGGTATTATGGCAAAAGTTTCCAGGACATTGACAACCTATATATGTATGTACTTGTCGGCACTGGAGT--------AC---------TAAA-TATATTGCACATGTTCATGCATGTTCAACATATTTAGGAGCTCAAGTACCGAA-AA----------|--------|---ATGAACAACTAAAA-------GCGG---AGAATACGAAAGTG-C
droSim2	x:18341756-18341796 +		T----------TGGTATTATGGCAACAAGTTTCCAGGACATCGAG----------|----------CTGTGT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------
droSec2	scaffold_8:1734626-1734666 +		T----------TGGTATTATGGCAACAAGTTTCCAGGACATCGAG----------|----------CTGTGT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------
droYak3	X:11886139-11886241 -	dya_51	T----------TGGTATTATGGCAACAAGTTTCCGGGACTTCGTA----------|----------CTGTATG--------AGAG---ACTATATA-TACAATACGA--------AGCCTCTGAAATTTTCTGCGCTCAAGTACCAAA-AAGTAC----------|--------|----------|-----|-------|----------
droEre2	scaffold_4690:9688639-9688679 +		T----------TGGTATTAAGGCAACAAGTTTCAGGGACTTCGCA----------|----------CTGTAT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004909:7956376-7956580 +	dwi_140	TTAGCTTAAATGCACAATTTATGCACTATGGAAATAATTAATTGGATATTGGTTGGTATTATCGCAGCAAGTTTCCGGGATATCGTA----------CTGTATT--------TCTAAACATTTCATA-TACAATACGA--------AACCTCAGAAATTTGCTGCGGTTAGTTACCGTT-AACAACTCATAAGAAA-GGAGAGAA----------TAAAA-------ATGATCAATATACATGTGTGTGTG
droVir3	scaffold_13042:907857-907872 -		T----------GTGTGT----------|----------|-------|--------|----------|---------|--------|----------|----------|-------|----------|-----|-------|----------GTGTGTGTG
droMoj3	scaffold_6496:4195040-4195086 -		C----------AAAAAAAATGAGAAATACCT----------|----------|-------|--------|----------|---------|--------|----------ATACATA---------|----------|-------|----------|-----|-------|------CATATGCATGTGTGTGTG
droGri2	scaffold_15081:2044829-2044996 -	dgr_10	T----------GGTATTGCTGCAGCAATTTCCCGGTCTCGTA----------|----------TGTATTATCAAAATGGTAT---ACTCTGAACCACATACGA--------TTCCTCAGAAATTCGCTGGTGTAAGTTACCGTT-TTCAACCGTATAGCAACTGTGCCGATAAACCTATC-----CCAGTCTATCGA----TAGACA-ACGATTGTC
dp5	3:5184418-5184437 +		T----------CCAAGTCT----------|----------|-------|--------|----------|---------|--------|----------|----------|-------|----------|-----|-------|----------GTGTGTGTGTG
droAna3	scaffold_13417:2468029-2468191 -		T----------GGTATTATGGCAGCCAGTTTCCGGGATCTCGTA----------|----------CTGTATG--------AAGT---TTTCTATA-TACAATTCGA--------AAACTCAGAAACTTCCTGGCGTGAGTACCATTGATCAACGGCTGAGTATGCGACC-GGAAAGGGGACG-----CGAATGCGACGACTAAAGGATGGCGCGATGCGG
droBip1	scf7180000395874:40395-40520 -		G----------GGGAGTGCCTGGTATTATGGCAGCGAGTTTCCGGGATCTCGTA----------|----------GTGTATG--------AAGT---TTTATAAA-TACAATTCGA--------AAACTCAGAAACTTTCTGGCTTGAAGTACATTC-ATCAACGGCCGAGTA-|--------|----------|-----|-------|----------ATATA
droKik1	scf7180000302517:1183445-1183567 +		T----------GGTATAGCCGCAGAAAGTTTCCCAG-TTTCGTA----------|----------ATGTATG--------GTTA---TATTTGAAA-TACAGTACGA--------CAGATCAGAAATTTTCGGGAGTTAGTACCGTA-AACAACCAAAAATGGA-GCAAGGAG----------CA---|-------|----------|----------A
droFic1	scf7180000454073:1733616-1733722 +		T----------CGGTATTATCGCAGCAAGTTTCCGGGACTTCGTA----------|----------CTGTATG--------AAGA---ATTCTATA-TACAATACGA--------AACCTCAGAAATTTATTGCAATGAACCACGTTT-AAGTAATTGAT------|--------|----------|-----|-------|----------
droEle1	scf7180000490751:1118514-1118622 +		T----------TGGTATTATCGCAGCAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------AGAA---ATTCTATA-TACAATACGA--------AACCTTAGAAATTTTCTGAAGTTAGTACCATA-GAGTACCATAA----|--------|----------|-----|-------|----------
droRho1	scf7180000761121:190394-190496 -		T----------TGGTATTATCGCAGCAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------AGAA---ATTCTATA-TACAATACGA--------AACCTTAGAAATTTTCTGGAGTTATCTACGATT-AAGTAC----------|--------|----------|-----|-------|----------
droBia1	scf7180000302069:1151364-1151463 -		T----------TGGTATTATCGCAACACAAGTTTCCGGGATTTTGTA----------|----------TTGTATG--------ACTA---GATTCTATA-TACAATACGA--------AACCTCAGAAATTTTCTGGAGTTAGTACCATA-AA----------|--------|----------|-----|-------|----------
droTak1	scf7180000415169:845124-845246 -		T----------TGGTATTATCGCAACACAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------CTGA---ATTCTATA-TACAATACGA--------AAGCTCAGAAATTTTCTGGAGTTAGTACCATT-AAGTACTTACTTACGAA-GGATCGAT----------T----|-------|----------|----------A
droEug1	scf7180000409230:879979-880090 -		T----------TGGTATTATCGCAATAAGTTCCTGGGATTCGCA----------|----------CTGTATT--------ACGA---TTTTTACA-TACAATACGA--------AAGCTCAGAAACTAACTGGAATTAAGTACCGTA-AAGTACGGATCAGA---|--------|----------|-----|-------|----------A
dm3	chrX:19452595-19452757 +	dme-mir-4966-2	T----------TGGTATTATGGCAAAAGTTTCCAGGACATTGACAACCTATATATGTATGTACTTGTCGGCACTGGAGT--------AC---------TAAA-TATATTGCACATGTTCATGCATGTTCAACATATTTAGGAGCTCAAGTACCGAA-AA----------|--------|---ATGAACAACTAAAA-------GCGG---AGAATACGAAAGTG-C
~~droSim2~~	x:18341756-18341796 +		T----------TGGTATTATGGCAACAAGTTTCCAGGACATCGAG----------|----------CTGTGT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------
droSec2	scaffold_8:1734626-1734666 +		T----------TGGTATTATGGCAACAAGTTTCCAGGACATCGAG----------|----------CTGTGT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------
droYak3	X:11886139-11886241 -	dya_51	T----------TGGTATTATGGCAACAAGTTTCCGGGACTTCGTA----------|----------CTGTATG--------AGAG---ACTATATA-TACAATACGA--------AGCCTCTGAAATTTTCTGCGCTCAAGTACCAAA-AAGTAC----------|--------|----------|-----|-------|----------
droEre2	scaffold_4690:9688639-9688679 +		T----------TGGTATTAAGGCAACAAGTTTCAGGGACTTCGCA----------|----------CTGTAT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------

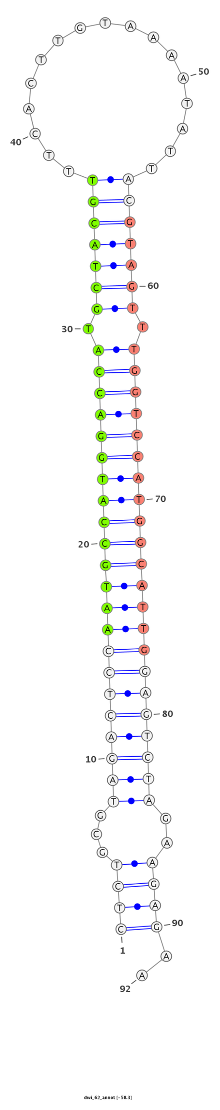
Generated: 09/08/2015 at 07:54 PM

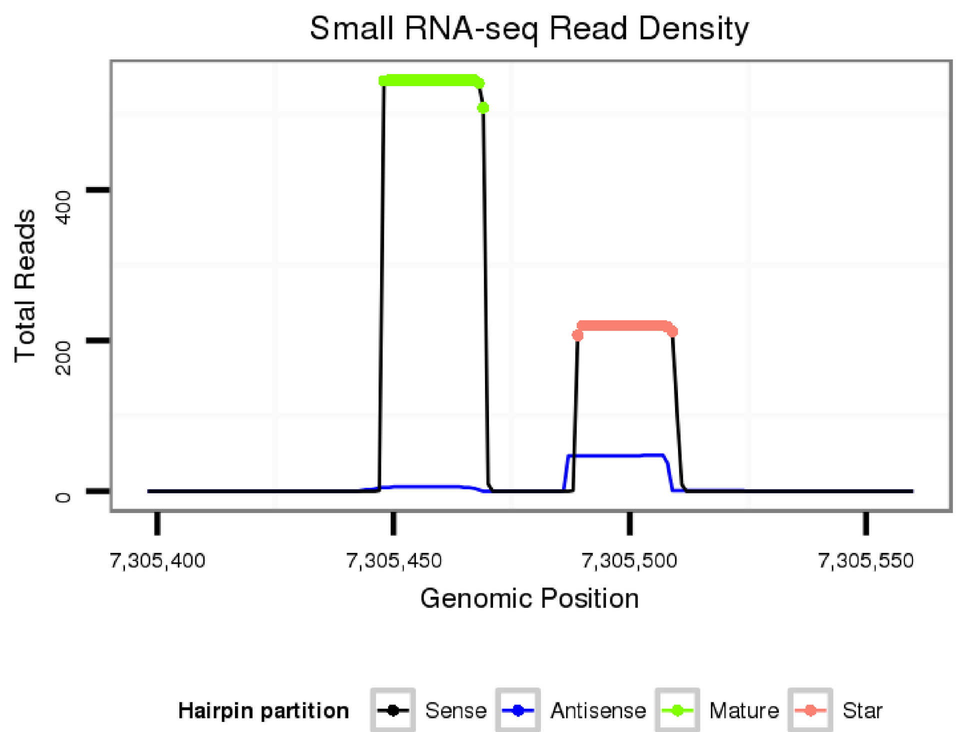
	PASS/FAIL		
crit.star	1	1	1
crit.loop	0	0	0
crit.mor	0	0	0
crit.half	0	0	0
crit.total	1	1	1
crit.pairing	1	1	1
crit.top3	1	1	1
crit.tptop3	1	1	1
crit.uri	0	0	0
crit.back	1	1	1
rescue.total	0	0	0
rescue.dominant	0	0	0
rescue.known	1	1	1
rescue.confident	5	5	6
rescue.candidate	0	0	0

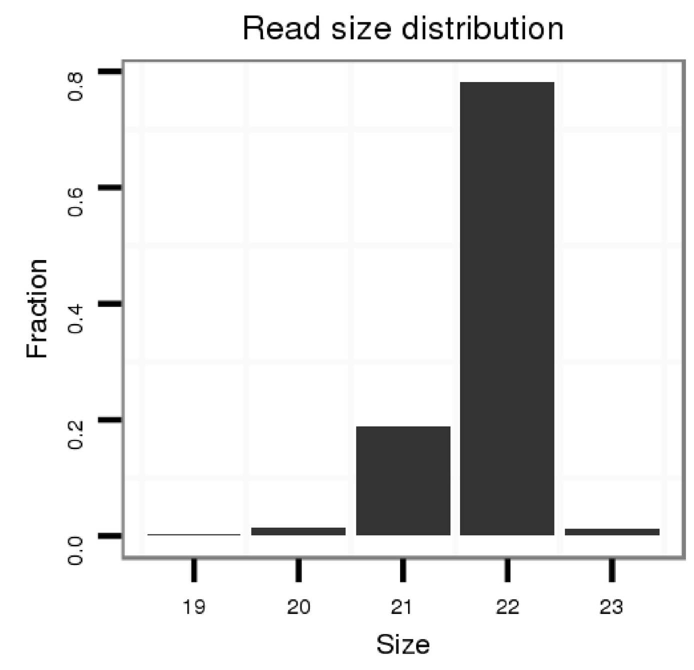
ID: dwi_62	Coordinate: scf2_1100000004902:7305448-7305510 +	Confidence: confident	Class: Canonical miRNA	Genomic Locale: intergenic	[View on UCSC Genome Browser {Cornell Mirror}]

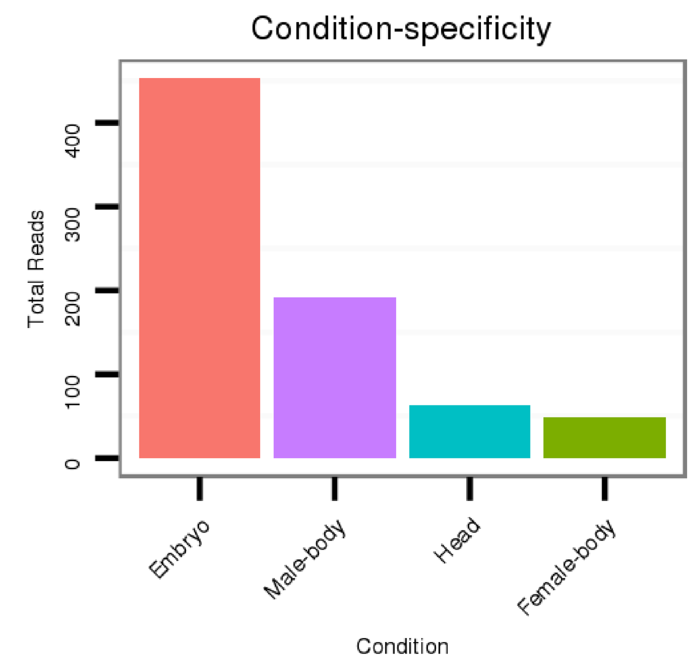
Legend: mature star mismatch in alignment mismatch in read

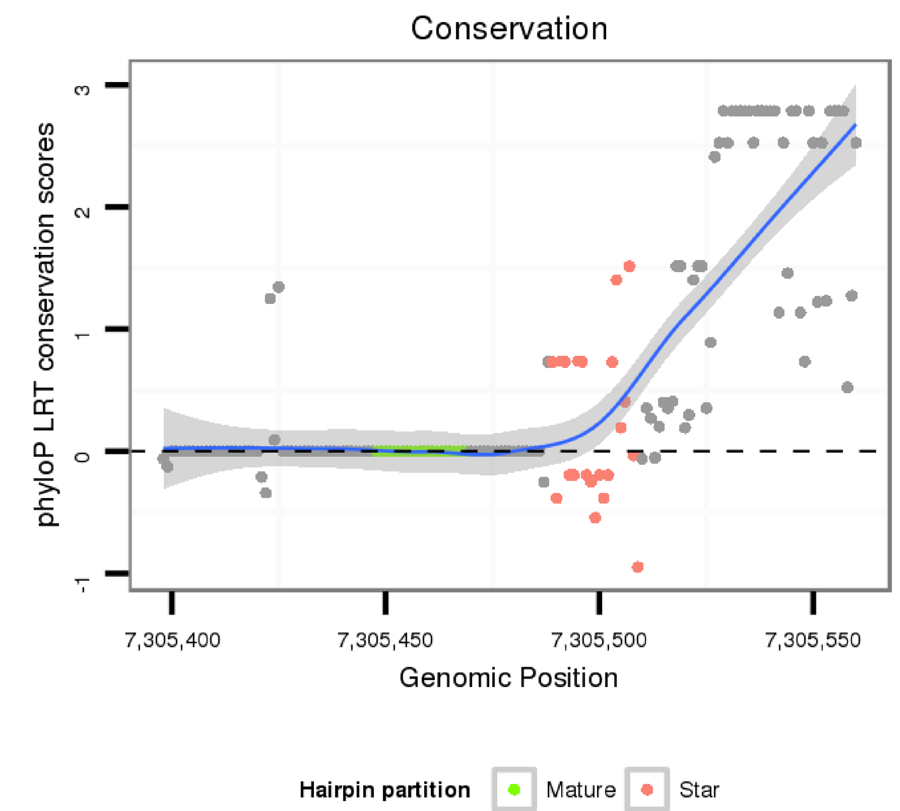
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AACCACTTTTTGGTCGCACTAGCTAGCTAGCTAGTCTCTGCGTAGACTCCAATGCCATGGACCATGCTACGTTTCACTTGTAAAATATTACGTAGTTTGGTCCATGGCATTGGAGTCTAGAAGAGAATGCCACTTAATCTTAATACATTTTACCGCTTAAGCC **********************************((((...((((((((((((((((((((((.(((((((.................))))))).))))))))))))))))))))))..))))..*************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	V117 male body	V119 head	M045 female body	M020 head
....AATGCCATGGACCATGCTACGT...	22	0	1	498.00	498	324	121	36	17	0
....GTAGTTTGGTCCATGGCATTG...	21	0	1	105.00	105	50	45	2	5	3
....GTAGTTTGGTCCATGGCATTGG..	22	0	1	92.00	92	65	9	8	10	0
....AATGCCATGGACCATGCTACG..	21	0	1	33.00	33	5	13	3	10	2
....AATGCCATGGACCATGCTACGTT..	23	0	1	10.00	10	7	1	0	2	0
....TAGTTTGGTCCATGGCATTGGA...	22	0	1	8.00	8	6	0	1	1	0
....GTAGTTTGGTCCATGGCATT..	20	0	1	6.00	6	0	0	0	2	4
....TAGTTTGGTCCATGGCATTGG..	21	0	1	3.00	3	0	0	1	2	0
....GTAGTTTGGTCCATGGCATTGC..	22	1	1	3.00	3	3	0	0	0	0
....AATGCCATGGACCATGCTACGC...	22	1	1	3.00	3	3	0	0	0	0
....AATGCCATGGACCATGCTAC...	20	0	1	3.00	3	1	2	0	0	0
....GTAGTTTGGTCCATGGCATTGGT...	23	1	1	2.00	2	1	1	0	0	0
....TAGTTTGGTCCATGGCATTG...	20	0	1	2.00	2	0	0	0	1	1
....GTAGTTTGGTCCATGGCAT...	19	0	1	2.00	2	0	0	0	0	2
....CGTAGTTTGGTCCATGGCATTG...	22	0	1	1.00	1	0	0	0	0	1
....GTAGTTTGGTCCATGGCATTT...	21	1	1	1.00	1	0	0	0	1	0
....TAGTTTGGTCCATGGCATTGC..	21	1	1	1.00	1	0	0	1	0	0
....GTAGTTTGGTCCATGGCATTGGA...	23	0	1	1.00	1	1	0	0	0	0
....ATGCCATGGACCATGCTACGT...	21	0	1	1.00	1	1	0	0	0	0
....CAATGCCATGGACCATGCTAC...	21	0	1	1.00	1	1	0	0	0	0
....AATGCCATGGACCATGCTACGTC..	23	1	1	1.00	1	0	0	1	0	0
....AATGCCATGGACCATGCTACGTA..	23	1	1	1.00	1	1	0	0	0	0
....GTAGTTTGGTCCATGGCATTGT..	22	1	1	1.00	1	0	0	0	0	1

Anti-sense strand reads

TTGGTGAAAAACCAGCGTGATCGATCGATCGATCAGAGACGCATCTGAGGTTACGGTACCTGGTACGATGCAAAGTGAACATTTTATAATGCATCAAACCAGGTACCGTAACCTCAGATCTTCTCTTACGGTGAATTAGAATTATGTAAAATGGCGAATTCGG **********************************((((...((((((((((((((((((((((.(((((((.................))))))).))))))))))))))))))))))..))))..*************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V119 head	M020 head	M045 female body	V118 embryo
....TGCATCAAACCAGGTACCGTAA..	22	0	1	36.00	36	31	3	1	1
....TGCATCAAACCAGGTACCGTA...	21	0	1	10.00	10	10	0	0	0
....GTTACGGTACCTGGTACGATGC..	22	0	1	2.00	2	0	2	0	0
....TGGTTACGGTACCTGGTACGAT..	22	1	1	1.00	1	1	0	0	0
....ACGGTACCTGGTACGATG...	18	0	1	1.00	1	0	1	0	0
....TGAGGTTACGGTACCTGGTACG..	22	0	1	1.00	1	1	0	0	0
....GGTTACGGTACCTGGTACGATG...	22	0	1	1.00	1	1	0	0	0
....ATGCATCAAACCAGGTACCGTA...	22	0	1	1.00	1	0	1	0	0
....GAGGTTACGGTACCTGGTACGAT..	23	0	1	1.00	1	1	0	0	0
....CCGTAACCTCAGATCTTCTCTT....................................	22	0	1	1.00	1	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004902:7305398-7305560 +	dwi_62	AACCACTTTTTGGTCGCACTAGCTAGCTAGCTAGTCTCTGCGTAGACTCCAATGCCATGGACCATGCTACGTTTCACTTGTAAAATATTACGTAGTTTGGTCCATG------GCATTGGAGTCTAGAAGAGAAT---GCCACTTAATCTTAATACATTTTACCGCTTA-AGCC
droVir3	scaffold_12855:6321406-6321444 +		GA---------------------AT--GCCACTTAATCTTAATACATTTTACAGTTTA-ACCC
droMoj3	scaffold_6540:6667618-6667656 +		GA---------------------AT--GCCACTTAATCTTAATACATTTTACAGTTTA-ACCC
droGri2	scaffold_14906:7769569-7769607 -		GA---------------------AT--GCCACTTAATCTTAATACATTTTACAGTTTA-ACCC
dp5	2:26813808-26813849 +		GG---------------------G-GGT---GCCACTTAATCTTAATGCATTCCACCGCTTAAATCC
droPer2	scaffold_6:2120586-2120627 +		GG---------------------G-GGT---GCCACTTAATCTTAATGCATTCCACCGCTTAAATCC
droAna3	scaffold_13340:3184506-3184595 +		AA---------------------ACGGT---TCGGAGCCTGAAGTCCGGAGTCTGGATCTGGTAGAGAAACCGAACCTGGCCACTTAATCTTAATGCTTTCTACCGCTTA-ACCC
droBip1	scf7180000396712:1174012-1174044 -		---CACTTAATCTTAATGCTTTCCACCGCTTA-ACCC
droKik1	scf7180000302706:192215-192249 +		G---CCACTTAATCTTAATGCATTCTACCGCTTA-ACCC
droFic1	scf7180000454063:218845-218906 -		TG--GGATCTGGGCCAGAAACAGAACCCGGCCACTTAATCTTAATGCATTCTACCGCTTA-ACCC
droEle1	scf7180000491104:917524-917556 -		---CACTTAATCTTAATGCATTCTACCGCTTA-ACCC
droRho1	scf7180000779821:25046-25080 -		G---CCACTTAATCTTAATGCATTCTACCGCTTA-ACTC
droBia1	scf7180000302155:1182993-1183053 -		G---GGATCCGGGCCAGAAACAGAACCAGGCCACTTAATCTTAATGCATTCTACCGCTTA-ACCC
droTak1	scf7180000415875:608997-609031 +		G---CCACTTAATCTTAATGCATTCTACCGCTTA-ACCC
droEug1	scf7180000409760:315887-315948 +		TG--GGATCTGGGCCAGAAACAGAACCCGGCCACTTAATCTTAATGCATTCTACCGCTTA-ACCC
dm3	chr3R:3413439-3413509 +		GC---------------------TGGGT--GCCTGGGTTGTGGCCAGAAACAGAACTCGACCACTTAATCTTAATGCATTCTACCGCTTA-ACCC
droSim2	3r:3327921-3327991 +		GC---------------------TGGGT--GCCTGGGTTGCGGCCAGAAACAGAACCCGACCACTTAATCTTAATGCATTCTACCGCTTA-ACCC
droSec2	scaffold_6:3505016-3505086 +		GC---------------------TGGGT--GCCTGGGTTGCGGCCAGAAACAGAACCCGACCACTTAATCTTAATGCATTCTACCGCTTA-ACCC
droYak3	v2_chr3R_random_116:1769-1803 +		G---CCACTTAATCTTAATGCATTCTACCGCTTA-ACCC
droEre2	scaffold_4770:3673377-3673411 +		G---CCACTTAATCTTAATGCATTCTACCGCTTA-ACCC

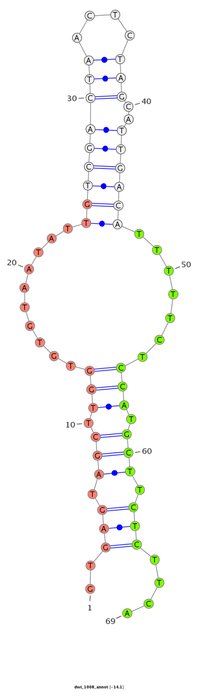
Generated: 09/08/2015 at 07:39 PM

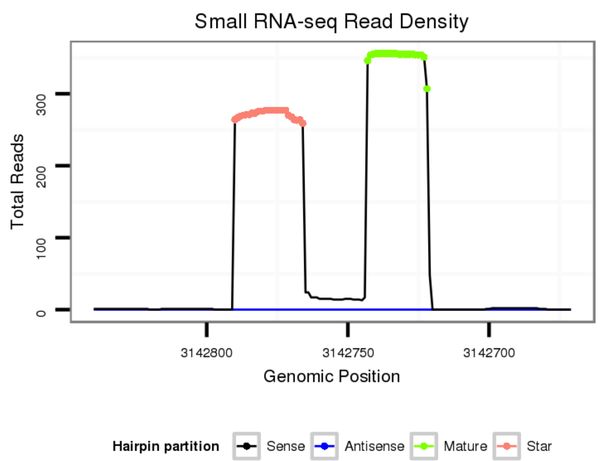
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

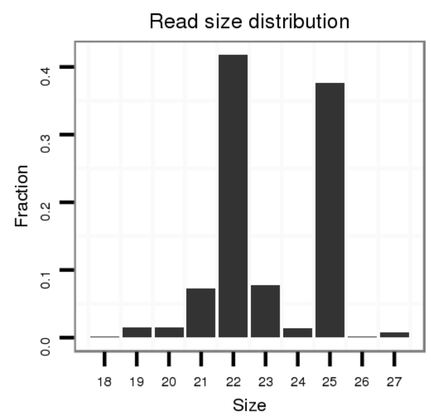
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_1008	**scf2_1100000004514:3142721-3142790 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

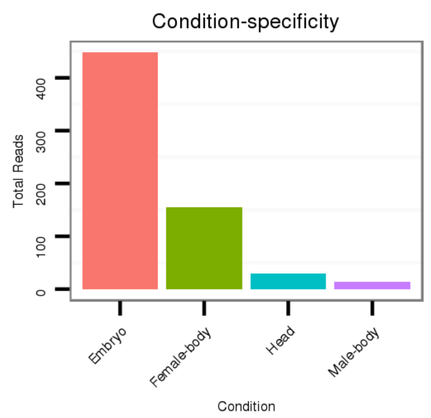
Legend: mature star mismatch in alignment mismatch in read

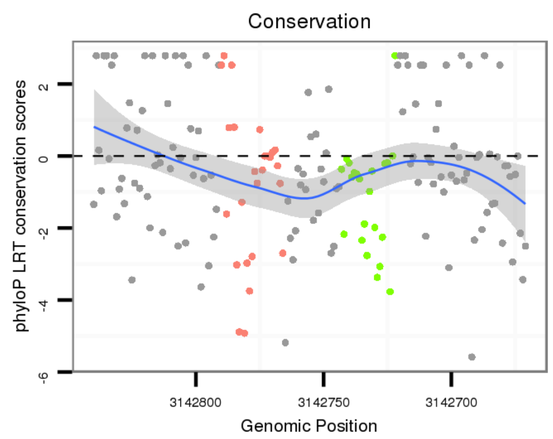
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK15642-in]; CDS [Dwil\GK15642-cds]; CDS [Dwil\GK15642-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TAATTATGAAGCAATCAAAGAACTGAAATACATTCAGCAAATATTCAATGGTGAGTAGCTTGGTGTGTAATATTGTCGACTAACTCTAGCATTGACATTTTTCTCCATGCTTCTCTTCAGAAACCTTGCGCAAATGGGCAATTCTTCCCATTTTGATTCGTGTAGCCGAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	M045 female body	V119 head	V117 male body	M020 head
**********..(((.(((.(((.........(((((((((....)))).)))))).....)))..))).))).....**********										
.....TTTTTCTCCATGCTTCTCTTCA.....	22	0	1	253.00	253	171	66	10	1	5
.....GTGAGTAGCTTGGTGTGTAATATTG.....	25	0	1	241.00	241	196	34	3	8	0
.....TTTTTCTCCATGCTTCTCTTCAG.....	23	0	1	46.00	46	32	12	2	0	0
.....TTTTTCTCCATGCTTCTCTTC.....	21	0	1	38.00	38	12	21	3	2	0
.....TCGACTAACTCTAGCATTGACA.....	22	0	1	10.00	10	8	1	0	0	1
.....GTGAGTAGCTTGGTGTGTA.....	19	0	1	7.00	7	5	1	0	1	0
.....GTGAGTAGCTTGGTGTGTAATATT.....	24	0	1	5.00	5	2	1	2	0	0
.....TTTTCTCCATGCTTCTCTTCA.....	21	0	1	5.00	5	1	4	0	0	0
.....ATTTTTCTCCATGCTTCTCTTC.....	22	0	1	4.00	4	3	1	0	0	0
.....GTGAGTAGCTTGGTGTGTAAT.....	21	0	1	4.00	4	3	0	0	1	0
.....GTGAGTAGCTTGGTGTGTAATATTGA.....	26	1	1	3.00	3	1	1	0	1	0
.....GTGAGTAGCTTGGTGTGTAATATTGTC.....	27	0	1	3.00	3	1	1	0	1	0
.....TTTTTCTCCATGCTTCTCTT.....	20	0	1	3.00	3	0	2	1	0	0
.....TTTTTCTCCATGCTTCTCTTCTT.....	22	1	2	3.00	6	3	3	0	0	0
.....GAGTAGCTTGGTGTGTAATATTG.....	23	0	1	2.00	2	2	0	0	0	0
.....GTGAGTAGCTTGGTGTGTAATATTTT.....	25	1	1	2.00	2	2	0	0	0	0
.....TGAGTAGCTTGGTGTGTAATATTG.....	24	0	1	2.00	2	0	2	0	0	0
.....TTTTTCTCCATGCTTCTCTTCAGT.....	24	1	1	2.00	2	0	2	0	0	0
.....TTTTCTCCATGCTTCTCTTC.....	20	0	1	2.00	2	0	2	0	0	0
.....GTGAGTAGCTTGGTGTGTAA.....	20	0	1	2.00	2	2	0	0	0	0
.....TTTTTCTCCATGCTTCTCTTCAA.....	23	1	1	1.00	1	1	0	0	0	0
.....CTTGGTGTGTAATATTGTC.....	19	0	1	1.00	1	1	0	0	0	0
.....TTTTTCTCCATGCTTCTCTTCC.....	22	1	1	1.00	1	0	0	1	0	0
.....TTTTTCTCCATGCTTCTCTTCAG.....	22	0	1	1.00	1	1	0	0	0	0
.....CTTGGTGTGTAATATTGTCGACTAACT.....	27	0	1	1.00	1	1	0	0	0	0
.....GACTAACTCTAGCATTGACA.....	20	0	1	1.00	1	0	1	0	0	0
.....AATTCTTCCCATTTTGATT.....	19	0	1	1.00	1	1	0	0	0	0
.....GTGAGTAGCTTGGTGTGTAATATCCC.....	26	3	1	1.00	1	0	0	1	0	0
.....TGAGTAGCTTGGTGTGTAATATTGTC.....	26	0	1	1.00	1	0	1	0	0	0
.....AGCTTGGTGTGTAATATTGTCGACT.....	25	0	1	1.00	1	0	0	0	0	1
.....TTTTTCTCCATGCTTCTCTTCG.....	22	1	1	1.00	1	1	0	0	0	0
.....AGCTTGGTGTGTAATATTGTCGAC.....	24	0	1	1.00	1	0	1	0	0	0
.....TTTTTCTCCATGCTTCTCTTT.....	21	1	1	1.00	1	0	1	0	0	0
TAATTATGAAGCAATCAAAG.....	20	0	1	1.00	1	1	0	0	0	0
.....AACTCTAGCATTGACATTTTTCTCCAT.....	27	0	1	1.00	1	0	1	0	0	0
.....GTAGCTTGGTGTGTAATATTGTC.....	23	0	1	1.00	1	1	0	0	0	0
.....TGTCGACTAACTCTAGCAT.....	19	0	1	1.00	1	1	0	0	0	0
.....TTTTCTCCATGCTTCTCTTCAGTT.....	24	2	1	1.00	1	0	1	0	0	0
.....GAAATACATTCAGCAAATA.....	19	0	1	1.00	1	0	1	0	0	0
.....TTCTCCATGCTTCTCTTCAG.....	20	0	1	1.00	1	0	1	0	0	0
.....TTGGTGTGTAATATTGTC.....	18	0	1	1.00	1	1	0	0	0	0
.....TTCTTCCCATTTTGATTCGT.....	20	0	1	1.00	1	1	0	0	0	0
.....GGTGTGTAATATTGTCGAC.....	19	0	1	1.00	1	0	1	0	0	0
.....CATTGACATTTTTCTCCATGCTTCT.....	25	0	1	1.00	1	1	0	0	0	0
.....AGTAGCTTGGTGTGTAATATTGTC.....	24	0	1	1.00	1	1	0	0	0	0
.....TGTCGACTAACTCTAGCATTGA.....	22	0	1	1.00	1	1	0	0	0	0
.....TTTTCTCCATGCTTCTCTTCAGT.....	23	1	1	1.00	1	0	0	0	1	0
.....GTGAGTAGCTTGGTGTGTAATA.....	22	0	1	1.00	1	0	1	0	0	0
.....TTTCTCCATGCTTCTCTTCA.....	20	0	1	1.00	1	1	0	0	0	0
.....GTGAGTAGCTTGGTGTGTAATAT.....	23	0	1	1.00	1	0	0	1	0	0
.....TTTTTCTCCATGCTTCTCTTTT.....	22	2	2	0.50	1	1	0	0	0	0

Anti-sense strand reads

ATTAATACTTCGTTAGTTTCTTGACTTTATGTAAGTCGTTTATAAGTTACCACTCATCGAACCACACATTATAACAGCTGATTGAGATCGTAACTGTAAAAAGAGGTACGAAGAGAAGTCTTTGGAACGCGTTTACCCGTTAAGAAGGGTAAAACTAAGCACATCGGCTT	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body
**********..(((.(((.(((.........(((((((((....)))).)))))).....)))..))).))).....**********						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004514:3142671-3142840 -	dwi_1008	TAATTATGAAGCAATCAAAGAACTGAAATACATTCAGCAAATATTCAATGGTGAGTAGCTTG------GTGTGTAATAT---TGTCGACT----------AACTCTAGCATTGA----------CATTT---------TTC------------TCCATGCT-----------TCTCTTCAGAAACCTTGCGCAAATGGGCAATTCTTCCCATTTTGATTCGTGTAGCCGAA
droVir3	scaffold_12822:3648577-3648729 +		TAACTATGACGCTATACAGACATGAAGTATTTGGAACTGTGCATTATGGGTAGGTAGAAGAATATTTTCCT----GAAATATCGT---------------------------C--ATAA----------------------------------AAATATTC-----------GTTGTCAGAGACCACTCGCAAATTATCGCGCGCTACCGATACTCAATCGTATGTCCAAC
droMoj3	scaffold_6496:17473448-17473616 +		TACCTATGAGTGTTATCAAAGATATGCAGTATTTGAACCAAGTCATTATCAGGTAAGCAGGAGA------GT---------C---AAATTATAT----------------------A-----C---AAAACT-T-----TGT---TATATATAATAAATTGTTTTTTTTT----------TTTTTCAGAGACCTTGCGACTATACAGGGTTCTTCGAATTCTCAATCGGAGGCCTTA
droGri2	scaffold_15245:17505776-17505943 +		CACCTATGAAGCGGTGCAGATCTAAAATTGTTGGAGCTGTGTATTATTGGGTAAGTTTCTTT------ACG----GTAACGC-TGGCCCA----------------------AGATCAAGCA---C-------CAATTCAT---------AAT----------TTTATCTT----------TTTTAACAGAAAGTATTCGAAAATATCTGCACTCGCTTTCTGAATCGCGAATGCACT
dp5	3:13267825-13267987 +		CACCTAGAGCGTATTAAAGAAATGAAATATCTGGAGCAGGTGGTAATGGGTGAGTACTCGT------GA---------G-GATTACATTTTGTTTCT------------------------------------TTTTCTCTAATATTTTATAATT----------CCTTCAGAAAGTCTTCGGAAGTACCGGTTCTTGCTCATCTAACGCGAAAGAGACAG
droPer2	scaffold_2:8357199-8357361 -		CACCTAGGAGCGTATCAAAGAAATGAAATATCTGGAGCAGGTGGTAATGGTGAGTATTCGT------GA---------G-GATTACATTTTGTTTCT------------------------------------TTTTCTCTAATATTTTATAATT----------CCTTTCAGAAAGTCTTCGGAAGTACCGTGCTCTTGCTCATTTAACGCGAAAGAGCGG
droAna3	scaffold_13266:1550971-1551126 +		CAGTTACGATGCCATAGCCGAAATGACATACGTGGAACAAGTCATAGCTGGTGAGTAGATCT------A----------AACACCACAT----------------------G-----AAAACT-----AAAT---CTAAT----------TCATTAAT----------TCCACATAGAAACCCTTCGAAAGCATCGTATTCTTCCCCACGTGACAAGCGGAAGCCAAT
droBip1	scf7180000396759:1609482-1609647 +		GACATATGAAAGCATGACAGAACTAGTCTACGTGGATCAGATAATAGCTGGTAAGTGACATC------A----------TTGT----AATCCA----------------------AATACTTAGACATTTTTGAGCTCAGGATAATTTAATTTTCAGAAACCCTTCGGCTTTATAGAGTCGTTCCTGTCCTGAATCGTGAATGCGTT
droKik1	scf7180000302277:316312-316471 +		CACGTAGGATGGCTTGGCTGAAATGACCTACGTGGAGCAGGTGGTGGCGGGTGAGTAAAACA------T----------TGCAGCTA----------TCCATATATCA----------TTGACT--------CTA----------ACTGAGTG----------TCTTTTGCAGAAACCCTGCGTAAGCATCGCATTATTGCCCAACTTCTGCGTGAAACCAAT
droFic1	scf7180000453809:467427-467583 +		CACCTACGAAGGTATCAAGGAGATGAAATATCTGGAGCAGGTCGTCATGGGTAAGTACTTAC------T----------TTA----TTGTCT---A-----T-----TGATTAGTTATT--AAT----------TCGTTTTC----------AACCCTCAGAAACCCTTCGCAAATATCGAGTTCTTGCGCATCTAACGAGAATAAGTGAC
droEle1	scf7180000491214:3605698-3605859 +		CACCTACGAGGGAATCAAGGAAATGAAGTATCTGGAGCAGGTCGTCATGGGTGAGTTTTCTA------AAGTT-------T---AACT-----GTGTTCTT----------AAG---TAA----------AAATTG--------ACT----------ATTGCTTT----------TGCTTACAGAAACCCTTCGAAGTATCCGTGCTGGCACATCTTACGAGAATGACCGAG
droRho1	scf7180000777223:19733-19894 -		TACCTATGAAAACATAAAGGAACTGGCTTACGTCAATCAAGTGATTTCTGGTAAGTATAGGA------GAA----ATGGTGC-AGTTTCG----------------------A-------AGTTTAT----------TAACTA--------CTT----------GTTCTATC----------GCCTCACAGAAAGACTTCGCATGTACAGTGTGGTTCGTATTTTAATCGCGAATGCCTG
droBia1	scf7180000302075:1623672-1623826 -		TACCTAGGAATGCATTCAAGATATTAAGTACCTGGACCAGGTTATAAATGGTAAGTGTAGCA------T----------TCAATACAT----------------------A-----AACACC-CAACTG--------ATT----------TGAAACC----------TCTTTACAGAAACCCTACGCCATTATACCATTGTACCCAATGTGGATCGAGTGGCCGCC
droTak1	scf7180000415260:152753-152908 +		AACTTAGGAAAGTATGAAGGAATTGGTATATTTAGACCAGGTAATAGCAGGTGAGTAAATGG------A----------GAA----TTTTCCATTAATGC----------TAAATA--------ACC----------TTATGATT----------CTTTTCAAGAAACCCTTCGCCTGTACACGCTTCTTCGTGTCTTGAATCGCGAATGCCTA
droEug1	scf7180000409770:780058-780213 +		TACCTATGAGTGCACGCAGGATCTTAAGTACCTGAACCAAGTATAAAGTGGTAAGTAAAGTT------C----------TGTT----AACTCAACTCATCC----------CAACTA--------ATT----------TACAAAC----------TTTTTTCAGAAACCTTACGCGCTTACACCATTATTCCCAATGTGGATCGAGTGGCCGCC
dm3	chr3R:23305481-23305639 +		TACCTACGAGTGCATCAAGGATCTAAAGTACCTGGACCAAGTTATAAATGGTGAGCGGTGTG------T----------TTT-AA----------AATTCCAGCGATCC----------CAAAGG--------ATC----------ATAAAATG----------TCCTTTCAGAAACTCTACGGCAATTATACCATTGTACGGAATGTGGATCGAGTGGCCGCC
droSim2	3r:22738306-22738462 +		TACATAGGAGTGCATCAAGGATCTAAAGTACCTTGACCAAGTTATAAATGGTAAGTCGTATG------T----------TTAA----------AATTCAAGCGATCC----------CAAAAG--------ATC----------ATTAAATG----------TCTTTTAGAAACTCTACGGCAATTATACCATTGTACGGATGTGGATCGAGTGGCCGCC
droSec2	scaffold_13:2048889-2049047 +		TACCTACGAGTGCATCAAGGATCTAAAGTACCTGGACCAAGTTATAAATGGTGAGTTGTGTG------T----------TTATTA----------AATTCAAGCGATCC----------CAAAAG--------ATC----------ATAAAATG----------TCGTTTCAGAAACCCTACGGCAATTATACCATAGTACCGAATGTGGATCGAGTGGCCGCC
droYak3	2R:10700140-10700299 +		CACCTACGAGGGAATCAAAGAAATGAAATACCTGGAGCAGGTGTGTAGTTAATT------A----------ATCGACT-----GTTTCGTTTTTTAGATTTATTGGATGC----------CT---------GCGTTTTAGAAACCCTACGAAAGTATCGAGTAGTGGCTCATCTTACAAGAATGAGTGAG
droEre2	scaffold_4845:15078063-15078225 -		TACTTAGGAGCGAATCAACAGATGAAGTACCTGGAACAGGTCGTCATGGGTGAGTGAAATC------A----------GCA-----------------------------------AATATCACAAATCCATGCCTAATTATC--ATT----------CTTATTTT----------GTCCGACAGAAACCCTTCGCAATATCAGTTCTGGCGCATCTTACGGTATGACCCAG

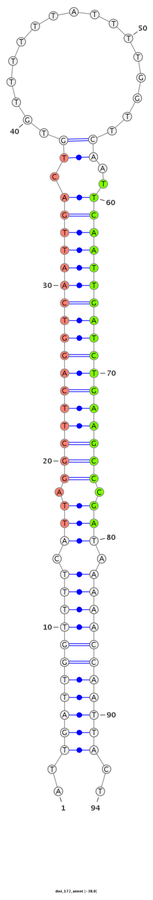
Generated: 09/08/2015 at 10:36 PM

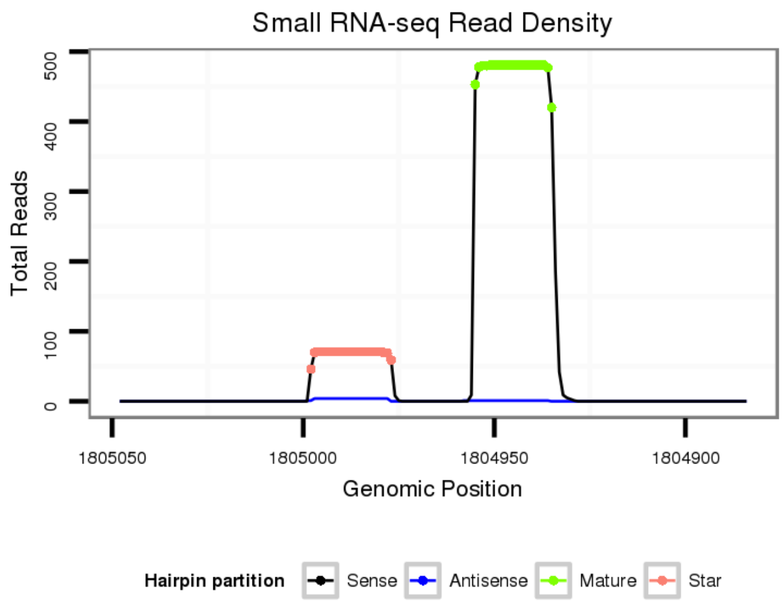
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	0
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

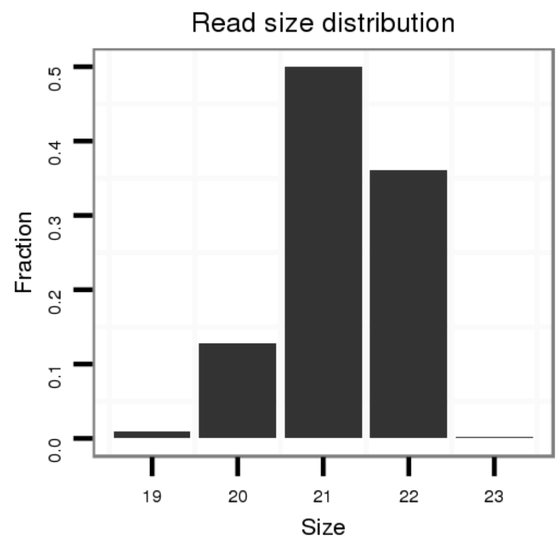
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_172	**scf2_1100000004577:1804934-1804998 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

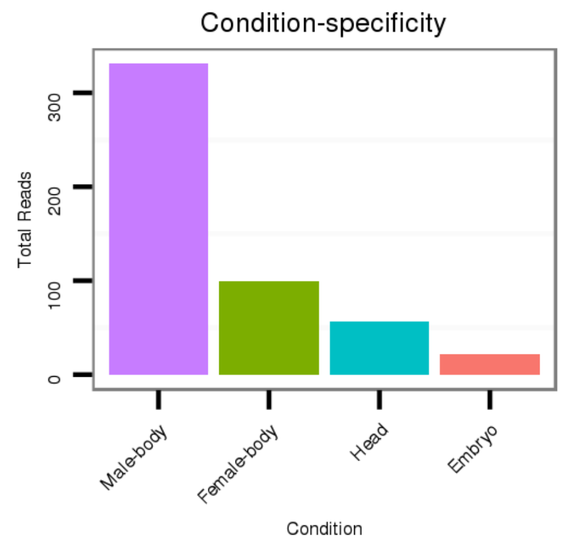
Legend: mature star **mismatch in alignment** mismatch in read

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

ATTAATGTAACATACATATATCTTAAAAATTATAAATTGATTGGTTTTCATTAGGCTTCAGGTCAATTGACTGTGTTTTTTATTTTGGTTCAATTCAATTGATCTGAAGCCCGATAAAAACCAATTACTACAACACAAAGGTCGCTTAAACAATTACAATAAATT	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	M045 female body	M020 head	V118 embryo	V119 head
**********..(((((((((((.(((.(((((((((((((((((.((.....)).))))))))))))))))).))).))))))))))..**********										
.....TTCAATTGATCTGAAGCCCGA.....	21	0	1	224.00	224	193	23	6	2	0
.....TTCAATTGATCTGAAGCCCGAT.....	22	0	1	134.00	134	96	33	0	5	0
.....TTCAATTGATCTGAAGCCCG.....	20	0	1	55.00	55	31	3	21	0	0
.....TTAGGCTTCAGGTCAATTGACT.....	22	0	1	37.00	37	1	18	6	9	3
.....TTCAATTGATCTGAAGCCCGATA.....	23	0	1	21.00	21	17	4	0	0	0
.....TAGGCTTCAGGTCAATTGACT.....	21	0	1	13.00	13	1	12	0	0	0
.....TCAATTGATCTGAAGCCCGATA.....	22	0	1	12.00	12	7	3	1	1	0
.....TTCAATTGATCTGAAGCCCGATTT.....	23	1	1	9.00	9	9	0	0	0	0
.....TTCAATTGATCTGAAGCCCGAA.....	22	1	1	9.00	9	9	0	0	0	0
.....TTAGGCTTCAGGTCAATTGAC.....	21	0	1	8.00	8	0	3	5	0	0
.....TCAATTGATCTGAAGCCCGAT.....	21	0	1	8.00	8	4	1	0	3	0
.....TAGGCTTCAGGTCAATTGACTG.....	22	0	1	7.00	7	0	2	4	1	0
.....ATTCAATTGATCTGAAGCCCGA.....	22	0	1	6.00	6	4	0	2	0	0
.....TTCAATTGATCTGAAGCCCGATC.....	23	1	1	5.00	5	3	2	0	0	0
.....TCAATTGATCTGAAGCCCGA.....	20	0	1	4.00	4	1	1	0	2	0
.....TTCAATTGATCTGAAGCCC.....	19	0	1	3.00	3	0	0	3	0	0
.....TTAGGCTTCAGGTCAATTGACTT.....	23	1	1	3.00	3	0	0	3	0	0
.....TTCAATTGATCTGAAGCCCGATCC.....	24	2	1	3.00	3	2	1	0	0	0
.....TTAGGCTTCAGGTCAATTGACTA.....	23	1	1	3.00	3	0	0	2	1	0
.....TTCAATTGATCTGAAGCCCGT.....	21	1	1	2.00	2	2	0	0	0	0
.....CAATTGATCTGAAGCCCGAT.....	20	0	1	2.00	2	0	2	0	0	0
.....TTCAATTGATCTGAAGCCCGATAAAA.....	26	0	1	2.00	2	1	1	0	0	0
.....TTCAATTGATCTGAAGCCCGATG.....	23	1	1	2.00	2	2	0	0	0	0
.....TTCAATTGATCTGAAGCCCGATAAA.....	25	0	1	2.00	2	1	1	0	0	0
.....TTCAATTGATCTGAAGCCCGATCT.....	24	2	1	2.00	2	1	0	0	0	1
.....TAGGCTTCAGGTCAATTGAC.....	20	0	1	2.00	2	0	0	2	0	0
.....TTCAATTGATCTGAAGCCCGATAA.....	24	0	1	2.00	2	1	1	0	0	0
.....ATTCAATTGATCTGAAGCCCG.....	21	0	1	2.00	2	0	0	2	0	0
.....TTCAATTGATCTGAAGCCCGATATT.....	24	1	1	2.00	2	1	1	0	0	0
.....TTCAATTGATCTGAAGCCCGTA.....	22	2	1	1.00	1	1	0	0	0	0
.....TTAGGCTTCAGGTCAATTGACA.....	22	1	1	1.00	1	0	0	0	1	0
.....TTCAATTGATCTGAAGCCCT.....	20	1	1	1.00	1	1	0	0	0	0
.....ATTGATCTGAAGCCCGATAA.....	20	0	1	1.00	1	0	1	0	0	0
.....TAGGCTTCAGGTCAATTGA.....	19	0	1	1.00	1	0	0	0	0	1
.....AGGCTTCAGGTCAATTGACT.....	20	0	1	1.00	1	0	1	0	0	0
.....TTCAATTGATCTGAAGCCCGG.....	21	1	1	1.00	1	0	0	1	0	0
.....TCAATTGATCTGAAGCCCGATAA.....	23	0	1	1.00	1	0	0	1	0	0
.....ATTCAATTGATCTGAAGCCCGAAT.....	24	2	1	1.00	1	1	0	0	0	0
.....TAGGCTTCAGGTCAATTGACTGT.....	23	0	1	1.00	1	0	0	1	0	0
.....ATTCAATTGATCTGAAGCCC.....	20	0	1	1.00	1	0	0	1	0	0
.....TTCAATTGATCTGAAGCCCGATAAAAA.....	27	0	1	1.00	1	0	1	0	0	0
.....TTAGGCTTCAGGTCAATTG.....	19	0	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

TAATTACATTGTATGTATATAGAATTTTTAATATTTAACTAACCAAAAGTAATCCGAAGTCCAGTTAACTGACACAAAAAATAAAACCAAGTTAAGTTAACTAGACTTCGGGCTATTTTTGGTTAATGATGTTGTGTTTCCAGCGAATTTGTTAATGTTATTTAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	M045 female body	V117 male body	M020 head
**********..(((((((((((.(((.(((((((((((((((((.((.....)).))))))))))))))))).))).))))))))))..**********									
.....ATCCGAAGTCCAGTTAACTG.....	20	0	1	3.00	3	3	0	0	0
.....TAATCCGAAGTCCAGTTAACTG.....	22	0	1	1.00	1	0	1	0	0
.....GTTAAGTTAACTAGACTTCGGGC.....	23	0	1	1.00	1	1	0	0	0
.....TCCGAAGTCCAGTTAACTG.....	19	0	2	0.50	1	0	0	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004577:1804884-1805048 -	dwi_172	ATTAATGTAACATACATATATCTTAAAAATTATAAATTGATTGGTTTTCATTAGGCTTCAGGTCAATTGACTGTGTTTTTTATTTTGGTTCAATTCAATTGATCTGAAGCCCGATAAAAACCAATTACTACAACACAAAGGTCGCTTAAACAATTACAATAAATT

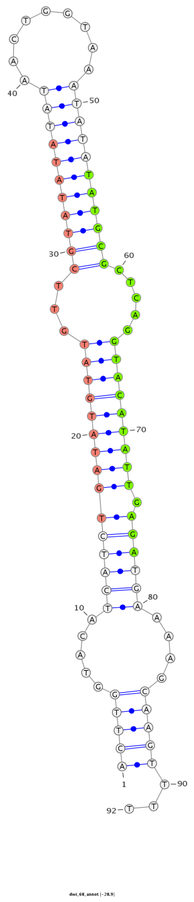
Generated: 09/08/2015 at 07:38 PM

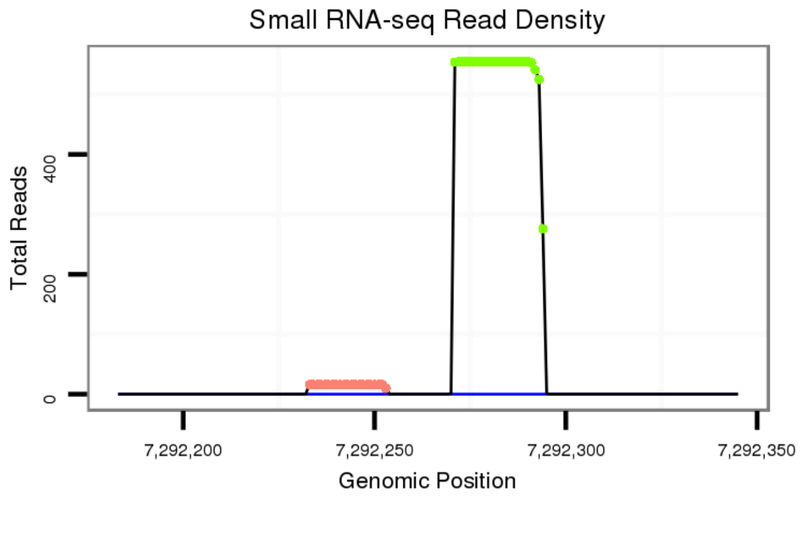
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

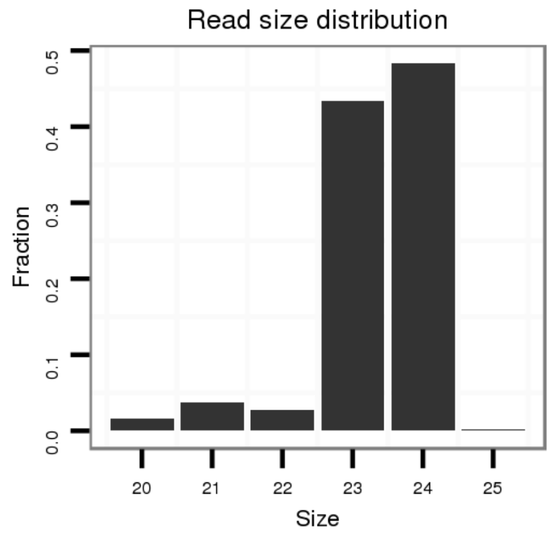
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_68	**scf2_1100000004902:7292233-7292295 +**	**confident**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

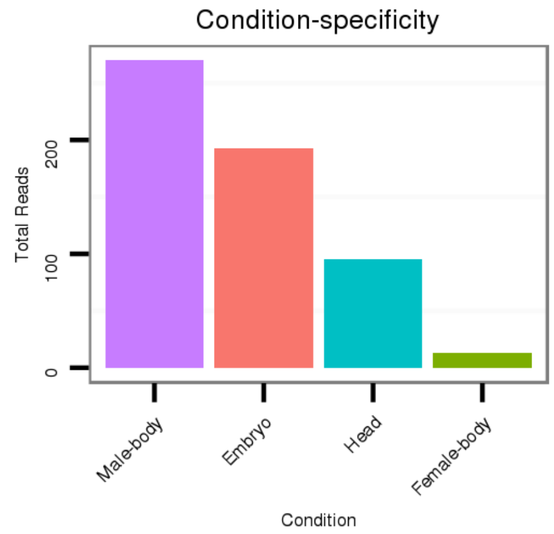
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK11063-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAGGGCTCTGTCGAGAGATGAGGCCAATGGCAAAAACTTGGTACATCATCTGATATGTATGTTCGTATATATATAACTGGTAAATATATATGCGCTCAGGTACATATTGAGATGAAAAGCAAGTTTTCTTCTGACTGTGGCAAAAGGCGTAAAAACTAAAAAC **********(((((.....(((((((((((((((...((((((((((.........))))))))))).....)))))))))..))))))....))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	V118 embryo	V119 head	M045 female body	M020 head
..........TATGCGCTCAGGTACATATTGAGA..........	24	0	1	275.00	275	155	107	8	5	0
..........TATGCGCTCAGGTACATATTGAG..........	23	0	1	248.00	248	88	74	80	2	4
..........TATGCGCTCAGGTACATATTGA..........	22	0	1	16.00	16	9	2	2	3	0
..........TATGCGCTCAGGTACATATTG..........	21	0	1	11.00	11	9	0	0	2	0
..........TGATATGTATGTTCGTATATA..........	21	0	1	10.00	10	3	7	0	0	0
..........TGATATGTATGTTCGTATAT..........	20	0	1	6.00	6	4	2	0	0	0
..........TATGCGCTCAGGTACATATTGAGAA.....	25	1	1	3.00	3	1	2	0	0	0
..........TATGCGCTCAGGTACATATT..........	20	0	1	2.00	2	1	0	1	0	0
..........TATGCGCTCAGGTACATATTGAC.......	23	1	1	1.00	1	1	0	0	0	0
..........ATGCGCTCAGGTACATATTG..........	20	0	1	1.00	1	0	0	0	1	0
..........ATATGCGCTCAGGTACATATTGAGAA.....	26	1	1	1.00	1	0	1	0	0	0
..........TATGCGCTCAGGTACATATA..........	20	1	1	1.00	1	1	0	0	0	0
..........TATGCGCTCAGGTACATATTGAGAT.....	25	0	1	1.00	1	1	0	0	0	0
..........TATGCGCTCAGGTACATATTGAGC......	24	1	1	1.00	1	0	0	1	0	0
..........ATATGCGCTCAGGTACATATTGAG......	24	0	1	1.00	1	0	1	0	0	0
..........TATGCGCTCAGGTACATATTGAGT......	24	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

TTCCCGAGACAGCTCTCTACTCCGGTTACCGTTTTTGAACCATGTAGTAGACTATACATACAAGCATATATATATTGACCATTTATATATACGCGAGTCCATGTATAACTCTACTTTTCGTTCAAAAGAAGACTGACACCGTTTTCCGCATTTTTGATTTTTG **********(((((.....(((((((((((((((...((((((((((.........))))))))))).....)))))))))..))))))....))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V119 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004902:7292183-7292345 +	dwi_68	AAGGGCTCTGTCGAGAGATGAGGCCAATGGCAAAAACTTGGTACATCATCTGATATGTATGTTCGTATATATATAACTGGTAAATATATATGCGCTCAGGTACATATTGAGATGAAAAGCAAGTTTTCTTCTGACTGTGGCAAAAGGCGTAAAAACTAAAAAC

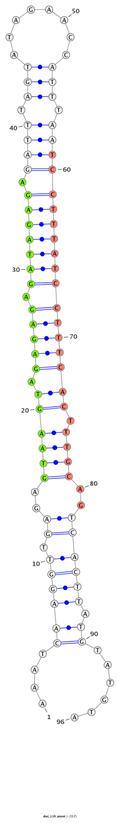
Generated: 09/08/2015 at 07:38 PM

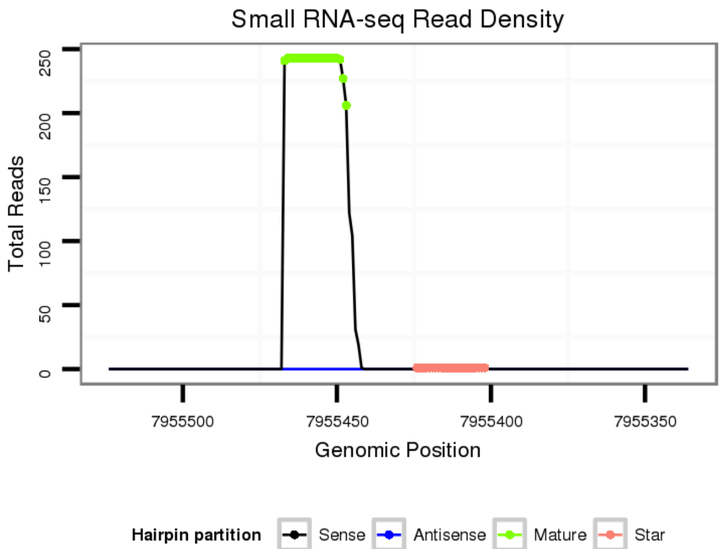
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

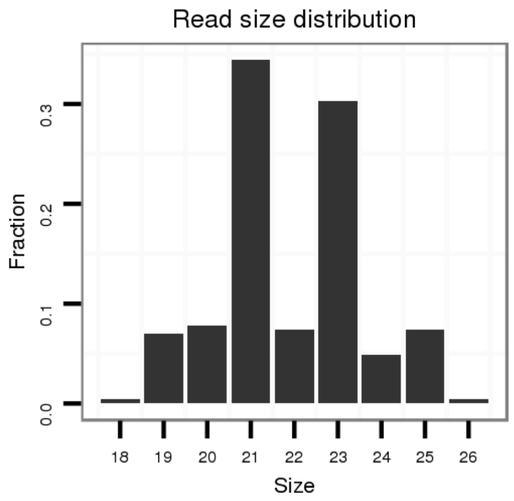
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_139	**scf2_1100000004909:7955386-7955474 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

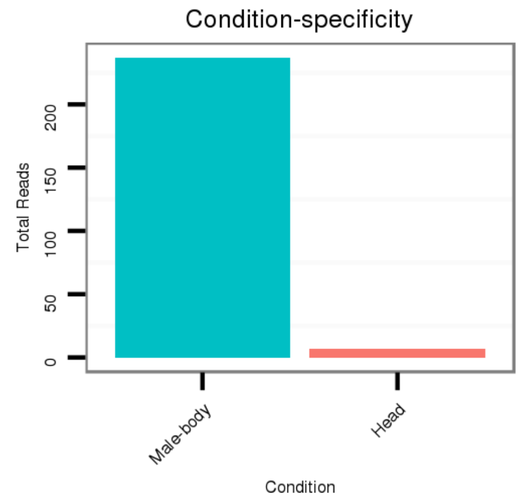
Legend: mature star **mismatch in alignment** mismatch in read

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

CACCATTCTCATAAAATTTCGTAGCAGCACAGCTTTAGAAGGAAATCAAGGTTGAGAGTAAGTAGAGAGAGATAGAGAGATTTAGTATAGAACCATTTAATCCTTTATCCTTTCACTTTGCAGTCACTTATGTATGTAACGGGACCAGTTTCTGCGATGGCGTTACAATGTTATTAAAGATACGATGTA	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	V119 head	M020 head	V118 embryo	M045 female body
....((((((.((..((((((.(((((.(((((((.((((.(((........))))..)))))))))))))))))))).))))..)))))).))......										
.....GTAAGTAGAGAGAGATAGAGA.....	21	0	1	84.00	84	82	2	0	0	0
.....GTAAGTAGAGAGAGATAGAGAGA.....	23	0	1	73.00	73	71	2	0	0	0
.....GTAAGTAGAGAGAGATAGAG.....	20	0	1	19.00	19	19	0	0	0	0
.....GTAAGTAGAGAGAGATAGAGAG.....	22	0	1	18.00	18	18	0	0	0	0
.....GTAAGTAGAGAGAGATAGAGAGATT.....	25	0	1	18.00	18	18	0	0	0	0
.....GTAAGTAGAGAGAGATAGA.....	19	0	1	15.00	15	13	2	0	0	0
.....GTAAGTAGAGAGAGATAGAGAGAT.....	24	0	1	12.00	12	12	0	0	0	0
.....GTAAGTAGAGAGAGATAGAGAA.....	22	1	1	4.00	4	3	1	0	0	0
.....TCCTTTATCCTTTCACTTTGCAGTT.....	25	1	1	3.00	3	0	1	2	0	0
.....GTAAGTAGAGAGAGATAGAGAGT.....	23	1	1	3.00	3	3	0	0	0	0
.....GTAAGTAGAGAGAGATAGAGT.....	21	1	1	3.00	3	3	0	0	0	0
.....GTAAGTAGAGAGAGATAGAGAGATTG.....	26	1	1	3.00	3	3	0	0	0	0
.....TAAGTAGAGAGAGATAGAG.....	19	0	1	2.00	2	2	0	0	0	0
.....GTAAGTAGAGAGAGATAGAGAGATC.....	25	1	1	2.00	2	2	0	0	0	0
.....GTAAGTAGAGAGAGATAGAGAGATTT.....	26	0	1	1.00	1	1	0	0	0	0
.....GTAAGTAGAGAGAGATAGAGAGATTTC.....	27	1	1	1.00	1	1	0	0	0	0
.....GTAAGTAGAGAGAGATAGAGAGATA.....	25	1	1	1.00	1	1	0	0	0	0
.....TCCTTTATCCTTTCACTTTGCAG.....	23	0	1	1.00	1	0	0	1	0	0
.....GTAAGTAGAGAGAGATAGAGAGATTC.....	26	1	1	1.00	1	1	0	0	0	0
.....GTAAGTAGAGAGAGATAGAGAGATTTCC.....	28	2	1	1.00	1	1	0	0	0	0
.....GTAAGTAGAGAGAGATAGAGAGAA.....	24	1	1	1.00	1	1	0	0	0	0
.....GTAAGTAGAGAGAGATAG.....	18	0	1	1.00	1	1	0	0	0	0
.....GTAAGTAGAGAGAGATAGAGAT.....	22	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

GTGGTAAGAGTATTTTAAAGCATCGTCGTGTCGAAATCTTCCTTTAGTTCCAACTCTCATTCATCTCTCTCTATCTCTCTAAATCATATCTTGGTAAATTAGGAAATAGGAAAGTGAAACGTCAGTGAATACATACATTGCCCTGGTCAAAGACGCTACCGCAATGTTACAATAATTTCTATGCTACAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V119 head	M045 female body
**********....((((((.((..((((((.(((((.(((((((.((((.(((........))))..)))))))))))))))))))).))))..)))))).))......**********							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004909:7955336-7955524 -	dwi_139	CACCATTCTCATAAAATTTCGTAGCAGCACAGCTTTAGAAGGAAATCAAGGTTGAGAGTAAGTAGAGAGAGATAGAGAGATTTAGTATAGAACCATTTAATCCTTTATCCTTTCACTTTGCAGTCACTTATGTATGTAACGGGACCAGTTTCTGCGATGGCGTTACAATGTTATTAAAGATACGATGTA

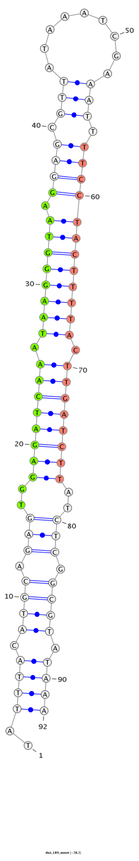
Generated: 09/08/2015 at 08:00 PM

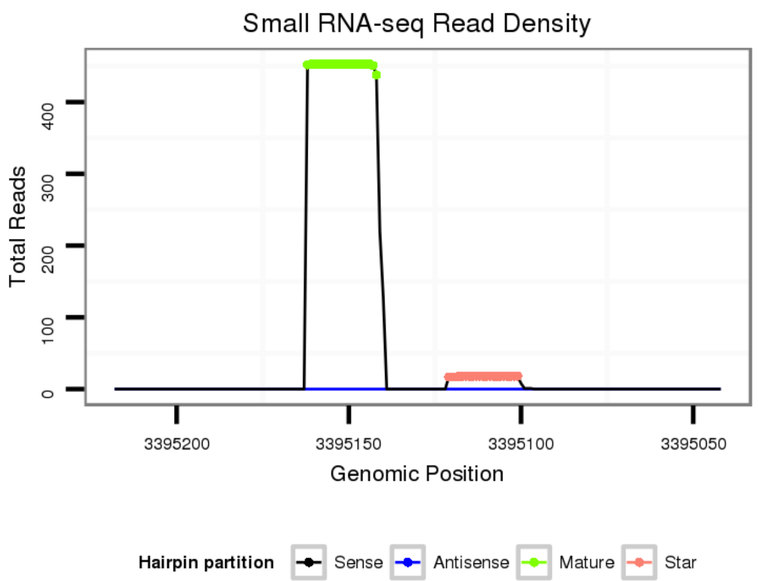
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

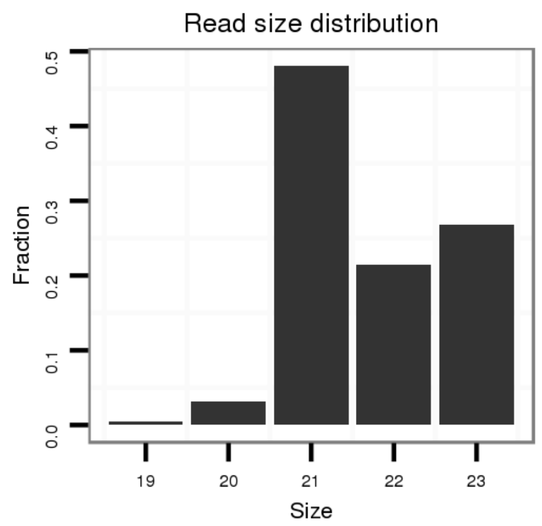
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_189	**scf2_1100000004511:3395092-3395168 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

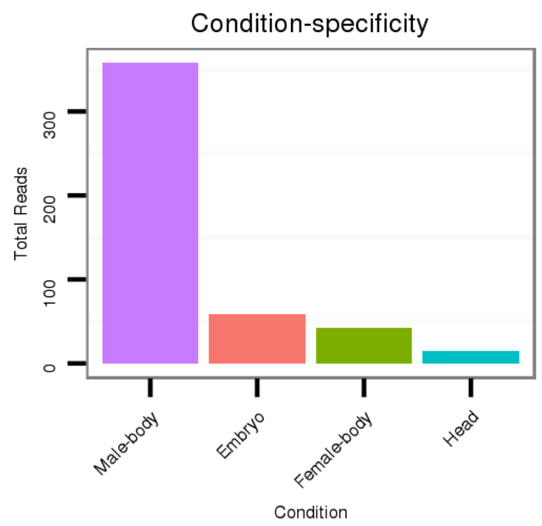
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

mature	star
	1. dwi_197 scf2_1100000004511:3392321-3392341 - 2. dwi_196 scf2_1100000004511:3392537-3392557 - 3. dwi_195 scf2_1100000004511:3392679-3392699 - 4. dwi_61 scf2_1100000004511:3393253-3393273 - 5. dwi_193 scf2_1100000004511:3393468-3393488 - 6. dwi_63 scf2_1100000004511:3393826-3393846 - 7. dwi_64 scf2_1100000004511:3394110-3394130 - 8. dwi_65 scf2_1100000004511:3394468-3394488 - 9. dwi_89 scf2_1100000004511:3394684-3394704 - 10. dwi_190 scf2_1100000004511:3394900-3394920 - 11. dwi_189 scf2_1100000004511:3395101-3395121 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AATTCTAGATAGAGAAAAACTTTGTGATCGTCGCAGGATCATATTTACATGCAGAGTGGAGATCAAATAAGGGTAAGGAGCGTTATAAATCGAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTAACAAAAATACAAATCAACATTTCTCTAATCATACC **********..((((.((((.(((..(((((((((.(((((((((.((((.(((.........))).))))))))))).)))))))..))).)))).))))********** Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	V118 embryo	M045 female body	V119 head	M020 head
.....TGGAGATCAAATAAGGGTAAG.....	21	0	1	217.00	217	203	2	11	1	0
.....TGGAGATCAAATAAGGGTAAGGA.....	23	0	1	127.00	127	72	41	6	8	0
.....TGGAGATCAAATAAGGGTAAGG.....	22	0	1	93.00	93	68	10	10	5	0
.....TGGAGATCAAATAAGGGTAA.....	20	0	1	13.00	13	12	0	1	0	0
.....TGGAGATCAAATAAGGGTAAGGAA.....	24	1	1	11.00	11	7	1	1	2	0
.....TTCCTACTTTTACTTGATCTT.....	21	0	11	10.73	118	5	8	94	8	3
.....TTCCTACTTTTACTTGATCTTA.....	22	0	11	7.73	85	2	43	40	0	0
.....TGGAGATCAAATAAGGGTAAGGAT.....	24	1	1	5.00	5	5	0	0	0	0
.....TGGAGATCAAATAAGGGTAAGA.....	22	1	1	3.00	3	1	0	0	2	0
.....TGGAGATCAAATAAGGGTAAGGT.....	23	1	1	3.00	3	2	0	1	0	0
.....TGGAGATCAAATAAGGGTAAGGATT.....	25	2	1	2.00	2	2	0	0	0	0
.....TGGAGATCAAATAAGGGTA.....	19	0	1	2.00	2	2	0	0	0	0
.....TGGAGATCAAATAAGGGTAAGT.....	22	1	1	2.00	2	2	0	0	0	0
.....CTACTTTTACTTGATCTTATCT.....	22	0	11	1.27	14	2	2	6	1	3
.....GGAGATCAAATAAGGGTAAG.....	20	0	1	1.00	1	0	0	1	0	0
.....TGGAGATCAAATAAGGGTAAA.....	21	1	1	1.00	1	1	0	0	0	0
.....TGGAGATCAAATAAGGGTAAGGTC.....	24	2	1	1.00	1	0	0	1	0	0
.....TTCCTACTTTTACTTGATCT.....	20	0	11	0.73	8	0	1	7	0	0
.....TTCCTACTTTTACTTGATCTTAA.....	23	1	11	0.64	7	1	0	6	0	0
.....TCCTACTTTTACTTGATCTT.....	20	0	11	0.27	3	0	0	3	0	0
.....CCTACTTTTACTTGATCTT.....	19	0	11	0.18	2	0	1	1	0	0
.....TTCCTACTTTTACTTGATCTC.....	21	1	11	0.18	2	0	0	0	0	2
.....TCCTACTTTTACTTGATCTTA.....	21	0	11	0.18	2	0	0	2	0	0
.....TTCCTACTTTTACTTGATCTTAAA.....	24	2	11	0.18	2	0	0	2	0	0
.....TTTTCCTACTTTTACTTGATCC.....	22	1	11	0.09	1	0	0	1	0	0
.....CTACTTTTACTTGATCTTATCTA.....	23	1	11	0.09	1	0	0	1	0	0
.....CTACTTTTACTTGATCTTATCC.....	22	1	11	0.09	1	1	0	0	0	0
.....TCCTACTTTTACTTGATCTTAA.....	22	1	11	0.09	1	0	0	1	0	0
.....CTACTTTTACTTGATCTTATCC.....	22	1	11	0.09	1	1	0	0	0	0
.....TCCTACTTTTACTTGATCTTAA.....	22	1	11	0.09	1	0	0	1	0	0
.....TCCTACTTTTACTTGATCT.....	19	0	11	0.09	1	0	0	1	0	0
.....CCTACTTTTACTTGATCTTA.....	20	0	11	0.09	1	0	1	0	0	0
.....CTACTTTTACTTGATCTTATC.....	21	0	11	0.09	1	0	1	0	0	0
.....TTCCTACTTTTACTTGATCTTT.....	22	1	11	0.09	1	0	0	1	0	0
.....CCTACTTTTACTTGATCTTATCTA.....	24	1	11	0.09	1	0	0	1	0	0

Anti-sense strand reads

TTAAGATCTATCTCTTTTTGAAACACTAGCAGCGTCCTAGTATAAATGTACGTCTCACCTCTAGTTTATTCCCATTCCTCGCAATATTTAGCTTTAAAAGGATGAAAATGAACTAGAATAGAGCCGCATATTTTTTGAGAATTGTTTTTATGTTTAGTTGTAAAGAGATTAGTATGG **********..((((.((((.(((..(((((((((.(((((((((.((((.(((.........))).))))))))))).)))))))..))).)))).))))********** Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo
.....TTAGCTTTAAAAGGATGAAAA.....	21	0	7	0.14	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3395042-3395218 -	dwi_189	AATTCTAGATAGAGAAAAACTTTGTGATCGTCGCAGGATCATATTTACATGCAGAGTGGAGATCAAATAAGGGTAAGGAGCGTTATAAATCGAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTAACAAAAATACAAATCAACATTTCTCTAATCATACC

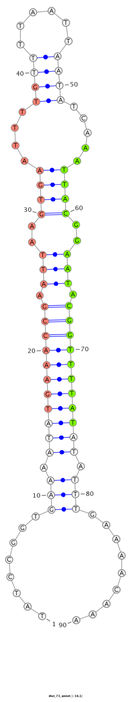
Generated: 09/08/2015 at 08:03 PM

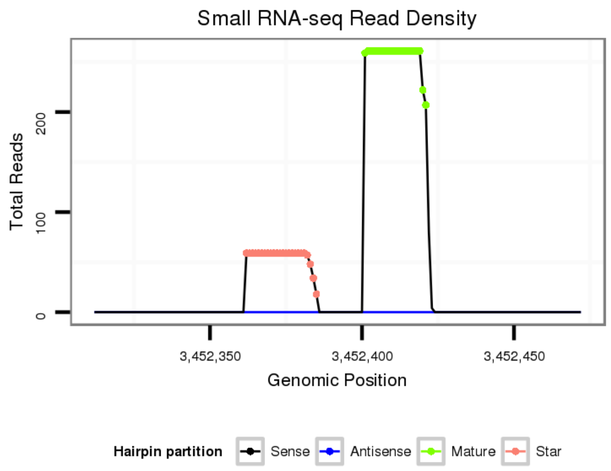
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

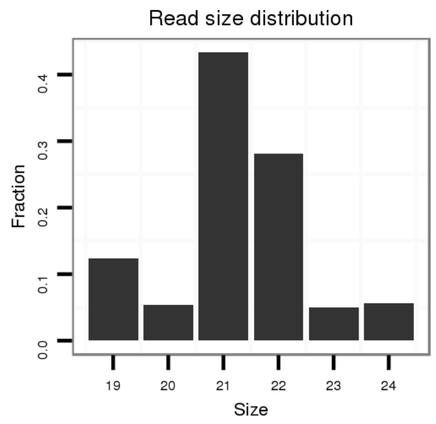
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_73	**scf2_1100000004513:3452362-3452422 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

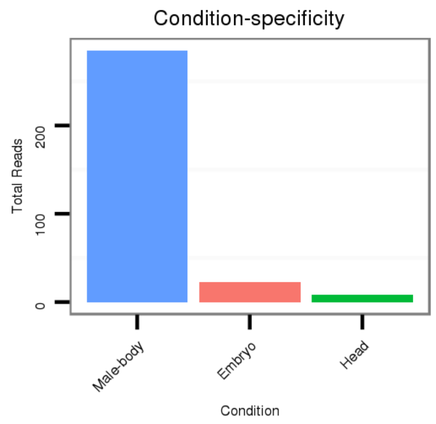
Legend: mature star mismatch in alignment mismatch in read

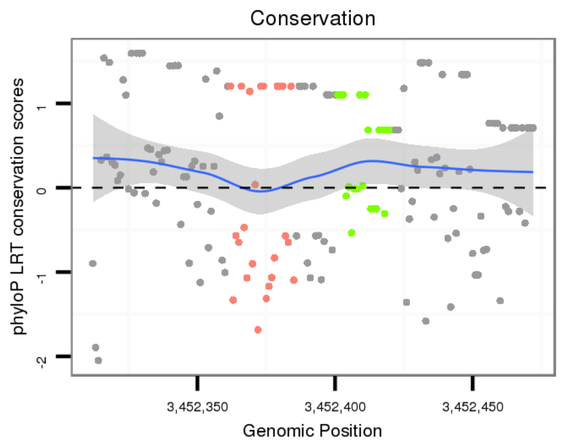
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGAAATAAACTAATTTTTTTTTATTGTAAAAAATTTATCCGGTGAAAATATGAAACCGAATTAAGTGAATTTTGTTTTAATTAATATCAAATTACGGAATACGGTTTTATATATTTGAAAACAAAATAACAACAATTTTCCATAAAATTTCTATTAACAAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	V118 embryo	M020 head	V119 head
..... AATTACGGAATACGGTTTTAT	21	0	1	127.00	127	123	3	1	0
..... AATTACGGAATACGGTTTTATA	22	0	1	75.00	75	60	14	0	1
..... AATTACGGAATACGGTTTT	19	0	1	39.00	39	38	0	0	1
..... AATTACGGAATACGGTTTTAA	21	1	1	20.00	20	20	0	0	0
..... TGAAACCGAATTAAGTGAATTTTG	24	0	1	18.00	18	11	4	3	0
..... AATTACGGAATACGGTTTTATAA	23	1	1	17.00	17	16	1	0	0
..... TGAAACCGAATTAAGTGAATTTT	23	0	1	16.00	16	14	2	0	0
..... AATTACGGAATACGGTTTTA	20	0	1	15.00	15	15	0	0	0
..... TGAAACCGAATTAAGTGAATTT	22	0	1	14.00	14	14	0	0	0
..... TGAAACCGAATTAAGTGAATT	21	0	1	9.00	9	7	0	2	0
..... AATTACGGAATACGGTTTTC	20	1	1	7.00	7	7	0	0	0
..... AATTACGGAATACGGTTTTATC	22	1	1	7.00	7	6	0	0	1
..... AATTACGGAATACGGTTTTATAT	23	0	1	3.00	3	3	0	0	0
..... TGAAACCGAATTAAGTGAAT	20	0	1	2.00	2	2	0	0	0
..... AATTACGGAATACGGTTTTT	20	1	1	2.00	2	2	0	0	0
..... AATTACGGAATACGGTTTTATCA	23	2	1	1.00	1	1	0	0	0
..... AATTACGGAATACGGTTTA	19	1	1	1.00	1	1	0	0	0
..... AATTACGGAATACGGTTTTATCC	23	2	1	1.00	1	1	0	0	0
..... ATTACGGAATACGGTTTTATAT	22	0	1	1.00	1	1	0	0	0
..... ATTACGGAATACGGTTTTATA	21	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

TCTTTATTTGATTAAAAAAAAATAACATTTTTTAAATAGGCCACTTTTATACTTTGGCTTAATTCACTTAAAACAAAATTAATTATAGTTTAATGCCTTATGCCAAAATATATAAACTTTTGTTTTATTGTTGTTAAAAGGTATTTTAAAGATAATTGTTT	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
droWil2	scf2_1100000004513:3452312-3452472 +	dwi_73	AGAAATAAACTAATTTTTTTTTATTGTAAAAAATTTATCCGGTGAAAATATGAAAC----------CGAATTAAG---TGAATTTTGTTTTAATTAAT----------ATCAAATTACGGAATACGGTTTTA-----TATATTTGAAAACAAAATAACAACAATTTTCCATAAAATTTCTATTAACAAA
droVir3	scaffold_12855:5684372-5684472 +		TT----------TTTTTTTTTTTGTTGTA--AAGTTCATTTAGCATA----------AACGTGAAGCGAAACTAAGCGCATGAAATCAAAAAATATAATTTATACAAAATTATGTTTAACAATAAAA----------
droMoj3	scaffold_6500:24526079-24526234 -		GAGAATAAAAAAAATATTTAAT----------AATAAAAAATATACGCAAGATTATAACGATATATA---CAAATTTTATTTTATTTATTTTTTTTTATTTTAATATCTTTATTATATTTTTT------------GCACGAAAATTAAAATGAGATTTAAATAA-----TTATTTAAAAA
droGri2	scaffold_15110:13655073-13655102 -		AAAAATAAAATA-TTTTTTTTTTTTGCAAA----------A----------
droPer2	scaffold_14:1399133-1399167 -		AA----------TTCTTTATTAGTGTCAAAAATTAATCAAGTGAA----------
droEle1	scf7180000490566:77707-77776 +		CGGGAAAAAATAAATTTTTTTAAAACTAAAAATGGTTTCT----------
dm3	chrUextra:7976877-7976919 +		TTAAAAA----------
droSec2	scaffold_40:188078-188152 -		TAGAAAATC----------AACAAAGTAAAAGAATCCAAC----------CGAAGTAGT---AGAATTTTATTTTCATTGTA----------ATAAAATTTTGGAGT---------A----------
droEre2	scaffold_4793:40700-40821 +		TTTAAA----------TGTAAAAA-------TAGCGAAAATATAATAC----------TGCACTATGATATAAATCATTCTTTAGTCACT------TAATATA---GGAAAATCACAGTTTTACAC----------GTGTAAAACAAAAAAAAAACAATTCACCACA----------

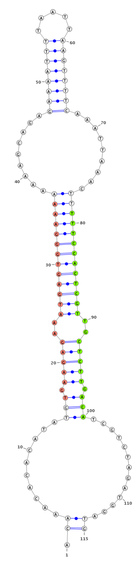
Generated: 09/08/2015 at 07:53 PM

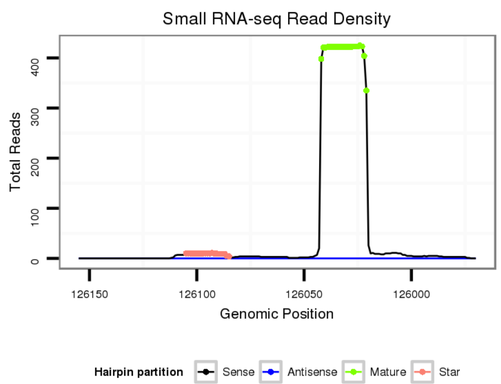
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

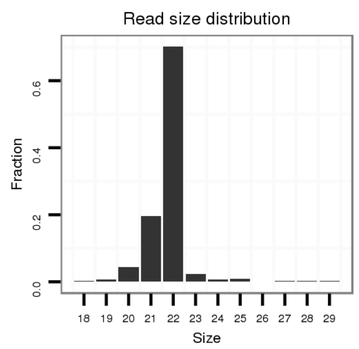
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_70	**scf2_1100000004514:126020-126105 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

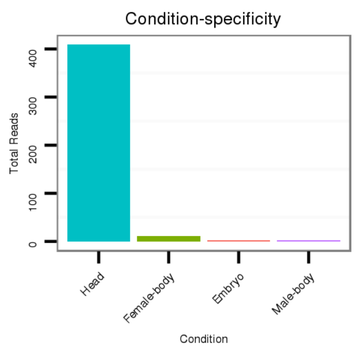
Legend: mature star mismatch in alignment mismatch in read

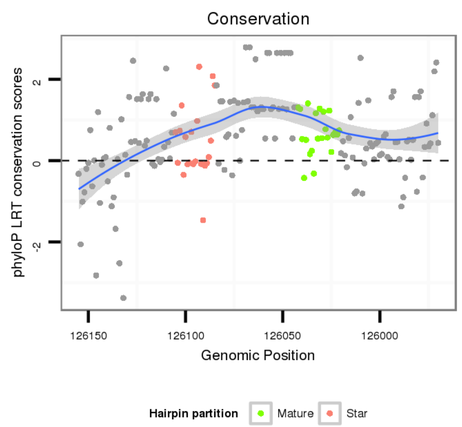
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CCTAGACATGCACTTACTCACACCTACACACACACACAAACACACATATGTGAAGAGAAATGAGTGGGAAAAAAAAGCAGAGAAAATTTTAATTAAGTTTTCAAAATTAAACTTTTTCCACTCGTTGCTCTTGACATCGTCTAGATGGATGTGTGTATGTGAGTGTAGACATGTGAGTATGTGTGTG	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V118 embryo	M045 female body	V119 head	V117 male body
********************************.((.....(((.(((((..(((((((((((((.....(((((((.....)))))))).....))))))))))))))..)))))).)))..............))*********************************											
..........TTTCCACTCGTTGCTCTTGACA..........	22	0	1	287.00	287	278	0	4	5	0
..........TTTCCACTCGTTGCTCTTGAC..........	21	0	1	67.00	67	65	0	2	0	0
..........TTTCCACTCGTTGCTCTTGA..........	20	0	1	19.00	19	19	0	0	0	0
..........TTCCACTCGTTGCTCTTGACA..........	21	0	1	13.00	13	10	0	3	0	0
..........TTCCACTCGTTGCTCTTGACAT..........	22	0	1	10.00	10	9	0	0	1	0
..........TTTCCACTCGTTGCTCTTGACG..........	22	1	1	5.00	5	5	0	0	0	0
..........TTTTCCACTCGTTGCTCTTGACA..........	23	0	1	5.00	5	5	0	0	0	0
..........TTTCCACTCGTTGCTCTTGACAT..........	23	0	1	4.00	4	4	0	0	0	0
..........CTTGACATCGTCTAGATGGATGT..........	23	0	1	2.00	2	0	2	0	0	0
..........CTTTTTCCACTCGTTGCTCTTGACA..........	25	0	1	2.00	2	2	0	0	0	0
..........TTTCCACTCGTTGCTCTTGACAA..........	23	1	1	2.00	2	2	0	0	0	0
..........TGAAGAGAAATGAGTGGGAAA..........	21	0	1	2.00	2	0	0	0	0	2
..........TTTTCCACTCGTTGCTCTTGAC..........	22	0	1	2.00	2	2	0	0	0	0
..........ATATGTGAAGAGAAATGAGTGGGAA..........	25	0	1	2.00	2	0	2	0	0	0
..........TTTTCCACTCGTTGCTCTTGACAT..........	24	0	1	2.00	2	2	0	0	0	0
..........ATATGTGAAGAGAAATGAGTGGGA..........	24	0	1	1.00	1	0	1	0	0	0
..........ATATGTGAAGAGAAATGA..........	18	0	1	1.00	1	0	1	0	0	0
..........GATGTGTGTATGTGAGTGTAGACA..........	24	0	1	1.00	1	0	0	0	1	0
..........TTTTCCACTCGTTGCTCTTGA..........	21	0	1	1.00	1	0	1	0	0	0
..........ATGTGAGTGTAGACATGTGAGTATGT.....	26	0	1	1.00	1	0	1	0	0	0
..........TATGTGAAGAGAAATGAGTGGGA..........	23	0	1	1.00	1	0	1	0	0	0
..........AGTGGGAAAAAAAAGCAGAGAAA..........	23	0	1	1.00	1	0	0	0	0	1
..........TTTTCCACTCGTTGCTCTTGACATCG..........	26	0	1	1.00	1	1	0	0	0	0
..........ATGGATGTGTGTATGTGAG..........	19	0	1	1.00	1	0	1	0	0	0
..........TGAAGAGAAATGAGTGGGA..........	19	0	1	1.00	1	0	0	1	0	0
..........TTTCCACTCGTTGCTCTTGAA..........	21	1	1	1.00	1	1	0	0	0	0
..........TTCAAATTAAACTTTTTCCACTCGTTGCT..........	29	0	1	1.00	1	1	0	0	0	0
..........GACATCGTCTAGATGGATGTGT..........	22	0	1	1.00	1	0	1	0	0	0
..........TTTTCCACTCGTTGCTCT..........	18	0	1	1.00	1	1	0	0	0	0
..........CTTGACATCGTCTAGATGGAT..........	21	0	1	1.00	1	1	0	0	0	0
..........ACATATGTGAAGAGAAATGAGTGGGA..........	26	0	1	1.00	1	0	1	0	0	0
..........TTTTCCACTCGTTGCTCTTGACG..........	23	1	1	1.00	1	1	0	0	0	0
..........AAAAAAGCAGAGAAAATTTTAATTAAGT..........	28	0	1	1.00	1	0	1	0	0	0
..........AATTAAACTTTTTCCACTCGTTGCT..........	25	0	1	1.00	1	0	1	0	0	0
..........GTCTAGATGGATGTGTGT..........	18	0	1	1.00	1	0	1	0	0	0
..........AACTTTTTCCACTCGTTGCTCTTGACA..........	27	0	1	1.00	1	1	0	0	0	0
..........ATGGATGTGTGTATGTGAGTGTAGA..........	25	0	1	1.00	1	0	0	0	1	0
..........TTTCCACTCGTTGCTCTTGACC..........	22	1	1	1.00	1	1	0	0	0	0
..........TTTCCACTCGTTGCTCTTG..........	19	0	1	1.00	1	0	0	1	0	0
..........CCACTCGTTGCTCTTGACA..........	19	0	1	1.00	1	1	0	0	0	0
..........TTTTTCCACTCGTTGCTCTTG..........	21	0	1	1.00	1	1	0	0	0	0
..........GTAGACATGTGAGTATGT.....	18	0	1	1.00	1	0	1	0	0	0
..........TTTCCACTCGTTGCTCTTGACT..........	22	1	1	1.00	1	1	0	0	0	0
..........TTTTTCCACTCGTTGCTCTTGACATCG..........	27	0	1	1.00	1	1	0	0	0	0
..........GTGTAGACATGTGAGTATGTGT...	22	0	1	1.00	1	0	0	0	0	1
..........CATCGTCTAGATGGATGTGTGTA..........	23	0	1	1.00	1	0	0	0	1	0
..........AGCAGAGAAAATTTTAATTAAGTT..........	24	0	1	1.00	1	0	0	0	1	0
..........TTTTCCACTCGTTGCTCTTGACATCGTCT..........	29	0	1	1.00	1	1	0	0	0	0
..........CATATGTGAAGAGAAATGAGT..........	21	0	1	1.00	1	0	0	1	0	0
..........TGACATCGTCTAGATGGATGTGT..........	23	0	1	1.00	1	0	1	0	0	0
..........AAAGCAGAGAAAATTTTAATTAAGT..........	25	0	1	1.00	1	0	0	0	1	0
..........GACATCGTCTAGATGGATGT..........	20	0	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

GGATCTGTACGTGAATGAGTGTGGATGTGTGTGTGTTTGTGTGTATACACTTCTCTTTACTCACCCTTTTTTTCGTCTCTTTTAAAATTAATTCAAAAGTTTAATTTGAAAAGGTGAGCAACGAGAACTGTAGCAGATCTACCTACACACATACACTCACATCTGTACACTCATACACACAC	Read size	# Mismatch	Hit Count	Total Norm	Total	V119 head	V118 embryo	V117 male body
********************************.((.....(((.(((((..(((((((((((((.....(((((((.....)))))))).....))))))))))))))..)))))).)))..............))*********************************								
..........GTGTGTGTGTTTGTGTGTAT..........	22	0	20	0.40	8	8	0	0
..........GTGTGTGTGTTTGTGTGTAT..........	20	0	20	0.15	3	3	0	0
..........TGTGTGTGTTTGTGTGTATA..........	24	0	15	0.07	1	0	1	0
..........TGTGTGTGTTTGTGTGTATA..........	20	0	20	0.05	1	0	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004514:125970-126155 -	dwi_70	-CCTA-----GACATGCACTTACTCACACCTACA----------CACACACACAAAC--ACACATA----------TGTGA----AGAG-AAA----------TGA----------GTGG--G--------A-------AAA--------AAAAGCAGAGAAAAT--TTTAATTAAGTTTTCAAATTAAACTTTTT--CCACTC----------GTTGCTCTTGACATCGTC--TAGAT--GGATGTGTGTATGTGAGTGTAGACATGTGAGTATG---TGTGTG
droVir3	scaffold_12932:454748-454916 +		-GTTA----GACACACACACACACGCACA----------CGCACACACAGCGCACA----------------------------------CAGA--G--------A-------AAAGCGAAAT-GCT--TTTAA-CATTTTCTAAGATTCAAATTTCG--TAAATT--------AT------CCCT---TTCGAGTTCCTGTG-----TGTAT--GAGTGTGTGTGTGTGTGTGTGCACGTGTGTGTATG---GTGTG
droMoj3	scaffold_6473:481468-481670 +		-CCGA-----GACGCGCGACACACACACACA----------CACACACACAGCACACAGA--------CGGCTGTG-AC---ACACTCCAA-----AAG-TAA----------AGA----------AAAA--A--------A-------AAA--------AATATATATA-TATATATAT-ATGTATTTATAAGTAAATAACTGAAGAAGTCG---GCTGCACGCATGCC--TGAC---GTGTGTGTGTGTGTGTGTGTGAGTGTATGAGTGTG---TGTGTG
droGri2	scaffold_15110:7129188-7129376 -		-GCAGA-----GACACACACACACACACATCCA----------CACACACTCAAGCGCTTAG---------TGCAA--------AATGTGTTA-----AATA-AATTA----------TGA----------GTGG--A--------A-------AAA--------AAAGTTAAAGA-AAT--TT----------ACATGGCTGCTTTGCT-TTACTTTTAA-GTGGTTTGCTTGCTTGCAGTT--TGGCT--GAGTGTGTGTGTGTGTGTGTGCGAGTGTGTGTGCTG---TGTGTG
dp5	3:3566677-3566848 +		-CACA-----GACACCACA----CAACCACT----------CAAA----------ACG---GTCCTCGTGGCAGCAGGCAGGCCATCTTGTTA-----GCGA-AAG----------TGA----------GCGG--GAAAAAATGA-------AAA--------ATAGCACAGA-AAT--TTTAATTAAGTTTTCAAATTAAACTTTTT--TCACTC----------ACTCGTGTGGCTGCTGTCTGGACAGCAGCCA----TGTC----------GTGTG
droPer2	scaffold_2:3755345-3755529 +		-CACC-----CGCACACGCACCACACACACT----------CACTCAAACACCGTCCTCG-----TGGCAGCAGGCAGGCCATCTTGTTA-----GCGA-AAG----------TGA----------GCGG--GAAAAAATGA-------AAA--------ATAGCACAGA-AAT--TTTAATTAAGTTTTCAAATTAAACTTTTT--TCACTC----------ACTCGTGTGGCTGCTGTCTGGACAGCAGCCA----TGTGG----------GTGTG
droAna3	scaffold_13266:4875360-4875567 +		-CATA-----AATATTG----------C----------ATACA----TGGTAGCA--------ATCTTGTTATGCCAAAAG-AAC----------TGAGCAAAAAAAAAATTAA-AGAAACAAAA-A-------A---GCAACCAAAGCACAGAA-AAT--TTTAATTAAGTTTTCAAATTAAACTTTTG--CTGTC----------GCTGCTGCTCCTCGTCGTCTGGACATACGTGA----GATGTAAGCTAGTGCCCAGTACGAGTGATGTGTTGTTG---TGTGTG
droBip1	scf7180000395751:673911-674119 +		-GGAG-----GACATAGGTAAATGTATATTCG----------C----------ATACA----TGGTAGCA--------ATCTTGTTATGCCAAAAG-AAC----------TGAGCACAAAAATAAGTAA-AGAAACAAAA-A-------AAA---ACGAACCAAGCACAGAA-AAT--TTTAATTAAGTTTTCAAATTAAACTTTTG--CT----------GTCGCTGCTCGCTGTCTGGACATACGTGA----GATGT--------AAGCTAGTGCGCCTGTACGAGTAAG---AGTGTG
droKik1	scf7180000302682:169963-170118 -		-CTTC-----AGCCTCCA---------CA----------C----------ACACA----TGGCCCCA-A-----AATCTTGTTA-----AAG-AGA----------GGA----------GCAG--A-----CAGA-------AAA--------AAAAGCACAGA-AAT--TTTAATTAAGTTTTCAAATTAAACTTTTT-TGCACTC----------GCACTGCTCTGCACATACTGA----TGGTT--GTGTGTGTGTGTG----------G---TGGGTG
droFic1	scf7180000453811:183784-183976 -		ATTTTTAT----TTGCGCCC-----GGGG----------CACAG----------ACACATC----------TTGTTA-----AGAAAGAAA-GAGAGAGA---------AAGCAAGCAAAA-AAAAAAGTGA-------AAA--A----AAGAAGCACAGAA-AAT--TTTAATTAAGTTTTCAAATTAAACTTTTT-GCACTG----------CTGCTGCTCTGCACATACGTGA----TATGTT---GCCATATGTATGTGTACGTGTGTGTTGTCTG---TGTGTA
droEle1	scf7180000491232:289464-289629 -		-TTTTTAT----TTGCGCCC----------C----------ACACATC----------TCGTT-----AAGGGAAA-GACAGAGATGC-------AAGACAA--A--------A-GGGGAAAAAAA----ACGAAGCACAGAA-AAT--TTTAATTAAGTTTTCAAATTAAACTTTTT-GCACTC--------C---------TGCTGCTCTGCTGTCTGGACAAACGTGA----TGTGTT---GCGA----------ACG--TTGTG
droRho1	scf7180000780219:64892-65064 +		-TTTTTAT----TTGAACCCGTACCCGC----------CACAG----------ATACATC----------TTGTTA-----AGAA-AAAGCGAGAGAGA---------GAGAAAGTAA--A--------A-------AAAAAA----ACGAAGCACAGAA-AAT--TTTAATTAAGTTTTCAAATTAAACTTTTT-GCACTC--------C---------TGCTCTGCTGTCTGGACAAACGTGA----TGTGTT---GCGA----------ACGAGTGTG
droBia1	scf7180000302143:1327514-1327620 -		-T---------------------------------------C----------TTCTTA-----AAAAGAA----------AG----------A--A--------A-------AAA--------AAGCAGCACAGAA-AAT--TTTAATTAAGTTTTCAAATTAAACTTTTT-GCACTG----------CTGCTGCTCTGCACATACGTGA----TGTGCA----GTGA----------TG---TGTGTG
droTak1	scf7180000410787:55415-55546 -		ATTTTTAT----TTGCTCCCCCTCTTTC-----------TC----------ACACATCTCC----------TTCTGA-----A--AGCA----------AGA----------AGCA--G--------A-------AAA--------AAGCAGCACAGAA-AAT--TTTAATTAAGTTTTCAAATTAAACTTTTT-GCACTG--------C---------TGCTCGTGCTGCACATACGTGA----TGTC----------GCGA----------ACG--TTGTG
droEug1	scf7180000409474:849774-849946 -		ATTTTTAT----TTGCGCCC----------CGC----------ACACATC----------TTGTGA-----AGAA-GAAAAGGGAGAGG---------GAC--AGAGA--GAAACAGAGCAAG-----A--------GGAAAAGCACGGAA-AAT--TTTAATTAAGTTTTCAAATTAAACTTTTT-GCACTG--------CT-----GCTGCTGCTCGCTGCTCTGACATACATGA----TGTGAT----GCGA----------TGCG--AGTGTG
dm3	chr2R:17096512-17096677 +		-CCGA-----GCGCCGGTCGACACGGACACA----------CACACACACACACGCGCCATC----------TTGTTA-----AAA-GAA----------TGA----------GCGA--G--------A-------AAA--------AAAGCAGAGA-AAT--TTTAATTAAGTTTTCAAATTAAACTTTTT-GCACTG--------CTGCTACTGCTACTGCTGCTGCTCTGCACATACGTGA----TGTGAT----GCGA----------ACG--TTGTG
droSim2	scf17651430-17651569 +		-CCAC-----AACATAG----------CACA----------CACA----------AGCCATC----------TTGTTA-----AAA-GAA----------TGA----------GCGA--G--------A-------AAA--------AAAGCAGAGA-AAT--TTTAATTAAGTTTTCAAATTAAACTTTTT-GCACTG--------CT---------GCTACTGCTACTGCTGCTGCTCTGCACATACGTGA----TGTGAT----GCGA----------ACG--TTGTG
droSec2	scaffold_9:422721-422867 +		-CGTGACAGCACA----------CACA----------CACA----------AGCCATC----------TTGTTA-----AAA-GAA----------TGA----------GCGA--G--------A-------AAA--------AAAGCAGAGA-AAT--TTTAATTAAGTTTTCAAATTAAACTTTTT-GCACTG--------CTGCTACTGCTGCTGCTCTGCACATACGTGA----TGTGAT----GCGA----------ACG--TTGTG
droYak3	2R:12099662-12099798 -		-CGCTTAC----TGAGAGCGATACAGCACA----------CACA----------ACGCAAC----------TTGTTA-----AAA-AAA----------TGA----------GCGA--G--------A-------AAA--------AAAGCAGAGA-AAT--TTTAATTAAGTTTTCAAATTAAACTTTTT-GCACTG--------CTGCTGCTCTGCACATACGTGA----TGTGTT---GCGA----------ACG--TTGTG
droEre2	scaffold_4845:11239078-11239234 +		-TTTTTAT----TTGCTCTCCCCTTACACCCACGCACACACACACA----------ACGCATC----------TTGCTG-----AAA-GAA----------TGA----------GCGG--G--------A-------AAA--------AAAGCAGAG--AAT--TTTAATTAAGTTTTCAAATTAAACTTTTT-GCACTT--------CT------GCTACTGCTCGCTGCTCTGACATACGTGC----TGTGAT----GCGA----------ACG--TTGTG

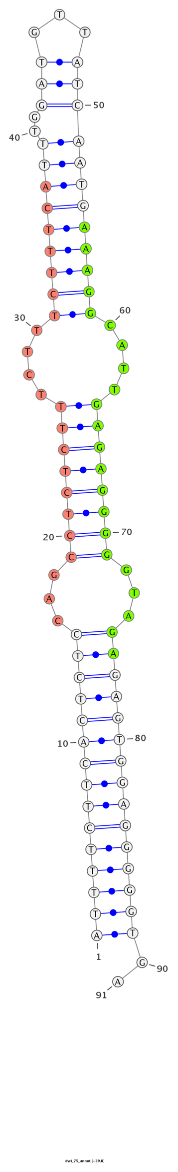
Generated: 09/08/2015 at 07:39 PM

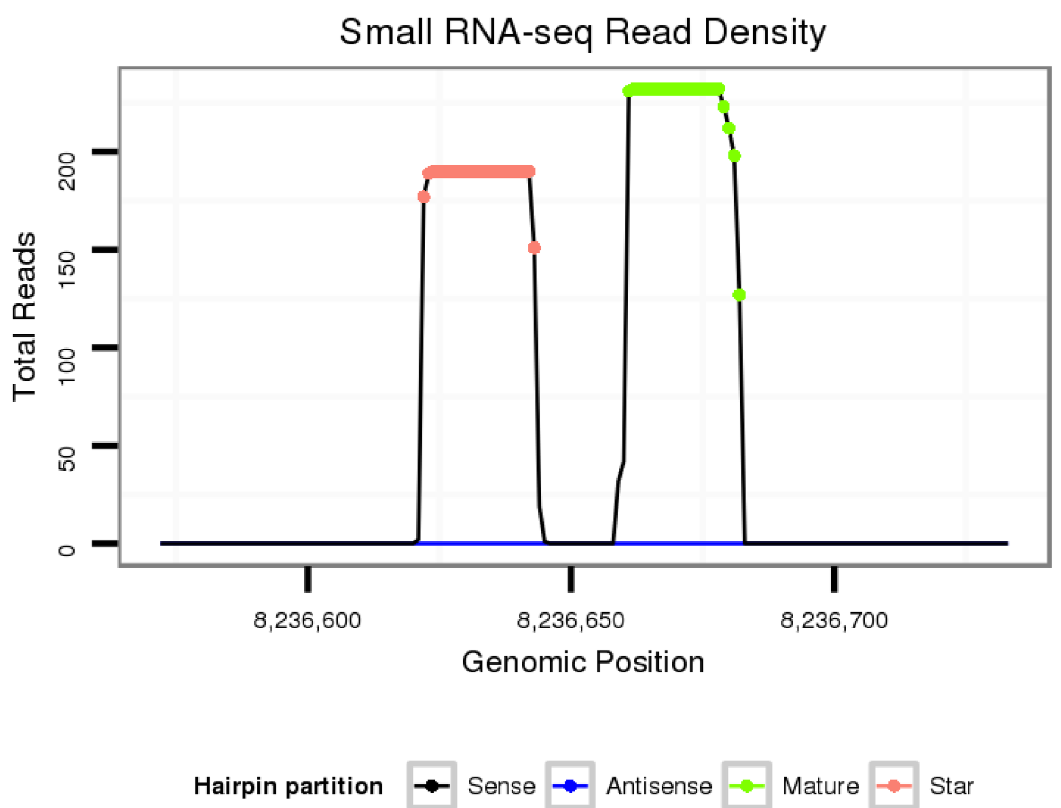
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

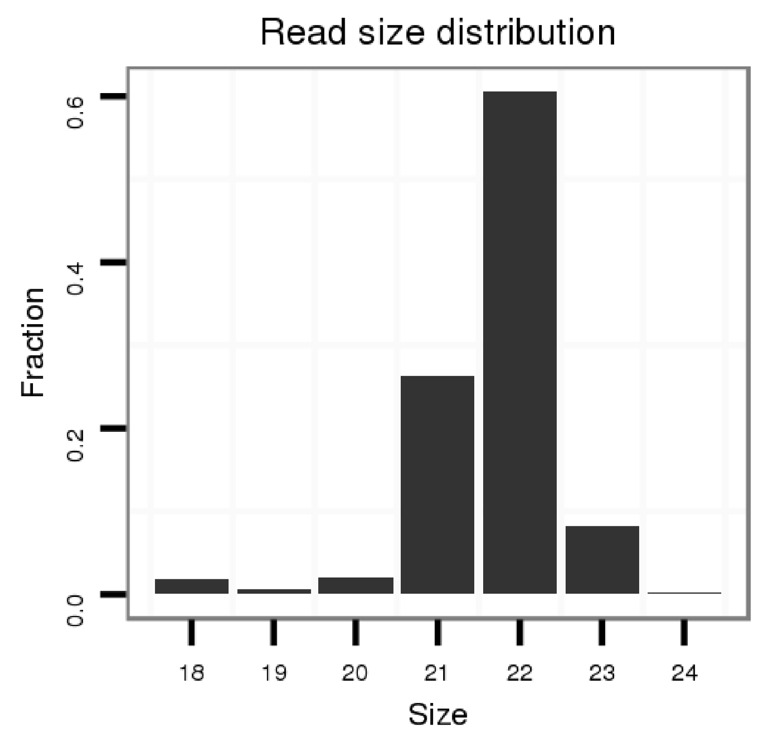
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_75	**scf2_1100000004943:8236622-8236683 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

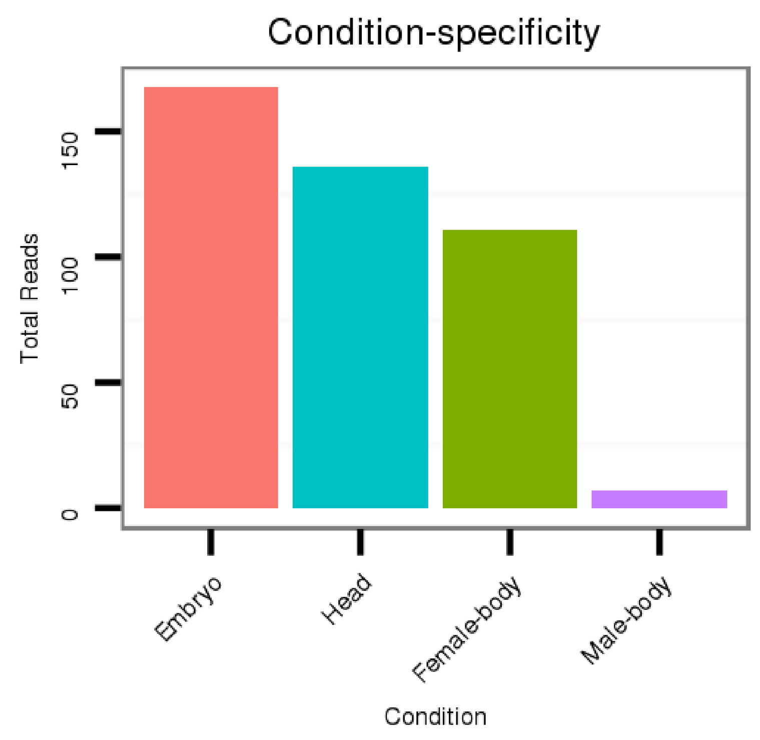
Legend: mature star mismatch in alignment mismatch in read

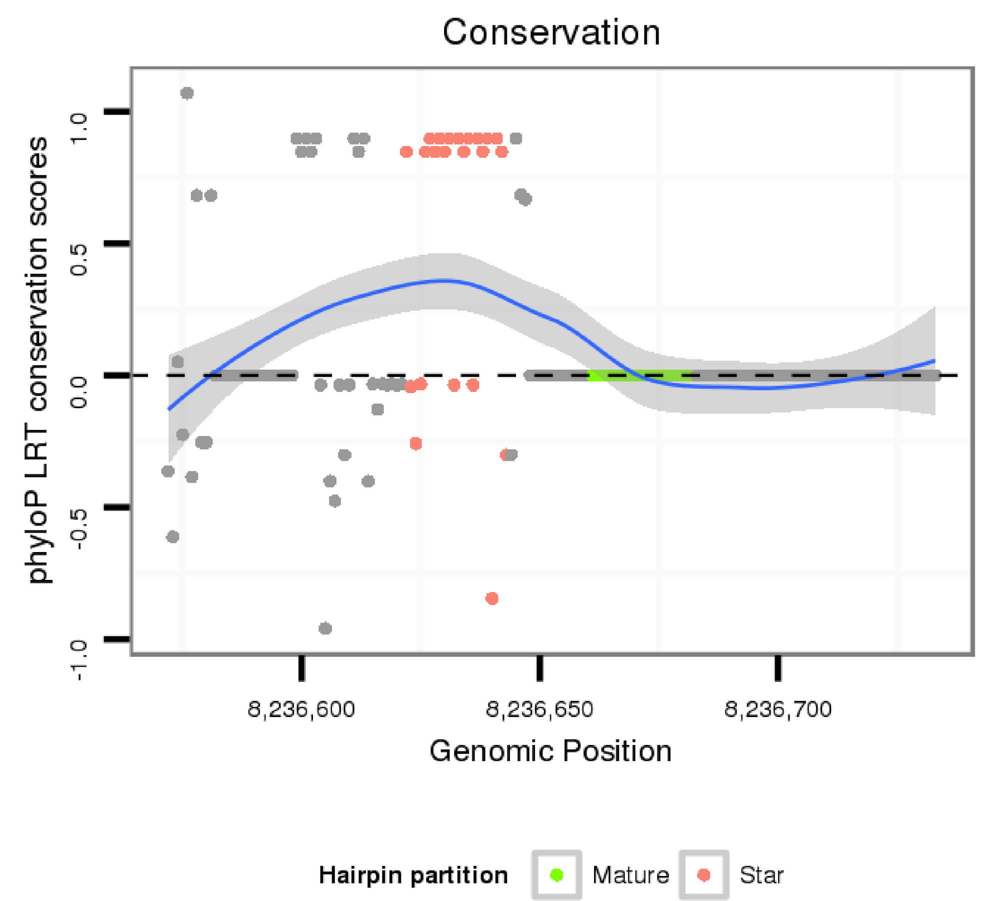
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK14047-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GGTTTTTCTATAAGATCTGGCTCTCTTTCTCTTCTATTTTCTTCACTCTCCAGCCTCTCTTTCTTTCTTTCATTTGGATGTTATCAATGAAAGGCATTGAGAGGGGGTAGAGAGTGGAGGGGGTGATCGTTTGAAGTGTGACCATTTGCTAGAAATTTGTCT ***********************************(((((((((((((((...((((((((....(((((((((..(((...))))))))))))....))))))))...)))))))))))))))..************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	M045 female body	V119 head	M020 head	V117 male body
....AAAGGCATTGAGAGGGGGTAGA...	22	0	1	121.00	121	67	4	26	20	4
....CAGCCTCTCTTTCTTTCTTTCA..	22	0	1	120.00	120	43	59	9	9	0
....AAAGGCATTGAGAGGGGGTAG..	21	0	1	54.00	54	21	7	17	8	1
....CAGCCTCTCTTTCTTTCTTTC...	21	0	1	38.00	38	5	18	8	7	0
....CAGCCTCTCTTTCTTTCTTTCAT...	23	0	1	16.00	16	7	6	1	2	0
....TGAAAGGCATTGAGAGGGGGTAG..	23	0	1	13.00	13	7	1	1	4	0
....AGCCTCTCTTTCTTTCTTTCA..	21	0	1	9.00	9	1	8	0	0	0
....TGAAAGGCATTGAGAGGGGGTA...	22	0	1	9.00	9	5	1	3	0	0
....TGAAAGGCATTGAGAGGGGGT..	21	0	1	9.00	9	1	2	5	0	1
....AAAGGCATTGAGAGGGGG...	18	0	1	8.00	8	0	0	0	8	0
....AAAGGCATTGAGAGGGGGTAGAA..	23	1	1	7.00	7	4	0	1	1	1
....GAAAGGCATTGAGAGGGGGTAGA...	23	0	1	6.00	6	3	0	1	2	0
....AAAGGCATTGAGAGGGGGTA...	20	0	1	4.00	4	3	0	1	0	0
....GAAAGGCATTGAGAGGGGGTAG..	22	0	1	3.00	3	1	0	1	1	0
....CAGCCTCTCTTTCTTTCTTTCAA...	23	1	1	3.00	3	0	3	0	0	0
....AGCCTCTCTTTCTTTCTTTCAA...	22	1	1	2.00	2	0	2	0	0	0
....CCAGCCTCTCTTTCTTTCTTTCA..	23	0	1	2.00	2	0	2	0	0	0
....AGCCTCTCTTTCTTTCTTTCAT...	22	0	1	2.00	2	1	1	0	0	0
....AAAGGCATTGAGAGGGGGTAGT...	22	1	1	2.00	2	0	0	1	1	0
....AAAGGCATTGAGAGGGGGT..	19	0	1	2.00	2	0	0	1	0	1
....TGAAAGGCATTGAGAGGGC..	19	1	1	1.00	1	0	0	1	0	0
....AGCCTCTCTTTCTTTCTTTC...	20	0	1	1.00	1	0	1	0	0	0
....TGAAAGGCATTGAGAGGGGGTT...	22	1	1	1.00	1	0	0	0	0	1
....GAAAGGCATTGAGAGGGGGTA...	21	0	1	1.00	1	1	0	0	0	0
....CAGCCTCTCTTTCTTTCTTTCATT..	24	0	1	1.00	1	1	0	0	0	0
....TGAAAGGCATTGAGAGGGGG...	20	0	1	1.00	1	0	0	1	0	0
....AAGGCATTGAGAGGGGGTAG..	20	0	1	1.00	1	0	1	0	0	0
....GCCTCTCTTTCTTTCTTTCA..	20	0	1	1.00	1	0	1	0	0	0
....AAAGGCATTGAGAGGGGGTAGAT..	23	1	1	1.00	1	0	1	0	0	0
....GAAAGGCATTGAGAGGGGGTAGG...	23	1	1	1.00	1	0	0	0	1	0
....AAAGGCATTGAGAGGGGGTAA..	21	1	1	1.00	1	1	0	0	0	0
....CAGCCTCTCTTTCTTTCTTTCAAA..	24	2	1	1.00	1	0	1	0	0	0
....CAGCCTCTCTTTCTTTCTT...	19	0	2	0.50	1	0	1	0	0	0
....CAGCCTCTCTTTCTTTCTTT..	20	0	2	0.50	1	1	0	0	0	0
....CAGCCTCTCTTTCTTTCA..	18	1	4	0.50	2	0	2	0	0	0

Anti-sense strand reads

CCAAAAAGATATTCTAGACCGAGAGAAAGAGAAGATAAAAGAAGTGAGAGGTCGGAGAGAAAGAAAGAAAGTAAACCTACAATAGTTACTTTCCGTAACTCTCCCCCATCTCTCACCTCCCCCACTAGCAAACTTCACACTGGTAAACGATCTTTAAACAGA ***********************************(((((((((((((((...((((((((....(((((((((..(((...))))))))))))....))))))))...)))))))))))))))..************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004943:8236572-8236733 +	dwi_75	GGTTTTTCTATAAGATCTGGCTCTCTTTCTCTTCTATTTTCTTCACTCTCCAGC----CTCTCTTTCTTTCTTTCATTTGGATGTTATCAATGAAAGGCATTGAGAGGGGGTAGAGAGTGGAGGGGGTGATCGTTTGAAGTGTGACCATTTGCTAGAAATTTGTCT
droVir3	scaffold_12855:8768849-8768907 -		TCTCTC---------------------TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTATCATTTG--
droMoj3	scaffold_6540:23940403-23940455 -		TCCCTT---------------------TCTCTCGTACCCTCTTTCTCTCTCTCT----CTCTCTCTCTCTCTCTCTCGCT--
droGri2	scaffold_14830:2446369-2446378 -		GGTTTCTTCA--

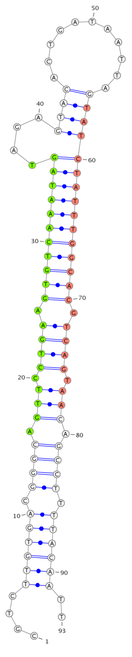
Generated: 09/08/2015 at 07:39 PM

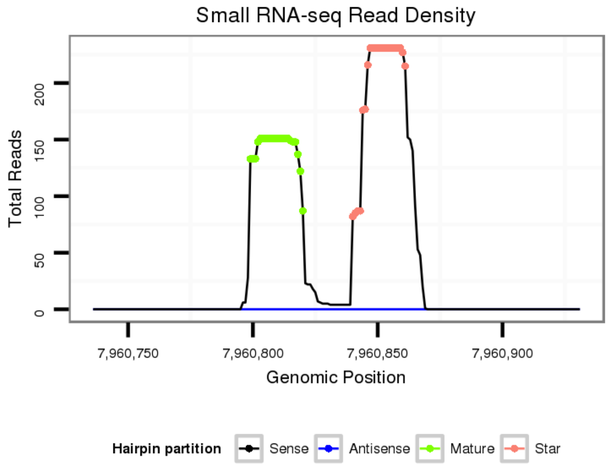
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

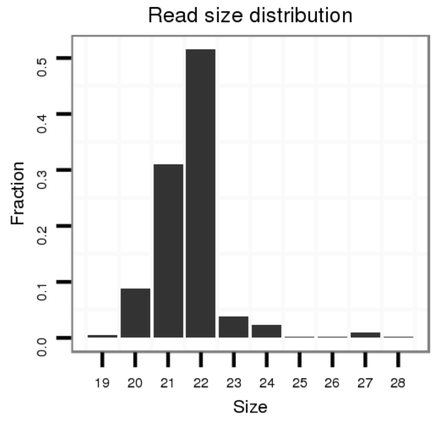
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_143	**scf2_1100000004909:7960786-7960881 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

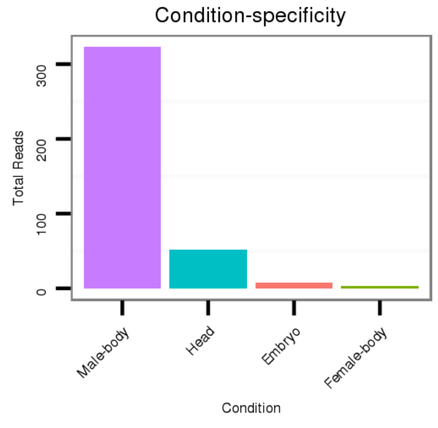
Legend: mature star mismatch in alignment mismatch in read

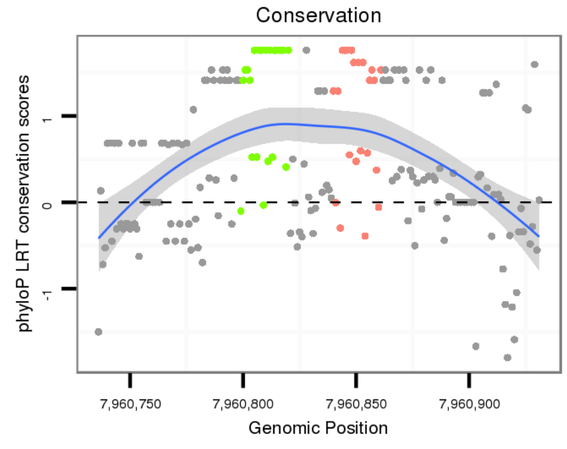
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AGCTAAAATTGTTATTGTGTTATACCAGAATCAAGAGCTACTAATTGGCGTCTTGTGACGGGCAGTTCCTGAAGTGTCAAATAGTAGAGTACACTGATAATTAGTATCTATTTGGCACGTCAGTAACAGCCTTTTACAATTAAATGCAAATGCGGCGAGAGCATGGCCTGCCTGCCAGACTGTGGATATGATTAAC	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	M020 head	V119 head	V118 embryo	M045 female body
**********....(((((((.(((((.(((.(((((.((((((((((((....((((..........))))))))))))))))).)))))..))))).)))))))..**********										
.....AGTTCCTGAAGTGTCAAATAGT.....	22	0	1	64.00	64	58	1	4	0	1
.....TATCTATTTGGCACGTCAGTAA.....	22	0	1	62.00	62	57	2	0	3	0
.....TATTTGGCACGTCAGTAACAG.....	21	0	1	47.00	47	37	5	5	0	0
.....AGTTCCTGAAGTGTCAAATAG.....	21	0	1	35.00	35	30	1	3	1	0
.....TATTTGGCACGTCAGTAACAGC.....	22	0	1	32.00	32	28	0	3	1	0
.....TTTGGCACGTCAGTAACAGCCT.....	22	0	1	22.00	22	8	12	2	0	0
.....CAGTTCCTGAAGTGTCAAATA.....	21	0	1	14.00	14	13	0	1	0	0
.....TATCTATTTGGCACGTCAGTA.....	21	0	1	12.00	12	12	0	0	0	0
.....TATTTGGCACGTCAGTAACA.....	20	0	1	10.00	10	9	0	0	1	0
.....TTTGGCACGTCAGTAACAGCCTT.....	23	0	1	10.00	10	9	0	0	0	1
.....TTGGCACGTCAGTAACAGCCTT.....	22	0	1	9.00	9	7	0	0	1	1
.....CAGTTCCTGAAGTGTCAAAT.....	20	0	1	8.00	8	8	0	0	0	0
.....TCCTGAAGTGTCAAATAGTAGAGT.....	24	0	1	8.00	8	7	0	0	1	0
.....TTGGCACGTCAGTAACAGCCT.....	21	0	1	6.00	6	2	4	0	0	0
.....TTTGGCACGTCAGTAACAGC.....	20	0	1	6.00	6	4	0	2	0	0
.....AGTTCCTGAAGTGTCAAATA.....	20	0	1	5.00	5	5	0	0	0	0
.....GTAGAGTACACTGATAATTAGTATCTA.....	27	0	1	4.00	4	0	4	0	0	0
.....TATCTATTTGGCACGTCAGT.....	20	0	1	4.00	4	3	0	1	0	0
.....TATTTGGCACGTCAGTAACAGT.....	22	1	1	4.00	4	4	0	0	0	0
.....TTTGGCACGTCAGTAACAGCC.....	21	0	1	4.00	4	2	2	0	0	0
.....GGCAGTTCCTGAAGTGTCAAAT.....	22	0	1	3.00	3	3	0	0	0	0
.....TCCTGAAGTGTCAAATAGTAGA.....	22	0	1	3.00	3	3	0	0	0	0
.....ATCTATTTGGCACGTCAGTAAC.....	22	0	1	2.00	2	2	0	0	0	0
.....GGCAGTTCCTGAAGTGTCA.....	19	0	1	2.00	2	2	0	0	0	0
.....TCCTGAAGTGTCAAATAGTAGAG.....	23	0	1	2.00	2	2	0	0	0	0
.....TTTGGCACGTCAGTAACAGCCC.....	22	1	1	2.00	2	0	2	0	0	0
.....TCTATTTGGCACGTCAGTAACAG.....	23	0	1	2.00	2	2	0	0	0	0
.....CCTGAAGTGTCAAATAGTAGAG.....	22	0	1	1.00	1	1	0	0	0	0
.....TTTGGCACGTCAGTAACAGCCG.....	22	1	1	1.00	1	0	1	0	0	0
.....TATTTGGCACGTCAGTAACAGCA.....	23	1	1	1.00	1	1	0	0	0	0
.....AGTTCCTGAAGTGTCAAATAGTA.....	23	0	1	1.00	1	1	0	0	0	0
.....ATCTATTTGGCACGTCAGTAACG.....	23	1	1	1.00	1	1	0	0	0	0
.....TTTGGCACGTCAGTAACAGCCTTT.....	24	0	1	1.00	1	1	0	0	0	0
.....CCTGAAGTGTCAAATAGTAGAGTACACT.....	28	0	1	1.00	1	1	0	0	0	0
.....GCAGTTCCTGAAGTGTCAAAA.....	21	1	1	1.00	1	1	0	0	0	0
.....TATCTATTTGGCACGTCAGTAAA.....	23	1	1	1.00	1	1	0	0	0	0
.....TTGGCACGTCAGTAACAGCCC.....	21	1	1	1.00	1	0	1	0	0	0
.....TATTTGGCACGTCAGTAACAA.....	21	1	1	1.00	1	1	0	0	0	0
.....TCCTGAAGTGTCAAATAGTAGAGTAA.....	26	1	1	1.00	1	1	0	0	0	0
.....TTGGCACGTCAGTAACAGCCG.....	21	1	1	1.00	1	0	1	0	0	0
.....CCTGAAGTGTCAAATAGTAGA.....	21	0	1	1.00	1	1	0	0	0	0
.....ATCTATTTGGCACGTCAGTAA.....	21	0	1	1.00	1	1	0	0	0	0
.....GGCAGTTCCTGAAGTGTCAA.....	20	0	1	1.00	1	1	0	0	0	0
.....TCCTGAAGTGTCAAATAGTAGAGTA.....	25	0	1	1.00	1	1	0	0	0	0
.....TATTTGGCACGTCAGTAACATT.....	22	2	1	1.00	1	1	0	0	0	0
.....TCCTGAAGTGTCAAATAGTAGAGTAC.....	26	0	1	1.00	1	1	0	0	0	0
.....ATTTGGCACGTCAGTAACAGCC.....	22	0	1	1.00	1	1	0	0	0	0
.....AGTTCCTGAAGTGTCAAATAT.....	21	1	1	1.00	1	1	0	0	0	0
.....TCCTGAAGTGTCAAATAGTAGAGTACC.....	27	1	1	1.00	1	0	1	0	0	0
.....AGTTCCTGAAGTGTCAAATAGTC.....	23	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

TCGATTTTAACAATAACACAATATGGTCTTAGTTCTCGATGATTAACCGCAGAACACTGCCCGTCAAGGACTTCACAGTTTATCATCTCATGTGACTATTAATCATAGATAAACCGTGCAGTCATTGTCGGAAAATGTTAATTTACGTTTACGCCGCTCTCGTACCGGACGGACGGTCTGACACCTATACTAATTG	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body
**********....(((((((.(((((.(((.(((((.((((((((((((....((((..........))))))))))))))))).)))))..))))).)))))))..**********						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004909:7960736-7960931 +	dwi_143	AGCT----AAAATTGTTATTGTGTTATACCAGAATCAAGAGCTAC---TA-ATTGGCGTCTTGTGACGGGCAGTTCCTGAAGTGTCAAATAGTAGAGTACACTGATAA----------TTAGTATCTATTTGGCACGTCAGTAACAGCCTTTTACAATTAAATGCAAATGCGGCGAGAGCATGGCCTGCCTGCCAGACTGTGG----------ATATGATTAAC---------
droVir3	scaffold_13042:902965-903164 -	dvi_45	ATAACGATAACAATAACGATAACTT-------AACGGATAACGATAACGATAAGCGCATCTGGTGACTAGCGTTCCTGAAGTGTCAAATAGTAGTACTACTCGTAAGAAAATGTACGTTGATTTTATTTGGCACATCAGTGACAGCATGTTACGAGTAATTGCACA-ACAGCCA---------GAGCGGAGACAGAT-CCGGAG----------ACAGATGAGT---------
droMoj3	scaffold_6328:2897600-2897724 -		--GCATCTGGTGACTAGCTGTTCCTGAAGTGTCAAATAGTGAGTACTACTCGTAAGAAAATGTACGTTGATTTTATTTGGCACATCAGTGACAGCATGTCACGAGTAATTGCACA-ACGACCA---------GAG----------C---------
droAna3	scaffold_13417:2460847-2461003 -	dan_75	G---TCGCGTCCGTGACGGGCAGTTCCTGAACTGTCAAATAGTGGAGCGGCATAAA---C---------------ATATTTGGCACGTCAGTAACAGCCTGTTACAAGTCAGCGCACG-ACCAGCA---------GTACGGCCACCCTCGGCGGAAGCTAGCAGGCACTAGGCGGTCCAGGACGATC---------
droBip1	scf7180000395874:32871-33025 -		CTGC--AAACGTCGCGTCCGTGACGGGCAGTTCCTGAACTGTCAAATAGTGGAGCGGCATAAA---C---------------ATATTTGGCACGTCAGTAACAGCCTGTTACAAGACAGCGCACG-ACCAGCA---------ATACGGCCACCTCG-ATGGAAGC----------GTACACG--GATGACTTTTGGT
droKik1	scf7180000302517:1186179-1186304 +		--TGGCGTCCGTGACAGGCAGTTCCTGAAGTGTCAAATAGTGGATGACATGAG---A---------------ATATTTGGCACCCAGAGACAGCCTGTTACTGGGCAGCGAACG-ACC---C---------ATGCCGGACACCGAA-ACAGAA----------ACAAC---------
droEug1	scf7180000409231:637-694 -		TT--TAAAATTTAAATACTGTATGCACTGATAC----------TCGGTATGTATGTGTCGCCT----------ACAGTGAGT---------

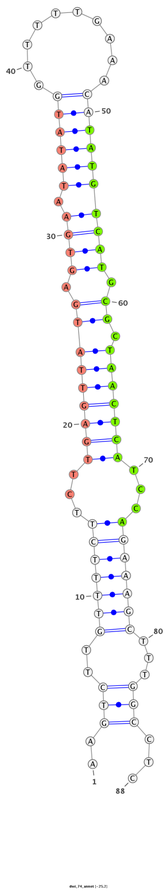
Generated: 09/08/2015 at 08:05 PM

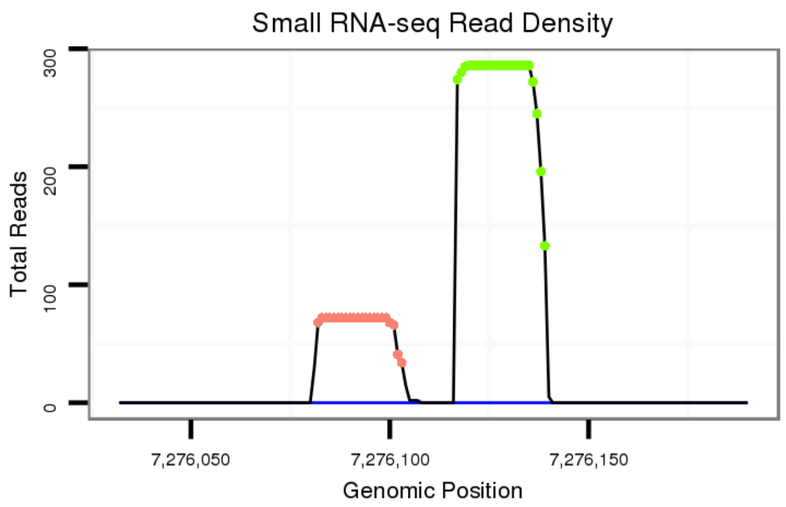
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	4
rescue.candidate	1

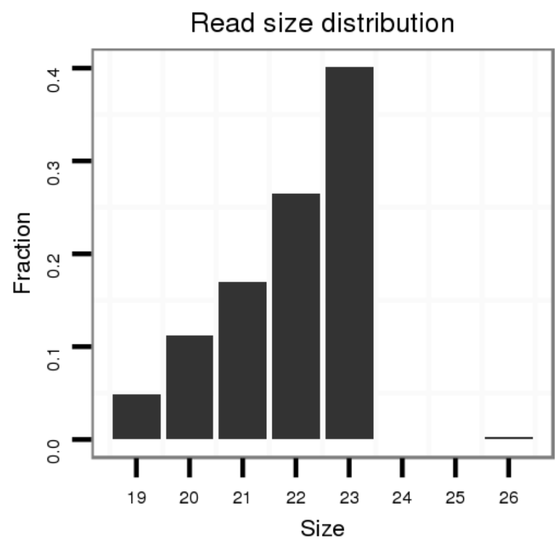
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_74	**scf2_1100000004902:7276082-7276140 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

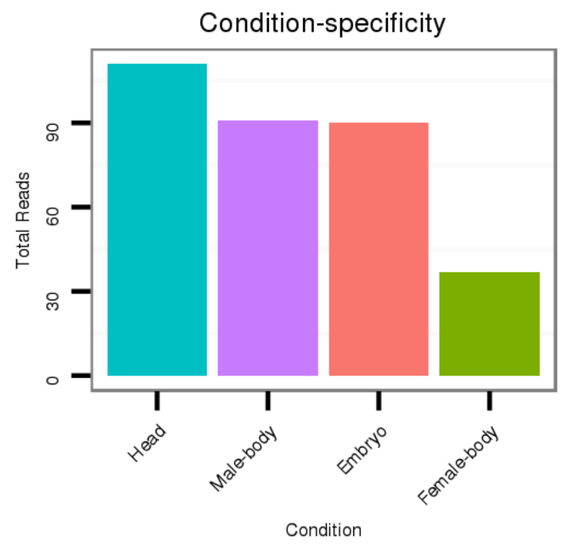
Legend: mature star **mismatch in alignment** mismatch in read

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

	Read size	# Mismatch	Hit Count	Total Norm	Total	male body	head	embryo	body	head
TTCATGTCTTAAAGTAATAATAACTTAACTCTAAAAAGTCTTGTTTTCTTCTTGAGTTATGAGTGAATATATGGTTTTTGAAACATATGTCATGCGCTAACTCATCCAGAAAGCTTTGGCCTCATGTAGTCGTTAAAAAGATTATGTAAAAGTTCTCAT						V117	M020	V118	M045 female	V119
..(((..(((((((...(((((((((.((((.((((((.........)))))))))).)))..)))))))...)))))))...)))....										
.....TATGTCATGCGCTAACTCATCCA.....	23	0	1	126.00	126	17	33	62	10	4
.....TATGTCATGCGCTAACTCATCC.....	22	0	1	60.00	60	13	29	9	5	4
.....TATGTCATGCGCTAACTCATC.....	21	0	1	49.00	49	16	21	5	5	2
.....TATGTCATGCGCTAACTCAT.....	20	0	1	25.00	25	11	2	2	9	1
.....CTTGAGTTATGAGTGAATATAT.....	22	0	1	17.00	17	13	0	2	1	1
.....TCTTGAGTTATGAGTGAATAT.....	21	0	1	14.00	14	13	0	1	0	0
.....TATGTCATGCGCTAACTCA.....	19	0	1	14.00	14	0	14	0	0	0
.....CTTGAGTTATGAGTGAATAT.....	20	0	1	11.00	11	11	0	0	0	0
.....TATGTCATGCGCTAACTCATCCT.....	23	1	1	9.00	9	0	9	0	0	0
.....CTTGAGTTATGAGTGAATATATG.....	23	0	1	6.00	6	1	0	5	0	0
.....TCTTGAGTTATGAGTGAATATAA.....	23	1	1	5.00	5	3	0	2	0	0
.....TGTCATGCGCTAACTCATCCAG.....	22	0	1	5.00	5	3	0	1	1	0
.....TCTTGAGTTATGAGTGAATAA.....	21	1	1	4.00	4	4	0	0	0	0
.....TATGTCATGCGCTAACTCATA.....	21	1	1	4.00	4	1	1	0	0	2
.....TCTTGAGTTATGAGTGAAT.....	19	0	1	4.00	4	4	0	0	0	0
.....TTGAGTTATGAGTGAATATATG.....	22	0	1	4.00	4	1	0	3	0	0
.....CTTGAGTTATGAGTGAATATAA.....	22	1	1	4.00	4	4	0	0	0	0
.....CTTGAGTTATGAGTGAATATA.....	21	0	1	4.00	4	4	0	0	0	0
.....TATGTCATGCGCTAACTCATCA.....	22	1	1	3.00	3	1	1	1	0	0
.....ATGTCATGCGCTAACTCATCC.....	21	0	1	3.00	3	0	0	1	2	0
.....TCTTGAGTTATGAGTGAATATATG.....	24	0	1	3.00	3	2	0	1	0	0
.....TCTTGAGTTATGAGTGAATATA.....	22	0	1	3.00	3	2	0	1	0	0
.....TATGTCATGCGCTAACTCATCCAT.....	24	1	1	2.00	2	1	0	1	0	0
.....TCTTGAGTTATGAGTGAATATAT.....	23	0	1	2.00	2	2	0	0	0	0
.....ATGTCATGCGCTAACTCAT.....	19	0	1	2.00	2	0	0	0	2	0
.....TCTTGAGTTATGAGTGAATA.....	20	0	1	2.00	2	2	0	0	0	0
.....ATGTCATGCGCTAACTCATCCAA.....	23	1	1	1.00	1	0	0	0	1	0
.....CTTGAGTTATGAGTGAATATC.....	21	1	1	1.00	1	1	0	0	0	0
.....TCTTGAGTTATGAGTGAATATAAA.....	24	2	1	1.00	1	1	0	0	0	0
.....GTCATGCGCTAACTCATCCA.....	20	0	1	1.00	1	0	0	0	1	0
.....TATGTCATGCGCTAACTCATCCC.....	23	1	1	1.00	1	0	1	0	0	0
.....ATGTCATGCGCTAACTCATCCA.....	22	0	1	1.00	1	0	0	0	1	0
.....TATGTCATGCGCTAACTCATCCAA.....	24	1	1	1.00	1	0	0	1	0	0
.....TCTTGAGTTATGAGTGAATATC.....	22	1	1	1.00	1	1	0	0	0	0
.....CTTGAGTTATGAGTGAATATATAAA.....	25	3	1	1.00	1	0	0	1	0	0
.....CTTGAGTTATGAGTGAATATATGGTT.....	26	0	1	1.00	1	1	0	0	0	0
.....TCTTGAGTTATGAGTGAATATATGGTT.....	27	0	1	1.00	1	0	0	1	0	0
.....TATGTCATGCGCTAACTCATCT.....	22	1	1	1.00	1	0	1	0	0	0
.....TTCTTGAGTTATGAGTGAATATAA.....	24	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body
AAGTACAGAATTTCATTATTATTGAATTGAGATTTTTCAGAACAAAAGAAGAACTCAATACTCACTTATATACCAAAAACTTTGTATACAGTACGCGATTGAGTAGGTCTTTCGAAACCGGAGTACATCAGCAATTTTTCTAATACATTTTCAAGAGTA						
**********..(((..(((((((...(((((((((.((((.((((((.........)))))))))).)))..)))))))...)))))))...)))...**********						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004902:7276032-7276190 +	dwi_74	TTCATGTCTTAAAGTAATAATAACTTAACTCTAAAAAGTCTTGTTTTCTTCTTGAGTTATGAGTGAATATATGGTTTTTGAAACATATGTCATGCGCTAACTCATCCAGAAAGCTTTGGCCTCATGTAGTCGTTAAAAAGATTATGTAAAAGTTCTCAT

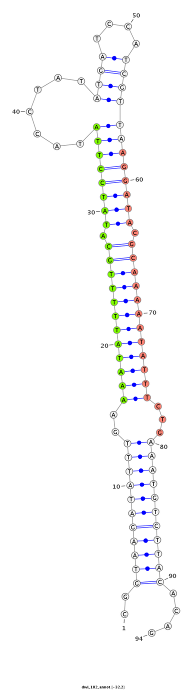
Generated: 09/08/2015 at 07:39 PM

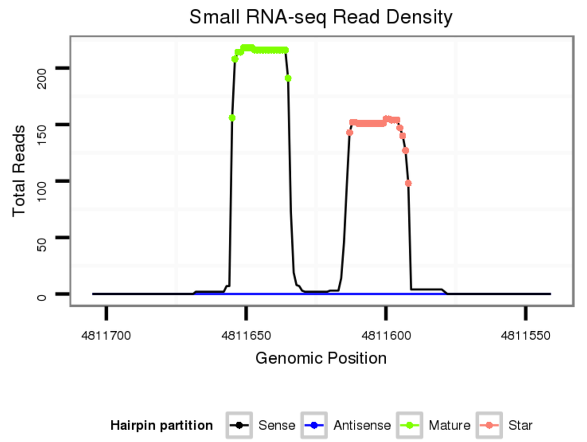
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

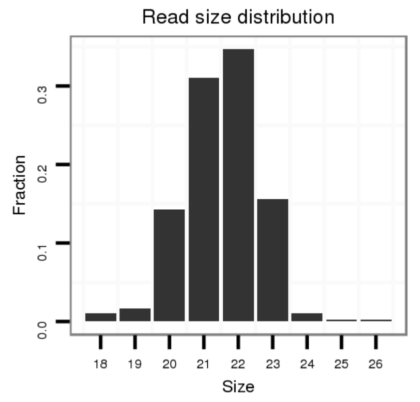
ID: dwi_102	Coordinate: scf2_1100000004521:4811591-4811655 -	Confidence: confident	Class: Canonical miRNA	Genomic Locale: intergenic	[View on UCSC Genome Browser {Cornell Mirror}]

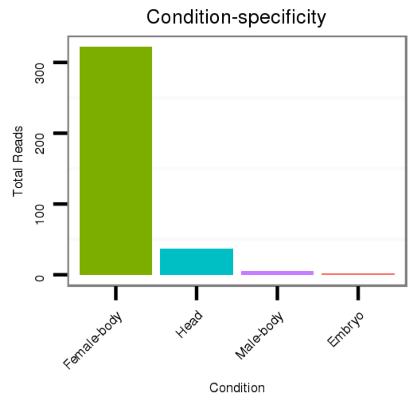
Legend: mature star mismatch in alignment mismatch in read

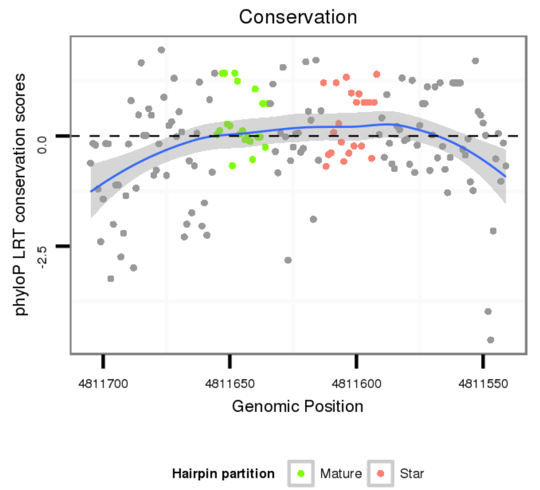
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

mature	star
1. dwi_102 scf2_1100000004521:4811635-4811655 - 2. scf2_1100000004961:1416511-1416531 +	

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TAAACATTATTTCAATTTGTTTATCTCAAAGTAAACGGTAAGATATTTGAAAATATTTTTGCATATCCTTATACCTATATGATCCATCGTTAAGGATACGCAAAAATATTTCTGAAATGTCTTACACAGCCTTTTCAAACGTAAATTTTATGTTAAACGAAAAA

**********************************..((((((((((..((((((((((((.((((((((.......((((....)))))))))))).))))))))))))...)))))))))))....***********************************

Read	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	M020 head	V117 male body	V118 embryo	V119 head
...AAATATTTTTGCATATCCTTA...	21	0	2	85.50	171	171	0	0	0	0
...AGGATACGCAAAAATATTTCTG...	22	0	1	45.00	45	38	7	0	0	0
...AAATATTTTTGCATATCCTTAT...	22	0	1	44.00	44	43	0	1	0	0
...AAGGATACGCAAAAATATTTCTG...	23	0	1	37.00	37	12	24	0	1	0
...AATATTTTTGCATATCCTTA...	20	0	2	32.00	64	64	0	0	0	0
...AAATATTTTTGCATATCCTT...	20	0	3	17.33	52	52	0	0	0	0
...TAAGGATACGCAAAAATATTTCT...	23	0	1	14.00	14	14	0	0	0	0
...AAGGATACGCAAAAATATTTCT...	22	0	1	12.00	12	10	0	2	0	0
...TAAGGATACGCAAAAATATTTC...	22	0	1	10.00	10	8	0	0	0	2
...GGATACGCAAAAATATTTCTG...	21	0	1	9.00	9	9	0	0	0	0
...AATATTTTTGCATATCCTTATA...	22	0	1	9.00	9	9	0	0	0	0
...AATATTTTTGCATATCCTTAT...	21	0	1	6.00	6	6	0	0	0	0
...GAAAATATTTTTGCATATCCTT...	22	0	1	5.00	5	5	0	0	0	0
...TTAAGGATACGCAAAAATATTT...	22	0	1	5.00	5	5	0	0	0	0
...ATTTTTGCATATCCTTAT...	18	0	1	4.00	4	4	0	0	0	0
...TTAAGGATACGCAAAAATATT...	21	0	1	4.00	4	2	0	2	0	0
...AATATTTTTGCATATCCTT...	19	0	3	3.67	11	11	0	0	0	0
...TAAGGATACGCAAAAATATT...	20	0	1	3.00	3	3	0	0	0	0
...AGGATACGCAAAAATATTTCT...	21	0	1	3.00	3	3	0	0	0	0
...TAAGGATACGCAAAAATATTTCTG...	24	0	1	3.00	3	0	3	0	0	0
...ATATTTTTGCATATCCTTA...	19	0	2	2.50	5	5	0	0	0	0
...GTAAGATATTTGAAAATATTT...	21	0	1	2.00	2	2	0	0	0	0
...ATATTTTTGCATATCCTTATACC...	23	0	1	2.00	2	2	0	0	0	0
...ATATTTCTGAAATGTCTTACA...	21	0	1	2.00	2	2	0	0	0	0
...ATATTTCTGAAATGTCTTACAC...	22	0	1	2.00	2	2	0	0	0	0
...TTAAGGATACGCAAAAATATTTC...	23	0	1	2.00	2	1	1	0	0	0
...TAAGGATACGCAAAAATATTT...	21	0	1	2.00	2	2	0	0	0	0
...GGATACGCAAAAATATTTCTGT...	22	1	1	2.00	2	2	0	0	0	0
...AAATATTTTTGCATATCCTTATACCT...	26	0	1	1.00	1	1	0	0	0	0
...AAATATTTTTGCATATCCTTATT...	23	1	1	1.00	1	1	0	0	0	0
...AAATATTTTTGCATATCCTTATACC...	24	0	1	1.00	1	1	0	0	0	0
...TAAGGATACGCAAAAATATTTCA...	23	1	1	1.00	1	1	0	0	0	0
...TACCTATATGATCCATCGTTA...	21	0	1	1.00	1	0	0	0	1	0
...AAGGATACGCAAAAATATTTC...	21	0	1	1.00	1	1	0	0	0	0
...AATATTTTTGCATATCCTTATAC...	23	0	1	1.00	1	1	0	0	0	0
...CTATATGATCCATCGTTAAGG...	21	0	1	1.00	1	1	0	0	0	0
...ATATTTTTGCATATCCTTATA...	21	0	1	1.00	1	1	0	0	0	0
...ATATTTTTGCATATCCTTATAC...	22	0	1	1.00	1	1	0	0	0	0
...ATCGTTAAGGATACGCAAAAAT...	22	0	1	1.00	1	1	0	0	0	0
...AAATATTTTTGCATATCCTTATACC...	25	0	1	1.00	1	1	0	0	0	0
...GATACGCAAAAATATTTCTGT...	21	1	1	1.00	1	1	0	0	0	0
...AAATATTTTTGCATATCCTTATA...	23	0	1	1.00	1	1	0	0	0	0
...AAAATATTTTTGCATATCCTTA...	22	0	2	0.50	1	1	0	0	0	0
...AAAATATTTTTGCATATCCTT...	21	0	3	0.33	1	1	0	0	0	0

Anti-sense strand reads

ATTTGTAATAAAGTTAAACAAATAGAGTTTCATTTGCCATTCTATAAACTTTTATAAAAACGTATAGGAATATGGATATACTAGGTAGCAATTCCTATGCGTTTTTATAAAGACTTTACAGAATGTGTCGGAAAAGTTTGCATTTAAAATACAATTTGCTTTTT

**********************************..((((((((((..((((((((((((.((((((((.......((((....)))))))))))).))))))))))))...)))))))))))....***********************************

Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004521:4811541-4811705 -	dwi_102	TAAACATTATTT-----CAA---TTT-GTTTATCTCA------AAGTAAAC----GGTAAGATATT---TG---AAAATATTTTTGCATATCCTTATACCTATATG---ATCCATCGTTA---AGGATACGCA-AA---AA---TATTTCTGAAATGTCTTACA---CAG--CCTTTTCA---AACGTAAATTT---TA---T-G---TTAAACGAAAAAA
droVir3	scaffold_12954:2009004-2009160 -		AAATTATTATTA---TAA---ATT---A---A---AAATAAAGTTTGAGAATAATTTAATAATATT---TGATATAAACAAT---TTGACCA---TA---GTTT---AAAGGATAAAAA--ATAACTCCA---T---AAGT-TCTAATATAAGGTATAAATCATATTGAACCTATAAAATTTGTTAAATTATATAA
droMoj3	scaffold_6680:16371250-16371414 +		TAAACATGTGTT---TAA---ATA-ATTTTTAAT---AAAT----GAAA---TCTACTAT---ATTTA---TGATATTTTTTCTTATCAA---ACACAAAAGTCTGAATATT---TAG---ATA-TTAAATATTAAATTTAAAATATATATTTA---TTATGGATTATA---CAT---TTTTAAAATTTCA---T-G---TTAAATGAAAAAA
droGri2	scaffold_14853:959308-959472 +		TATAATATCGATATTGCAAGCA---A---T---AA---CTAT---ATATA---ACTA---TATAA---CTATATA---TAAATATATGT---ATATATATATACATAC---ACATA---TACATATATAC-ATATATATAA---ATA--TAT--AG---TAATAATTTATA---TAC--CC---TTACCATGATATGATAA-ACGAAACA---AATACAAAAA
dp5	4_group1:272620-272777 -		TATACATTTTTA----CAA---ATT---A----AAGTAAAC----GAAG-------AGGAGGATATTTTTACTCGAAATGC---AGCTGTGATATATTTTTAATGAATGT---ATAGAGAGAGAAAAAC---ACAACAGAAATTATATGCAACAATTTTCCAACCA---ACAAAAAGTTAAA---ACA---AAACGAAACA
droPer2	scaffold_1:267767-267924 -		TATACATTTTTA----CAA---ATT---A----AAGTAAAC----GAGG-------AGGAGGATATTTTTACTCGAAATGC---AGCTGTGATATATTTTTAATGAATGT---ATAGAGAGAGAAAAAC---ACAACAGAAATTATATGCAACAATTTTCCAACCA---ACAAAAAGTTAAA---ACA---AAACGAAACA
droAna3	scaffold_13266:19162040-19162210 -		TTATTTTAATAG----TTA---GA-GGCTTGGTTTTA---AAGA----AAAA---CAAAATAT---GTTTG---GAAAAATTCGTTGTTGAGA---T---ATC---A---ATCGTA---C---GTGTAT---TTGGGAG---TG---ATG---GGAT---TAAAGTTGCAAAAAGTGATATTTTATTC--TTAG--TAAAAAACATA--CAATAATTC---TA---T-GCA---AAAGTAACAA
droBip1	scf7180000396571:260583-260745 +		AAAAAAATATA---TAT---A---TATAA-AAAAAT---GATATTATAA---TGAA---ATAA---AATTATTTATATT---A---TTT---ATT---ATTTATA---TTATTTATTA---TTTATATTATTTAT---TATTTATATTA-T---TTATTATTTA--TAT--TATTTATAT---TATTAAAAAAATAATAAT---ATA---AACAAACCAA
droKik1	scf7180000302398:184960-185131 -		TTAATATCAAGA----AAATA---A-TTTATTTC---TCAAAAAAAT---AT---C---TAT---TTAAAAAATAAAAACT---ACAATAAAAATATTTATAAATATATTTAAATATTTAAACATACAT---TAAAAATATTC-ATTTATTTAA---AAA--TAT--TT---TA---AAT---ATTTGAAA---ATATATTTTAA-ATT---AAGAAAATAA
droFic1	scf7180000454055:298728-298865 -		TTATTTTTTAA---ATT---TTTAAA---AACA----AAAA---TAAA---ATAA---AAT---TTTGAATATA---TAT---ATA---ATATACA---TAATAAATGA---TTCAGTTTATAAAT---TAAAAATGTTTTT---TTTTTATATC--TTT--TTTTTAAA---T-A---TTAAAAATTAAC
droEle1	scf7180000490644:689682-689822 +		TAAAATTTTAAT---TTT---TAT---ATTCAAATTGA---AGTTAAATAATAATATTATTGATTTCATCATTTAAATTGATTTATAATTA---TAAAT---AAAA---T---ATTTCTTTT--TTTC--TAAAGTCCCTA-GATA---TGACTT-TCAAATAT---ACGGAAAAAC
droRho1	scf7180000779688:491-671 -		TGAGGTTTCTTT----CAA---GAA-ACTTTA---AAATA--C---AGTTA---AA-TTA---A---TATTGGAATTTAAAATATATTTATTTCTCCTAAATACCAATCTT---ATAAATGTCA---ACAAAATGAAAA---AAAATACAAAT---TCCGTTAGTTTTCCAGTG---TTTTTTAAAAACTAAAAATCGTAATTC---GT---T-A---TTAAACCTAAAGA
droBia1	scf7180000301226:13109-13249 -		AAAATTTTTTTA----AG---TT---TGTAA-AA---AGCTAGTTTC---A---AAAAGTACCCTCTGTTTG---CAA---GTCTACATCTC---C---ATGTTT---C---ATATATCTGCATAA---AA---TCCTCTGAATT---CT---CTACTTTTA---AATA---AATTTTTTAA-A---TCCACAAAAA
droTak1	scf7180000415386:7640-7787 +		AATTTAATTTTA---AA---TT---T---AAATTAAATGT---ATTAA---ACTG---TGACCTATACTATTTAAATTAAATACGAATATCATCATATCTAATATTATCATCCTGCATTTAAATATTTTTAATCA---CACAGTTTTA---TATG---TAT---TG---T-G---TTAAAAGATATGT
droEug1	scf7180000409472:177205-177358 +		TATCCAATAACT----GTT---A---AAGTTAAC----ATTA---AAGTTAAAATATAAATTAAATAT---ATTTA---CGAA---TGGTTATCATT---ATTAATTTTAG---TAATAC---TAAA---GATATTAATAT---TAT---ACATTTCAATT---TT---ATC---GTAT---TGGGGTCGGTAT--ACGACTTTT---T---AAGTT
dm3	chr3L:19002298-19002382 +		CACACGACCCGA----AAGTA---G---G---AACAC---T---TTTTG---CAA---ATGCAACATGTTGCGGATGCT---G---ATG---CCACATGGCTAAG---GGG---AGGCCAAAAAT
droSim2	4:201328-201399 -		AAAACATAAATT----GTATATTTTAATAATTAAA-AA---TTACAATAAG---C---TAAACTAA---ATGTTT---TACCATTTT---CTCAT
droSec2	scaffold_8:3569152-3569311 -		TTATCATAACTT----AGTCATCTTTAAAGTCATA-CG---GTAAAATCTC---A---AAAAATAA---ATG-TAGCGTTTGTACTTCCAA---TTGTTTAGTTATTGTATA---GCACCGGATATTATTTCTGGT---CG---A---TACGACAAAACCTTATA---AATA---GGATCT-CTGA-A---TGAAGAAGCTGTA
droYak3	v2_chr2L_random_028:300364-300552 -		TAAACATTGTTT----TTA---TTT-TTTTTTTT---ACAT---TAAC---TAA---TAATA---ACAA---ATTTA---TAATTTATAGAACAGTTTTTATTTTTTATTCTTAGTTTCGTTATCCT---ATCCTG---C---GCGTAC---TGGA---AA---TA---TTTTGTGTAA---TGCGGTCGAAATAAGCGTCCTCC---AACGCCAATTTATT---CTTA-AAA---GCGACTGTAAC
droEre2	scaffold_4770:6417207-6417362 -		AAAAACTTGTTT----TAA---ATT---A---TTCA---AAATGTATCTTCGG---CCT---AAATAAACCATGAAGAAAATATTGTAAAGTATTGTATGAACTT---AACCACCATCT---TAATTT---ATTTCAGACACTATTTTAGACTTGTTTTTGAACG---TCATATGTT---TTGGATAATTAAA

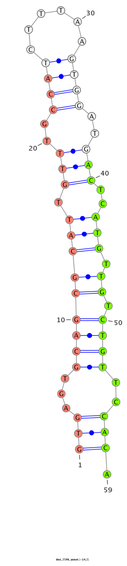
Generated: 09/08/2015 at 07:42 PM

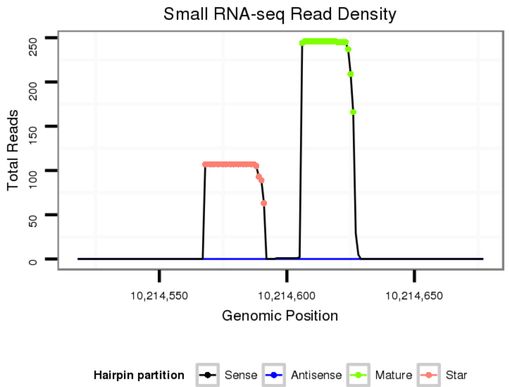
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

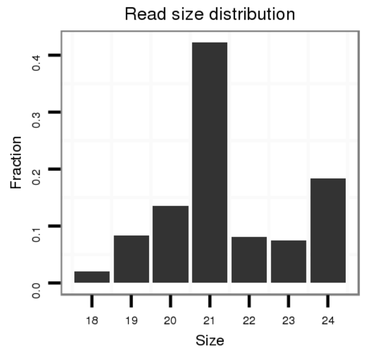
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_2596	**scf2_1100000004902:10214568-10214627 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

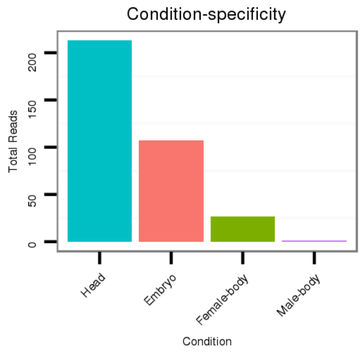
Legend: mature star mismatch in alignment mismatch in read

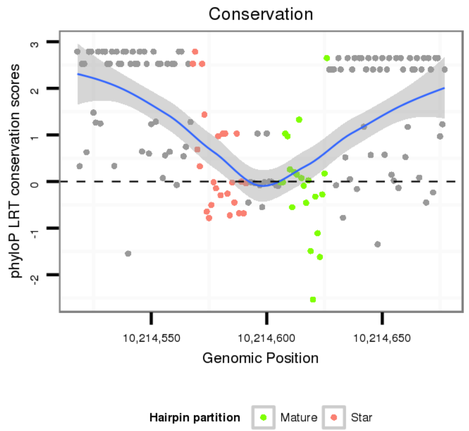
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK12160-in]; CDS [Dwil\GK12160-cds]; CDS [Dwil\GK12160-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATGCGAAATTGATGCTTAGCATACTCGATTGCCTGCCAAGGGCGAATAGGGTGAGTGCAGCGCATTGTTTGCCACTCTTTAAGTGGATGACTCATGTTGTCTGTTCCACAGGCTACTCTCGTTTTCCTGCTAGATCATTTGTCGCTGGTCGTTTCGAATTC	Read size	# Mismatch	Hit Count	Total Norm	Total	V119 head	V118 embryo	M020 head	M045 female body	V117 male body
**********(((...(((((((((.(((..((((.....))))..))))..)))).))).))))..))))**********										
..ACTCATGTTGTCTGTTCCACAGT..	23	1	1	2146.00	2146	1009	1054	49	33	1
..ACTCATGTTGTCTGTTCCACA..	21	0	1	135.00	135	92	16	11	16	0
..GTGAGTGCAGCGCATTGTTTGCCA..	24	0	1	63.00	63	11	52	0	0	0
..ACTCATGTTGTCTGTTCCAC..	20	0	1	43.00	43	27	8	8	0	0
..ACTCATGTTGTCTGTTCCA..	19	0	1	28.00	28	12	0	14	2	0
..GTGAGTGCAGCGCATTGTTTGCC..	23	0	1	26.00	26	3	23	0	0	0
..ACTCATGTTGTCTGTTCCACAG..	22	0	1	24.00	24	6	2	8	8	0
..ACTCATGTTGTCTGTTCCACAGA..	23	1	1	12.00	12	7	5	0	0	0
..GTGAGTGCAGCGCATTGTTTG..	21	0	1	12.00	12	9	3	0	0	0
..ACTCATGTTGTCTGTTCCACAGC..	23	1	1	12.00	12	2	1	9	0	0
..ACTCATGTTGTCTGTTCCACAGTT..	24	2	1	11.00	11	9	2	0	0	0
..ACTCATGTTGTCTGTTCC..	18	0	1	7.00	7	0	0	7	0	0
..ACTCATGTTGTCTGTTCCACAGG..	23	0	1	5.00	5	2	0	3	0	0
..GTGAGTGCAGCGCATTGTTTGC..	22	0	1	4.00	4	2	2	0	0	0
..ATGTTGTCTGTTCCACAGT..	19	1	1	3.00	3	2	0	0	1	0
..GTGAGTGCAGCGCATTGTTTGCCC..	24	1	1	2.00	2	1	1	0	0	0
..TCATGTTGTCTGTTCCACAGT..	21	1	1	2.00	2	1	0	0	1	0
..ACTCATGTTGTCTGTTCCACC..	21	1	1	2.00	2	1	0	1	0	0
..ACTCATGTTGTCTGTTCCACT..	21	1	1	2.00	2	0	0	2	0	0
..GTGAGTGCAGCGCATTGTTT..	20	0	1	2.00	2	0	1	0	0	1
..CTCATGTTGTCTGTTCCACA..	20	0	1	2.00	2	1	0	0	1	0
..ACTCATGTTGTCTGTTCCACAAT..	23	2	1	2.00	2	2	0	0	0	0
..ACTCATGTTGTCTGTTCCACAGTA..	24	2	1	2.00	2	2	0	0	0	0
..ACTCATGTTGTCTGTTCCG..	19	1	1	1.00	1	0	0	1	0	0
..GACTCATGTTGTCTGTTCC..	19	0	1	1.00	1	1	0	0	0	0
..ACTCATGTTGTCTGTTCCACAGAAA..	25	3	1	1.00	1	1	0	0	0	0
..ACTCATGTTGTCTGTTCCACAA..	22	1	1	1.00	1	1	0	0	0	0
..TCATGTTGTCTGTTCCACAGTT..	22	2	1	1.00	1	0	0	0	1	0
..ACTCATGTTGTCTGTTCCACAGT..	23	2	1	1.00	1	1	0	0	0	0
..CATGTTGTCTGTTCCACAGT..	20	1	1	1.00	1	1	0	0	0	0
..TAAGTGGATGACTCATGTTGTCTG..	24	0	1	1.00	1	1	0	0	0	0
..ACTCATGTTGTCTGTTCCACATT..	23	2	2	1.00	2	0	2	0	0	0
..ACTCATGTTGTCTGTTCCAGT..	21	2	3	1.00	3	2	1	0	0	0

Anti-sense strand reads

TACGCTTTAACTACGAATCGTATGAGCTAACGGACGGTTCCCGCTTATCCCACTCACGTCGCGTAACAAACGGTAGAAATTCACCTACTGAGTACAACAGACAAGGTGTCCGATGAGAGCAAAAGGACGATCTAGTAAACAGCGACCAGCAAAGCTTAAG	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
droWil2	scf2_1100000004902:10214518-10214677 +	dwi_2596	ATGCGAAATTGATGCTTAGCATACTCGATTGCCTGCCAAGGGCGAATAGGGTGAG-TGCA-GCGCATTGTTTGCCATCTTTAAGTGGATGACTCATG----------TTGT----------CT-------GTTCCACAGGCTACTCTCGTTTTCCTGCTAGATCATTTGTCGCTGGTCGTTTCGAATTC
droVir3	scaffold_13047:14849044-14849215 +		ATGCGAAACTGATGCTTAGCATACTCGACTGTTTGCCCAGACGCGAATAGGGTGCCG-TTTA----------AT-TTATGACTGTGGTTC----TTT-T-TAATGGAT----------A------AA------T---------ATC-TAA---------CAA----------TTCCATTAACTC---------------TAATTTTAGGCTACCTTGGTATTCCTGCTTGACCATCTTCGCTGGTTGTGTCTCAATGC
droMoj3	scaffold_6540:18301856-18302020 +		ATGCGAAACTGATGCTTAGCATACTCGACTGTTTGCCACGGGCGAATAGGGTGAG-TCTA----------AT-CTC--AACGTGA---GTCTGCTGGGT----------A------AA------T---------C-TGAAAATGTTGTTC----------------GACTATCAATAGGCCACCTTGGTGTTCCTGCTTGACCACTTGTGTTCTGGTTGTGTCTCAATGC
droGri2	scaffold_14830:5132856-5132921 -		ATGCGAAACTGATGCTTAGCATACTCGACTGTTTGCCAGGGCGAATAGGGTGAG-TACA----------AC-AT----------ATT
dp5	2:16132388-16132547 -		ATGCAAAACTGATGCTTAGCATCTCGATTGCCTGCCAGGGCGAACAGGGTGAG-TGGA-AAGCATACAGTACTAGTATTCCATGGAGGTTCTCA----------TTCC----------CT-------GTCCTTTAGGCCACTCTTGTGATTCCTGCTGGACCACCTGTCGCTGGTCGTTTCCAACTC
droPer2	scaffold_0:4273201-4273360 +		ATGCAAAACTGATGCTTAGCATCTCGATTGCCTGCCAGGGCGAACAGGGTGAG-TGGA-AAGCATACAGTACTAGTATTCCATGGAGGTTCTCA----------TTCC----------CT-------GTCCTTTAGGCCACTCTTGTGATTCCTGCTGGACCACCTGTCGCTGGTCGTTTCCAACTC
droAna3	scaffold_13340:284903-285070 -		ATGCGAAACTGATGCTTAGCATCTCGACTGTCTGCCGCGGGCAAACCGGGTATG-TTTCA----------GAGTAGC----------A------TTTTTGCGTTTATTCCACCGAGGTTTTCTGATTCG----------CGGCTT------CTCTCGCTAGGCCACGCTTGTGTTCCTGCTGGACCACTTGTCGCTGGTTGTGTCTCAACTC
droBip1	scf7180000394085:684606-684770 +		ACGCGAAACTGATGCTCAGCATCTCGACTGTCTGCCGCGGGCGAACCGGGTACG-TTTGAAACGAT-TATTCTGGTTACTCTATTAAGGTTTTCTGA----------TTC-----------C----------CGTCTT------CTCTCAATAGGCCAACGCTGGTGTTCCTGCTGGACCACTTGTCGCTGGTTGTGTCTCGAACTC
droKik1	scf7180000302475:2208727-2208892 -		ATGCGAAACTGATGCTTAGCATCTCGACTGCCTGCCGCGGGCGAACAGGGTAAG-TTTCA----------ATTGGA----------A------TCCGACGAA----------TCCCAAC----------CAG----------AAATC-TGATCAAAATTGTTAC------ATTAATAGGCCACCTTGGTGTTCCTGCTGGACCACTTGTCGCTGGTTGTGTCTCAACTC
droFic1	scf7180000454097:97371-97538 +		ACGCTAAGGCTGATGCTCAGCATCTCGACTGCCTGCCGCGGGCGAACAGAGTAAG-ATCC----------GCACTCCGCCTGTCG----------C---TCAGC----------TG---ACATTTGTA-----CATGTAACTAATGC-AA----------T------CCATCTGCAGGCCACGCTGTGGTGTTCTGCTGGACCACCTGTCGCTGGTCGTCTCGAACTC
droEle1	scf7180000491196:16912-17067 +		ACGCGAAACTCATGCTTAGCATACTCGACTGCCTGCCGCGACGAACCGGGTAAG-AATA----------GC-TG----------ATGC----------TGGTAAGAAAA----------TCGTGACCCATAC----------CACAGA------ATTCTACAGGCCACGCTGTGATTCCTGCTGGACCATCTGTCGCTGGTCGTTTCCAACTC
droRho1	scf7180000779322:12005-12160 -		ATGCGAAACTCATGCTTAGCATACTCGACTGCCTGCCGCGGGCGAACAGGGTAAG-AAAA----------GC-TG----------GCAT----------ATAAAAGAAAA----------TGTTGACCCTTAC----------CGCATA------ACGATTATAGGCCACGCTGTGATTCCTGCTGGACCATCTGTCGCTGGTCGTTTCCAACTC
droBia1	scf7180000302035:336181-336339 +		ATGCGAAACTGATGCTTAGCATCTCGACTGCCTGCCGCGGGCGAATAGGGTAAG-ATTA----------G-GT----------TTT-T-CCGCCTGA----------AGATACA----------TTTTTACCGA----------CC----------CGCCTT------CCCCACAGGCCACCTGTGGTATTCCTGCTGGACCACCTTTCGCTGGTCGTTTCCAACTC
droTak1	scf7180000415712:771848-772001 +		ATGCGAAACTGATGCTTAGCATACTCGACTGCCTGCCGCGGGCAAACAGGGTAAGCATTA----------GC-CA----------TTTTC-CATTTTAA----------AAGTAGA----------T------T----------CTC-AAA----------C----------AT------ATTTTACAGGCCACTCTGGTATTCCTGCTGGACCACCTGTCGCTGGTCGTCTCGAACTC
droEug1	scf7180000409488:240924-241083 -		ATGCGAAACTGATGCTTAGCATACTCGACTGCCTGCCGCGGGCGAACAGGGTAAG-ATCA----------GC-TT----------TTA----------AACATTCGAAAGTACA----------TTTTTACCGAACT----------CGGGGT------CTGCTGCAGGCCACCTGTGATTCCTGCTAGACCACCTGTCACTGGTCGTTTCCAACTC
dm3	chr3R:27662474-27662643 +		ATGCGAAACTGATGCTTAGCATACTCGACTGCCTACGCGGGCGAACAGGGTGAG-ACGG----------GT-CG----------TTTTT-AAATTTAA----------G------AA------A---------CGT-AAT---------CTA----------TAATCTGTATAACAATTTCGTA------ATGACACGGCCACCTGTGGTATTCCTTCTTGATCACCTGTCGCTGGTCGTTTCAACTC
droSim2	3r:26938395-26938571 +	dsi_16839	ATGCGAAACTGATGCTTAGCATTCTCGACTGCCTGCCGCGGGCGAACAGGGTAAG-ACCA----------G-CG----------CTTTT-AAGTTTAA----------A------AA------A---------CTT-TAA---------CTA----------TAGTATGTATTCCAATTTCGTAATTGGAATAATTACAGGCCACCTGTGGTATTCCTTCTTGATCACCTGTCGCTGGTCGTTTCAACTC
droSec2	scaffold_31:325803-325978 +		ATGCGAAACTGATGCTTAGCATTCTCGACTGCCTGCCGCGGGCGAACAGGGTAAG-ACCA----------G-CG----------TTT-T-AAATTTAA----------A------AA------T---------CTT-TAA---------CTA----------TAGTTTTTATTCCAATTTCGTAATTGGAATCATAACAGGCCACCTGTGGTATTCCTTCTTGATCACCTGTCGCTGGTCGTTTCAAACTC
droYak3	3R:28598401-28598556 +		ATGCGAAACTGATGCTTAGCATTCTCGACTGCCTGCCGCGGGCAAACAGGGTAAG-ATGG----------GC-CG----------TTTCTTAATTTTAA----------A------CA------A---------CTT-TAA---------ATA----------TAATTTGTA----------TTGCAGGCCACCTGTGGTATTCCTCTTGATCACCTGTCGCTGGTCGTTTCAAACTC
droEre2	scaffold_4820:305943-306118 -		ATGCGAAACTGATGCTTAGCATACTCGACTGCCTGCCGCGGGCAAACAGGGTAAG-ATGG----------GC-CG----------TTTCT-TAACTTAA----------A------AATTACATA---------CAT-GAA---------CTC----------TAATTTGTACTCCAATTGCGTA------ACTCTACAGGCCACCTGTGGTATTCCTTCTTGGTCACACCTGTCGCTGGTCGTTTCAAACTC

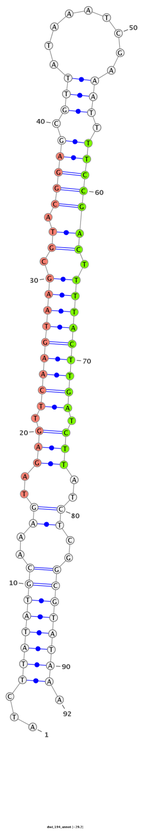
Generated: 09/08/2015 at 10:35 PM

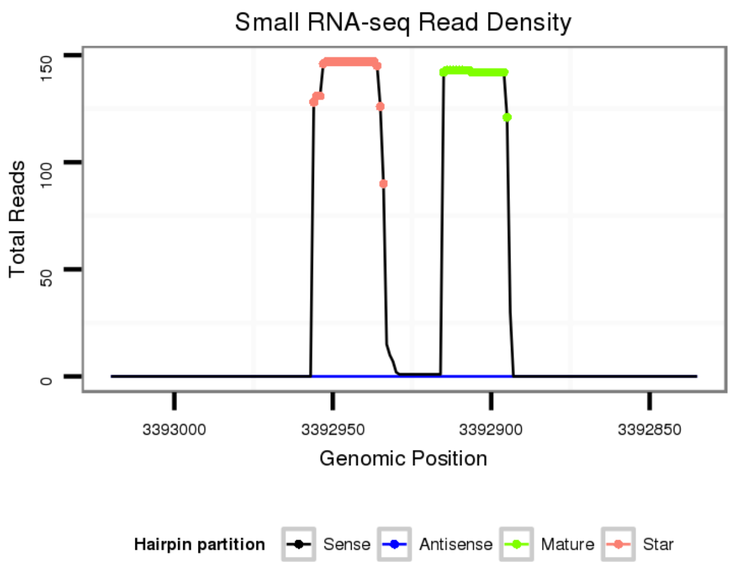
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

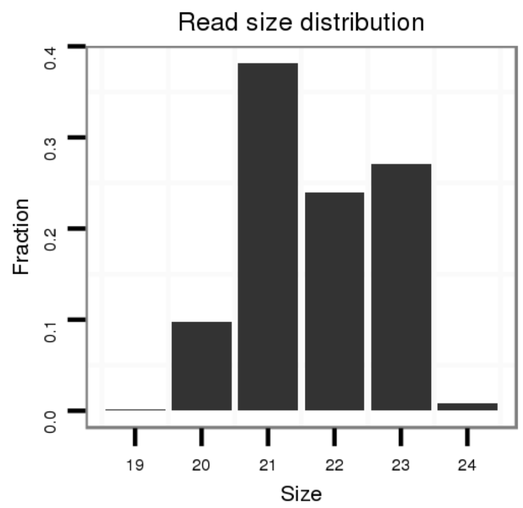
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_194	**scf2_1100000004511:3392885-3392970 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

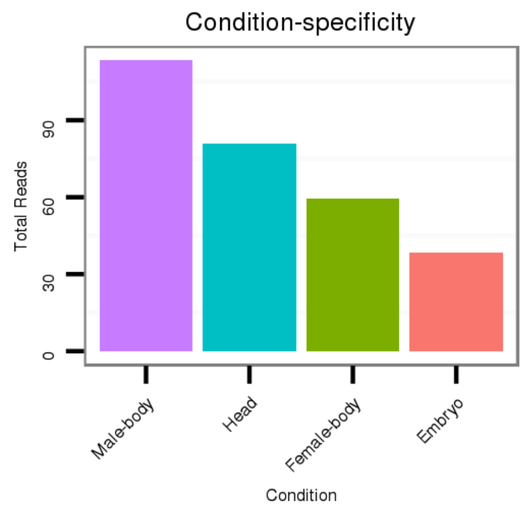
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

mature	star
1. dwi_194 scf2_1100000004511:3392895-3392915 - 2. dwi_72 scf2_1100000004511:3393111-3393131 - 3. dwi_157 scf2_1100000004511:3393968-3393988 -	

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GAATTGGCAGAGAAAAACTTAGTGATAGTCGCAGGATCATAAAAATCACATCTTATATGCAAAGTAGAGTTCAAGTAAGCGTACGGAGCGTTATAAATCGAAATTTTCCGACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCATAAAAAAAAATACAAATCAACATTTTTCTAATCATCCCA	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	M020 head	M045 female body	V118 embryo	V119 head
**********...(((((((..((..(((.(((((((((.((.(((((.(((.....))).)))))).)))))))).)))..))..)))))).**********										
.....TTCCGACTTTTACTTGATCTT.....	21	0	3	90.00	270	24	165	62	11	8
.....TAGAGTTCAAGTAAGCGTACGGA.....	23	0	1	73.00	73	45	0	7	21	0
.....TAGAGTTCAAGTAAGCGTACGG.....	22	0	1	36.00	36	26	0	9	1	0
.....TTCCGACTTTTACTTGATCTTA.....	22	0	3	30.00	90	15	5	35	35	0
.....TTCCGACTTTTACTTGATCT.....	20	0	3	21.00	63	4	55	3	0	1
.....TAGAGTTCAAGTAAGCGTACG.....	21	0	1	17.00	17	12	0	4	0	1
.....TAGAGTTCAAGTAAGCGTACGGAA.....	24	1	1	14.00	14	13	0	0	1	0
.....AGTTCAAGTAAGCGTACGGAGCG.....	23	0	1	6.00	6	5	0	0	1	0
.....TAGAGTTCAAGTAAGCGTACGGAT.....	24	1	1	6.00	6	6	0	0	0	0
.....TTCCGACTTTTACTTGATCTTAA.....	23	1	3	4.67	14	0	2	10	1	1
.....AGTTCAAGTAAGCGTACGGAG.....	21	0	1	4.00	4	4	0	0	0	0
.....AGTTCAAGTAAGCGTACGGAGC.....	22	0	1	3.00	3	3	0	0	0	0
.....AGAGTTCAAGTAAGCGTACG.....	20	0	1	2.00	2	0	0	2	0	0
.....TAGAGTTCAAGTAAGCGTAC.....	20	0	1	2.00	2	2	0	0	0	0
.....TCCGACTTTTACTTGATCTT.....	20	0	3	1.67	5	0	0	5	0	0
.....TTATAAATCGAAATTTTCCGACTT.....	24	0	2	1.50	3	0	3	0	0	0
.....AGTTCAAGTAAGCGTACGGAGCGT.....	24	0	1	1.00	1	1	0	0	0	0
.....AGTTCAAGTAAGCGTACGGA.....	20	0	1	1.00	1	1	0	0	0	0
.....TAGAGTTCAAGTAAGCGTACGGAAA.....	25	2	1	1.00	1	1	0	0	0	0
.....AGAGTTCAAGTAAGCGTACGGA.....	22	0	1	1.00	1	0	0	1	0	0
.....GTTCAAGTAAGCGTACGGAG.....	20	0	1	1.00	1	0	0	1	0	0
.....AGTTCAAGTAAGCGTACGAG.....	20	2	1	1.00	1	1	0	0	0	0
.....TTCCGACTTTTACTTGATCTTC.....	22	1	3	0.67	2	0	1	1	0	0
.....TCCGACTTTTACTTGATCTTA.....	21	0	3	0.33	1	0	0	1	0	0
.....TCCGACTTTTACTTGATCTTAA.....	22	1	3	0.33	1	0	0	1	0	0
.....CGACTTTTACTTGATCTTATCTA.....	23	1	3	0.33	1	0	0	0	1	0
.....TTCCGACTTTTACTTGATCTC.....	21	1	3	0.33	1	0	1	0	0	0
.....TTCCGACTTTTACTTGATC.....	19	0	3	0.33	1	0	0	0	0	1
.....TTCCGACTTTTACTTGATCTTT.....	22	1	3	0.33	1	0	0	0	1	0
.....TTCCGACTTTTACTTGATCC.....	20	1	3	0.33	1	0	1	0	0	0
.....TTCCGACTTTTACTTGATCG.....	20	1	3	0.33	1	0	1	0	0	0

Anti-sense strand reads

CTTAACCGTCTCTTTTTGAATCACTATCAGCGTCCTAGTATTTTTAGTGTAGAATATACGTTTCATCTCAAGTTCATTCGCATGCCTCGCAATATTTAGCTTTAAAAGGCTGAAAATGAACTAGAATAGAGCCGCATATTTTTTGAGTATTTTTTTTATGTTTAGTTGTAAAAAGATTAGTAGGGT	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo
...(((((((((..((..(((.(((((((((.((.(((((.(((.....))).)))))).)))))))).)))..))..)))))).********						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3392835-3393020 -	dwi_194	GAATTGGCAGAGAAAAACTTAGTGATAGTCGCAGGATCATAAAAATCACATCTTATATGCAAAGTAGAGTTCAAGTAAGCGTACGGAGCGTTATAAATCGAAATTTTCCGACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCATAAAAAAAAATACAAATCAACATTTTTCTAATCATCCCA

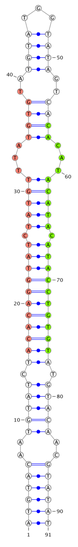
Generated: 09/08/2015 at 08:03 PM

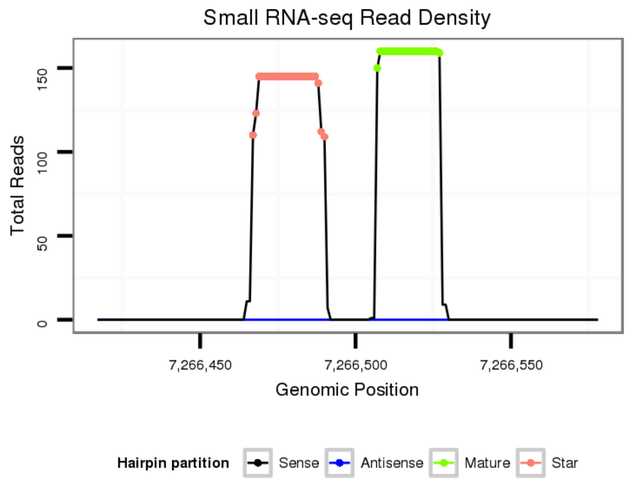
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

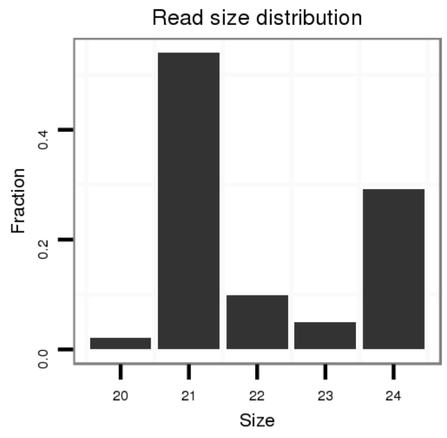
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_170	**scf2_1100000004902:7266467-7266528 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

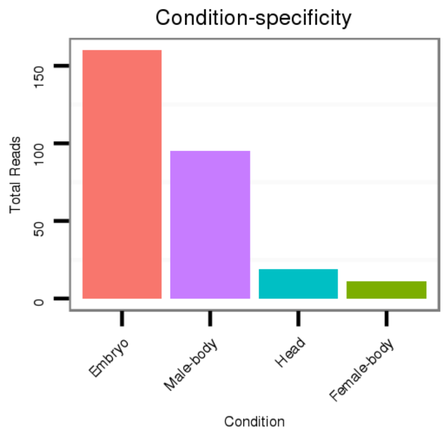
Legend: mature star mismatch in alignment mismatch in read

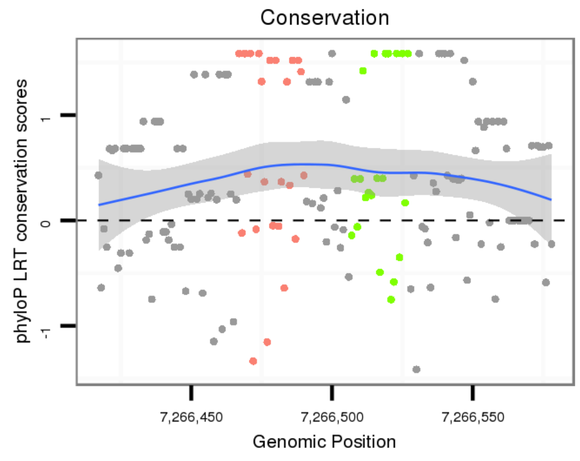
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
Galileo_DM	DNA	P	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGCCTCTAATTTAAAAAACGAAAAATTCTATGTATATGTACAATGTATCTACACAGGTATCTATGTTTATGTGTATGTATGGTATAGTCACACATACATACATACCTGTGTATGTACAACGTATATACATACATCACGTAAATTTTCTGTCAAGTGTGCCAG **********(((((((..(((((.((((((((((.(((((...((((..((((...))))..))))...))))).))))))))))).)))))..)))))))**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	V117 male body	V119 head	M045 female body	M020 head
..........CACATACATACATACCTGTGT..........	21	0	1	146.00	146	73	60	8	5	0
..........ACACAGGTATCTATGTTTATGTGT..........	24	0	1	81.00	81	62	13	4	2	0
..........ACACAGGTATCTATGTTTATGT..........	22	0	1	15.00	15	7	5	2	1	0
..........ACAGGTATCTATGTTTATGTGT..........	22	0	1	13.00	13	7	5	1	0	0
..........CTACACAGGTATCTATGTTTATGT..........	24	0	1	11.00	11	6	4	1	0	0
..........CACAGGTATCTATGTTTATGTGT..........	23	0	1	8.00	8	1	6	1	0	0
..........ACATACATACATACCTGTGTAT..........	22	0	1	7.00	7	2	0	0	5	0
..........ACAGGTATCTATGTTTATGTGTA..........	23	0	1	5.00	5	4	1	0	0	0
..........ACAGGTATCTATGTTTATGTG..........	21	0	1	3.00	3	2	1	0	0	0
..........ACACAGGTATCTATGTTTATG..........	21	0	1	3.00	3	0	2	0	1	0
..........ACATACATACATACCTGTGT..........	20	0	1	3.00	3	1	2	0	0	0
..........CACAGGTATCTATGTTTATGTGTA..........	24	0	1	2.00	2	2	0	0	0	0
..........CACATACATACATACCTGTGTAT..........	23	0	1	2.00	2	0	0	1	1	0
..........CACAGGTATCTATGTTTATGT..........	21	0	1	2.00	2	0	0	1	1	0
..........CACAGGTATCTATGTTTATG..........	20	0	1	1.00	1	0	0	0	0	1
..........CACATACATACATACCTGTGTT..........	22	1	1	1.00	1	1	0	0	0	0
..........ACAGGTATCTATGTTTATGT..........	20	0	1	1.00	1	0	0	0	1	0
..........ACACAGGTATCTATGTTTATGTCC..........	24	2	1	1.00	1	0	0	0	1	0
..........CTACACAGGTATCTATGTTTATGTC..........	25	1	1	1.00	1	0	1	0	0	0
..........ACACAGGTATCTATGTTTATGTAA..........	24	2	1	1.00	1	1	0	0	0	0
..........CACATACATACATACCTGTG..........	20	0	1	1.00	1	0	0	0	0	1
..........CACACATACATACATACCTGTGT..........	23	0	1	1.00	1	1	0	0	0	0
..........CACAGGTATCTATGTTTATGTGTC..........	24	1	1	1.00	1	0	1	0	0	0
..........CACATACATACATACCTGTGG..........	21	1	2	0.50	1	0	0	0	0	1
..........CACATACATACATACCTGTGTC..........	22	1	2	0.50	1	0	1	0	0	0

Anti-sense strand reads

ACGGAGATTAAATTTTTTGCTTTTTAAGATACATATACATGTTACATAGATGTGTCCATAGATACAAATACACATACATACCATATCAGTGTGTATGTATGTATGGACACATACATGTTGCATATATGTATGTAGTGCATTTAAAAGACAGTTCACACGGTC **********(((((((..(((((.((((((((((.(((((...((((..((((...))))..))))...))))).))))))))))).)))))..)))))))**********	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
droWil2	scf2_1100000004902:7266417-7266578 +	dwi_170	TGCCTCTAATTTAAAAAACGAAA----------AATTCTATGTATATGTAC--AATGTATCTACACAGGT------ATCTATGTTTATGTGT--------ATGTATGGTATAGTCACACATACATACATACCTGTGTATGTACA-ACGTATATACA--TACATCACGTAAATTTTCTGTCAAGTGTGCCAG
droMoj3	scaffold_6328:617841-617984 +		AAA----------AGAGAAATATCATAAATGCGTGTATGGTTTACCCA----------|--|--------ACATAAATAGATA--CATGTACATATATGAATATATGT--------AATTACATACATATATACATACCTGTGTACGTGCAACCATATGTACA--TACAT-ATGTGAGTAT--------TATGCGAA
droGri2	scaffold_15110:13506305-13506443 -		TGTTTCTCTTTAAAAAAACAAA----------CCTATTGTACATAAATAT--AATATACATATATATGT------ATGTGTATCTGTGTGT--------GTGTATGATACTGT--TGTG----TTGTTATTTTGTGTCTTGT-ACATATATGCA--AAACTCA-GTGATTTTT----------
droPer2	scaffold_5:929044-929150 +		TCT----------|----------|--------ATGTGTATATTCGATATATATATATATAT--ATATATGTGTAT--ATATGT------ATATATACGATATATA--TATATATATATATGTATATATATATT-TCGTATATAAA--TA----------
dm3	chrU:8430656-8430761 -		TAT----------|----------|--------GTATATATGT--CATCTATGTACATATGT------ATCTATGTATATATGTATATATGT---------ATATACGTATATATGTATATACGTATATATGTATATATGTATATATGTATATG--TATAT----------
droEre2	scaffold_4784:25382740-25382831 -		TAT----------|----------|--------ATATATGTAT--AGTATATACACATAAGTATATA----------T--------ATGTATAGTATATACACATATGTATATATATGTATATATATACA--GTATATACACAT----------

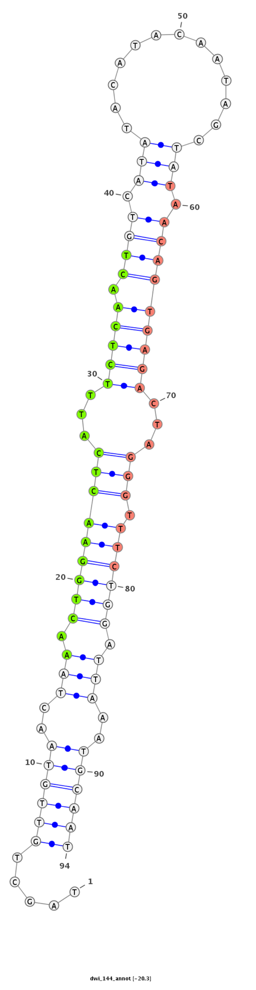
Generated: 09/08/2015 at 07:39 PM

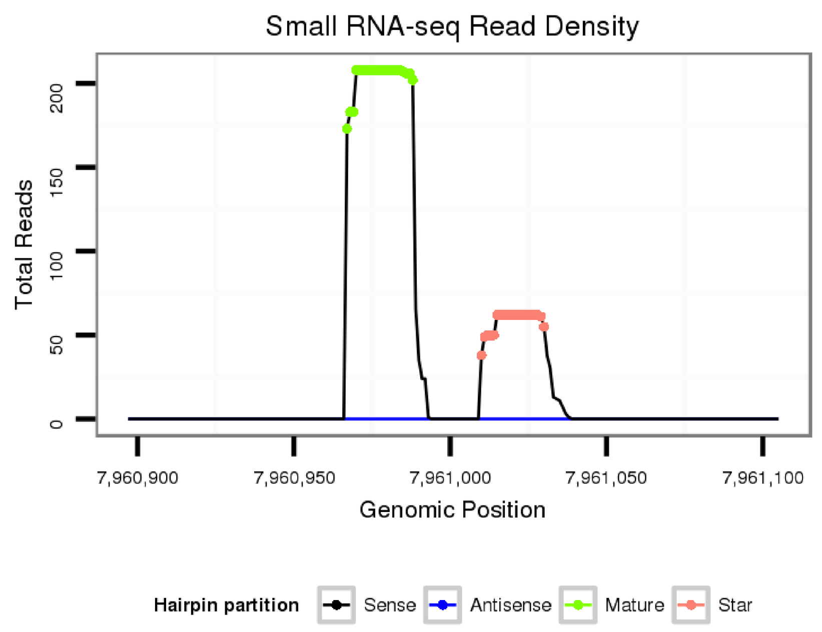
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

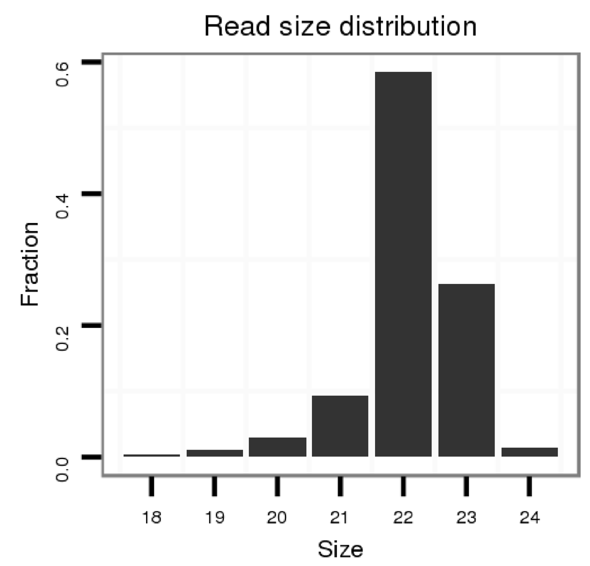
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_144	**scf2_1100000004909:7960947-7961055 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

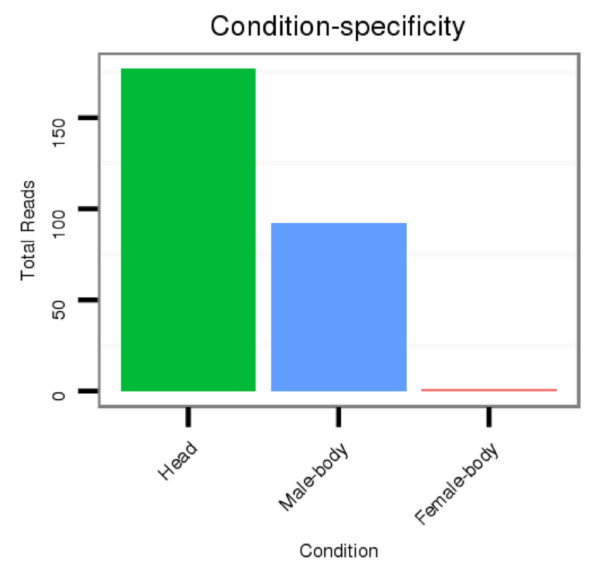
Legend: mature star mismatch in alignment mismatch in read

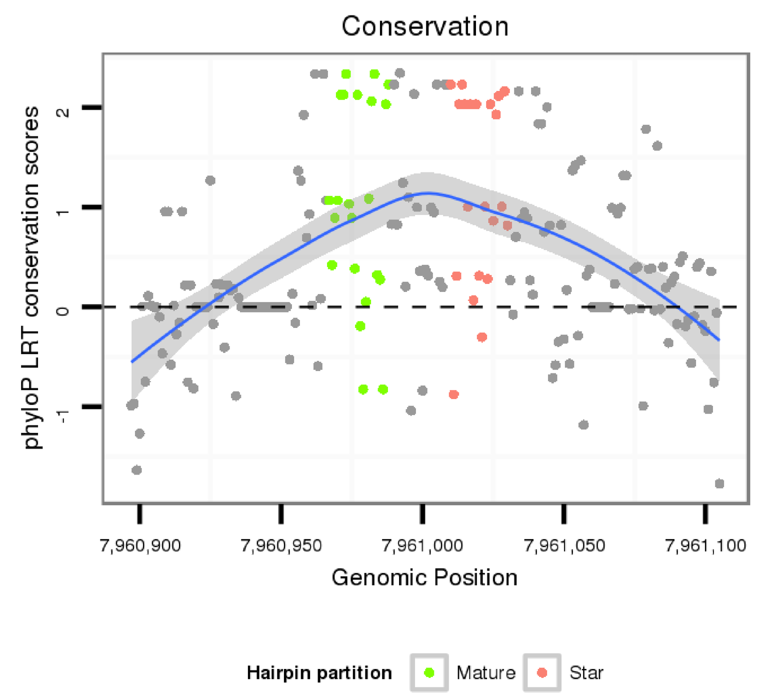
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
(CTAA)n	Simple_repeat	Simple_repeat	+
(CATA)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CATGGCCTGCCTGCCAGACTGTGGATATGATTAACCAACCAACCAACTAACTAACTAGCTGTTGTAACTAAACTGGAACTCATTTCTCAACTGTCATATACATACAATAGCTATAACAGTGAGACTAGGGTTTCTGGATTAAATGCAATAAGTGAAACAACGTACATACATACATACATATATACATCTCGAAACATACATACATATAT **.....((((((..(((.(((((((((...(((((.((((.(((............))).)))))))))...))).)))))).))).))))))**	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V117 male body	V119 head	V118 embryo	M045 female body
........AACTGGAACTCATTTCTCAACT........	22	0	1	137.00	137	132	3	2	0	0
........AACTGGAACTCATTTCTCAACTG........	23	0	1	28.00	28	17	10	0	0	1
........TGGAACTCATTTCTCAACTGTCA........	23	0	1	23.00	23	0	21	2	0	0
........TAACAGTGAGACTAGGGTTTC........	21	0	1	15.00	15	2	9	4	0	0
........TAACAGTGAGACTAGGGTTTCTG........	23	0	1	10.00	10	2	7	1	0	0
........ACTGGAACTCATTTCTCAACTGT........	23	0	1	8.00	8	3	5	0	0	0
........TAACAGTGAGACTAGGGTTTCT........	22	0	1	7.00	7	1	3	3	0	0
........AACAGTGAGACTAGGGTTTCTG........	22	0	1	7.00	7	0	6	1	0	0
........TAACAGTGAGACTAGGGTTT........	20	0	1	5.00	5	0	5	0	0	0
........GTGAGACTAGGGTTTCTGGAT........	21	0	1	4.00	4	0	4	0	0	0
........AACTGGAACTCATTTCTCAACC........	22	1	1	4.00	4	4	0	0	0	0
........GTGAGACTAGGGTTTCTGGATT........	22	0	1	4.00	4	0	4	0	0	0
........AACTGGAACTCATTTCTCAAC........	21	0	1	4.00	4	3	1	0	0	0
........AACTGGAACTCATTTCTCAACTGT........	24	0	1	2.00	2	1	1	0	0	0
........AACAGTGAGACTAGGGTTTC........	20	0	1	2.00	2	0	2	0	0	0
........GTGAGACTAGGGTTTCTGGATTA........	23	0	1	2.00	2	0	2	0	0	0
........ACTGGAACTCATTTCTCAACTG........	22	0	1	2.00	2	1	1	0	0	0
........AACTGGAACTCATTTCTCAACTGA........	24	1	1	1.00	1	0	0	0	1	0
........ACAGTGAGACTAGGGTTTCTGG........	22	0	1	1.00	1	0	1	0	0	0
........AACTGGAACTCATTTCTCA........	19	0	1	1.00	1	1	0	0	0	0
........TAACAGTGAGACTAGGGTTTCCT........	23	2	1	1.00	1	0	1	0	0	0
........GTGAGACTAGGGTTTCTGGATTAA........	24	0	1	1.00	1	0	1	0	0	0
........TAACAGTGAGACTAGGGTTCTG........	22	3	1	1.00	1	0	1	0	0	0
........AACAGTGAGACTAGGGTTT........	19	0	1	1.00	1	0	1	0	0	0
........GTGAGACTAGGGTTTCTGGA........	20	0	1	1.00	1	0	1	0	0	0
........TAACAGTGAGACTAGGGTT........	19	0	1	1.00	1	0	1	0	0	0
........ACTGGAACTCATTTCTCAACTGC........	23	1	1	1.00	1	1	0	0	0	0
........TGGAACTCATTTCTCAACTGT........	21	0	1	1.00	1	0	1	0	0	0
........AACAGTGAGACTAGGGTTTCT........	21	0	1	1.00	1	0	1	0	0	0
........AACTGGAACTCATTTCTCAACTGG........	24	1	1	1.00	1	1	0	0	0	0
........AACTGGAACTCATTTCTC........	18	0	1	1.00	1	1	0	0	0	0
........AACTGGAACTCATTTCTCAACG........	22	1	1	1.00	1	1	0	0	0	0
........TGGAACTCATTTCTCAACTGTCAT........	24	0	1	1.00	1	0	1	0	0	0
........TACATACATACATACATATATACAT........	25	0	20	0.05	1	0	0	0	0	1
........TACATACATACATATATACAT........	21	0	20	0.05	1	0	0	0	0	1

Anti-sense strand reads

GTACCGGACGGACGGTCTGACACCTATACTAATTGGTTGGTTGGTTGATTGATTGATCGACAACATTGATTTGACCTTGAGTAAAGAGTTGACAGTATATGTATGTTATCGATATTGTCACTCTGATCCCAAAGACCTAATTTACGTTATTCACTTTGTTGCATGTATGTATGTATGTATATATGTAGAGCTTTGTATGTATGTATATA **.....((((((..(((.(((((((((...(((((.((((.(((............))).)))))))))...))).)))))).))).))))))**	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	V118 embryo
........TGGTTGGTTGGTTGATTGATT........	21	0	4	0.25	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004909:7960897-7961105 +	dwi_144	CATG----------------------GCCTGCCTGCCAGAC--------------------------TGTGGATATGATTAAC---CAACCAACCAACTAACTAACTAGCTGTTGTAACTAAACTGGAACTCATTTCTCAACTGTCATATACATACAATAGCTATAACAGTGAGACTAGGGTTTCTGGATTAAATGCAATAAG--TGA-----------------------------A---------------------------------------ACAACGTACATACATACATACATATAT---ACATCTCG----AAACATAC-----------ATACATATAT
droVir3	scaffold_13042:902849-902992 -	dvi_76	CCGG-A---------------------GA------------C------AGATCCGGAGACAGATGAGTCTT-----GGATGAT---AACG----------------CGATGTGGCATCTAAGCTGGAACTCGATTCTCCTCTGTCATATGCGGACGATAACTATGGCAGTGAGGGTGGGGTTTCCTTATTAGATGCGATAC---TCA---AAAC
droMoj3	scaffold_6328:2897203-2897283 -		--GCATCTAAGCTGGAACTCGATTCTCCTCTGTCATATGCAGCCGACAACTATGGCAGTGAGGGTGGGGTTTCCCTATTGGAT---
droGri2	scaffold_15203:434426-434468 -		TACATA--CA---TACATATGTATGT---ACATTT------ATATAC-----------ATACATATAT
droPer2	scaffold_14:1995439-1995512 -		AATA---AAATATGTGACGGACACCATTTCTA--------TA--TACATACATATAT---ACATTTCTTGATAACCTAAT-----------GTACATATAT
droAna3	scaffold_13417:2460624-2460876 -	dan_231	CTAGCAGGCACTAGGCGGTCCAGGACGATCC--AGGCGGTGCAA-TAGCGG----------GGATCACTTTG-----GGTCGGC---CAGC---------------GATTGTTGTAGCTAAACTGGAACTCGTTTCTCAGCTGTCATATACATTCGATAGCTATAACAGTGAGGATGGGGTTTCTGGATTAAGTGCAATGG---TAT-TA----------------------------CGGGCCGACCACTGTGACTGGGTCCCACCGTGAAGTGGGT--------------G----CGGGTGTCGGCACTCCCG----GAGCAGTC------TCCGGAGTGCGGACAG
droBip1	scf7180000395874:32689-32909 -		CGGCCA-----------------------------CCTCGATGGAAGCGTACAGGGATCACTTTT-----GGTCGAC---CAAC---------------GATTGTTGTAGCTAAACTGGAACTCGTTTCTCACCTGTCATATACATCCGATAGCTATAACAGTGAGGATTGGGTTTCTGGATTAAGTGCAATGG---TGT-TA----------------------------CGGGCCGACTACTGTGACTGGGGCCCACC---AAGTGGGT--------------G----CGGGGCTCGGCCTTCCCG----GAGCAGTC------TCCG------GCGAAC
droKik1	scf7180000302517:1186271-1186452 +		AACG--------------------ACCC--ATGCCGGACACCCAAAGAGAAAC----------AACACG-----GATCGGCGGTCCAC---------------AATTGTTGCAACTAAACTGGAACTCGCTCCTCATCTGTCATGTGCATTCGTTAGCTATTACAGTGAGGTTGGAGTTTCTGGATTAAGTGCAATGG---TGATTA-----------------------------CCG---TACCAATATGGC---------------------CAAGGT---------------------------------------CTTCA-------TGCC
droFic1	scf7180000454073:1735829-1735969 +		TG---TTGCAGCTAAACTGGAACTCAAATCTCAGCTGTCATATGCATTCAATAG-TATCGCAGTGGGGTGGG--TTCTAGAACAAGTGCAATCC---TC----CCGGGCA--ATCGCTTCCGTGTCAAA-AAAGAAAGG--------------------------------------ACGAACT-----------------------------GCGGC----------GG--AAT
droEle1	scf7180000490751:1121746-1121835 +		C---AGCTCTCAAACACATGCGATAGGTATGACAGTGTGAATGGGGTC--------------------------GAGTCGATCGCGACA---AAAAGAATGG---A---------------------------------------AC--GGA----------------AGT----------------GAATCCCCA----------AA
droRho1	scf7180000761121:187390-187525 -		TG---TTGCAGCTAAACTGGAACTCATGTCTCAGCTGTCATATACATTTGATAGGTATAACAGTGAGGATGGGGTTTCTGGAATAAGTGCAATGG---CGA--CCAGAGCAAGATCGGGTTTGTTGCGGC---AGAAAGG---------------------------------------ACGAAGT---
droBia1	scf7180000302069:1148267-1148395 -		T---TGCAGCTAAACTGGAACCCTGGTCTCAACTGTCATGTGCACTTGATATGTATAACAGTGAGGACGGGGTTTCTGGAATAA-TGCAATGG---TGG---CAGAGTG--ATCGAGTCCATCGCGAGG-----GGGAA---------------------------------------ACGAGG---T
droTak1	scf7180000415169:842162-842309 -		TG---TTGCAGCTAAACTGGAACCCAACT-TGCGCTGTGATATTCATTTGATAGGTATAACAGCGGGATGGGGTTTTCGGAATAGGTGCAATAG---TGAGTGCAGAGCA--ATCGATCCTA--GCAGGCTAAGAAAGG---------------------------------------ACGAAGT-----------------------------GACGA----------AGGATCC
droEug1	scf7180000409230:877463-877613 -		G---TTGCAGCTAAACTGGAACTCAAGTCTCAGCTGTCATATTCATTTGATAGTTATGACAGTGAGGATGGGGTTTCTGGAATAACTGCAACAATTGTGA--GCAGTGAG--ATCGAGTTTATCGCAAGGAAACAAATG---------------------------------------ACAAAGT-----------------------------AGTGA----------TAGATCC
dm3	chrX:19454271-19454313 +		TATGTA---TG---TATGTATAT---ACATCTAT----ATGCATAT-----------ATATGTATGT
droEre2	scaffold_4690:9690267-9690305 +		TATATA-----------------------CAT--ATGTACATAT--AT-------------ATGCATAT-----------ACATATATGT

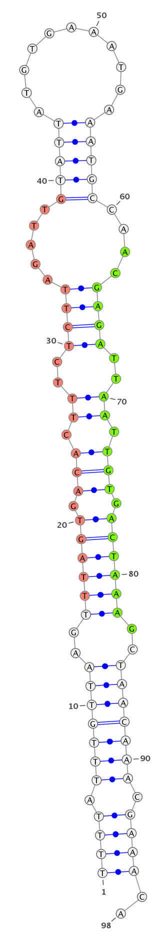
Generated: 09/08/2015 at 08:01 PM

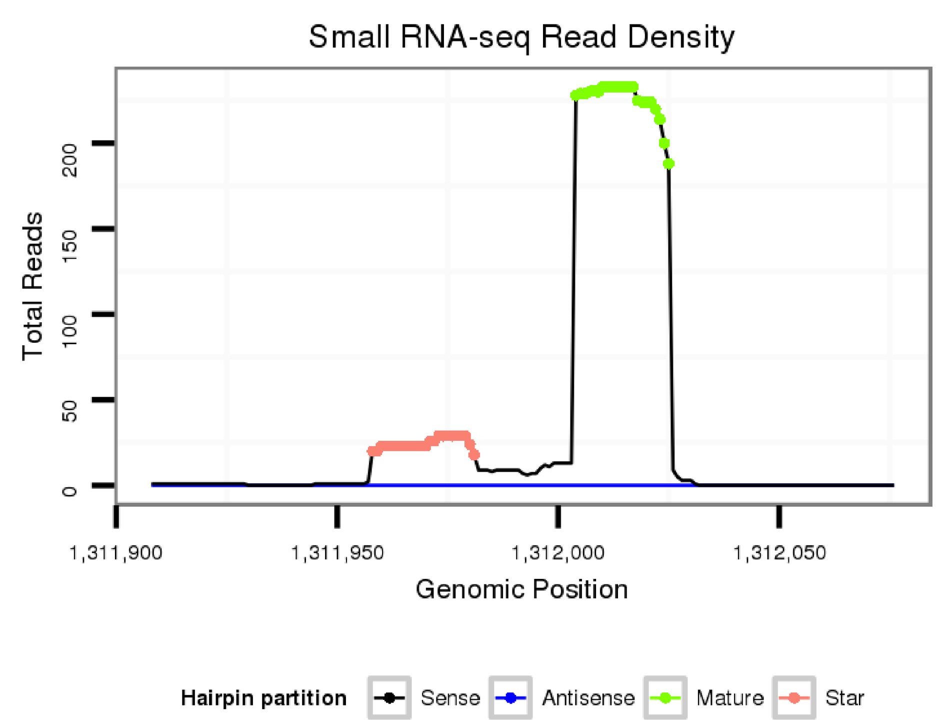
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	4
rescue.candidate	0

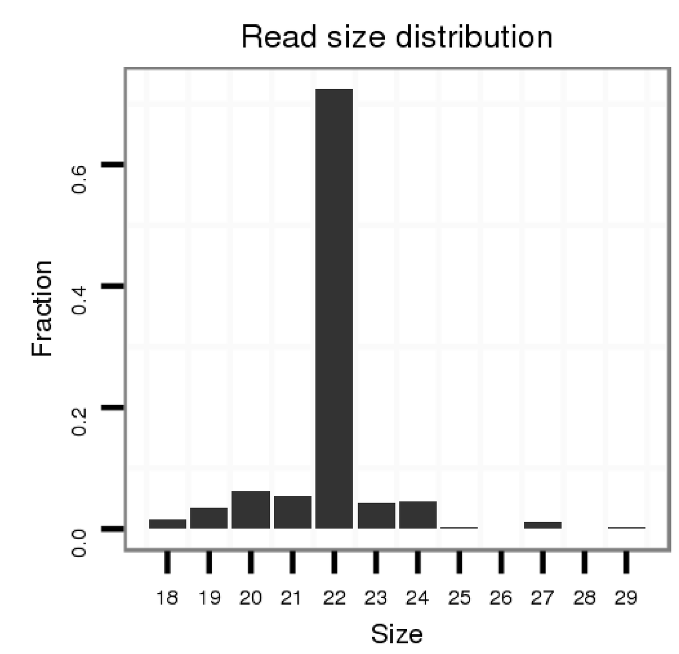
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_81	**scf2_1100000004540:1311958-1312026 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

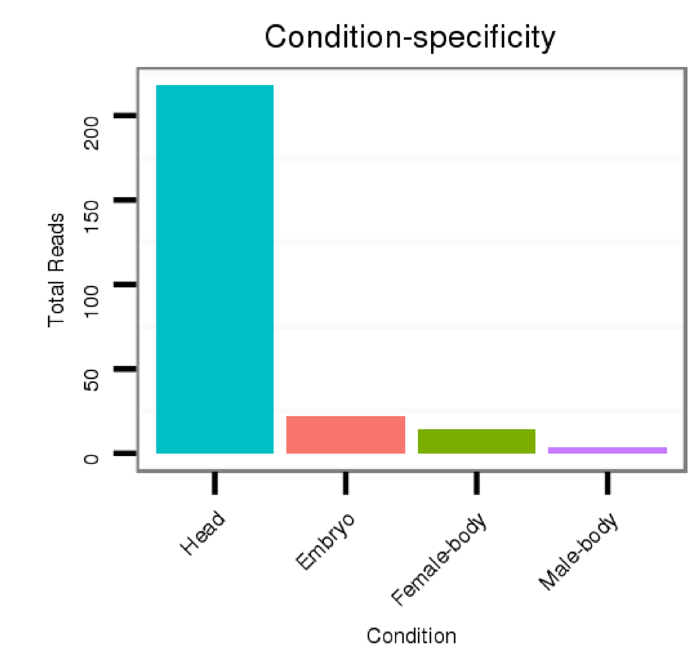
Legend: mature star mismatch in alignment mismatch in read

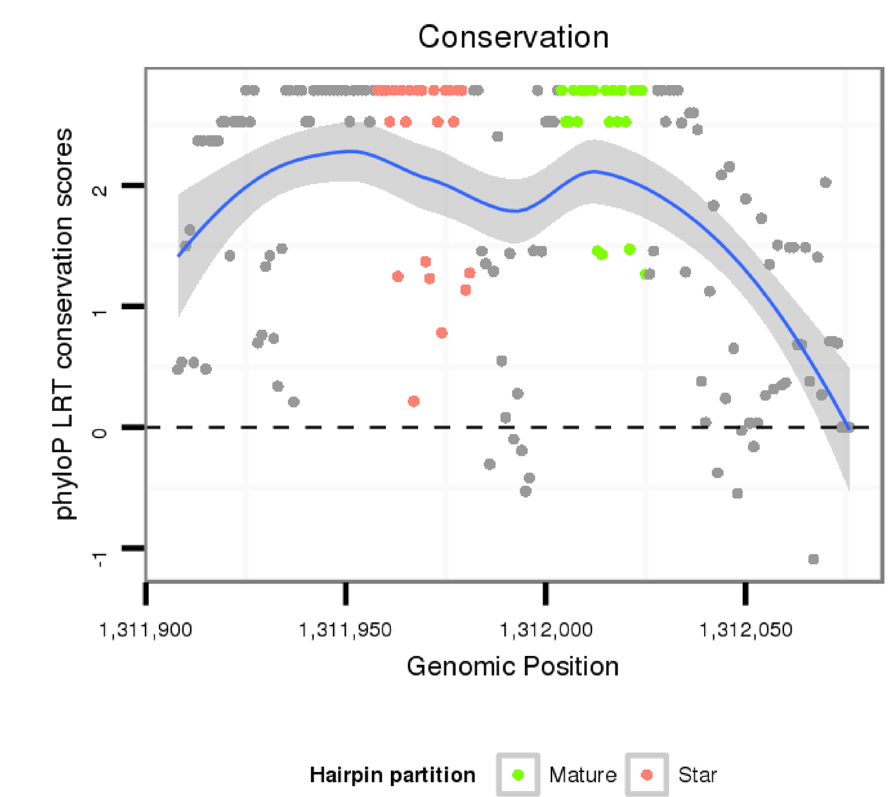
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
A-rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

CGAGACGGCGGCGAGGCTGACAAATTTTTTTAGCATTTTATTTGTTAAGTTTAGTGACACTTTCTCTTAGATTGTATTATGTGAAATGAAATGCCAACGAGATTAATTGTGACTAAAGCTAACAAACGAAACAAATACAAGTACATATATACATATATAAACAAAGAAA **********************************((((.(((((((..((((((.(((.((..((((.....(((((..........)))))....))))..)).))).))))))..))))))).))))..**************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V118 embryo	M045 female body	V119 head	V117 male body
....ACGAGATTAATTGTGACTAAAG...	22	0	1	177.00	177	162	6	7	2	0
....ACGAGATTAATTGTGACTAA...	20	0	1	14.00	14	13	0	1	0	0
....ACGAGATTAATTGTGACTAAA..	21	0	1	11.00	11	9	1	1	0	0
....TTAGTGACACTTTCTCTTAGATTG...	24	0	1	8.00	8	8	0	0	0	0
....TTAGTGACACTTTCTCTTAGATT..	23	0	1	6.00	6	3	2	0	1	0
....ACGAGATTAATTGTGACTA..	19	0	1	6.00	6	6	0	0	0	0
....TTAGTGACACTTTCTCTTAGAT...	22	0	1	4.00	4	3	0	1	0	0
....ACGAGATTAATTGTGACTAAAGC..	23	0	1	4.00	4	3	1	0	0	0
....ACGAGATTAATTGTGACT...	18	0	1	3.00	3	3	0	0	0	0
....AAATGCCAACGAGATTAATTGT...	22	0	1	3.00	3	0	1	0	2	0
....CTTAGATTGTATTATGTGAAATGAAAT...	27	0	1	2.00	2	0	2	0	0	0
....AATGCCAACGAGATTAATTGT...	21	0	1	2.00	2	0	2	0	0	0
....GATTAATTGTGACTAAAGCT...	20	0	1	2.00	2	1	1	0	0	0
....ACGAGATTAATTGTGACTAAAGT..	23	1	1	2.00	2	0	1	1	0	0
....TTAATTGTGACTAAAGCTAAC..	21	0	1	2.00	2	1	1	0	0	0
....ACGAGATTAATTGTGACTAAAC...	22	1	1	1.00	1	1	0	0	0	0
....GCCAACGAGATTAATTGTGACT...	22	0	1	1.00	1	0	0	1	0	0
....ATGTGAAATGAAATGCCAACGAG..	23	0	1	1.00	1	0	1	0	0	0
....AGTGACACTTTCTCTTAGATTGTAT..	25	0	1	1.00	1	0	0	1	0	0
....GCCAACGAGATTAATTGT...	18	0	1	1.00	1	0	1	0	0	0
....ACGAGATTAATTGTGACC...	18	1	1	1.00	1	1	0	0	0	0
....AGATTAATTGTGACTAAAG...	19	0	1	1.00	1	1	0	0	0	0
....TTATGTGAAATGAAATGCCAACGA...	24	0	1	1.00	1	0	1	0	0	0
....AGTGACACTTTCTCTTAGATTG...	22	0	1	1.00	1	1	0	0	0	0
....TTAATTGTGACTAAAGCTAACA...	22	0	1	1.00	1	0	1	0	0	0
....TGCCAACGAGATTAATTGTG..	20	0	1	1.00	1	0	1	0	0	0
....CTCTTAGATTGTATTATGTGAA..	22	0	1	1.00	1	0	0	0	0	1
....TGCCAACGAGATTAATTGT...	19	0	1	1.00	1	0	1	0	0	0
....CTTAGATTGTATTATGTGA...	19	0	1	1.00	1	0	1	0	0	0
....CTCTTAGATTGTATTATGTGA...	21	0	1	1.00	1	0	0	0	0	1
....AGTGACACTTTCTCTTAGATTGTA...	24	0	1	1.00	1	0	0	1	0	0
....CTCTTAGATTGTATTATGTGAAATGAA...	27	0	1	1.00	1	0	0	0	0	1
.....................................TTATTTGTTAAGTTTAGTGACACTTTCT..	28	0	1	1.00	1	0	1	0	0	0
....TGAAATGCCAACGAGATTAATTGT...	24	0	1	1.00	1	0	1	0	0	0
....TTTAGTGACACTTTCTCTTAGAT...	23	0	1	1.00	1	0	0	0	1	0
....CGAGATTAATTGTGACTAAA..	20	0	1	1.00	1	0	0	1	0	0
CGAGACGGCGGCGAGGCTGACA...	22	0	1	1.00	1	0	0	1	0	0
....ACGAGATTAATTGTGACTAAAGA..	23	1	1	1.00	1	1	0	0	0	0
....CTTAGATTGTATTATGTGAAATGAAATGC...	29	0	1	1.00	1	0	0	0	0	1
....CAACGAGATTAATTGTGACTAAAG...	24	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

GCTCTGCCGCCGCTCCGACTGTTTAAAAAAATCGTAAAATAAACAATTCAAATCACTGTGAAAGAGAATCTAACATAATACACTTTACTTTACGGTTGCTCTAATTAACACTGATTTCGATTGTTTGCTTTGTTTATGTTCATGTATATATGTATATATTTGTTTCTTT **********************************((((.(((((((..((((((.(((.((..((((.....(((((..........)))))....))))..)).))).))))))..))))))).))))..**************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	V119 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004540:1311908-1312076 +	dwi_81	-----CGAG-ACGGCGGCGAGGCTGAC-A-AA-TTTTTTTAGCATTTTATTTGTTAAGTTTAGTGACACTTTCT--CTTAGATTGTATTATGTGA-AATG--AA-----ATGCCAACGAGATTAATTGTGACTAAAGCTA------------ACAAACGAAA--CAA-----A------------TACAAGTAC--ATATATA------------------CATATATA---AACAAAGAAA
droVir3	scaffold_13049:7754231-7754384 -		-----------CGACGGCGGCGAGGCTGAA----A--TTTTGTAGCATTTTATTTGTTAAGTTTAGTGACATTTTT--CTTAGATTGTATTTTGTGAAGAGC---AA-GTGAAGCCAACGAGATTAATTGTGACTAAAGCTA------------ACAAACAAAA--TTATAT---TTATTTTATATATA--TATA-TAT-------
droMoj3	scaffold_6680:6000941-6001116 -		-----------CGACGGCGGCGAGGCTGAA----A--TTTTGTAGCATTTTATTTGTTAAGTTTAGTGACATTT-TT--CTTAGATTGTATT-TGTGA-GAGATGCGA-GCGAAGCCAACGAGATTAATTGTGACTAAAATTA------------ACAAACAAAA--TCATAT---TTATTTTAAAAACATA--TAT--CAA-------TG-----------ATATATA--TGTATCACAAAG---
droGri2	scaffold_15110:5128834-5128987 +		-----TG-GTTCGACGGCGGCGAGGCTGAA----A--TTTTGTAGCATTTTATTTGTTAAGTTTAGTGACAATTTTTGCATAGATTGTAC----C-------AAGTTGAAGCCAACGAGATTATGTGTGACTAAAGCAA------------ACAAACAAAA--TTA-----------------TAAAT-TAT--------------TTATTTT---TTTATATA---AATA------
dp5	XR_group6:3178374-3178487 -		---------------CGCGGCTGAC----A--TTTTGTAGCATTTTATTTGTTAAGTTTAGTAACACTTTCT--CTTAGATCGTATT--GCAA-AAGA--AA-ATGAAGCCAACGAGATTAATTGTGACTAAAGCTA------------ACAAAC--
droPer2	scaffold_9:1472985-1473098 -		---------------CGCGGCTGAC----A--TTTTGTAGCATTTTATTTGTTAAGTTTAGTAACACTTTCT--CTTAGATCGTATT--GCAA-AAGA--AA-ATGAAGCCAACGAGATTAATTGTGACTAAAGCTA------------ACAAAC--
droAna3	scaffold_13337:1258773-1258936 +		-----------CGGCGGCGAGGCTGAA---C--TTTTGTAGCATTTTATTTGTTAAGTTTAGTAACACTTTCT--CTTAGATCGTATT--GC---------AA-ATGAAGCCAACGAGATTAATTGTGACTAAAGCTA------------ACAAACAAAA--CAA-----A-------------T-CAA--AC--GCATACACCATGTAATTTATTTTATATATA--TATA--CA------
droBip1	scf7180000396371:1591343-1591515 +		-----------CGGCGGCGAGGCTGAA--AC--TTTTGTAGCATTTTATTTGTTAAGTTTAGTAACACTTTCT--CTTAGATCGTATT--GC---------AA-ATGAAGCCAACGAGATTAATTGTGACTAAAGCTA------------ACAAACAAAAAACAA-----ATCAAA--CAAA--CACA--------TACACCATGTAATTTATTTTATATATA--TATA-CACA------
droKik1	scf7180000302686:95001-95136 +		-----------CGGCGGCGAGGCTGAA----A--TTTTGTAGCATTTTATTTGTTAAGTTTAGTAACATTTTCT--CCTAGATCGTATC--GCAACGCAA--AA-AGAAAGCCAACGAGATTAATTGTGACTAAAGCTAAATAACAAACAAACAAACAAA--
droFic1	scf7180000453839:648516-648658 +		-----------CGGCGGCGAGGCTGAA--AA--AATTGTAGCATTTTATTTGTTAAGTTTAGTAACACTTTCT--CTTAGATCGTATT--GC---------AA-TTGAAGCCAACGAGATTAATTGTGACTAAAGCTA------------ACAAACAAAA--CAA-----A-------------CACAACAACACCCACACA----------------------CA------
droEle1	scf7180000491255:759133-759268 -		-----CAAGTTCGACGGCGGCGAGGCTGAA---ACTTTTGTAGCATTTTATTTGTTAAGTTTAGTAACACTTTCT--CTTAGATCGTATT--GC---------AA-TTGAAGCCAACGAGATTAATTGTGACTAAAGCTA------------ACAAACAAAA--CAC----AA-------------CACAA---
droRho1	scf7180000767448:22855-22997 +		-----CAAGTTCGGCGGCGAGGCTGAA----A--TTTTTTAGCATTTTATTTGTTAAGTTTAGTAACACTTTCT--CTTAGATCGTATT--GC---------AA-TTGAAGCCAACGAGATTAATTGTGACTAAAGCTA------------ACAAACAAAA--CAA-----A-------------CACAA-CAT--CCA--CA-----------------------CA------
droBia1	scf7180000302428:4667239-4667370 -		-----CAAGTTCGGCGGCGAGGCTGAA----A--TTTTGTAGCATTTTATTTGTTAAGTTTAGTAACACTTTCT--CTTAGATCGTATT--GC---------AA-TTGAAGCCAACGAGATTAATTGTGACTAAAGCTA------------ACAAACAAAAAACAA-----A---CA------
droTak1	scf7180000415703:291690-291815 +		-----CAAGTTCGGCGGCGAGGCTGAA----A--TTTTTTAGCATTTTATTTGTTAAGTTTAGTAACACTTTCT--CTTAGATCGTATT--GC---------AA-TTGAAGCCAACGAGATTAATTGTGACTAAAGCTA------------ACAAACAAAA--AA---
droEug1	scf7180000409466:4488824-4488963 -		TTGAACAAGTTCGGCGGCGAGGCTGAA----A--TTTTGTAGCATTTTATTTGTTAAGTTTAGTAACACTTTCT--CTTAGATCATATT-TGC---------AATTTGAAGCCAACGAGATTAATTGTGACTAAAGCTA------------ACAAACAAAA--CAA-----A-------------AACAA---
dm3	chr3L:12396058-12396213 -	dme_427	T-GAGCAAGTTCGGCGGCGAGGCTGAAGAAAA--CTTTGTAGCATTTTATTTGTTAAGTTTAGTAACACTTCCT--CTTAGATCGTATT--GC---------AA-TTGAAGCCAACGAGATTAATTGTGACGAAAGCTA------------ACAAACAAAA--CAAAACCAA-------------CACAA-TAC--CCAT--A-------------------CA------
droSim2	3l:12096643-12096775 -		T-GAGCAAGTTCGGCGGCGAGGCTGAA--AA--CTTTGTAGCATTTTATTTGTTAAGTTTAGTAACACTTTCT--CTTAGATCGTATT--GC---------AA-TTGAAGCCAACGAGATTAATTGTGACGAAAGCTA------------ACAAACAAAA--CAA-----A---
droSec2	scaffold_0:4580052-4580175 -		T-GAGCAAGTTCGGCGGCGAGGCTGAA--AA--CTTTGTAGCATTTTATTTGTTAAGTTTAGTAACACTTTCT--CTTAGATCGTATT--GC---------AA-TTGAAGCCAACGAGATTAATTGTGACGAAAGCTA------------ACAAA--
droYak3	3L:12451772-12451920 -	dya_1642	---AGCAAGTTCGGCGGCGAGGCTGAA--AA--TTTTGTAGCATTTTATTTGTTAAGTTTAGTAACACTTTCT--CTTAGATCGTATT--GC---------AA-TTGAAGCCAACGAGATTAATTGTGACTAAAGCTA------------ACAAACAAAAA-CCA-----A-------------CACAA-TAC--CCATACA-------------------CA------
droEre2	scaffold_4784:12390945-12391090 -		---AGCAAGTTCGGCGGCGAGGCTGAA----A--ATTTGTAGCATTTTATTTGTTAAGTTTAGTAACACTTTCT--CTTAGATCGTATT--GC---------AA-TTGAAGCCAACGAGATTAATTGTGACTAAAGCTA------------ACAAACAAAA--CCA-----A-------------CACAA-TAC--CCATACA--------------------C------

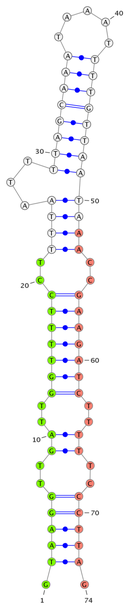
Generated: 09/08/2015 at 07:39 PM

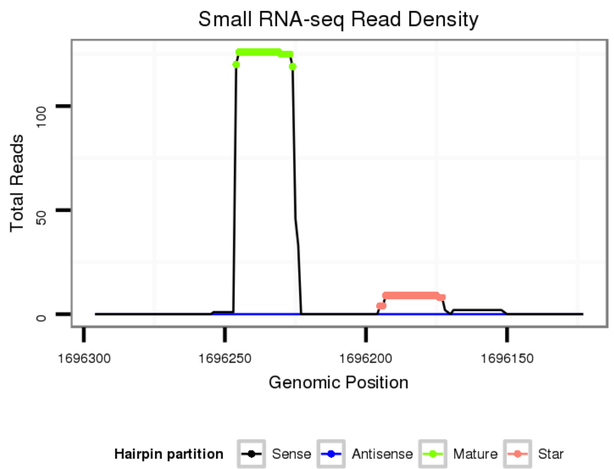
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

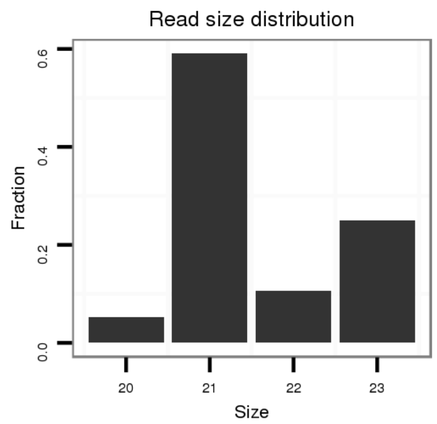
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_82	**scf2_1100000004963:1696173-1696246 -**	**confident**	**Mirtron**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

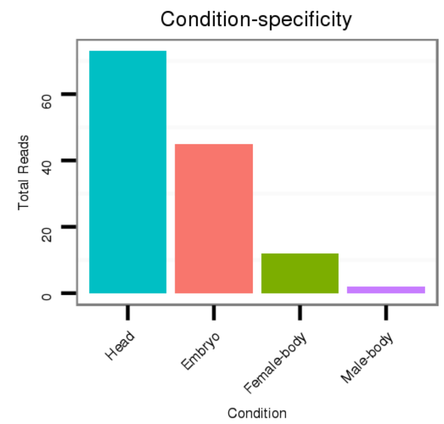
Legend: mature star mismatch in alignment mismatch in read

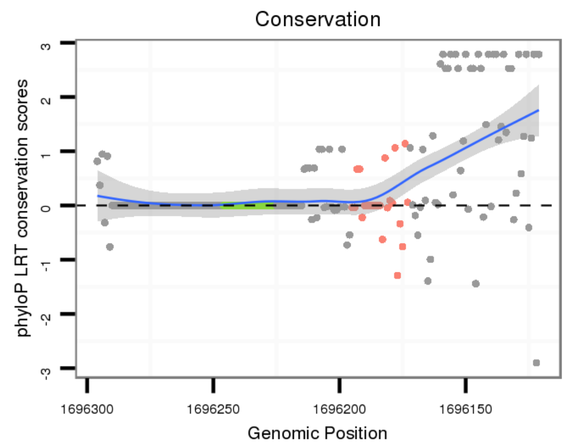
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dwil\GK15941-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATACCAAAAACTCTATTTAATTAATTGTCAAAAAAATAAAAATTTAAGCAGTAAGGTTGATTGGTTTTCCTTTTAATTTTAGCAAATAAATTTTGTTAATAAACCGAAGATCTTTTTCCCTTAGCTAGTTGATAAAATGGTGTGTGTGCCTTGCTTCATAATTCCGTTGCTCCT **********.(((((..((..(((((((..((((...(((((((((.....)))))))))).))))))).))..)))).********** **Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V118 embryo**	**V119 head**	**M045 female body**	**M020 head**	**V117 male body**
..........CCGAAGATCTTTTTCCCTTAGT..........	22	1	1	106.00	106	62	31	6	0	7
..........GTAAGGTTGATTGGTTTTCCT..........	21	0	1	72.00	72	15	46	4	7	0
..........GTAAGGTTGATTGGTTTTCCTTT..........	23	0	1	30.00	30	20	9	1	0	0
..........GTAAGGTTGATTGGTTTTCCTT..........	22	0	1	11.00	11	4	2	2	2	1
..........CCGAAGATCTTTTTCCCTTAGA..........	22	1	1	11.00	11	6	3	2	0	0
..........GTAAGGTTGATTGGTTTTCC..........	20	0	1	6.00	6	1	3	0	1	1
..........AACCGAAGATCTTTTTCCCTTAGT..........	24	1	1	3.00	3	1	1	0	1	0
..........AACCGAAGATCTTTTTCCCTTAG..........	23	0	1	3.00	3	2	1	0	0	0
..........TAAGGTTGATTGGTTTTCCTTT..........	22	0	1	3.00	3	1	0	2	0	0
..........CCGAAGATCTTTTTCCCTTAG..........	21	0	1	3.00	3	1	0	1	1	0
..........TAAGGTTGATTGGTTTTCCTT..........	21	0	1	2.00	2	1	1	0	0	0
..........TTTAAGCAGTAAGGTTGATTGGTT..........	24	0	1	1.00	1	0	1	0	0	0
..........CCGAAGATCTTTTTCCCTTAGC..........	22	0	1	1.00	1	1	0	0	0	0
..........TAAGGTTGATTGGTTTTCCT..........	20	0	1	1.00	1	0	0	1	0	0
..........GTTGATAAAATGGTGTGT..........	18	0	1	1.00	1	1	0	0	0	0
..........AACCGAAGATCTTTTTCCCTTAGA..........	24	1	1	1.00	1	0	1	0	0	0
..........AACCGAAGATCTTTTTCCCTT..........	21	0	1	1.00	1	0	0	1	0	0
..........GTTGATAAAATGGTGTGTG..........	19	0	1	1.00	1	0	1	0	0	0
..........GTAAGGTTGATTGGTTTTCCC..........	21	1	1	1.00	1	0	0	0	1	0
..........CCGAAGATCTTTTTCCCTTAGCT..........	23	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

TATGGTTTTTGAGATAAATTAATTAACAGTTTTTTTATTTTTAAATTCGTCATTCCAACTAACCAAAAGGAAAATTAAAATCGTTTATTTAAAACAATTATTTGGCTTCTAGAAAAAGGGAATCGATCAACTATTTTACCACACACACGGAACGAAGTATTAAGGCAACGAGGA **********.(((((..((..(((((((..((((...(((((((((.....)))))))))).))))))).))..)))).********** **Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V117 male body**
..........GTTGATAAAATGGTGTGT..........	18	0	1	1.00	1	1	0	0	0	0
..........AACCGAAGATCTTTTTCCCTTAGA..........	24	1	1	1.00	1	0	1	0	0	0
..........AACCGAAGATCTTTTTCCCTT..........	21	0	1	1.00	1	0	0	1	0	0
..........GTTGATAAAATGGTGTGTG..........	19	0	1	1.00	1	0	1	0	0	0
..........GTAAGGTTGATTGGTTTTCCC..........	21	1	1	1.00	1	0	0	0	1	0
..........CCGAAGATCTTTTTCCCTTAGCT..........	23	0	1	1.00	1	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004963:1696121-1696296 -	dwi_82	ATACCAAAAACTCTATTTAATTAATTGTCAAAAAAATAAAAATTTAAGCAGTAAGGTTGATTGGTTTTCCTTTTAATTTTAGCAAATAAATTTTGTTAATAAACCGAAGATCTTTTTCCCTTAGCTAGTT-GATAAAATGGTGTGTGTGCCTTGCTTCATAATTCCGTTGCTCCTCT
droVir3	scaffold_12726:472689-472731 -		AA----------AATGGTTTGCGTGCCCTGTTTCATCATCCGGTGCTGCTGT
droMoj3	scaffold_6308:2156393-2156435 -		AA----------AATGGTTTGCGTGCCCTGCTTCATCGTCCGGTGCTGCTCT
droGri2	scaffold_15203:5760491-5760533 +		AA----------GATGGTTTGCCCTGCCCTGCTTCATCATCCCATTGCTGCTGT
dp5	XL_grouple:2573957-2574043 -		AA----------CAATTGCAATATTAGTAACCAACCA----------CCCGGCAGCTGTTTAAGGAAAATGGTGTGCGTGCCGTGCTTTATCATTCCGGTGCTGCTCT
droPer2	scaffold_18:1472057-1472143 -		AA----------CAATTGCAATATTAGTAACCAACCA----------CCCGGCAGCTGTTTAAGGAAAATGGTGTGCGTGCCGTGCTTTATCATTCCGGTGCTGCTCT
droAna3	scaffold_12613:350547-350589 +		AA----------AATGGTGTGTGTTCCGTGTTTTATCATTCCATTGTTGCTGT
droBip1	scf7180000393900:45327-45367 -		A----------ATGGTTTGTGTACCGTGTTTTATCATTCCGCTCTTGTTGT
droKik1	scf7180000302344:1724766-1724808 +		AA----------GATGGTGTGCGTGCCCTGTTTTATCATTCCCCTGCTCCTAT
droFic1	scf7180000454072:198291-198330 +		A----------TGGTGTGCGTGCCCTGCTTCATCATTCCACTGCTCCTTT
droEle1	scf7180000491001:209812-209852 -		A----------ATGGTGTGCGTACCCTGTTTTATCATTCCACTGCTGCTCT
droRho1	scf7180000779337:249479-249518 -		A----------TGGTGTGCGTACCGTGCTTTATCATTCCACTGCTACTAT
droBia1	scf7180000302126:2167982-2168061 +		AAATCC----------AAAATCGGCAGGTTT----------CTCCCCAAAACT----ACCACTATGGTGTGCGTACCTTGCTTTATCATTCCACTGCTGCTGT
droTak1	scf7180000415769:1569688-1569752 -		TT----------TTCCTCGACAACAAACT-AGCACAATGGTGTGCGTACCGTGCTTTATCATTCCGCTGCTCCTTT
droEug1	scf7180000408825:187988-188028 +		A----------ATGGTGTGCGTACCGTGCTTTATCATTCCACTTCTGCTATT
dm3	chrX:3066973-3067013 -		A----------ATGGTTTGCGTGCCCTGTATTATCATTCCACTGCTTCTGT
droSim2	x:2839108-2839148 -		A----------ATGGTTTGCGTGCCCTGTTTCATCATTCCACTGCTACTGT
droSec2	scaffold_10:2796360-2796400 -		A----------ATGGTTTGCGTGCCCTGTTTCATCATTCCACTGCTTCTGT
droYak3	X:5301308-5301348 +		A----------ATGGTGTGCGTGCCCTGTTTCATCATTCCACTGCTGCTGT
droEre2	scaffold_4690:493127-493177 -		TAACCA----------AAACAATGGTGTGCGTGCCCTGTTTCATCATTCCACTGCTGCTGT

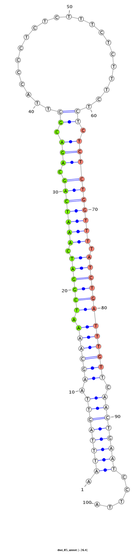
Generated: 09/08/2015 at 10:36 PM

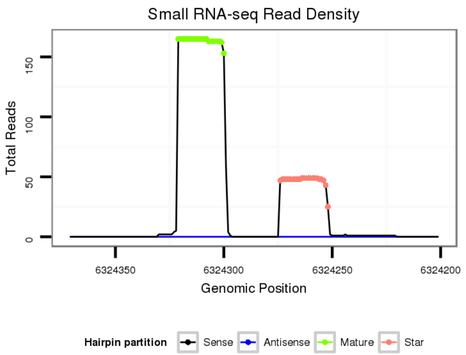
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

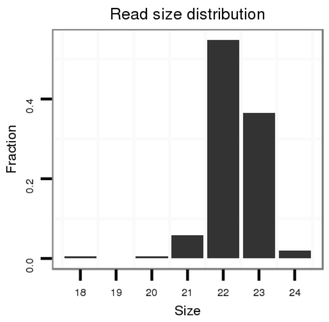
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_85	**scf2_1100000004902:6324251-6324321 -**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

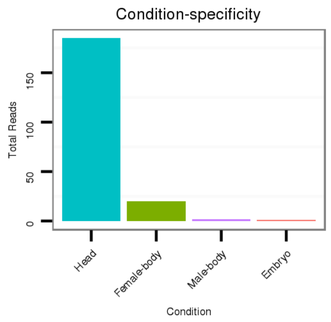
Legend: mature star mismatch in alignment mismatch in read

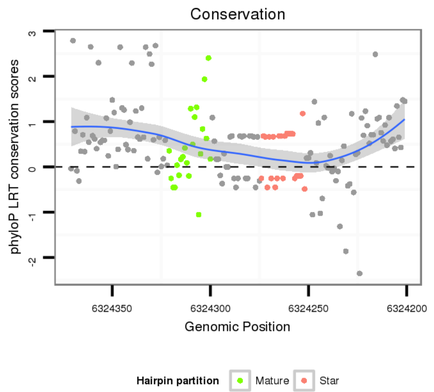
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK11118-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CAACGTAACGAGTGCATTGCATGAGAATCGGTGTTAATTTAGTTAAGCAAAATCGGATCAAATCAGCAGACGGTTACCCCTCTCTTTCTCTTTCTCTCTCTTGGTTTTATCTGATTTGTTCAACTGAATCCTTAAAGCTTTTTTTTGTTTGTAAAATTTTGCATGTAGTT	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	M045 female body	V119 head	V117 male body	V118 embryo
**********.(((((((((.(((((((.(((((((.(((((((.(((.((.....................)).)))))))))).)))))))))))).)))))))).**********										
.....AATCGGATCAAATCAGCAGACG.....	22	0	1	95.00	95	93	2	0	0	0
.....AATCGGATCAAATCAGCAGACGG.....	23	0	1	54.00	54	49	4	1	0	0
.....CTCTCTGGTTTTATCTGATTTGT.....	23	0	1	22.00	22	16	1	3	2	0
.....CTCTCTGGTTTTATCTGATTTG.....	22	0	1	18.00	18	6	8	3	0	1
.....AATCGGATCAAATCAGCAGAC.....	21	0	1	8.00	8	8	0	0	0	0
.....CTCTCTGGTTTTATCTGATTT.....	21	0	1	4.00	4	1	3	0	0	0
.....AATCGGATCAAATCAGCAGACGGT.....	24	0	1	3.00	3	3	0	0	0	0
.....AATCGGATCAAATCAGCAGACGGA.....	24	1	1	2.00	2	2	0	0	0	0
.....CTCTCTGGTTTTATCTGATTTGA.....	23	1	1	2.00	2	2	0	0	0	0
.....GTTAAGCAAAATCGGATCAAATC.....	23	0	1	2.00	2	2	0	0	0	0
.....AATCGGATCAAATCAGCAGACT.....	22	1	1	2.00	2	1	1	0	0	0
.....CTCTCTGGTTTTATCTGATTTG.....	23	1	1	2.00	2	2	0	0	0	0
.....AAAATCGGATCAAATCAGCAGAC.....	23	0	1	1.00	1	1	0	0	0	0
.....CTCTCTGGTTTTATCTGATTTGTT.....	24	0	1	1.00	1	0	1	0	0	0
.....CTCTCTGGTTTTATCTGATTTT.....	22	1	1	1.00	1	0	1	0	0	0
.....AAAATCGGATCAAATCAGCAGA.....	22	0	1	1.00	1	1	0	0	0	0
.....TTATCTGATTTGTTCAACTGA.....	21	0	1	1.00	1	1	0	0	0	0
.....AAATCGGATCAAATCAGCAGACGGTT.....	26	0	1	1.00	1	1	0	0	0	0
.....TCTCTGGTTTTATCTGATTTGT.....	22	0	1	1.00	1	0	1	0	0	0
.....CTCTCTGGTTTTATCTGATTTGG.....	23	1	1	1.00	1	1	0	0	0	0
.....CTCTCTGGTTTTATCTGA.....	18	0	1	1.00	1	1	0	0	0	0
.....AATCCTTAAAGCTTTTTTTTGTTT.....	24	0	1	1.00	1	0	1	0	0	0
.....CTCTCTGGTTTTATCTGATT.....	20	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

GTTGCATTGCTCACGTAACGTACTCTTAGCCACAATTAAATCAATTCGTTTTAGCCTAGTTTAGTCGTCTGCCAATGGGGAGAGAAAGAGAAAGAGAGAGACCAAAATAGACTAAACAAGTTGACTTAGGAATTTCGAAAAAAAACAAACATTTTAAAACGTACATCAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo
**********.(((((((((.(((((((.(((((((.(((((((.(((.((.....................)).)))))))))).)))))))))))).)))))))).**********						
.....AGAGAAAGAGAAAGAGAGA.....	21	0	20	0.05	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004902:6324201-6324371 -	dwi_85	CAACGTAACGA-----GTGCATTGCATGAGAATCGGTGT--------TAATTTAGTTAAGCAA--------A----ATC-GGAT--C-AAATCA-GCAGA----------CGGTTACCCCTCTCTTTCTCTTTCTCTCTCTTGGTTTTATCTGATTT-GTTCAACTGAAT----------CC---------TTAAAGCTTT------T-TTTTGT-TTG----------TAAAA-TTTTGCATGTAGTT
droVir3	scaffold_13049:6504180-6504304 +		CAAAAAGAATATACAAAA----AGATGACAATAGATT--------CAATT----------------------TTTGGCGCACCCTCTC--AC-----TCTCTGC--CTCTCTCTACTACCCGC----------T----------C--------T----------C--------AGCTCT--GTTTTGTTGTCT----------AACTCTAAATC
droMoj3	scaffold_6328:2379624-2379771 -		AAACGTACAAA-----ATGC-CCAATTTGT----------T----------TGATAT-A----------C-----AGAGCAACGTT-C----------CCCGCTCCTGTT----------CC-CC-CCCTCTCTCTCTCTCTGTCTCTCTCTGTCTCTCT----------AGCTCT-GT------TGTTTTG-T-TTGCCGGCATGTTTTGTTTCCAAATATTTACAAATGTTT
droGri2	scaffold_14853:8680615-8680786 -		TATTTTTT---------GCATGCTATTTCG--CTCACTCGCTCGCTCAGTTGCCTC----------G-----GGA-GTGT--C-AAAGCA-GCTCTCTTCT----------TCTT----------CTTGCTCTTCG-GAATGCGCTCTTCA----------T-----------TCT----------TCTTCTTCTTCTGATCGTTTTCTAT-TTGAAGTTTG-------T-CATTTTC-TTG----------T--AAGTTTTG-GTTTGTT
dp5	2:23119427-23119603 +		CAAAGTAACGA-----ATGCATTGCATGAGAATCGGTGT--------TAATTTAGTTGAAAGTTTGGAGGAAGCT---TCTTCCC-CAAAGAATTG---------------GCTTA-----CATCGTTCC--CGTT-GCGGCACAACTGGCTTTTCAATGAATGA----------AGAATCTGTGTCATCCTCC----------C----------T--------C--------T--------AC------TG---CC-TTG----------T--AATTATTGCATGTAGTT
droPer2	scaffold_3:5890248-5890424 +		CAAAGTAACGA-----ATGCATTGCATGAGAATCGGTGT--------TAATTTAGTTGAAAGTTTGGAGGAAGCT---TCTTCCC-CAAAGAATTG---------------GCTTA-----CATCGTTCC--CGTT-GCGGCACAACTGGCTTTTCAATGAATGA----------AGAATCTGTGTCATCCTCC----------C----------T--------C--------T--------AC------TG---CC-TTG----------T--AATTATTGCATGTAGTT
droAna3	scaffold_13340:3437746-3437910 -		CAAAGTAACGA-----ATGCATTGCATGAGAATCGGTGT--------TAATTTAGTTGAAAAA-------E----C---AAGTC--G-GAAGAATCAGATCTAACT--------G-GATGG----TATCATTCC--TGTT-GCGGCACAAC--TCTTTTCAAATGAATCCC----------C-------C----T--CTGCATTTGAAGGCGT------G-T----C-TTG----------A--AATTACTGCATGTAGTT
droBip1	scf71800000396712:915689-915843 +		CAAAGTAACGA-----ATGCATTGCATGAGAATCGGTGT--------TAATTTAGTTGAAAA--------AAACC---AAGTC--C-AAAGAATCG---------------G----A-----TATCATTCC--TGTT-GCGGCACAAC--TCTTTTCAATGAATCCC----------C-------C----T--CAGCATTTGAAGGCGT------G-----GT-TTG----------T--AATTACTGCAGTAGTT
droKik1	scf71800000302639:1891652-1891820 +		CAAAGTAACGA-----ATGCATTGCATGAGAATCGGTGT--------TAATTTAGTTGAAAG--------A-----GGTC--C-CCGAATCTCA----------TTGC-G--------AATCATTTT--CCTTGGCGGCACAACTGACTTTTCAGTGAATCTA----------C-------C-AGCTCTCTTC-G----------CCCTCTCTA--TCTG--T----------TA---------T--TCTGT-GTG----------T--AATTATGCATGTAGTT
droFic1	scf71800000454106:2505587-2505775 +		CAGAGTAACGA-----ATGCATTGCATGAGAATCGGTGT--------TAATTTAGTTGAAAG--------E-----G---AGTC--C-AGAGAATCCAGATCTGATCTGATTAATCG-GATTA-----AGTCACTCC--ACTT-GGGGCACAAT-CGCTTTTCAATGAATCTA----------C-------C----T--CTGTTCCC-GAATCCGTGAAT----------TC---------ACATCG-GGC------TGTGTAAT-TTG----------T--AAGTATGCATGTAGTT
droEle1	scf71800000491212:1126043-1126216 +		CAAAGTAACGA-----ATGCATTGCATGAGAATCGGTGT--------TAATTTAGTTGAAAG--------E-----G---AGTC--C-AGAGAATCCAGATCTGATCTTAT----TG-GATTACTGAAAATCATTCC--CCTT-GGGGCACAAG--ACTTTTCAATGAATAT----------C-------GTGATCCAA----------C---------A----C-CTTCT---GTT---C-GTG----------T--AATTATGCATGTAGTT
droRho1	scf71800000777243:3160-3314 =		CAAAGTAACGA-----ATGCATTGCATGAGAATCGGTGT--------TAATTTAGTTGAAAG--------E-----G---AGTC--C-AGAGAATCCAGATCTGATTT-------CG-GATTA-TAAAGAGCATTCC--CCTT-GGGGCACAAC--ACTTTTCAATGAATAT----------C-------TCATCCTAC----------C---------A----C-CTTCC---G-----E---TG----------T--AATTATGCATGTAGTT
droBia1	scf71800000301501:579239-579324 +		TAATTCAGCGA-----ATGCATTGTTGCGAA-------T----------TAATTCAGATACAACG--------E-----G---AGC--C-------A----------AAAGAAATT----------C---------T---------TTATCTTCC----------T---------A----C-CTTCC---GT---C-TG----------T--AA---------TATTT
droTak1	scf71800000414009:150057-150189 +		CAAAGTAACGA-----ATGCATTGCATGAGAATCGGTGT--------TAATTTAGTTGAAAG--------E-----G---GGTC--C-AGAGA-----------------------TCATTCT--CGTT-GGGACACAGG--ACTCTTCAATGAATGTT----------C-------C-TCATCCAAC----------C---------TA----C-CTTCC---G-----E---TG----------T--AA---AATGCATGTAGTT
droEug1	scf71800000407691:79592-79708 -		AAAGAAAACGA-----AGCGCAAGAACCCGAAGCC--TT---------ACACTCAGCTGAGCAG--------E-----G---AGC--CGCAGAAACC----------------------------------TATAATGGGGTGT----------C-------C-TCCTCTAG-TCCCTGTCTTTCGCTCTCTCGCT----------C-------C-TTCT---G-----E---TG----------T--AATTATGCATGTAGTT
dm3	chr3R:4662156-4662334 -		CAAAGTAACGA-----ATGCATTGCATGAGAATCGGTGT--------TAATTTAGTTGAAAG--------E-----G---TGTC--C-AGAAA-CCAGATCTAATT-TATAGATCTGATT----------TATTCCGATCTT-GGGCCACAAG--ACTTTTCAATGAATG----------GTATCTC-TCTCATCCTTC----------C---------TA--TCAG----------C---------CCGT-------TCT---TG-TG----------T--AATTATGCATGTAGTT
droSim2	3r:16329712-16329891 +		CAAAGTAACGA-----ATGCATTGCATGAGAATCGGTGT--------TAATTTAGTTGAAAG--------E-----G---TGTC--C-AGAGA-CCAGATCTGATTCTATAAATCTGATA---------TATTCCGATCTT-GGGGCACAAG--TCTTTTCAATGAATC----------GAATCTC-TCATCCTTC----------C---------TA--TCAG----------C---------CCGT-------TCT---TG-TG----------T--AATTATGCATGTAGTT
droSec2	scaffold_0:17195438-17195617 +		CAAAGTAACGA-----ATGCATTGCATGAGAATCGGTGT--------TAATTTAGTTGAAAG--------E-----G---TGTC--C-AGAGA-GCCAGATCTGATTCTATAAATCTGATA---------TATTCCGATCTT-GGGGCACAAG--ACTTTTCAATGAATC----------GAATCTC-TCATCCTTC----------C---------TA--TCAG----------C---------CCGT-------ACT---TG-TG----------T--AATTATGCGCATGTAGTT
droYak3	3R:8724250-8724420 -		CAAACTAACGA-----ATGCATTGCATGAGAATCGGTGT--------TAATTTAGTTGAAAG--------E-----G---TGTC--C-AGAGA-GCCAGATCTGATT----------TATATAGATCAATTC--GCTG-GGGGCACAAG--ACTTTTCAATGAATCTC----------T-------C-TCATCCTTC----------T---------TA--CCAAA----------C---------GCCGT-------TCT---CG-TG----------T--AATTATGCGCATGTAGTT
droEre2	scaffold_4770:16923820-16923979 +		CAAAGTAACGA-----ATGCATTGCATGAGAATCGGTGT--------TAATTTAGTTGAAAG--------E-----G---TGTC--C-AAAGAATCCAGAT----------CATTCC--GCTT-GGGGCACAAG--ACTTTTCAATGAATCTC----------C-------C-TCATCCTTC----------C---------TA--TCAG----------C---------CCTTGTGTAATCT---TG-TG----------T--AATTACGCATGTAGTT

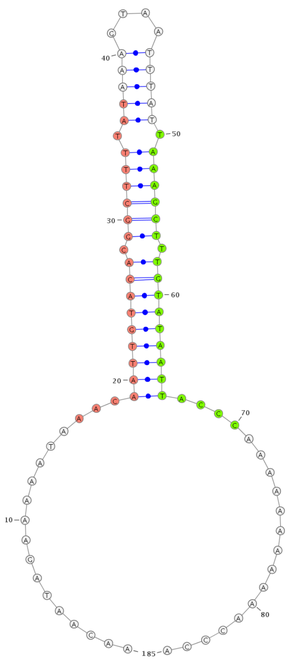
Generated: 09/08/2015 at 07:40 PM

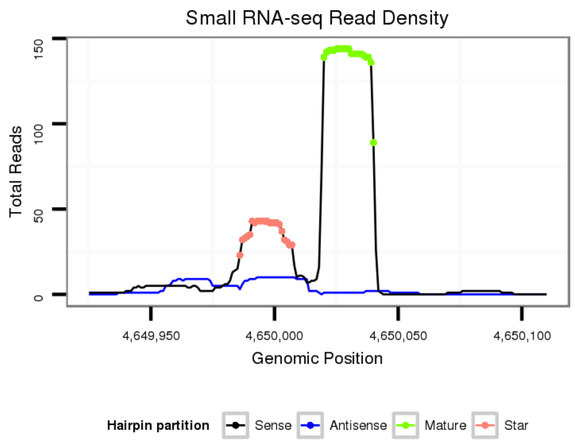
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

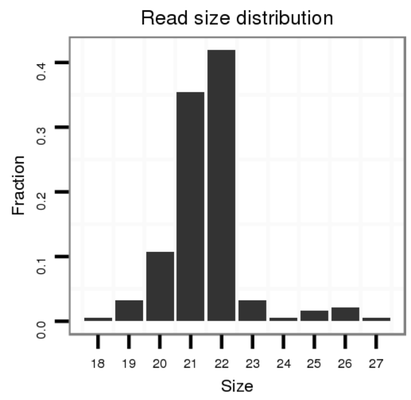
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_5415	**scf2_1100000004902:4649975-4650060 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

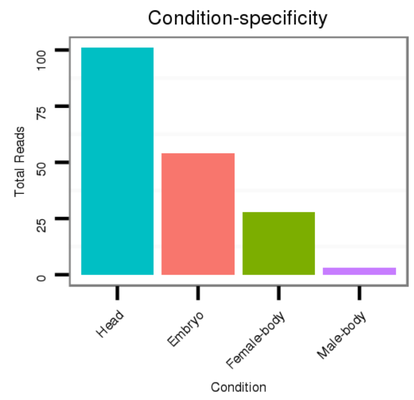
Legend: mature star mismatch in alignment mismatch in read

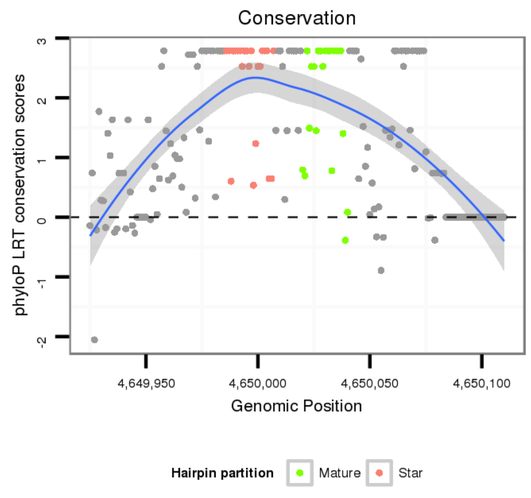
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
A-rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAGAAAAGAAAAGTTTAAAAAATCAAAACAACCAACCAACCAACAAAACAATAGAAAAATAAACAATTGTACACGGCTTTTATAAAGTAATTTATTAAAGCTTTGTATAATTACCCAAAAAAAAAAACCCAAAAATTTTTGTTTTTATTTGTTAGTAGATTTCCTCATCTCTTTTAAGTTTCTTTT **********.....(((((((((.(((((((.(((((....))))).)))))))..)))))))).....********** **Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M020 head**	**V118 embryo**	**V119 head**	**M045 female body**	**V117 male body**
.....TAAAGCTTTGTATAATTACCC..... 21	0	1	31.00	31	20	5	2	4	0
.....TTAAAGCTTTGTATAATTACCC..... 22	0	1	30.00	30	20	4	4	2	0
.....TTAAAGCTTTGTATAATTACC..... 21	0	1	25.00	25	17	4	3	1	0
.....TAAAGCTTTGTATAATTACCCA..... 22	0	1	22.00	22	0	8	7	7	0
.....TAAAGCTTTGTATAATTACC..... 20	0	1	12.00	12	4	2	5	0	1
.....AACAATTGTACACGGCTTTTAT..... 22	0	1	7.00	7	1	4	2	0	0
.....ACAATTGTACACGGCTTTTATA..... 22	0	1	6.00	6	0	3	2	1	0
.....ATTAAAGCTTTGTATAATTACC..... 22	0	1	6.00	6	4	2	0	0	0
.....TTAAAGCTTTGTATAATTACT..... 21	1	1	4.00	4	2	1	1	0	0
.....TTGTACACGGCTTTTATAAAGT..... 22	0	1	3.00	3	1	0	2	0	0
.....ACAATTGTACACGGCTTTTAT..... 21	0	1	3.00	3	0	0	1	2	0
.....TTAAAGCTTTGTATAATTACCT..... 22	1	1	3.00	3	3	0	0	0	0
.....ATTAAAGCTTTGTATAATTACT..... 22	1	1	3.00	3	1	0	0	1	1
.....AGTAATTTATTAAAGCTTTGT..... 21	0	1	2.00	2	0	2	0	0	0
.....TTAAAGCTTTGTATAATTACG..... 21	1	1	2.00	2	0	0	2	0	0
.....TAAAGCTTTGTATAATTACCT..... 21	1	1	2.00	2	2	0	0	0	0
.....ATAAACAATTGTACACGGCT..... 20	0	1	2.00	2	0	2	0	0	0
.....TAAAGCTTTGTATAATTACA..... 20	1	1	2.00	2	0	0	2	0	0
.....ATAAACAATTGTACACGGCTT..... 21	0	1	2.00	2	0	1	0	1	0
.....AATAAACAATTGTACACGGCTT..... 22	0	1	2.00	2	0	0	0	0	2
.....CAATTGTACACGGCTTTTATA..... 21	0	1	1.00	1	0	0	0	1	0
.....TAAAGCTTTGTATAATTACCA..... 21	1	1	1.00	1	0	0	1	0	0
.....AATCAAAACAACCAACCAACCAACA..... 25	0	1	1.00	1	0	0	0	1	0
.....ACAAAACAATAGAAAAATAAACAAT..... 25	0	1	1.00	1	0	0	0	1	0
.....CTTTGTATAATTACCCAAA..... 19	0	1	1.00	1	0	0	0	1	0
.....TTGTACACGGCTTTTATAAAGTAATT..... 26	0	1	1.00	1	0	0	1	0	0
.....AATTGTACACGGCTTTTAT..... 19	0	1	1.00	1	0	1	0	0	0
.....AAAGCTTTGTATAATTACC..... 19	0	1	1.00	1	0	1	0	0	0
.....TTAAAGCTTTGTATAATTAC..... 20	0	1	1.00	1	1	0	0	0	0
.....AAAGCTTTGTATAATTACCCT..... 21	1	1	1.00	1	0	0	0	1	0
.....AACAATTGTACACGGCTTTT..... 20	0	1	1.00	1	0	0	0	1	0
.....AAACAATTGTACACGGCTTTTAT..... 23	0	1	1.00	1	0	1	0	0	0
.....ATTAAAGCTTTGTATAATTACCC..... 23	0	1	1.00	1	0	1	0	0	0
.....CAAAACAACCAACCAACCAACAA..... 23	0	1	1.00	1	0	0	0	0	1
.....TAAAGCTTTGTATAATTACCCAA..... 23	0	1	1.00	1	0	1	0	0	0
.....ATTTATTAAAGCTTTGTATAATTACC..... 26	0	1	1.00	1	0	0	0	1	0
.....TAAAAAATCAAAACAACCAACCAAC..... 25	0	1	1.00	1	0	0	0	1	0
.....TATTAAAGCTTTGTATAATTACA..... 23	1	1	1.00	1	0	1	0	0	0
.....AAAGCTTTGTATAATTACCC..... 20	0	1	1.00	1	0	1	0	0	0
.....AAAATCAAAACAACCAACCAACCAAC..... 26	0	1	1.00	1	0	0	0	1	0
.....TAAACAATTGTACACGGCTT..... 20	0	1	1.00	1	0	1	0	0	0
.....TTGTACACGGCTTTTATAAAGTAAT..... 25	0	1	1.00	1	0	0	1	0	0
.....AAAAATAAACAATTGTACACGGCTTT..... 26	0	1	1.00	1	0	1	0	0	0
.....TAGAAAAATAAACAATTGTACACGGCT..... 27	0	1	1.00	1	0	0	0	1	0
.....AAGCTTTGTATAATTACCCA..... 20	0	1	1.00	1	0	1	0	0	0
.....TATTAAAGCTTTGTATAATTACT..... 23	1	1	1.00	1	0	1	0	0	0
.....AACAATAGAAAAATAAACAATTGTACA..... 27	0	1	1.00	1	0	0	0	1	0
AAGAAAAGAAAAGTTTAAAAA..... 21	0	1	1.00	1	0	1	0	0	0
.....ATTAAAGCTTTGTATAAT..... 18	0	1	1.00	1	0	1	0	0	0
.....TATTAAAGCTTTGTATAATTAC..... 22	0	1	1.00	1	0	1	0	0	0
.....TTGTACACGGCTTTTATAAAGTA..... 23	0	1	1.00	1	1	0	0	0	0
.....GTACACGGCTTTTATAAAGTAATTT..... 25	0	1	1.00	1	0	0	0	1	0
.....TAAAGCTTTGTATAATTACCCT..... 22	1	1	1.00	1	1	0	0	0	0
.....TTTATTAAAGCTTTGTATAATTACC..... 25	0	1	1.00	1	0	1	0	0	0
.....TTGTACACGGCTTTTATAA..... 19	0	1	1.00	1	0	0	0	1	0
.....TTATTAAAGCTTTGTATAATTACC..... 24	0	1	1.00	1	1	0	0	0	0
.....AAAATAAACAATTGTACACGGCT..... 23	0	1	1.00	1	0	1	0	0	0
.....TAAAGCTTTGTATAATTAC..... 19	0	1	1.00	1	0	0	1	0	0
.....TATTAAAGCTTTGTATAATT..... 20	0	1	1.00	1	0	1	0	0	0
.....TTGTACACGGCTTTTATAAAG..... 21	0	1	1.00	1	0	0	0	1	0
.....TAAAGCTTTGTATAATTACCTT..... 22	2	1	1.00	1	0	0	1	0	0
.....AAAATCAAAACAACCAACCAACCAACA..... 27	0	1	1.00	1	0	0	0	1	0
.....AAAGCTTTGTATAATTACCCA..... 21	0	1	1.00	1	0	0	0	1	0
.....ATTGTACACGGCTTTTATA..... 19	0	1	1.00	1	0	1	0	0	0
.....AAGTAATTTATTAAAGCTTTGT..... 22	0	1	1.00	1	0	1	0	0	0
.....TTAAAGCTTTGTATAATTACA..... 21	1	1	1.00	1	0	0	1	0	0
.....TAGAAAAATAAACAATTGTACACGGC..... 26	0	1	1.00	1	0	0	0	1	0
.....TAAAGCTTTGTATAATTACCG..... 21	1	1	1.00	1	0	0	1	0	0
.....TTAAAGCTTTGTATAATTACCA..... 22	1	1	1.00	1	0	0	1	0	0
.....ATAAACAATTGTACACGGCTTTT..... 23	0	1	1.00	1	0	1	0	0	0
.....TTAGTAGATTTCCTCATCTCT..... 21	0	1	1.00	1	1	0	0	0	0
.....TATTTGTTAGTAGATTTCCTCA..... 22	0	1	1.00	1	0	0	0	1	0
.....TATTAAAGCTTTGTATAATTATT..... 23	2	2	0.50	1	1	0	0	0	0
.....TTAAAGCTTTGTATAATTACTT..... 22	2	2	0.50	1	0	0	1	0	0
.....TTAAAGCTTTGTATAATTATT..... 21	2	5	0.20	1	0	0	1	0	0
.....ATTAAAGCTTTGTATAATTATT..... 22	2	5	0.20	1	0	0	0	1	0

Anti-sense strand reads

TTCTTTTCTTTTCAAATTTTTTAGTTTTGTTGGTTGGTTGGTTGTTTTGTTATCTTTTTATTTGTTAACATGTGCCGAAAATATTTCATTAAATAATTTCGAAACATATTAATGGGTTTTTTTTTTTGGGTTTTTAAAAACAAAAATAAACAATCATCTAAAGGAGTAGAGAAAATTCAAAGAAAA **********.....(((((((((.(((((((.(((((....))))).)))))))..)))))))).....********** **Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M045 female body**	**V117 male body**	**V119 head**	**M020 head**	**V118 embryo**
.....TGTTAACATGTGCCGAAAATATTTCAT..... 27	0	1	3.00	3	3	0	0	0	0
.....GTTAACATGTGCCGAAAATATTTCAT..... 26	0	1	2.00	2	2	0	0	0	0
.....TGGTTGGTTGTTTTGTTATCTTTTTAT..... 27	0	1	2.00	2	2	0	0	0	0
.....GGTTGGTTGGTTGTTTTGT..... 19	0	1	2.00	2	1	1	0	0	0
.....CAAATTTTTTAGTTTTGTTGGTTGGT..... 26	0	1	1.00	1	1	0	0	0	0
.....TAACATGTGCCGAAAATATTTCATTAAAT..... 29	0	1	1.00	1	1	0	0	0	0
.....TGGGTTTTTTTTTTGGGTTTT..... 22	0	1	1.00	1	0	0	1	0	0
.....GGTTGTTTTGTTATCTTTTTATTTGT..... 26	0	1	1.00	1	1	0	0	0	0
.....GGTTGGTTGGTTGTTTTG..... 18	0	1	1.00	1	1	0	0	0	0
.....TTGGTTGGTTGTTTTGTTATCTT..... 23	0	1	1.00	1	1	0	0	0	0
.....GTTGGTTGTTTTGTTATCTTTTTAT..... 25	0	1	1.00	1	1	0	0	0	0
.....TAACATGTGCCGAAAATATTTCAT..... 24	0	1	1.00	1	1	0	0	0	0
.....TTTATTTGTTAACATGTGCCGAAAATAT..... 28	0	1	1.00	1	1	0	0	0	0
.....TTGTTAACATGTGCCGAAAATATTTCAT..... 28	0	1	1.00	1	1	0	0	0	0
.....CATGTGCCGAAAATATTTCATTAAA..... 25	0	1	1.00	1	1	0	0	0	0
.....TTGGTTGGTTGGTTGTTTTGT..... 21	0	1	1.00	1	1	0	0	0	0
.....ATTTCGAAACATATTAATGGGTTTTTT..... 27	0	1	1.00	1	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004902:4649925-4650110 +	dwi_5415	AA-GAAAA--GAA--------AAGTTTA----AAAAATCAAAACA----ACC----AACCAAC--CAACAAAACAATAGAAA----------------AATAAAC-AATTGTACACGGCTTTTATAAAGTAATTTATTAAAGCTTTGTATAATTACCCAAAAAAAAAAACCCAAAAA-TTTTTGTTTTTATTTGTTAGTAGATTTCCTCATCTCTTTTAAGTTTCTTTT
droVir3	scaffold_13047:1835005-1835158 +	dvi_24634	AA-TGAGC--AA-------AA-------AGAG-----AACAA---CCC----AACC---AACAA--AAAACAATAGAAAA-AAAAACATAAAAAAAAAATAATAATTGTACACGGCTTTCGTAAAGAATTTATTGAAGCTTTGTATAATTAAGAAAAAAA-AAAACCTTGAAC-TTTGTGTTTTTATTT----------
droMoj3	scaffold_6540:3761902-3762063 +	dmo_3126	AA-TGAAAGAAA-------GA------AGAG-----ATGAA---CCCAACCAACA-ACAAAAAAAAAAACCAATAGAAAAAACTAAAA-AAAAAAAAAATAAACAAC-ATTGTACACTGCTTTCGTAAAGAATTTATTGAAGCTTTGTATAATTAAAAAAAAAA----AAACTGAACTTTTGTGTTTTTATTTG----------
droGri2	scaffold_14906:8668153-8668293 +	dgr_462	AA-AAAAA--AA-------AA------AGTG-----AACAA---CCC----AACC---A--ACAAAACAATAGAAA----------AAAATAAAC-AATTGTACACGGCTTTCGTAAAGAATTTATTGCGAAGCTTTGTATAATTAGCAAAAAAAAACAACCTGATC-TTTGTGTTATTATTTGCT----------
dp5	2:27294876-27295016 -	dps_3827	AC-CA-----------------------AA---TCC----ATTCAACAG--AAAAAACAATAGAAGA-ACAAAAA-AAAAAGAAAATAAAA-AATTGTACACGGCTTTTATGAAGTAATTTGTTAAAGCTTTGTATAATTACCCAAAAAAAAAA--AAAACCAAA-TTTGTGTTTTTATTTG----------
droPer2	scaffold_6:2585075-2585217 -	dpe_2481	AC-CA-----------------------AA---TCC----ATTCAACAG--AAAAAACAATAGAAGA-ACAAAAA-AAAAAGAAAATAAAA-AATTGTACACGGCTTTTATGAAGTAATTTGTTAAAGCTTTGTATAATTACAAAAAAAAAAAACCCCAAA-TTTGTGTTTTTATTTG----------
droAna3	scaffold_13340:11049288-11049440 -	dan_90	AA-AAAAA--CAA--------ATATTTGAAAAAGAA-----ATCAA-CCCTC----AACC---AACCACACAAACCAATAGAAA----------AAATAAC-AATTGTACACGGCTTTCGTAAAGTGATTTATTAAAGCTTGTATAATTAAGAAAAA--------GAACAAA-TTTGTGTTTTTATTTCCAATAGA----------
droBip1	scf7180000396374:34265-34385 +		AA-GA-----------------------AATCCCTC----AACC---AACCACACAAACCAATAGAAA----------AAATAAC-AATTGTACACGGCTTTCGTAAAGTGATTTATTAAAGCTTGTATAATTAAGAAAAACA--------ACAAA-TTTGTGTTTTTATTT----------
droKik1	scf7180000302247:250358-250491 +		AA-----------------------ACGAACCAACC---ATCAACAAACAATAGAAGA-AA------AAAAACAAAATAAAC-AATTGTACATGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAAAAAAAAGA-A--CAACGAAAA-TTTGTGTTTTTATTTG----------
droFic1	scf7180000454106:2527568-2527712 +		GAATGA-----AAACCCCACAA-------AGCC-----AACC----ACC----AACC---AACACAAAACAATAGAAA----------AACAAATAAAC-AATTGTACACGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAAGAAAAAAA----AACCTCCAA-ATTTGTGTTTTTATTTG----------
droEle1	scf7180000491212:1154186-1154310 +		AA-GC-----------------------A---TCCACCAACC---AGCA-----ACAATAAAA----------AAACAAATAAAC-AATTGTACACGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAAGAAAAAAG--AACCCCAAA-TTTGTGTTTTTATTTG----------
droRho1	scf7180000778307:14071-14198 +		AA-----------------------ACGAACCAACC---AACATCAAAACAATAGAAA----------AAAACAAATAAAC-AATTGTACACGGCTTTCGTAAAGCAATTTATTGAAGCTTTGTATAATTAAGAAAAAAA----AACCTCAAA-TTTGTGTTTTTATTTG----------
droBia1	scf7180000302402:7353521-7353643 -		AA-----------------------ACC----AACC---AACAACAAATCCATAGAAA----------AAA-CAATAAAC-AATTGTACACGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAAGAAAAAAAA--CAACGAAAA-TTTGTGTTTTTATTTG----------
droTak1	scf7180000414009:179087-179216 +		TA-TAA-----------------------A---ACGAACCAACC---AACAAGAAAACAATAGAAA----------AAACAAATAAAC-AATTGTACACGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAAAAAAAA---A--AACCTCAAA-TTTGTGTTTTTATTTG----------
droEug1	scf7180000409490:80968-81096 +		AA-----------------------ACGAACCAACC---AACAACAAAACAATAGAAA----------AAAAATCAAATAAAC-AATTGTACATGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAAGAAAAAAA----AACCTCAAA-TTTGTGTTTTGCATTTG----------
dm3	chr3R:4640258-4640386 -	dme_421	CA-----------------------A---ACGAAACAAACAAC---AACAACAAAACAATAGAAA----------AAAGAAATAAAC-AATTGTACATGGCTTTCGTAAAGAAATTTATCAAGGCTTTGTATGATTAACCAAAAAAAA--ATCCACAAA-TTTGTGTTTTTATTTG----------
droSim2	3r:16351750-16351875 +	dsi_75	AC-----------------------AA---CC----A-ACC---AACAACAAAACAATAGAAA----------AAAAAACAAATAAAC-AATTGTACATGGCTTTCGTAAAGAAATTTATTAAAGCTTTGTATGATTAACCAAAAAA-A--ATCCTGAAA-TTTGTGTTTTTATTTG----------
droSec2	scaffold_0:17217390-17217519 +	dse_1844	CA-----------------------A---ACGAAACAAACAAC---AACAACAAAACAATAGAAA----------AAAAACAAATAAAC-AATTGTACATGGCTTTCGTAAAGAAATTTATTAAAGCTTTGTATGATTAACCAAAAAA-A--ATTCTGAAA-TTTGTGTTTTTATTTG----------
droYak3	3R:8702192-8702322 -	dya_1796	T--------------------------CAA---ACC----AAACCAAC---AACAACAAAACAATAGAAGA---------AAAAAACAAATAAAC-AATTGTACATGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACCAAAAAAAA--ATCCTCAAA-TTTGTGTTTTGCATTTG----------
droEre2	scaffold_4770:16945913-16946037 +	der_1521	CA-----------------------A---ACC----AAACCAAC---AACAACAAAACAATAGAAA----------AAAACAAATAAAC-AATTGTACATGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACCAAAAAA----ATCCTCAAA-TTTGTGTTTTTATTTG----------

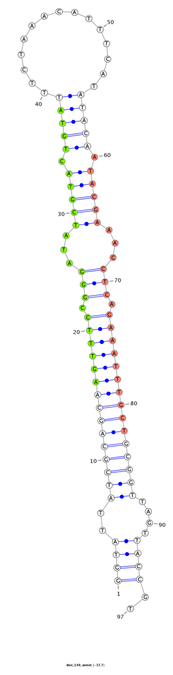
Generated: 09/08/2015 at 07:40 PM

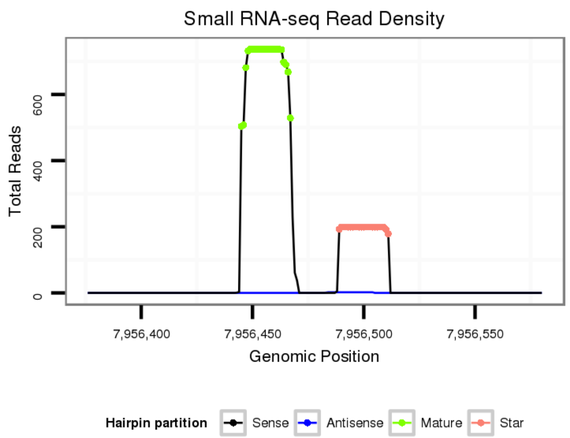
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	8
rescue.candidate	4

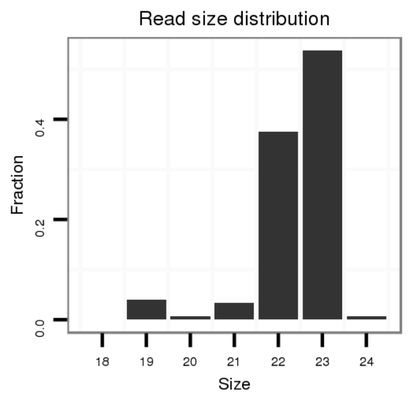
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_140	**scf2_1100000004909:7956426-7956530 +**	**Known Ortholog**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

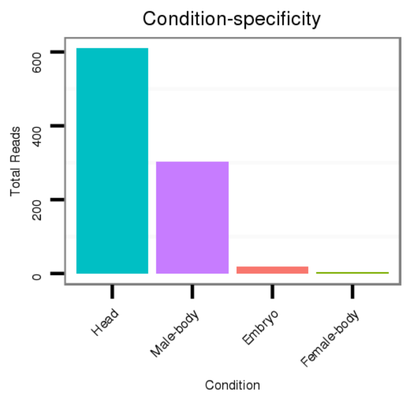
Legend: mature star mismatch in alignment mismatch in read

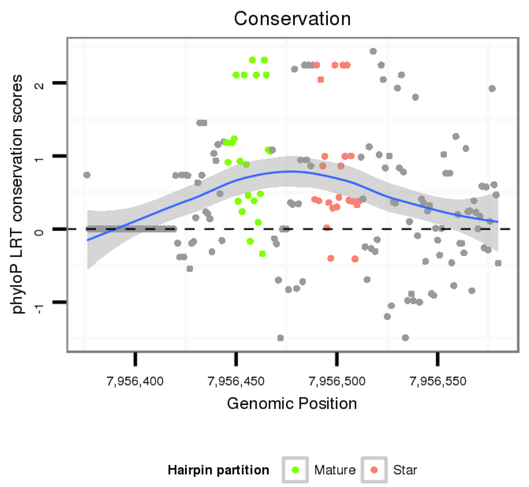
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTAGCTTAAATGCACAATTTATGCACTATGGAAATAATTAATTGGATATTGGTTGGTATTATCGCAGCAAGTTTCCGGGATATCGTACTGTATTTCTAAACATTTCATATACAATACGAAACCTCAGAAATTTGCTGCGGTTAGTTACCGTTAACAACTCATAAGAAAGGAGAGAATAAAAATGATCAATATACATGTGTGTGTG	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V117 male body	V119 head	V118 embryo	M045 female body
**********(((((..(((((((((((((((.(((...(((((.(((((.....)))))..)))))...)))).)))))))))))))))....)))))..**********										
.....AGTTTCCGGGATATCGTACTGTA.....	23	0	1	290.00	290	236	53	0	1	0
.....ATACGAAACCTCAGAAATTTGCT.....	23	0	1	173.00	173	10	81	66	15	1
.....TTTCCGGGATATCGTACTGTAT.....	22	0	1	161.00	161	123	34	2	0	2
.....AGTTTCCGGGATATCGTACTGT.....	22	0	1	139.00	139	49	89	1	0	0
.....AGTTTCCGGGATATCGTACTGTAA.....	24	1	1	124.00	124	103	21	0	0	0
.....AGTTTCCGGGATATCGTAC.....	19	0	1	38.00	38	38	0	0	0	0
.....TTCCGGGATATCGTACTGTATTT.....	23	0	1	33.00	33	30	3	0	0	0
.....AGTTTCCGGGATATCGTACTG.....	21	0	1	21.00	21	0	20	1	0	0
.....TTCCGGGATATCGTACTGTATT.....	22	0	1	16.00	16	13	3	0	0	0
.....ATACGAAACCTCAGAAATTTGC.....	22	0	1	13.00	13	3	3	4	2	1
.....TTTCCGGGATATCGTACTGTATT.....	23	0	1	7.00	7	5	2	0	0	0
.....AGTTTCCGGGATATCGTACTGTC.....	23	1	1	7.00	7	6	1	0	0	0
.....TACGAAACCTCAGAAATTTGCT.....	22	0	1	6.00	6	0	4	2	0	0
.....AGTTTCCGGGATATCGTACTGC.....	22	1	1	6.00	6	6	0	0	0	0
.....AGTTTCCGGGATATCGTACT.....	20	0	1	6.00	6	1	5	0	0	0
.....TTTCCGGGATATCGTACTGTAC.....	22	1	1	6.00	6	6	0	0	0	0
.....AGTTTCCGGGATATCGTACTGTAT.....	24	0	1	6.00	6	5	0	1	0	0
.....TTTCCGGGATATCGTACTGTA.....	21	0	1	5.00	5	4	1	0	0	0
.....AATACGAAACCTCAGAAATTTG.....	22	0	1	5.00	5	3	2	0	0	0
.....TCCGGGATATCGTACTGTATTT.....	22	0	1	5.00	5	5	0	0	0	0
.....GTTTCCGGGATATCGTACTGTA.....	22	0	1	4.00	4	3	1	0	0	0
.....AGTTTCCGGGATATCGTACTGC.....	22	1	1	4.00	4	4	0	0	0	0
.....AGTTTCCGGGATATCGTACTGTAC.....	24	1	1	3.00	3	3	0	0	0	0
.....ATACGAAACCTCAGAAATTTGCTT.....	24	1	1	3.00	3	0	2	1	0	0
.....AGTTTCCGGGATATCGTACTGTAAA.....	25	2	1	2.00	2	1	1	0	0	0
.....AGTTTCCGGGATATCGTACTGTT.....	23	1	1	2.00	2	0	2	0	0	0
.....ATACGAAACCTCAGAAATTTG.....	21	0	1	2.00	2	1	1	0	0	0
.....TTTCCGGGATATCGTACTGTATAA.....	24	2	1	2.00	2	2	0	0	0	0
.....ATACGAAACCTCAGAAATTTGCTA.....	24	1	1	2.00	2	0	1	1	0	0
.....ATACGAAACCTCAGAAATTTGCC.....	23	1	1	2.00	2	1	1	0	0	0
.....TTCCGGGATATCGTACTGTAT.....	21	0	1	2.00	2	2	0	0	0	0
.....TTTCCGGGATATCGTACTGTAA.....	22	1	1	1.00	1	1	0	0	0	0
.....CAAGTTTCCGGGATATCGTACT.....	22	0	1	1.00	1	1	0	0	0	0
.....AGTTTCCGGGATATCGTACTGTAG.....	24	1	1	1.00	1	1	0	0	0	0
.....AGTTTCCGGGATATCGTA.....	18	0	1	1.00	1	0	1	0	0	0
.....AATACGAAACCTCAGAAATTTGT.....	23	1	1	1.00	1	0	0	1	0	0
.....AGTTTCCGGGATATCGTACTGTCA.....	24	2	1	1.00	1	1	0	0	0	0
.....GTTTCCGGGATATCGTACTGTAAA.....	24	2	1	1.00	1	1	0	0	0	0
.....TTCCGGGATATCGTACTGTATTA.....	23	1	1	1.00	1	1	0	0	0	0
.....AAGTTTCCGGGATATCGTACTA.....	22	1	1	1.00	1	0	1	0	0	0
.....GTTTCCGGGATATCGTACTGTAA.....	23	1	1	1.00	1	1	0	0	0	0
.....AAGTTTCCGGGATATCGTACTG.....	22	0	1	1.00	1	0	1	0	0	0
.....AAGTTTCCGGGATATCGTACT.....	21	0	1	1.00	1	0	0	1	0	0
.....AGTTTCCGGGATATCGTACTGTCC.....	24	2	1	1.00	1	1	0	0	0	0
.....TTTCCGGGATATCGTACTGTATTAA.....	25	2	1	1.00	1	1	0	0	0	0
.....TTTCCGGGATATCGTACTGTAG.....	22	1	1	1.00	1	1	0	0	0	0
.....AGTTTCCGGGATATCGTACTGA.....	22	1	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

AATCGAATTTACGTGTTAAATACGTGATACCTTTATTAATTAACCTATAACCAACCATAATAGCGTCGTTCAAAGGCCCTATAGCATGACATAAAGATTTGTAAAGTATATGTTATGCTTTGGAGTCTTTAAACGACGCCAATCAATGGCAATTGTTGAGTATTCTTTCCTCTCTTATTTTTACTAGTTATATGTACACACACAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V118 embryo	M045 female body
**********(((((..(((((((((((((((.(((...(((((.(((((.....)))))..)))))...)))).)))))))))))))))....)))))..**********								
.....ATATGTTATGCTTTGGAGTCTT.....	22	0	1	1.00	1	0	1	0
.....TATGTTATGCTTTGGAGTCTT.....	21	0	1	1.00	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004909:7956376-7956580 +	dwi_140	TTAGCTTAAATGCACAATTTATGCACTATGGAAATAATTAATTGGATATTGGTTGGTATTATCGCAGCAAGTTTCCGGGATATCGTA----------CTGTATT--------TCTAAACATTTCATA-TACAATACGA--------AACCTCAGAAATTTGCTGCGGTTAGTTACCGTT-AACAACTCATAAGAAA-GGAGAGAA----------TAAAA-------ATGATCAATATACATGTGTGTGTG
droVir3	scaffold_13042:907857-907872 -		T----------GTGTGT----------|----------|-------|--------|----------|---------|--------|----------|----------|-------|----------|-----|-------|----------GTGTGTGTG
droMoj3	scaffold_6496:4195040-4195086 -		C----------AAAAAAAATGAGAAATACCT----------|----------|-------|--------|----------|---------|--------|----------ATACATA---------|----------|-------|----------|-----|-------|------CATATGCATGTGTGTGTG
droGri2	scaffold_15081:2044829-2044996 -	dgr_10	T----------GGTATTGCTGCAGCAATTTCCCGGTCTCGTA----------|----------TGTATTATCAAAATGGTAT---ACTCTGAACCACATACGA--------TTCCTCAGAAATTCGCTGGTGTAAGTTACCGTT-TTCAACCGTATAGCAACTGTGCCGATAAACCTATC-----CCAGTCTATCGA----TAGACA-ACGATTGTC
dp5	3:5184418-5184437 +		T----------CCAAGTCT----------|----------|-------|--------|----------|---------|--------|----------|----------|-------|----------|-----|-------|----------GTGTGTGTGTG
droAna3	scaffold_13417:2468029-2468191 -		T----------GGTATTATGGCAGCCAGTTTCCGGGATCTCGTA----------|----------CTGTATG--------AAGT---TTTCTATA-TACAATTCGA--------AAACTCAGAAACTTCCTGGCGTGAGTACCATTGATCAACGGCTGAGTATGCGACC-GGAAAGGGGACG-----CGAATGCGACGACTAAAGGATGGCGCGATGCGG
droBip1	scf7180000395874:40395-40520 -		G----------GGGAGTGCCTGGTATTATGGCAGCGAGTTTCCGGGATCTCGTA----------|----------GTGTATG--------AAGT---TTTATAAA-TACAATTCGA--------AAACTCAGAAACTTTCTGGCTTGAAGTACATTC-ATCAACGGCCGAGTA-|--------|----------|-----|-------|----------ATATA
droKik1	scf7180000302517:1183445-1183567 +		T----------GGTATAGCCGCAGAAAGTTTCCCAG-TTTCGTA----------|----------ATGTATG--------GTTA---TATTTGAAA-TACAGTACGA--------CAGATCAGAAATTTTCGGGAGTTAGTACCGTA-AACAACCAAAAATGGA-GCAAGGAG----------CA---|-------|----------|----------A
droFic1	scf7180000454073:1733616-1733722 +		T----------CGGTATTATCGCAGCAAGTTTCCGGGACTTCGTA----------|----------CTGTATG--------AAGA---ATTCTATA-TACAATACGA--------AACCTCAGAAATTTATTGCAATGAACCACGTTT-AAGTAATTGAT------|--------|----------|-----|-------|----------
droEle1	scf7180000490751:1118514-1118622 +		T----------TGGTATTATCGCAGCAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------AGAA---ATTCTATA-TACAATACGA--------AACCTTAGAAATTTTCTGAAGTTAGTACCATA-GAGTACCATAA----|--------|----------|-----|-------|----------
droRho1	scf7180000761121:190394-190496 -		T----------TGGTATTATCGCAGCAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------AGAA---ATTCTATA-TACAATACGA--------AACCTTAGAAATTTTCTGGAGTTATCTACGATT-AAGTAC----------|--------|----------|-----|-------|----------
droBia1	scf7180000302069:1151364-1151463 -		T----------TGGTATTATCGCAACACAAGTTTCCGGGATTTTGTA----------|----------TTGTATG--------ACTA---GATTCTATA-TACAATACGA--------AACCTCAGAAATTTTCTGGAGTTAGTACCATA-AA----------|--------|----------|-----|-------|----------
droTak1	scf7180000415169:845124-845246 -		T----------TGGTATTATCGCAACACAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------CTGA---ATTCTATA-TACAATACGA--------AAGCTCAGAAATTTTCTGGAGTTAGTACCATT-AAGTACTTACTTACGAA-GGATCGAT----------T----|-------|----------|----------A
droEug1	scf7180000409230:879979-880090 -		T----------TGGTATTATCGCAATAAGTTCCTGGGATTCGCA----------|----------CTGTATT--------ACGA---TTTTTACA-TACAATACGA--------AAGCTCAGAAACTAACTGGAATTAAGTACCGTA-AAGTACGGATCAGA---|--------|----------|-----|-------|----------A
dm3	chrX:19452595-19452757 +	dme-mir-4966-2	T----------TGGTATTATGGCAAAAGTTTCCAGGACATTGACAACCTATATATGTATGTACTTGTCGGCACTGGAGT--------AC---------TAAA-TATATTGCACATGTTCATGCATGTTCAACATATTTAGGAGCTCAAGTACCGAA-AA----------|--------|---ATGAACAACTAAAA-------GCGG---AGAATACGAAAGTG-C
droSim2	x:18341756-18341796 +		T----------TGGTATTATGGCAACAAGTTTCCAGGACATCGAG----------|----------CTGTGT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------
droSec2	scaffold_8:1734626-1734666 +		T----------TGGTATTATGGCAACAAGTTTCCAGGACATCGAG----------|----------CTGTGT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------
droYak3	X:11886139-11886241 -	dya_51	T----------TGGTATTATGGCAACAAGTTTCCGGGACTTCGTA----------|----------CTGTATG--------AGAG---ACTATATA-TACAATACGA--------AGCCTCTGAAATTTTCTGCGCTCAAGTACCAAA-AAGTAC----------|--------|----------|-----|-------|----------
droEre2	scaffold_4690:9688639-9688679 +		T----------TGGTATTAAGGCAACAAGTTTCAGGGACTTCGCA----------|----------CTGTAT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004909:7956376-7956580 +	dwi_140	TTAGCTTAAATGCACAATTTATGCACTATGGAAATAATTAATTGGATATTGGTTGGTATTATCGCAGCAAGTTTCCGGGATATCGTA----------CTGTATT--------TCTAAACATTTCATA-TACAATACGA--------AACCTCAGAAATTTGCTGCGGTTAGTTACCGTT-AACAACTCATAAGAAA-GGAGAGAA----------TAAAA-------ATGATCAATATACATGTGTGTGTG
droVir3	scaffold_13042:907857-907872 -		T----------GTGTGT----------|----------|-------|--------|----------|---------|--------|----------|----------|-------|----------|-----|-------|----------GTGTGTGTG
droMoj3	scaffold_6496:4195040-4195086 -		C----------AAAAAAAATGAGAAATACCT----------|----------|-------|--------|----------|---------|--------|----------ATACATA---------|----------|-------|----------|-----|-------|------CATATGCATGTGTGTGTG
droGri2	scaffold_15081:2044829-2044996 -	dgr_10	T----------GGTATTGCTGCAGCAATTTCCCGGTCTCGTA----------|----------TGTATTATCAAAATGGTAT---ACTCTGAACCACATACGA--------TTCCTCAGAAATTCGCTGGTGTAAGTTACCGTT-TTCAACCGTATAGCAACTGTGCCGATAAACCTATC-----CCAGTCTATCGA----TAGACA-ACGATTGTC
dp5	3:5184418-5184437 +		T----------CCAAGTCT----------|----------|-------|--------|----------|---------|--------|----------|----------|-------|----------|-----|-------|----------GTGTGTGTGTG
droAna3	scaffold_13417:2468029-2468191 -		T----------GGTATTATGGCAGCCAGTTTCCGGGATCTCGTA----------|----------CTGTATG--------AAGT---TTTCTATA-TACAATTCGA--------AAACTCAGAAACTTCCTGGCGTGAGTACCATTGATCAACGGCTGAGTATGCGACC-GGAAAGGGGACG-----CGAATGCGACGACTAAAGGATGGCGCGATGCGG
droBip1	scf7180000395874:40395-40520 -		G----------GGGAGTGCCTGGTATTATGGCAGCGAGTTTCCGGGATCTCGTA----------|----------GTGTATG--------AAGT---TTTATAAA-TACAATTCGA--------AAACTCAGAAACTTTCTGGCTTGAAGTACATTC-ATCAACGGCCGAGTA-|--------|----------|-----|-------|----------ATATA
droKik1	scf7180000302517:1183445-1183567 +		T----------GGTATAGCCGCAGAAAGTTTCCCAG-TTTCGTA----------|----------ATGTATG--------GTTA---TATTTGAAA-TACAGTACGA--------CAGATCAGAAATTTTCGGGAGTTAGTACCGTA-AACAACCAAAAATGGA-GCAAGGAG----------CA---|-------|----------|----------A
droFic1	scf7180000454073:1733616-1733722 +		T----------CGGTATTATCGCAGCAAGTTTCCGGGACTTCGTA----------|----------CTGTATG--------AAGA---ATTCTATA-TACAATACGA--------AACCTCAGAAATTTATTGCAATGAACCACGTTT-AAGTAATTGAT------|--------|----------|-----|-------|----------
droEle1	scf7180000490751:1118514-1118622 +		T----------TGGTATTATCGCAGCAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------AGAA---ATTCTATA-TACAATACGA--------AACCTTAGAAATTTTCTGAAGTTAGTACCATA-GAGTACCATAA----|--------|----------|-----|-------|----------
droRho1	scf7180000761121:190394-190496 -		T----------TGGTATTATCGCAGCAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------AGAA---ATTCTATA-TACAATACGA--------AACCTTAGAAATTTTCTGGAGTTATCTACGATT-AAGTAC----------|--------|----------|-----|-------|----------
droBia1	scf7180000302069:1151364-1151463 -		T----------TGGTATTATCGCAACACAAGTTTCCGGGATTTTGTA----------|----------TTGTATG--------ACTA---GATTCTATA-TACAATACGA--------AACCTCAGAAATTTTCTGGAGTTAGTACCATA-AA----------|--------|----------|-----|-------|----------
droTak1	scf7180000415169:845124-845246 -		T----------TGGTATTATCGCAACACAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------CTGA---ATTCTATA-TACAATACGA--------AAGCTCAGAAATTTTCTGGAGTTAGTACCATT-AAGTACTTACTTACGAA-GGATCGAT----------T----|-------|----------|----------A
droEug1	scf7180000409230:879979-880090 -		T----------TGGTATTATCGCAATAAGTTCCTGGGATTCGCA----------|----------CTGTATT--------ACGA---TTTTTACA-TACAATACGA--------AAGCTCAGAAACTAACTGGAATTAAGTACCGTA-AAGTACGGATCAGA---|--------|----------|-----|-------|----------A
dm3	chrX:19452595-19452757 +	dme-mir-4966-2	T----------TGGTATTATGGCAAAAGTTTCCAGGACATTGACAACCTATATATGTATGTACTTGTCGGCACTGGAGT--------AC---------TAAA-TATATTGCACATGTTCATGCATGTTCAACATATTTAGGAGCTCAAGTACCGAA-AA----------|--------|---ATGAACAACTAAAA-------GCGG---AGAATACGAAAGTG-C
~~droSim2~~	x:18341756-18341796 +		T----------TGGTATTATGGCAACAAGTTTCCAGGACATCGAG----------|----------CTGTGT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------
droSec2	scaffold_8:1734626-1734666 +		T----------TGGTATTATGGCAACAAGTTTCCAGGACATCGAG----------|----------CTGTGT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------
droYak3	X:11886139-11886241 -	dya_51	T----------TGGTATTATGGCAACAAGTTTCCGGGACTTCGTA----------|----------CTGTATG--------AGAG---ACTATATA-TACAATACGA--------AGCCTCTGAAATTTTCTGCGCTCAAGTACCAAA-AAGTAC----------|--------|----------|-----|-------|----------
droEre2	scaffold_4690:9688639-9688679 +		T----------TGGTATTAAGGCAACAAGTTTCAGGGACTTCGCA----------|----------CTGTAT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------

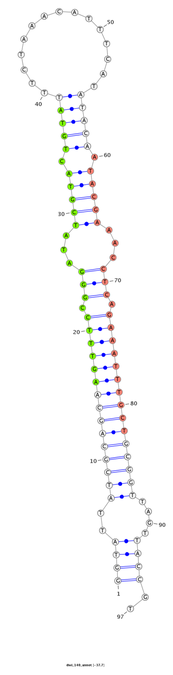
Generated: 09/08/2015 at 07:54 PM

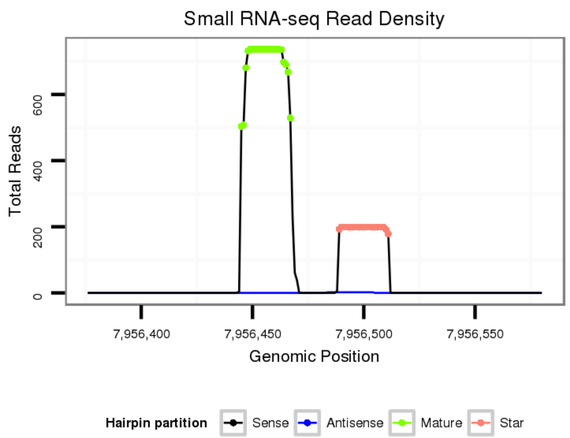
	PASS/FAIL		
crit.star	1	1	1
crit.loop	0	0	0
crit.mor	0	0	0
crit.half	0	0	0
crit.total	1	1	1
crit.pairing	1	1	1
crit.top3	1	1	1
crit.tptop3	1	1	1
crit.uri	0	0	0
crit.back	1	1	1
rescue.total	0	0	0
rescue.dominant	0	0	0
rescue.known	1	1	1
rescue.confident	5	5	6
rescue.candidate	0	0	0

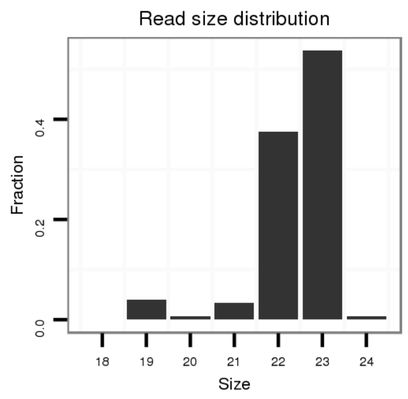
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_140	**scf2_1100000004909:7956426-7956530 +**	**Known Ortholog**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

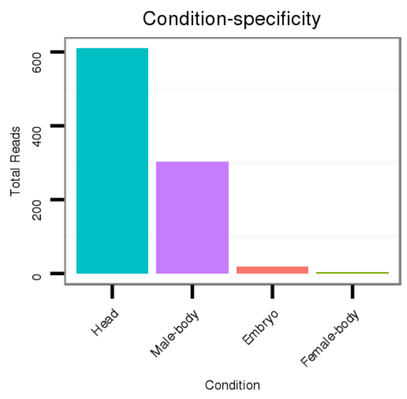
Legend: mature star mismatch in alignment mismatch in read

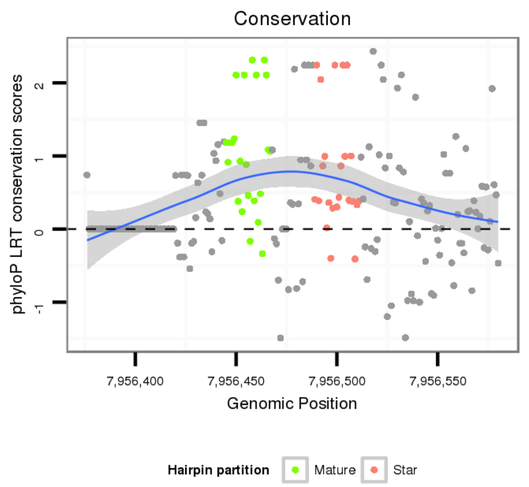
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTAGCTTAAATGCACAATTTATGCACTATGGAAATAATTAATTGGATATTGGTTGGTATTATCGCAGCAAGTTTCCGGGATATCGTACTGTATTTCTAAACATTTCATATACAATACGAAACCTCAGAAATTTGCTGCGGTTAGTTACCGTTAACAACTCATAAGAAAGGAGAGAATAAAAATGATCAATATACATGTGTGTGTG	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V117 male body	V119 head	V118 embryo	M045 female body
**********(((((..(((((((((((((((.(((...(((((.(((((.....)))))..)))))...)))).)))))))))))))))....)))))..**********										
.....AGTTTCCGGGATATCGTACTGTA.....	23	0	1	290.00	290	236	53	0	1	0
.....ATACGAAACCTCAGAAATTTGCT.....	23	0	1	173.00	173	10	81	66	15	1
.....TTTCCGGGATATCGTACTGTAT.....	22	0	1	161.00	161	123	34	2	0	2
.....AGTTTCCGGGATATCGTACTGT.....	22	0	1	139.00	139	49	89	1	0	0
.....AGTTTCCGGGATATCGTACTGTAA.....	24	1	1	124.00	124	103	21	0	0	0
.....AGTTTCCGGGATATCGTAC.....	19	0	1	38.00	38	38	0	0	0	0
.....TTCCGGGATATCGTACTGTATTT.....	23	0	1	33.00	33	30	3	0	0	0
.....AGTTTCCGGGATATCGTACTG.....	21	0	1	21.00	21	0	20	1	0	0
.....TTCCGGGATATCGTACTGTATT.....	22	0	1	16.00	16	13	3	0	0	0
.....ATACGAAACCTCAGAAATTTGC.....	22	0	1	13.00	13	3	3	4	2	1
.....TTTCCGGGATATCGTACTGTATT.....	23	0	1	7.00	7	5	2	0	0	0
.....AGTTTCCGGGATATCGTACTGTC.....	23	1	1	7.00	7	6	1	0	0	0
.....TACGAAACCTCAGAAATTTGCT.....	22	0	1	6.00	6	0	4	2	0	0
.....AGTTTCCGGGATATCGTACTGC.....	22	1	1	6.00	6	6	0	0	0	0
.....AGTTTCCGGGATATCGTACT.....	20	0	1	6.00	6	1	5	0	0	0
.....TTTCCGGGATATCGTACTGTAC.....	22	1	1	6.00	6	6	0	0	0	0
.....AGTTTCCGGGATATCGTACTGTAT.....	24	0	1	6.00	6	5	0	1	0	0
.....TTTCCGGGATATCGTACTGTA.....	21	0	1	5.00	5	4	1	0	0	0
.....AATACGAAACCTCAGAAATTTG.....	22	0	1	5.00	5	3	2	0	0	0
.....TCCGGGATATCGTACTGTATTT.....	22	0	1	5.00	5	5	0	0	0	0
.....GTTTCCGGGATATCGTACTGTA.....	22	0	1	4.00	4	3	1	0	0	0
.....AGTTTCCGGGATATCGTACTGC.....	22	1	1	4.00	4	4	0	0	0	0
.....AGTTTCCGGGATATCGTACTGTAC.....	24	1	1	3.00	3	3	0	0	0	0
.....ATACGAAACCTCAGAAATTTGCTT.....	24	1	1	3.00	3	0	2	1	0	0
.....AGTTTCCGGGATATCGTACTGTAAA.....	25	2	1	2.00	2	1	1	0	0	0
.....AGTTTCCGGGATATCGTACTGTT.....	23	1	1	2.00	2	0	2	0	0	0
.....ATACGAAACCTCAGAAATTTG.....	21	0	1	2.00	2	1	1	0	0	0
.....TTTCCGGGATATCGTACTGTATAA.....	24	2	1	2.00	2	2	0	0	0	0
.....ATACGAAACCTCAGAAATTTGCTA.....	24	1	1	2.00	2	0	1	1	0	0
.....ATACGAAACCTCAGAAATTTGCC.....	23	1	1	2.00	2	1	1	0	0	0
.....TTCCGGGATATCGTACTGTAT.....	21	0	1	2.00	2	2	0	0	0	0
.....TTTCCGGGATATCGTACTGTAA.....	22	1	1	1.00	1	1	0	0	0	0
.....CAAGTTTCCGGGATATCGTACT.....	22	0	1	1.00	1	1	0	0	0	0
.....AGTTTCCGGGATATCGTACTGTAG.....	24	1	1	1.00	1	1	0	0	0	0
.....AGTTTCCGGGATATCGTA.....	18	0	1	1.00	1	0	1	0	0	0
.....AATACGAAACCTCAGAAATTTGT.....	23	1	1	1.00	1	0	0	1	0	0
.....AGTTTCCGGGATATCGTACTGTCA.....	24	2	1	1.00	1	1	0	0	0	0
.....GTTTCCGGGATATCGTACTGTAAA.....	24	2	1	1.00	1	1	0	0	0	0
.....TTCCGGGATATCGTACTGTATTA.....	23	1	1	1.00	1	1	0	0	0	0
.....AAGTTTCCGGGATATCGTACTA.....	22	1	1	1.00	1	0	1	0	0	0
.....GTTTCCGGGATATCGTACTGTAA.....	23	1	1	1.00	1	1	0	0	0	0
.....AAGTTTCCGGGATATCGTACTG.....	22	0	1	1.00	1	0	1	0	0	0
.....AAGTTTCCGGGATATCGTACT.....	21	0	1	1.00	1	0	0	1	0	0
.....AGTTTCCGGGATATCGTACTGTCC.....	24	2	1	1.00	1	1	0	0	0	0
.....TTTCCGGGATATCGTACTGTATTAA.....	25	2	1	1.00	1	1	0	0	0	0
.....TTTCCGGGATATCGTACTGTAG.....	22	1	1	1.00	1	1	0	0	0	0
.....AGTTTCCGGGATATCGTACTGA.....	22	1	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

AATCGAATTTACGTGTTAAATACGTGATACCTTTATTAATTAACCTATAACCAACCATAATAGCGTCGTTCAAAGGCCCTATAGCATGACATAAAGATTTGTAAAGTATATGTTATGCTTTGGAGTCTTTAAACGACGCCAATCAATGGCAATTGTTGAGTATTCTTTCCTCTCTTATTTTTACTAGTTATATGTACACACACAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V118 embryo	M045 female body
**********(((((..(((((((((((((((.(((...(((((.(((((.....)))))..)))))...)))).)))))))))))))))....)))))..**********								
.....ATATGTTATGCTTTGGAGTCTT.....	22	0	1	1.00	1	0	1	0
.....TATGTTATGCTTTGGAGTCTT.....	21	0	1	1.00	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004909:7956376-7956580 +	dwi_140	TTAGCTTAAATGCACAATTTATGCACTATGGAAATAATTAATTGGATATTGGTTGGTATTATCGCAGCAAGTTTCCGGGATATCGTA----------CTGTATT--------TCTAAACATTTCATA-TACAATACGA--------AACCTCAGAAATTTGCTGCGGTTAGTTACCGTT-AACAACTCATAAGAAA-GGAGAGAA----------TAAAA-------ATGATCAATATACATGTGTGTGTG
droVir3	scaffold_13042:907857-907872 -		T----------GTGTGT----------|----------|-------|--------|----------|---------|--------|----------|----------|-------|----------|-----|-------|----------GTGTGTGTG
droMoj3	scaffold_6496:4195040-4195086 -		C----------AAAAAAAATGAGAAATACCT----------|----------|-------|--------|----------|---------|--------|----------ATACATA---------|----------|-------|----------|-----|-------|------CATATGCATGTGTGTGTG
droGri2	scaffold_15081:2044829-2044996 -	dgr_10	T----------GGTATTGCTGCAGCAATTTCCCGGTCTCGTA----------|----------TGTATTATCAAAATGGTAT---ACTCTGAACCACATACGA--------TTCCTCAGAAATTCGCTGGTGTAAGTTACCGTT-TTCAACCGTATAGCAACTGTGCCGATAAACCTATC-----CCAGTCTATCGA----TAGACA-ACGATTGTC
dp5	3:5184418-5184437 +		T----------CCAAGTCT----------|----------|-------|--------|----------|---------|--------|----------|----------|-------|----------|-----|-------|----------GTGTGTGTGTG
droAna3	scaffold_13417:2468029-2468191 -		T----------GGTATTATGGCAGCCAGTTTCCGGGATCTCGTA----------|----------CTGTATG--------AAGT---TTTCTATA-TACAATTCGA--------AAACTCAGAAACTTCCTGGCGTGAGTACCATTGATCAACGGCTGAGTATGCGACC-GGAAAGGGGACG-----CGAATGCGACGACTAAAGGATGGCGCGATGCGG
droBip1	scf7180000395874:40395-40520 -		G----------GGGAGTGCCTGGTATTATGGCAGCGAGTTTCCGGGATCTCGTA----------|----------GTGTATG--------AAGT---TTTATAAA-TACAATTCGA--------AAACTCAGAAACTTTCTGGCTTGAAGTACATTC-ATCAACGGCCGAGTA-|--------|----------|-----|-------|----------ATATA
droKik1	scf7180000302517:1183445-1183567 +		T----------GGTATAGCCGCAGAAAGTTTCCCAG-TTTCGTA----------|----------ATGTATG--------GTTA---TATTTGAAA-TACAGTACGA--------CAGATCAGAAATTTTCGGGAGTTAGTACCGTA-AACAACCAAAAATGGA-GCAAGGAG----------CA---|-------|----------|----------A
droFic1	scf7180000454073:1733616-1733722 +		T----------CGGTATTATCGCAGCAAGTTTCCGGGACTTCGTA----------|----------CTGTATG--------AAGA---ATTCTATA-TACAATACGA--------AACCTCAGAAATTTATTGCAATGAACCACGTTT-AAGTAATTGAT------|--------|----------|-----|-------|----------
droEle1	scf7180000490751:1118514-1118622 +		T----------TGGTATTATCGCAGCAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------AGAA---ATTCTATA-TACAATACGA--------AACCTTAGAAATTTTCTGAAGTTAGTACCATA-GAGTACCATAA----|--------|----------|-----|-------|----------
droRho1	scf7180000761121:190394-190496 -		T----------TGGTATTATCGCAGCAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------AGAA---ATTCTATA-TACAATACGA--------AACCTTAGAAATTTTCTGGAGTTATCTACGATT-AAGTAC----------|--------|----------|-----|-------|----------
droBia1	scf7180000302069:1151364-1151463 -		T----------TGGTATTATCGCAACACAAGTTTCCGGGATTTTGTA----------|----------TTGTATG--------ACTA---GATTCTATA-TACAATACGA--------AACCTCAGAAATTTTCTGGAGTTAGTACCATA-AA----------|--------|----------|-----|-------|----------
droTak1	scf7180000415169:845124-845246 -		T----------TGGTATTATCGCAACACAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------CTGA---ATTCTATA-TACAATACGA--------AAGCTCAGAAATTTTCTGGAGTTAGTACCATT-AAGTACTTACTTACGAA-GGATCGAT----------T----|-------|----------|----------A
droEug1	scf7180000409230:879979-880090 -		T----------TGGTATTATCGCAATAAGTTCCTGGGATTCGCA----------|----------CTGTATT--------ACGA---TTTTTACA-TACAATACGA--------AAGCTCAGAAACTAACTGGAATTAAGTACCGTA-AAGTACGGATCAGA---|--------|----------|-----|-------|----------A
dm3	chrX:19452595-19452757 +	dme-mir-4966-2	T----------TGGTATTATGGCAAAAGTTTCCAGGACATTGACAACCTATATATGTATGTACTTGTCGGCACTGGAGT--------AC---------TAAA-TATATTGCACATGTTCATGCATGTTCAACATATTTAGGAGCTCAAGTACCGAA-AA----------|--------|---ATGAACAACTAAAA-------GCGG---AGAATACGAAAGTG-C
droSim2	x:18341756-18341796 +		T----------TGGTATTATGGCAACAAGTTTCCAGGACATCGAG----------|----------CTGTGT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------
droSec2	scaffold_8:1734626-1734666 +		T----------TGGTATTATGGCAACAAGTTTCCAGGACATCGAG----------|----------CTGTGT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------
droYak3	X:11886139-11886241 -	dya_51	T----------TGGTATTATGGCAACAAGTTTCCGGGACTTCGTA----------|----------CTGTATG--------AGAG---ACTATATA-TACAATACGA--------AGCCTCTGAAATTTTCTGCGCTCAAGTACCAAA-AAGTAC----------|--------|----------|-----|-------|----------
droEre2	scaffold_4690:9688639-9688679 +		T----------TGGTATTAAGGCAACAAGTTTCAGGGACTTCGCA----------|----------CTGTAT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004909:7956376-7956580 +	dwi_140	TTAGCTTAAATGCACAATTTATGCACTATGGAAATAATTAATTGGATATTGGTTGGTATTATCGCAGCAAGTTTCCGGGATATCGTA----------CTGTATT--------TCTAAACATTTCATA-TACAATACGA--------AACCTCAGAAATTTGCTGCGGTTAGTTACCGTT-AACAACTCATAAGAAA-GGAGAGAA----------TAAAA-------ATGATCAATATACATGTGTGTGTG
droVir3	scaffold_13042:907857-907872 -		T----------GTGTGT----------|----------|-------|--------|----------|---------|--------|----------|----------|-------|----------|-----|-------|----------GTGTGTGTG
droMoj3	scaffold_6496:4195040-4195086 -		C----------AAAAAAAATGAGAAATACCT----------|----------|-------|--------|----------|---------|--------|----------ATACATA---------|----------|-------|----------|-----|-------|------CATATGCATGTGTGTGTG
droGri2	scaffold_15081:2044829-2044996 -	dgr_10	T----------GGTATTGCTGCAGCAATTTCCCGGTCTCGTA----------|----------TGTATTATCAAAATGGTAT---ACTCTGAACCACATACGA--------TTCCTCAGAAATTCGCTGGTGTAAGTTACCGTT-TTCAACCGTATAGCAACTGTGCCGATAAACCTATC-----CCAGTCTATCGA----TAGACA-ACGATTGTC
dp5	3:5184418-5184437 +		T----------CCAAGTCT----------|----------|-------|--------|----------|---------|--------|----------|----------|-------|----------|-----|-------|----------GTGTGTGTGTG
droAna3	scaffold_13417:2468029-2468191 -		T----------GGTATTATGGCAGCCAGTTTCCGGGATCTCGTA----------|----------CTGTATG--------AAGT---TTTCTATA-TACAATTCGA--------AAACTCAGAAACTTCCTGGCGTGAGTACCATTGATCAACGGCTGAGTATGCGACC-GGAAAGGGGACG-----CGAATGCGACGACTAAAGGATGGCGCGATGCGG
droBip1	scf7180000395874:40395-40520 -		G----------GGGAGTGCCTGGTATTATGGCAGCGAGTTTCCGGGATCTCGTA----------|----------GTGTATG--------AAGT---TTTATAAA-TACAATTCGA--------AAACTCAGAAACTTTCTGGCTTGAAGTACATTC-ATCAACGGCCGAGTA-|--------|----------|-----|-------|----------ATATA
droKik1	scf7180000302517:1183445-1183567 +		T----------GGTATAGCCGCAGAAAGTTTCCCAG-TTTCGTA----------|----------ATGTATG--------GTTA---TATTTGAAA-TACAGTACGA--------CAGATCAGAAATTTTCGGGAGTTAGTACCGTA-AACAACCAAAAATGGA-GCAAGGAG----------CA---|-------|----------|----------A
droFic1	scf7180000454073:1733616-1733722 +		T----------CGGTATTATCGCAGCAAGTTTCCGGGACTTCGTA----------|----------CTGTATG--------AAGA---ATTCTATA-TACAATACGA--------AACCTCAGAAATTTATTGCAATGAACCACGTTT-AAGTAATTGAT------|--------|----------|-----|-------|----------
droEle1	scf7180000490751:1118514-1118622 +		T----------TGGTATTATCGCAGCAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------AGAA---ATTCTATA-TACAATACGA--------AACCTTAGAAATTTTCTGAAGTTAGTACCATA-GAGTACCATAA----|--------|----------|-----|-------|----------
droRho1	scf7180000761121:190394-190496 -		T----------TGGTATTATCGCAGCAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------AGAA---ATTCTATA-TACAATACGA--------AACCTTAGAAATTTTCTGGAGTTATCTACGATT-AAGTAC----------|--------|----------|-----|-------|----------
droBia1	scf7180000302069:1151364-1151463 -		T----------TGGTATTATCGCAACACAAGTTTCCGGGATTTTGTA----------|----------TTGTATG--------ACTA---GATTCTATA-TACAATACGA--------AACCTCAGAAATTTTCTGGAGTTAGTACCATA-AA----------|--------|----------|-----|-------|----------
droTak1	scf7180000415169:845124-845246 -		T----------TGGTATTATCGCAACACAAGTTTCCGGGATTCGTA----------|----------CTGTATG--------CTGA---ATTCTATA-TACAATACGA--------AAGCTCAGAAATTTTCTGGAGTTAGTACCATT-AAGTACTTACTTACGAA-GGATCGAT----------T----|-------|----------|----------A
droEug1	scf7180000409230:879979-880090 -		T----------TGGTATTATCGCAATAAGTTCCTGGGATTCGCA----------|----------CTGTATT--------ACGA---TTTTTACA-TACAATACGA--------AAGCTCAGAAACTAACTGGAATTAAGTACCGTA-AAGTACGGATCAGA---|--------|----------|-----|-------|----------A
dm3	chrX:19452595-19452757 +	dme-mir-4966-2	T----------TGGTATTATGGCAAAAGTTTCCAGGACATTGACAACCTATATATGTATGTACTTGTCGGCACTGGAGT--------AC---------TAAA-TATATTGCACATGTTCATGCATGTTCAACATATTTAGGAGCTCAAGTACCGAA-AA----------|--------|---ATGAACAACTAAAA-------GCGG---AGAATACGAAAGTG-C
~~droSim2~~	x:18341756-18341796 +		T----------TGGTATTATGGCAACAAGTTTCCAGGACATCGAG----------|----------CTGTGT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------
droSec2	scaffold_8:1734626-1734666 +		T----------TGGTATTATGGCAACAAGTTTCCAGGACATCGAG----------|----------CTGTGT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------
droYak3	X:11886139-11886241 -	dya_51	T----------TGGTATTATGGCAACAAGTTTCCGGGACTTCGTA----------|----------CTGTATG--------AGAG---ACTATATA-TACAATACGA--------AGCCTCTGAAATTTTCTGCGCTCAAGTACCAAA-AAGTAC----------|--------|----------|-----|-------|----------
droEre2	scaffold_4690:9688639-9688679 +		T----------TGGTATTAAGGCAACAAGTTTCAGGGACTTCGCA----------|----------CTGTAT--------|----------|-------|----------|----------|-------|----------|-----|-------|----------

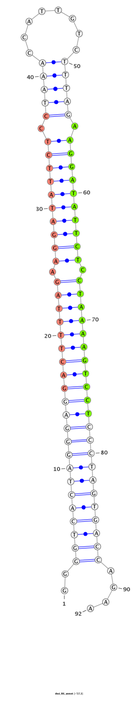
Generated: 09/08/2015 at 07:54 PM

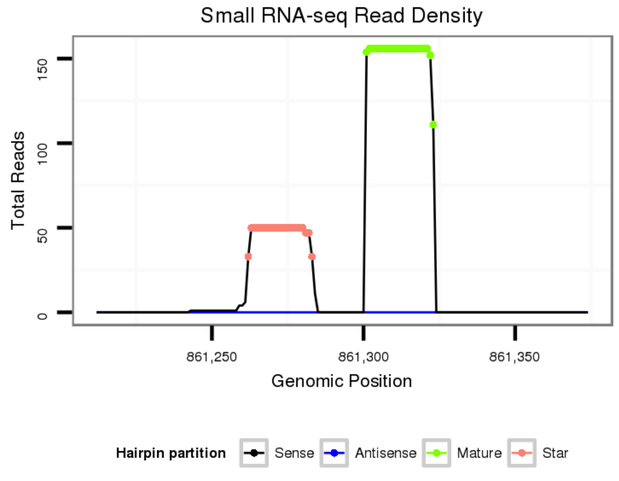
	PASS/FAIL		
crit.star	1	1	1
crit.loop	0	0	0
crit.mor	0	0	0
crit.half	0	0	0
crit.total	1	1	1
crit.pairing	1	1	1
crit.top3	1	1	1
crit.tptop3	1	1	1
crit.uri	0	0	0
crit.back	1	1	1
rescue.total	0	0	0
rescue.dominant	0	0	0
rescue.known	1	1	1
rescue.confident	5	5	6
rescue.candidate	0	0	0

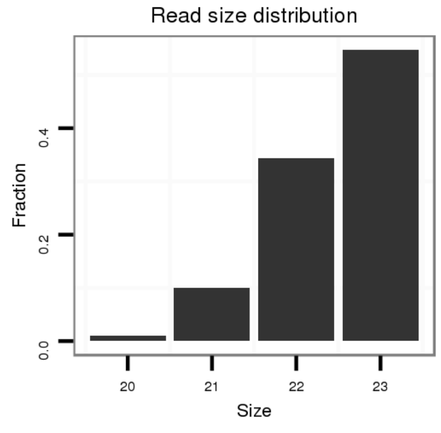
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_86	**scf2_1100000004513:861262-861324 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

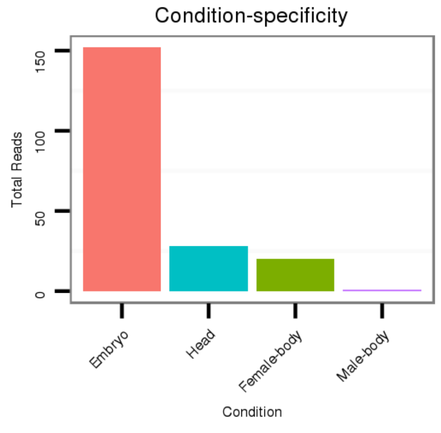
Legend: mature star mismatch in alignment mismatch in read

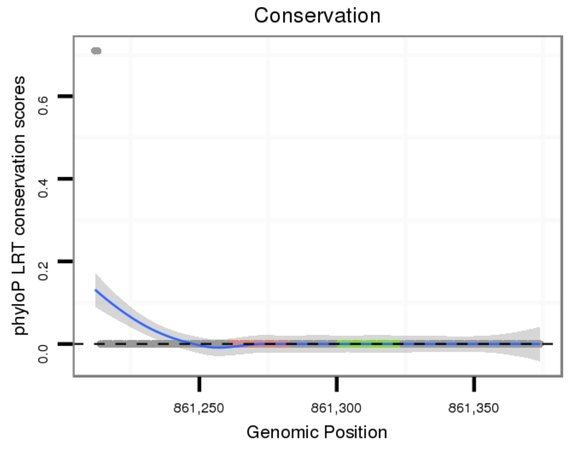
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK21702-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATAAAGGACAAATGACCTCTCTGCTTGGTAAAAAAGGGGTCACTAGGGAGGACTTTTAGAAGGATATTCTCCTAAACCATTGTCTTTAGAAGGATATTCTCCTAAAAGTCCTCCCTAGTGACCAGAAACTACTTTACGACCTAGTTAATATATACTATATACT	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	M045 female body	V119 head	M020 head	V117 male body
**********..((((((((((((((((((((((.((((((((((.(((((.....)))))..)))))))))).))))))))))))))))))))....**********										
.....AAGGATATTCTCCTAAAAGTCCT.....	23	0	1	109.00	109	92	8	7	1	1
.....AAGGATATTCTCCTAAAAGTCC.....	22	0	1	41.00	41	30	5	6	0	0
.....GACTTTTAGAAGGATATTCTCC.....	22	0	1	16.00	16	9	4	3	0	0
.....GACTTTTAGAAGGATATTCTC.....	21	0	1	11.00	11	8	1	0	2	0
.....ACTTTTAGAAGGATATTCTCCT.....	22	0	1	10.00	10	8	0	2	0	0
.....ACTTTTAGAAGGATATTCTCC.....	21	0	1	5.00	5	3	1	1	0	0
.....AAGGATATTCTCCTAAAAGTC.....	21	0	1	4.00	4	2	0	2	0	0
.....GAGGACTTTTAGAAGGATATTC.....	22	0	1	3.00	3	1	0	0	2	0
.....ACTTTTAGAAGGATATTCTC.....	20	0	1	2.00	2	0	0	0	2	0
.....AGGATATTCTCCTAAAAGTCCT.....	22	0	1	2.00	2	0	1	0	1	0
.....GGACTTTTAGAAGGATATTCTCC.....	23	0	1	1.00	1	0	1	0	0	0
.....GACTTTTAGAAGGATATTCTCCT.....	23	0	1	1.00	1	0	0	1	0	0
.....AAGGATATTCTCCTAAAAGTCCA.....	23	1	1	1.00	1	1	0	0	0	0
.....AAAAGGGGTCACTAGGGAG.....	19	0	1	1.00	1	1	0	0	0	0
.....GGACTTTTAGAAGGATATTCTC.....	22	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

TATTTCCTGTTTACTGGAGAGACGAACCATTTTTTCCCCAGTGATCCCTCCTGAAAATCTTCCTATAAGAGGATTTGGTAACAGAAATCTTCCTATAAGAGGATTTTCAGGAGGGATCACTGGTCTTTGATGAAATGCTGGATCAATTATATATGATATATGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	M020 head	V119 head	V117 male body
**********..((((((((((((((((((((((.((((((((((.(((((.....)))))..)))))))))).))))))))))))))))))))....**********									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004513:861212-861374 +	dwi_86	ATAAAGGACAAATGACCTCTCTGCTTGGTAAAAAAGGGGTCACTAGGGAGGACTTTTAGAAGGATATTCTCCTAAACCATTGTCTTTAGAAGGATATTCTCCTAAAAGTCCTCCCTAGTGACCAGAAACTACTTTACGACCTAGTTAATATATACTATATACT
droMoj3	scaffold_6496:12614707-12614708 +		AT----------

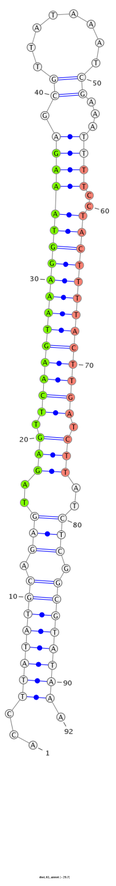
Generated: 09/08/2015 at 03:39:12 PM

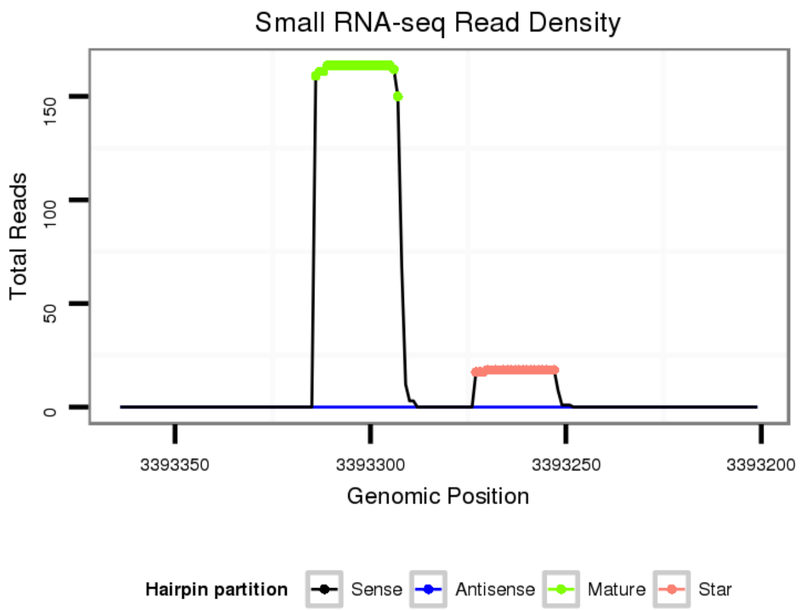
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

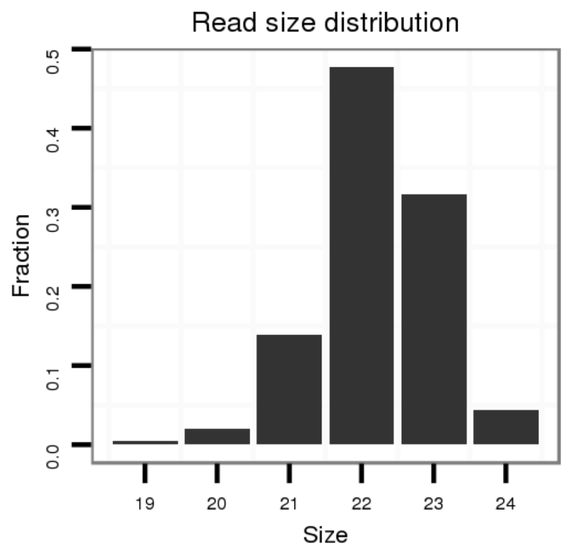
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_61	**scf2_1100000004511:3393251-3393314 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

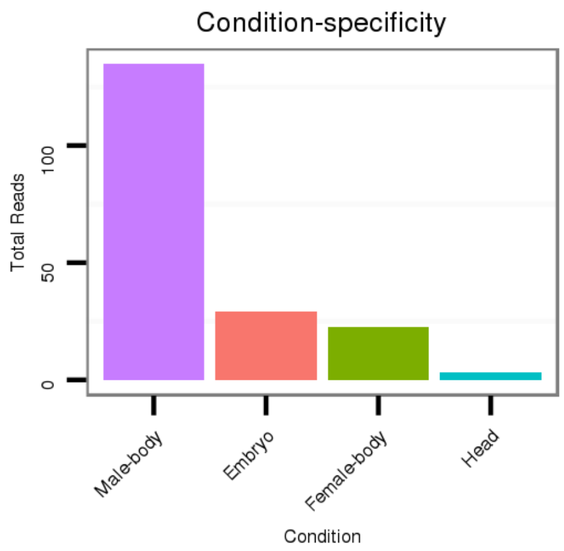
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

mature	**star**
1. dwi_61 scf2_1100000004511:3393293-3393314 - 2. dwi_63 scf2_1100000004511:3393866-3393887 - 3. dwi_64 scf2_1100000004511:3394150-3394171 - 4. dwi_65 scf2_1100000004511:3394508-3394529 -	1. dwi_197 scf2_1100000004511:3392321-3392341 - 2. dwi_196 scf2_1100000004511:3392537-3392557 - 3. dwi_195 scf2_1100000004511:3392679-3392699 - 4. dwi_61 scf2_1100000004511:3393253-3393273 - 5. dwi_193 scf2_1100000004511:3393468-3393488 - 6. dwi_63 scf2_1100000004511:3393826-3393846 - 7. dwi_64 scf2_1100000004511:3394110-3394130 - 8. dwi_65 scf2_1100000004511:3394468-3394488 - 9. dwi_89 scf2_1100000004511:3394684-3394704 - 10. dwi_190 scf2_1100000004511:3394900-3394920 - 11. dwi_189 scf2_1100000004511:3395101-3395121 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAACTTAGTGATAGTCGCAGTATCATCAAAATCATACCTTATATGCAGAGTAGAGTTCAAGTAAAGGTAAAGAGCGTTATAAATCGAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTAAGAGAAAAACTAAGTGATCGTCGCAGGA **********...(((((((.(((..(((.((((((((((((((((.((.....)).)...)))))..)))))))))))))).)))..)))..)))))))).**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V117 male body**	**V118 embryo**	**M045 female body**	**V119 head**	**M020 head**
..........TAGAGTTCAAGTAAAGGTAAAG..........	22	0	4	81.00	324	291	17	10	6	0
..........TAGAGTTCAAGTAAAGGTAAAGA..........	23	0	4	56.50	226	153	62	11	0	0
..........TAGAGTTCAAGTAAAGGTAAA..........	21	0	5	13.40	67	58	3	5	1	0
..........TTCCTACTTTTACTTGATCTT..........	21	0	11	10.73	118	5	8	94	8	3
..........TAGAGTTCAAGTAAAGGTAAAGAG..........	24	0	4	8.25	33	26	5	1	1	0
..........TTCCTACTTTTACTTGATCTTA..........	22	0	11	7.73	85	2	43	40	0	0
..........TAGAGTTCAAGTAAAGGTAAAGAA..........	24	1	4	5.50	22	18	4	0	0	0
..........AGTTCAAGTAAAGGTAAAGAGCG..........	23	0	4	3.25	13	3	8	2	0	0
..........TAGAGTTCAAGTAAAGGTAA..........	20	0	5	2.60	13	11	0	1	1	0
..........AGAGTTCAAGTAAAGGTAAAG..........	21	0	4	1.50	6	2	1	3	0	0
..........CTACTTTTACTTGATCTTATCT..........	22	0	11	1.27	14	2	2	6	1	3
..........TAGAGTTCAAGTAAAGGTAAAGAAA..........	25	2	4	1.25	5	4	1	0	0	0
..........AGAGTTCAAGTAAAGGTAAAGA..........	22	0	4	1.00	4	0	0	4	0	0
..........TAGAGTTCAAGTAAAGGTAAAGAGA..........	25	1	4	0.75	3	3	0	0	0	0
..........AGTTCAAGTAAAGGTAAAGAGC..........	22	0	4	0.75	3	2	0	1	0	0
..........TAGAGTTCAAGTAAAGGTAAAGAT..........	24	1	4	0.75	3	2	1	0	0	0
..........TTCCTACTTTTACTTGATCT..........	20	0	11	0.73	8	0	1	7	0	0
..........TTCCTACTTTTACTTGATCTTAA..........	23	1	11	0.64	7	1	0	6	0	0
..........TAGAGTTCAAGTAAAGGTA..........	19	0	5	0.60	3	3	0	0	0	0
..........TAGAGTTCAAGTAAAGGTAAAA..........	22	1	5	0.60	3	3	0	0	0	0
..........TCCTACTTTTACTTGATCTT..........	20	0	11	0.27	3	0	0	3	0	0
..........GAGTTCAAGTAAAGGTAAAGA..........	21	0	4	0.25	1	0	1	0	0	0
..........AGTTCAAGTAAAGGTAAAGAG..........	21	0	4	0.25	1	1	0	0	0	0
..........TAGAGTTCAAGTAAAGGTAAAGG..........	23	1	4	0.25	1	1	0	0	0	0
..........GAGTTCAAGTAAAGGTAAAGAA..........	22	1	4	0.25	1	1	0	0	0	0
..........TAGAGTTCAAGTAAAGGTAAAGAGT..........	25	1	4	0.25	1	1	0	0	0	0
..........AGAGTTCAAGTAAAGGTAAAGAG..........	23	0	4	0.25	1	1	0	0	0	0
..........TTCCTACTTTTACTTGATCTC..........	21	1	11	0.18	2	0	0	0	0	2
..........TCCTACTTTTACTTGATCTTA..........	21	0	11	0.18	2	0	0	2	0	0
..........CCTACTTTTACTTGATCTT..........	19	0	11	0.18	2	0	1	1	0	0
..........TTCCTACTTTTACTTGATCTTAAA..........	24	2	11	0.18	2	0	0	2	0	0
..........CCTACTTTTACTTGATCTTATCTA..........	24	1	11	0.09	1	0	0	1	0	0
..........CTACTTTTACTTGATCTTATC..........	21	0	11	0.09	1	0	1	0	0	0
..........CCTACTTTTACTTGATCTTA..........	20	0	11	0.09	1	0	1	0	0	0
..........TTCCTACTTTTACTTGATCTTT..........	22	1	11	0.09	1	0	0	1	0	0
..........TTTTCCTACTTTTACTTGATCC..........	22	1	11	0.09	1	0	0	1	0	0
..........TCCTACTTTTACTTGATCTTAA..........	22	1	11	0.09	1	0	0	1	0	0
..........TCCTACTTTTACTTGATCT..........	19	0	11	0.09	1	0	0	1	0	0
..........CTACTTTTACTTGATCTTATCTA..........	23	1	11	0.09	1	0	0	1	0	0
..........CTACTTTTACTTGATCTTATCC..........	22	1	11	0.09	1	1	0	0	0	0

Anti-sense strand reads

TTTGAATCACTATCAGCGTCATAGTAGTTTTAGTATGGAATATACGTCTCATCTCAAGTTCATTTCCATTTCTCGCAATATTTAGCTTTAAAAGGATGAAAATGAACTAGAATAGAGCCGCATATTTTTTGAGAATTCTCTTTTTGATTCACTAGCAGCGTCCT **********...(((((((.(((..(((.((((((((((((((((.((.....)).)...)))))..)))))))))))))).)))..)))..)))))))).**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V118 embryo**
..........TTAGCTTTAAAAGGATGAAAA..........	21	0	7	0.14	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3393201-3393364 -	dwi_61	AAACTTAGTGATAGTCGCAGTATCATCAAAATCATACCTTATATGCAGAGTAGAGTTCAAGTAAAGGTAAAGAGCGTTATAAATCGAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTAAGAGAAAAACTAAGTGATCGTCGCAGGA

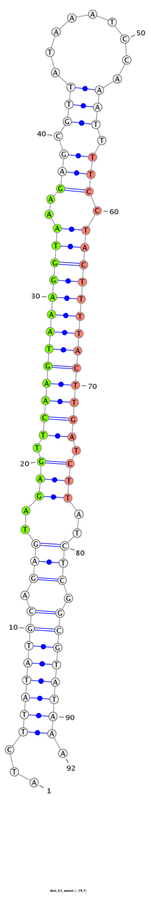
Generated: 09/08/2015 at 08:00 PM

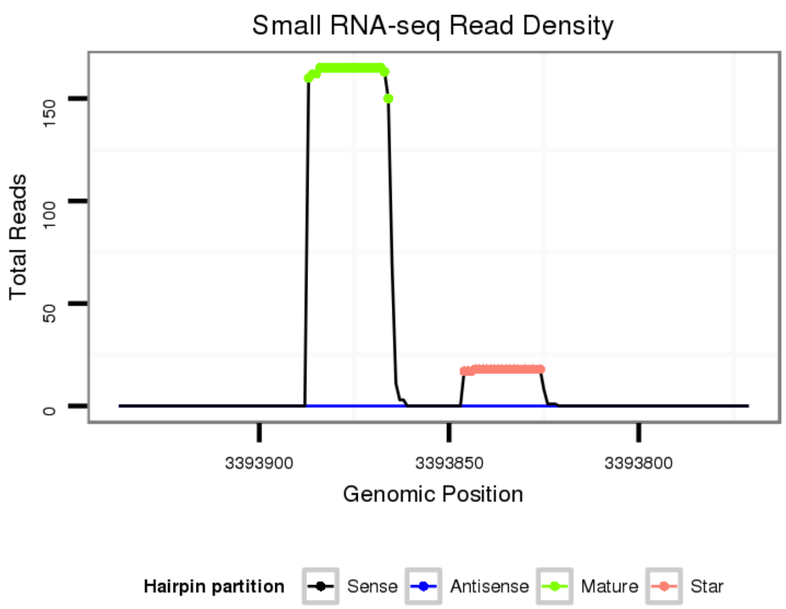
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

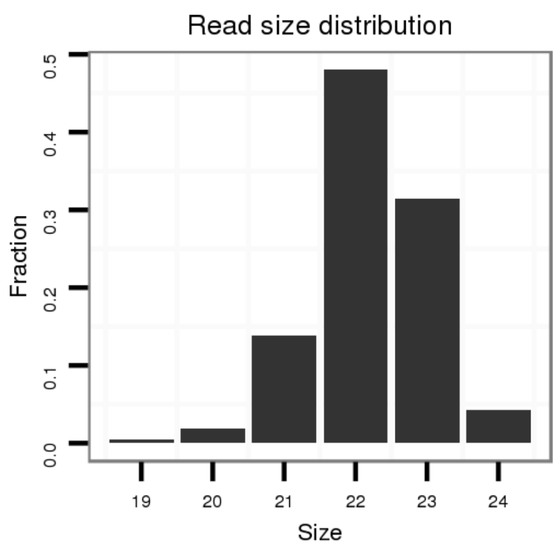
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_63	**scf2_1100000004511:3393821-3393887 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

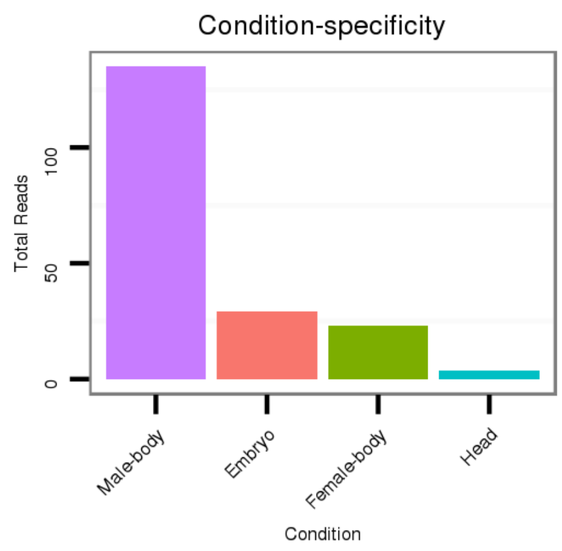
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

mature	star
1. dwi_61 scf2_1100000004511:3393293-3393314 - 2. dwi_63 scf2_1100000004511:3393866-3393887 - 3. dwi_64 scf2_1100000004511:3394150-3394171 - 4. dwi_65 scf2_1100000004511:3394508-3394529 -	1. dwi_197 scf2_1100000004511:3392321-3392341 - 2. dwi_196 scf2_1100000004511:3392537-3392557 - 3. dwi_195 scf2_1100000004511:3392679-3392699 - 4. dwi_61 scf2_1100000004511:3393253-3393273 - 5. dwi_193 scf2_1100000004511:3393468-3393488 - 6. dwi_63 scf2_1100000004511:3393826-3393846 - 7. dwi_64 scf2_1100000004511:3394110-3394130 - 8. dwi_65 scf2_1100000004511:3394468-3394488 - 9. dwi_89 scf2_1100000004511:3394684-3394704 - 10. dwi_190 scf2_1100000004511:3394900-3394920 - 11. dwi_189 scf2_1100000004511:3395101-3395121 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAACTAAGTGATCGTCGCAGGATCATAAAAATCATATCTTATATGCAGAGTAGAGTTCAAGTAAAGGTAAAGAGCGTTATAAATCCAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTAAGAGAAAAACTAAGTGATCGTCGCAGGATCA **********...(((((((((.(((..(((.((((.(((((((((((((..(((.(((.........))).)))).)))))))))))))).)))..)))).)))))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	V118 embryo	M045 female body	V119 head	M020 head
.....TAGAGTTCAAGTAAAGGTAAAG.....	22	0	4	81.00	324	291	17	10	6	0
.....TAGAGTTCAAGTAAAGGTAAAGA.....	23	0	4	56.50	226	153	62	11	0	0
.....TAGAGTTCAAGTAAAGGTAAA.....	21	0	5	13.40	67	58	3	5	1	0
.....TTCCTACTTTTACTTGATCTT.....	21	0	11	10.73	118	5	8	94	8	3
.....TAGAGTTCAAGTAAAGGTAAAGAG.....	24	0	4	8.25	33	26	5	1	1	0
.....TTCCTACTTTTACTTGATCTTA.....	22	0	11	7.73	85	2	43	40	0	0
.....TAGAGTTCAAGTAAAGGTAAAGAA.....	24	1	4	5.50	22	18	4	0	0	0
.....AGTTCAAGTAAAGGTAAAGAGCG.....	23	0	4	3.25	13	3	8	2	0	0
.....TAGAGTTCAAGTAAAGGTAA.....	20	0	5	2.60	13	11	0	1	1	0
.....AGAGTTCAAGTAAAGGTAAAG.....	21	0	4	1.50	6	2	1	3	0	0
.....CTACTTTTACTTGATCTTATCT.....	22	0	11	1.27	14	2	2	6	1	3
.....TAGAGTTCAAGTAAAGGTAAAGAAA.....	25	2	4	1.25	5	4	1	0	0	0
.....AGAGTTCAAGTAAAGGTAAAGA.....	22	0	4	1.00	4	0	0	4	0	0
.....TAGAGTTCAAGTAAAGGTAAAGAGA.....	25	1	4	0.75	3	3	0	0	0	0
.....TAGAGTTCAAGTAAAGGTAAAGAT.....	24	1	4	0.75	3	2	1	0	0	0
.....AGTTCAAGTAAAGGTAAAGAGC.....	22	0	4	0.75	3	2	0	1	0	0
.....TTCCTACTTTTACTTGATCT.....	20	0	11	0.73	8	0	1	7	0	0
.....TTCCTACTTTTACTTGATCTTAA.....	23	1	11	0.64	7	1	0	6	0	0
.....TAGAGTTCAAGTAAAGGTA.....	19	0	5	0.60	3	3	0	0	0	0
.....TAGAGTTCAAGTAAAGGTAAAA.....	22	1	5	0.60	3	3	0	0	0	0
.....TCCTACTTTTACTTGATCTT.....	20	0	11	0.27	3	0	0	3	0	0
.....AGTTCAAGTAAAGGTAAAGAG.....	21	0	4	0.25	1	1	0	0	0	0
.....TAGAGTTCAAGTAAAGGTAAAGG.....	23	1	4	0.25	1	1	0	0	0	0
.....AGAGTTCAAGTAAAGGTAAAGAG.....	23	0	4	0.25	1	1	0	0	0	0
.....GAGTTCAAGTAAAGGTAAAGAA.....	22	1	4	0.25	1	1	0	0	0	0
.....TAGAGTTCAAGTAAAGGTAAAGAGT.....	25	1	4	0.25	1	1	0	0	0	0
.....GAGTTCAAGTAAAGGTAAAGA.....	21	0	4	0.25	1	0	1	0	0	0
.....TCCTACTTTTACTTGATCTTA.....	21	0	11	0.18	2	0	0	2	0	0
.....TTCCTACTTTTACTTGATCTC.....	21	1	11	0.18	2	0	0	0	0	2
.....CCTACTTTTACTTGATCTT.....	19	0	11	0.18	2	0	1	1	0	0
.....TTCCTACTTTTACTTGATCTTAAA.....	24	2	11	0.18	2	0	0	2	0	0
.....CTACTTTTACTTGATCTTATCC.....	22	1	11	0.09	1	1	0	0	0	0
.....TCCTACTTTTACTTGATCT.....	19	0	11	0.09	1	0	0	1	0	0
.....CTACTTTTACTTGATCTTATCTA.....	23	1	11	0.09	1	0	0	1	0	0
.....TTTTCCTACTTTTACTTGATCC.....	22	1	11	0.09	1	0	0	1	0	0
.....CTACTTTTACTTGATCTTATC.....	21	0	11	0.09	1	0	1	0	0	0
.....CCTACTTTTACTTGATCTTATCTA.....	24	1	11	0.09	1	0	0	1	0	0
.....TTCCTACTTTTACTTGATCTTT.....	22	1	11	0.09	1	0	0	1	0	0
.....CCTACTTTTACTTGATCTTA.....	20	0	11	0.09	1	0	1	0	0	0
.....TCCTACTTTTACTTGATCTTAA.....	22	1	11	0.09	1	0	0	1	0	0

Anti-sense strand reads

TTTGATTCACTAGCAGCGTCCTAGTATTTTAGTATAGAATATACGTCTCATCTCAAGTTCATTTCCATTTCTCGCAATATTTAGGTTTAAAAGGATGAAAATGAACTAGAATAGAGCCGCATATTTTTTGAGAATTCTCTTTTTGATTCACTAGCAGCGTCCTAGT **********...(((((((((.(((..(((.((((.(((((((((((((..(((.(((.........))).)))).)))))))))))))).)))..)))).)))))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3393771-3393937 -	dwi_63	AAACTAAGTGATCGTCGCAGGATCATAAAAATCATATCTTATATGCAGAGTAGAGTTCAAGTAAAGGTAAAGAGCGTTATAAATCCAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTAAGAGAAAAACTAAGTGATCGTCGCAGGATCA

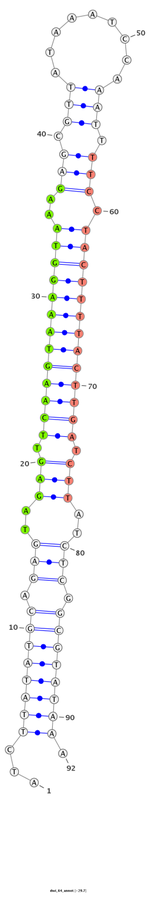
Generated: 09/08/2015 at 08:06 PM

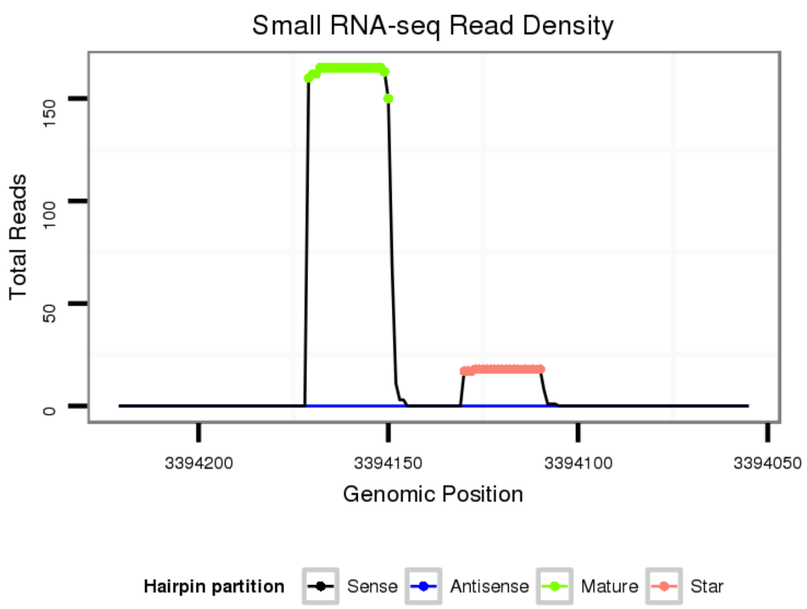
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

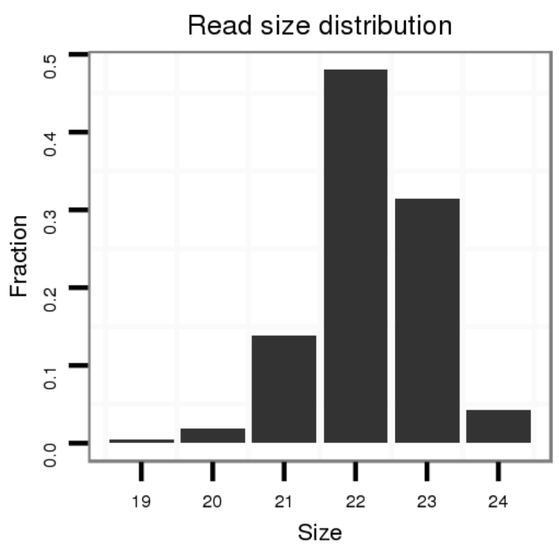
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_64	**scf2_1100000004511:3394105-3394171 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

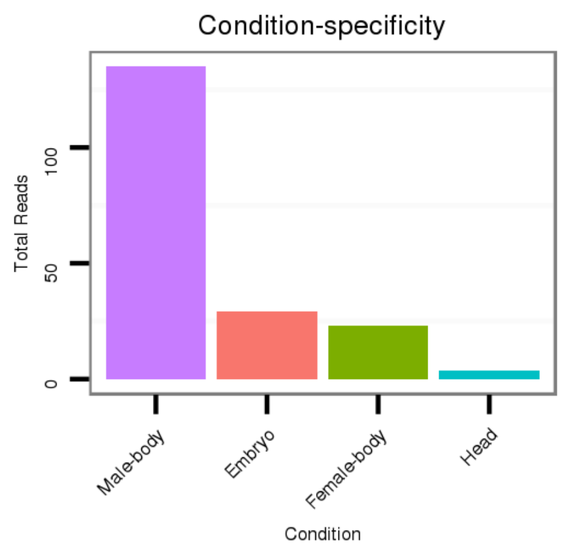
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

mature	star
1. dwi_61 scf2_1100000004511:3393293-3393314 - 2. dwi_63 scf2_1100000004511:3393866-3393887 - 3. dwi_64 scf2_1100000004511:3394150-3394171 - 4. dwi_65 scf2_1100000004511:3394508-3394529 -	1. dwi_197 scf2_1100000004511:3392321-3392341 - 2. dwi_196 scf2_1100000004511:3392537-3392557 - 3. dwi_195 scf2_1100000004511:3392679-3392699 - 4. dwi_61 scf2_1100000004511:3393253-3393273 - 5. dwi_193 scf2_1100000004511:3393468-3393488 - 6. dwi_63 scf2_1100000004511:3393826-3393846 - 7. dwi_64 scf2_1100000004511:3394110-3394130 - 8. dwi_65 scf2_1100000004511:3394468-3394488 - 9. dwi_89 scf2_1100000004511:3394684-3394704 - 10. dwi_190 scf2_1100000004511:3394900-3394920 - 11. dwi_189 scf2_1100000004511:3395101-3395121 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAACTTAGTGATAGTCGCAGGATCATAAAGATCATATCTTATATGCAGAGTAGAGTTCAAGTAAAGGTAAAGAGCGTTATAAATCCAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTAAGAGAAAAACTAAGTGATCATCGCAGGATCA **********...(((((((((.(((..(((.((((((((((((((..(((.(((.........))))).))).)))))))))))))).)))..)))).)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	V118 embryo	M045 female body	V119 head	M020 head
.....TAGAGTTCAAGTAAAGGTAAAG.....	22	0	4	81.00	324	291	17	10	6	0
.....TAGAGTTCAAGTAAAGGTAAAGA.....	23	0	4	56.50	226	153	62	11	0	0
.....TAGAGTTCAAGTAAAGGTAAA.....	21	0	5	13.40	67	58	3	5	1	0
.....TTCCTACTTTTACTTGATCTT.....	21	0	11	10.73	118	5	8	94	8	3
.....TAGAGTTCAAGTAAAGGTAAAGAG.....	24	0	4	8.25	33	26	5	1	1	0
.....TTCCTACTTTTACTTGATCTTA.....	22	0	11	7.73	85	2	43	40	0	0
.....TAGAGTTCAAGTAAAGGTAAAGAA.....	24	1	4	5.50	22	18	4	0	0	0
.....AGTTCAAGTAAAGGTAAAGAGCG.....	23	0	4	3.25	13	3	8	2	0	0
.....TAGAGTTCAAGTAAAGGTAA.....	20	0	5	2.60	13	11	0	1	1	0
.....AGAGTTCAAGTAAAGGTAAAG.....	21	0	4	1.50	6	2	1	3	0	0
.....CTACTTTTACTTGATCTTATCT.....	22	0	11	1.27	14	2	2	6	1	3
.....TAGAGTTCAAGTAAAGGTAAAGAAA.....	25	2	4	1.25	5	4	1	0	0	0
.....AGAGTTCAAGTAAAGGTAAAGA.....	22	0	4	1.00	4	0	0	4	0	0
.....TAGAGTTCAAGTAAAGGTAAAGAT.....	24	1	4	0.75	3	2	1	0	0	0
.....TAGAGTTCAAGTAAAGGTAAAGAGA.....	25	1	4	0.75	3	3	0	0	0	0
.....AGTTCAAGTAAAGGTAAAGAGC.....	22	0	4	0.75	3	2	0	1	0	0
.....TTCCTACTTTTACTTGATCT.....	20	0	11	0.73	8	0	1	7	0	0
.....TTCCTACTTTTACTTGATCTTAA.....	23	1	11	0.64	7	1	0	6	0	0
.....TAGAGTTCAAGTAAAGGTAAAA.....	22	1	5	0.60	3	3	0	0	0	0
.....TAGAGTTCAAGTAAAGGTA.....	19	0	5	0.60	3	3	0	0	0	0
.....TCCTACTTTTACTTGATCTT.....	20	0	11	0.27	3	0	0	3	0	0
.....GAGTTCAAGTAAAGGTAAAGAA.....	22	1	4	0.25	1	1	0	0	0	0
.....TAGAGTTCAAGTAAAGGTAAAGG.....	23	1	4	0.25	1	1	0	0	0	0
.....AGAGTTCAAGTAAAGGTAAAGAG.....	23	0	4	0.25	1	1	0	0	0	0
.....TAGAGTTCAAGTAAAGGTAAAGAGT.....	25	1	4	0.25	1	1	0	0	0	0
.....GAGTTCAAGTAAAGGTAAAGA.....	21	0	4	0.25	1	0	1	0	0	0
.....AGTTCAAGTAAAGGTAAAGAG.....	21	0	4	0.25	1	1	0	0	0	0
.....CCTACTTTTACTTGATCTT.....	19	0	11	0.18	2	0	1	1	0	0
.....TTCCTACTTTTACTTGATCTC.....	21	1	11	0.18	2	0	0	0	0	2
.....TTCCTACTTTTACTTGATCTTAAA.....	24	2	11	0.18	2	0	0	2	0	0
.....TCCTACTTTTACTTGATCTTA.....	21	0	11	0.18	2	0	0	2	0	0
.....TCCTACTTTTACTTGATCTTAA.....	22	1	11	0.09	1	0	0	1	0	0
.....TTCCTACTTTTACTTGATCTTT.....	22	1	11	0.09	1	0	0	1	0	0
.....TTTTCCTACTTTTACTTGATCC.....	22	1	11	0.09	1	0	0	1	0	0
.....TTCCTACTTTTACTTGATCTTT.....	22	1	11	0.09	1	0	0	1	0	0
.....TTTTCCTACTTTTACTTGATCC.....	22	1	11	0.09	1	0	0	1	0	0
.....TTCCTACTTTTACTTGATCTTT.....	22	1	11	0.09	1	0	0	1	0	0
.....TTTTCCTACTTTTACTTGATCC.....	22	1	11	0.09	1	0	0	1	0	0
.....CCTACTTTTACTTGATCTTA.....	24	1	11	0.09	1	0	0	1	0	0
.....CTACTTTTACTTGATCTTATC.....	21	0	11	0.09	1	0	1	0	0	0
.....CTACTTTTACTTGATCTTATCTA.....	23	1	11	0.09	1	0	0	1	0	0
.....TCCTACTTTTACTTGATCT.....	19	0	11	0.09	1	0	0	1	0	0
.....CCTACTTTTACTTGATCTTA.....	20	0	11	0.09	1	0	1	0	0	0
.....CTACTTTTACTTGATCTTATCC.....	22	1	11	0.09	1	1	0	0	0	0

Anti-sense strand reads

TTTGAATCACTATCAGCGTCCTAGTATTTCTAGTATAGAATATACGTCTCATCTCAAGTTCATTTCCATTTCTCGCAATATTTAGGTTTAAAAGGATGAAAATGAACTAGAATAGAGCCGCATATTTTTTGAGAATTCTCTTTTTGATTCACTAGTAGCGTCCTAGT **********...(((((((((.(((..(((.((((((((((((((..(((.(((.........))))).))).)))))))))))))).)))..)))).)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	V119 head
.....AGTTCAAGTAAAGGTAAAGAGC.....	22	0	4	0.75	3	2	0	1	0	0
.....TTCCTACTTTTACTTGATCT.....	20	0	11	0.73	8	0	1	7	0	0
.....TTCCTACTTTTACTTGATCTTAA.....	23	1	11	0.64	7	1	0	6	0	0
.....TAGAGTTCAAGTAAAGGTAAAA.....	22	1	5	0.60	3	3	0	0	0	0
.....TAGAGTTCAAGTAAAGGTA.....	19	0	5	0.60	3	3	0	0	0	0
.....TCCTACTTTTACTTGATCTT.....	20	0	11	0.27	3	0	0	3	0	0
.....GAGTTCAAGTAAAGGTAAAGAA.....	22	1	4	0.25	1	1	0	0	0	0
.....TAGAGTTCAAGTAAAGGTAAAGG.....	23	1	4	0.25	1	1	0	0	0	0
.....AGAGTTCAAGTAAAGGTAAAGAG.....	23	0	4	0.25	1	1	0	0	0	0
.....TAGAGTTCAAGTAAAGGTAAAGAGT.....	25	1	4	0.25	1	1	0	0	0	0
.....GAGTTCAAGTAAAGGTAAAGA.....	21	0	4	0.25	1	0	1	0	0	0
.....AGTTCAAGTAAAGGTAAAGAG.....	21	0	4	0.25	1	1	0	0	0	0
.....CCTACTTTTACTTGATCTT.....	19	0	11	0.18	2	0	1	1	0	0
.....TTCCTACTTTTACTTGATCTC.....	21	1	11	0.18	2	0	0	0	0	2
.....TTCCTACTTTTACTTGATCTTAAA.....	24	2	11	0.18	2	0	0	2	0	0
.....TCCTACTTTTACTTGATCTTA.....	21	0	11	0.18	2	0	0	2	0	0
.....TCCTACTTTTACTTGATCTTAA.....	22	1	11	0.09	1	0	0	1	0	0
.....TTCCTACTTTTACTTGATCTTT.....	22	1	11	0.09	1	0	0	1	0	0
.....TTTTCCTACTTTTACTTGATCC.....	22	1	11	0.09	1	0	0	1	0	0
.....TTCCTACTTTTACTTGATCTTT.....	22	1	11	0.09	1	0	0	1	0	0
.....TTTTCCTACTTTTACTTGATCC.....	22	1	11	0.09	1	0	0	1	0	0
.....CCTACTTTTACTTGATCTTA.....	24	1	11	0.09	1	0	0	1	0	0
.....CTACTTTTACTTGATCTTATC.....	21	0	11	0.09	1	0	1	0	0	0
.....CTACTTTTACTTGATCTTATCTA.....	23	1	11	0.09	1	0	0	1	0	0
.....TCCTACTTTTACTTGATCT.....	19	0	11	0.09	1	0	0	1	0	0
.....CCTACTTTTACTTGATCTTA.....	20	0	11	0.09	1	0	1	0	0	0
.....CTACTTTTACTTGATCTTATCC.....	22	1	11	0.09	1	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3394055-3394221 -	dwi_64	AAACTTAGTGATAGTCGCAGGATCATAAAGATCATATCTTATATGCAGAGTAGAGTTCAAGTAAAGGTAAAGAGCGTTATAAATCCAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTAAGAGAAAAACTAAGTGATCATCGCAGGATCA

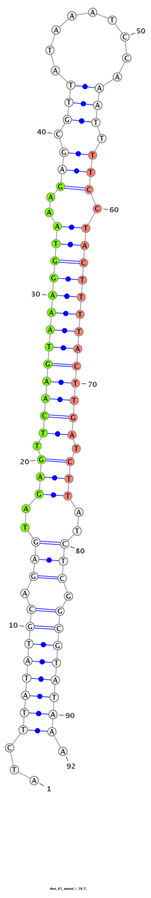
Generated: 09/08/2015 at 08:07 PM

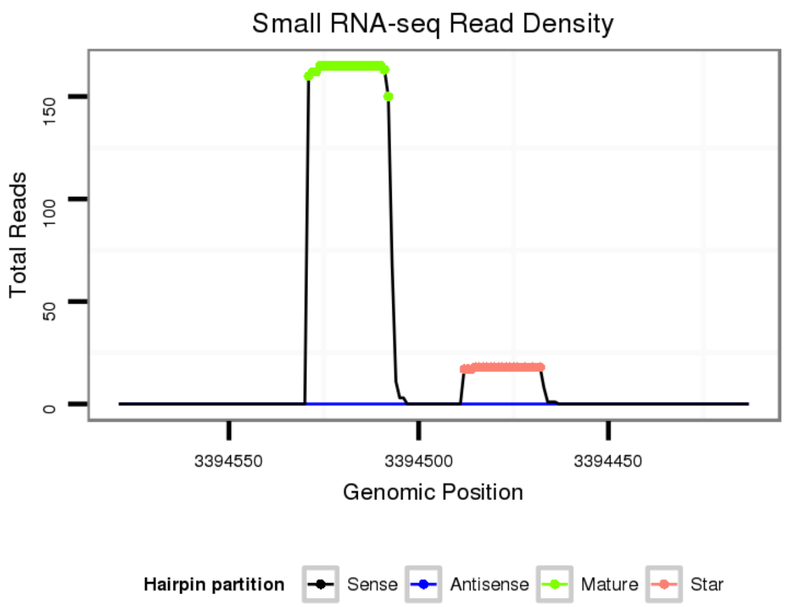
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

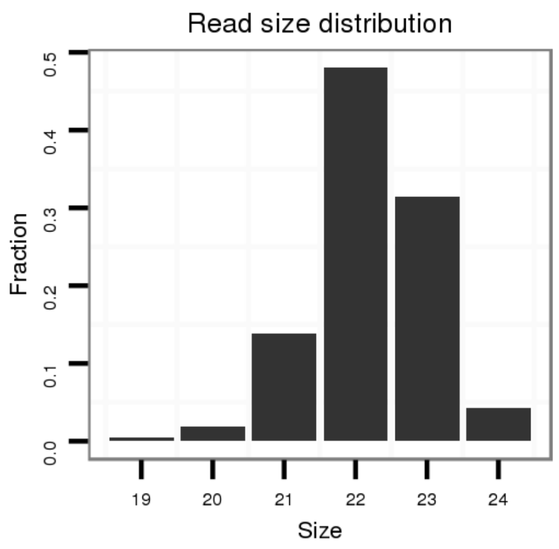
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_65	**scf2_1100000004511:3394463-3394529 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

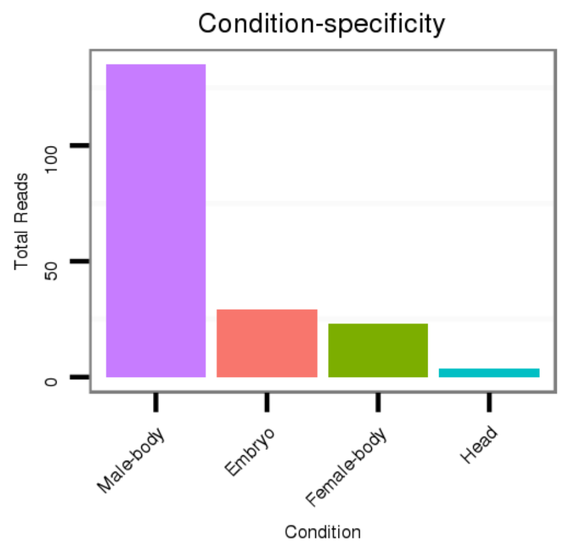
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

mature	star
1. dwi_61 scf2_1100000004511:3393293-3393314 - 2. dwi_63 scf2_1100000004511:3393866-3393887 - 3. dwi_64 scf2_1100000004511:3394150-3394171 - 4. dwi_65 scf2_1100000004511:3394508-3394529 -	1. dwi_197 scf2_1100000004511:3392321-3392341 - 2. dwi_196 scf2_1100000004511:3392537-3392557 - 3. dwi_195 scf2_1100000004511:3392679-3392699 - 4. dwi_61 scf2_1100000004511:3393253-3393273 - 5. dwi_193 scf2_1100000004511:3393468-3393488 - 6. dwi_63 scf2_1100000004511:3393826-3393846 - 7. dwi_64 scf2_1100000004511:3394110-3394130 - 8. dwi_65 scf2_1100000004511:3394468-3394488 - 9. dwi_89 scf2_1100000004511:3394684-3394704 - 10. dwi_190 scf2_1100000004511:3394900-3394920 - 11. dwi_189 scf2_1100000004511:3395101-3395121 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAACTTAGTGATAGTCGCAGGATCATAAAAATCATATCTTATATGCAGAGTAGAGTTCAAGTAAAGGTAAAGAGCGTTATAAATCCAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTAAGAGAAAAACTAAGTGATCGTCGCAGGATCA **********...(((((((((.(((..(((.(((((((((((((..(((.(((.........))).))).)))))))))))))).)))..)))..)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	V118 embryo	M045 female body	V119 head	M020 head
.....TAGAGTTCAAGTAAAGGTAAAG.....	22	0	4	81.00	324	291	17	10	6	0
.....TAGAGTTCAAGTAAAGGTAAAGA.....	23	0	4	56.50	226	153	62	11	0	0
.....TAGAGTTCAAGTAAAGGTAAA.....	21	0	5	13.40	67	58	3	5	1	0
.....TTCCTACTTTTACTTGATCTT.....	21	0	11	10.73	118	5	8	94	8	3
.....TAGAGTTCAAGTAAAGGTAAAGAG.....	24	0	4	8.25	33	26	5	1	1	0
.....TTCCTACTTTTACTTGATCTTA.....	22	0	11	7.73	85	2	43	40	0	0
.....TAGAGTTCAAGTAAAGGTAAAGAA.....	24	1	4	5.50	22	18	4	0	0	0
.....AGTTCAAGTAAAGGTAAAGAGCG.....	23	0	4	3.25	13	3	8	2	0	0
.....TAGAGTTCAAGTAAAGGTAA.....	20	0	5	2.60	13	11	0	1	1	0
.....AGAGTTCAAGTAAAGGTAAAG.....	21	0	4	1.50	6	2	1	3	0	0
.....CTACTTTTACTTGATCTTATCT.....	22	0	11	1.27	14	2	2	6	1	3
.....TAGAGTTCAAGTAAAGGTAAAGAAA.....	25	2	4	1.25	5	4	1	0	0	0
.....AGAGTTCAAGTAAAGGTAAAGA.....	22	0	4	1.00	4	0	0	4	0	0
.....TAGAGTTCAAGTAAAGGTAAAGAT.....	24	1	4	0.75	3	2	1	0	0	0
.....TAGAGTTCAAGTAAAGGTAAAGAGA.....	25	1	4	0.75	3	3	0	0	0	0
.....AGTTCAAGTAAAGGTAAAGAGC.....	22	0	4	0.75	3	2	0	1	0	0
.....TTCCTACTTTTACTTGATCT.....	20	0	11	0.73	8	0	1	7	0	0
.....TTCCTACTTTTACTTGATCTTAA.....	23	1	11	0.64	7	1	0	6	0	0
.....TAGAGTTCAAGTAAAGGTA.....	19	0	5	0.60	3	3	0	0	0	0
.....TAGAGTTCAAGTAAAGGTAAAA.....	22	1	5	0.60	3	3	0	0	0	0
.....TCCTACTTTTACTTGATCTT.....	20	0	11	0.27	3	0	0	3	0	0
.....AGTTCAAGTAAAGGTAAAGAG.....	21	0	4	0.25	1	1	0	0	0	0
.....TAGAGTTCAAGTAAAGGTAAAGG.....	23	1	4	0.25	1	1	0	0	0	0
.....GAGTTCAAGTAAAGGTAAAGA.....	21	0	4	0.25	1	0	1	0	0	0
.....GAGTTCAAGTAAAGGTAAAGAA.....	22	1	4	0.25	1	1	0	0	0	0
.....AGAGTTCAAGTAAAGGTAAAGAG.....	23	0	4	0.25	1	1	0	0	0	0
.....TAGAGTTCAAGTAAAGGTAAAGAGT.....	25	1	4	0.25	1	1	0	0	0	0
.....TTCCTACTTTTACTTGATCTC.....	21	1	11	0.18	2	0	0	0	0	2
.....TTCCTACTTTTACTTGATCTTAAA.....	24	2	11	0.18	2	0	0	2	0	0
.....CCTACTTTTACTTGATCTT.....	19	0	11	0.18	2	0	1	1	0	0
.....TCCTACTTTTACTTGATCTTA.....	21	0	11	0.18	2	0	0	2	0	0
.....CTACTTTTACTTGATCTTATC.....	21	0	11	0.09	1	0	1	0	0	0
.....CCTACTTTTACTTGATCTTA.....	20	0	11	0.09	1	0	1	0	0	0
.....CTACTTTTACTTGATCTTATCC.....	22	1	11	0.09	1	1	0	0	0	0
.....CCTACTTTTACTTGATCTTATCTA.....	24	1	11	0.09	1	0	0	1	0	0
.....CTACTTTTACTTGATCTTATCTA.....	23	1	11	0.09	1	0	0	1	0	0
.....TTTTCCTACTTTTACTTGATCC.....	22	1	11	0.09	1	0	0	1	0	0
.....TCCTACTTTTACTTGATCT.....	19	0	11	0.09	1	0	0	1	0	0
.....TTCCTACTTTTACTTGATCTTT.....	22	1	11	0.09	1	0	0	1	0	0
.....TCCTACTTTTACTTGATCTTAA.....	22	1	11	0.09	1	0	0	1	0	0

Anti-sense strand reads

TTTGAATCACTATCAGCGTCCTAGTATTTTAGTATAGAATATACGTCTCATCTCAAGTTCATTTCCATTTCTCGCAATATTTAGGTTTAAAAGGATGAAAATGAACTAGAATAGAGCCGCATATTTTTTGAGAATTCTCTTTTTGATTCACTAGCAGCGTCCTAGT **********...(((((((((.(((..(((.(((((((((((((..(((.(((.........))).))).)))))))))))))).)))..)))..)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3394413-3394579 -	dwi_65	AAACTTAGTGATAGTCGCAGGATCATAAAAATCATATCTTATATGCAGAGTAGAGTTCAAGTAAAGGTAAAGAGCGTTATAAATCCAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTAAGAGAAAAACTAAGTGATCGTCGCAGGATCA

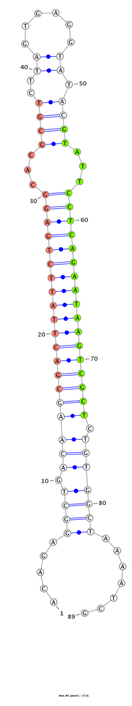
Generated: 09/08/2015 at 08:07 PM

	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	1
rescue.candidate	0

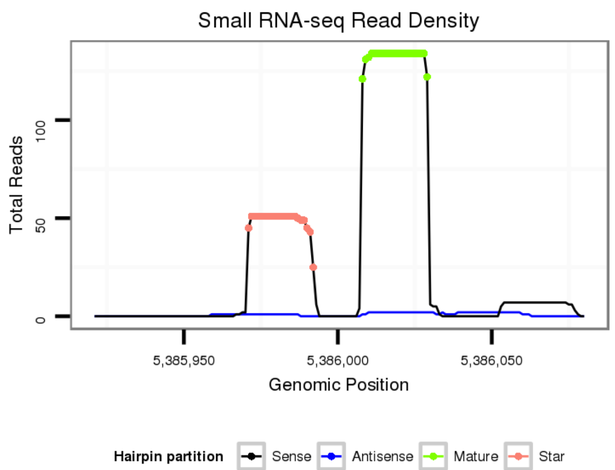
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_84	**scf2_1100000004961:5385971-5386030 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

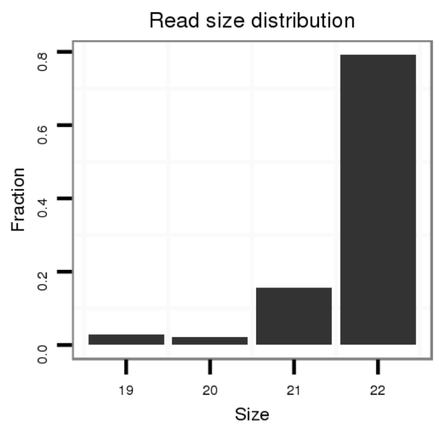
Legend: mature star mismatch in alignment mismatch in read

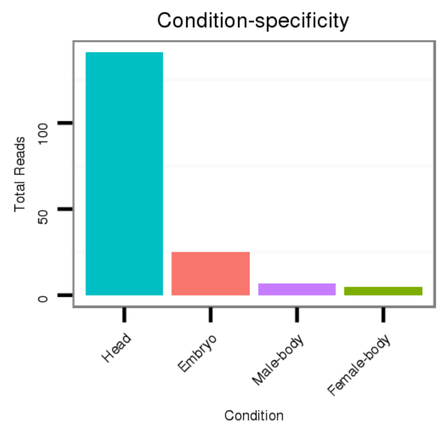
Predicted structure

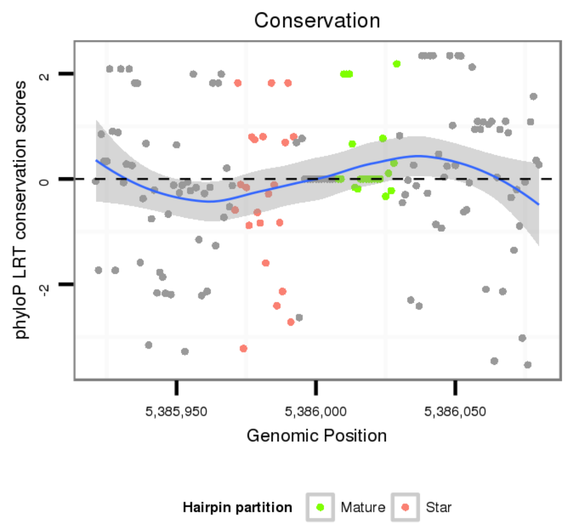


Show Alternate Folds









Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GGGAAAACATGAAAGGTCAGCCCTCTTCAGTAATAACAGAGGCTGACAAGCGACTTATTCTGAGGCACGCGTCTTAGTGAGGTATACGTATTCCTCAGAATAAGTCGCTCTGTGGCTAAAATCGAGCAAAAATCTGGTGTTAAATCGATTGTGCGGACTA	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V119 head	V118 embryo	M045 female body	V117 male body
**********.....((((.((((((((((((((((((((...((((..((.....)).))))...)))))))))))))))))).)))))))).....**********											
.....GTATTCCTCAGAATAAGTCGCT.....	22	0	1	111.00	111	18	63	22	3	5
.....CGACTTATTCTGAGGCACGCGT.....	22	0	1	19.00	19	16	2	1	0	0
.....CGACTTATTCTGAGGCACGCG.....	21	0	1	18.00	18	18	0	0	0	0
.....GTATTCCTCAGAATAAGTCGCC.....	22	1	1	8.00	8	8	0	0	0	0
.....GACTTATTCTGAGGCACGCGTC.....	22	0	1	6.00	6	1	4	1	0	0
.....GTATTCCTCAGAATAAGTCGC.....	21	0	1	6.00	6	1	3	0	0	2
.....TATTCCTCAGAATAAGTCGCT.....	21	0	1	4.00	4	1	2	0	1	0
.....CGTATTCCTCAGAATAAGTCGC.....	22	0	1	4.00	4	2	1	1	0	0
.....CGACTTATTCTGAGGCACG.....	19	0	1	4.00	4	4	0	0	0	0
.....TCTGGTGTTAAATCGATTGTGCGG....	24	0	1	3.00	3	0	0	0	3	0
.....GTATTCCTCAGAATAAGTCGCG.....	22	1	1	2.00	2	2	0	0	0	0
.....CGACTTATTCTGAGGCACGC.....	20	0	1	2.00	2	2	0	0	0	0
.....TATTCCTCAGAATAAGTCGC.....	20	0	1	2.00	2	0	1	0	1	0
.....TATTCCTCAGAATAAGTCGCTCTG.....	24	0	1	2.00	2	2	0	0	0	0
.....GTATTCCTCAGAATAAGTCGCTT.....	23	1	1	2.00	2	0	0	1	1	0
.....TCTGGTGTTAAATCGATTGTGCGGA...	25	0	1	1.00	1	0	0	0	0	1
.....TATTCCTCAGAATAAGTCGCTCTGT.....	25	0	1	1.00	1	1	0	0	0	0
.....TTCCTCAGAATAAGTCGCTCTG.....	22	0	1	1.00	1	1	0	0	0	0
.....CGACTTATTCTGAGGCACGCGTT.....	23	1	1	1.00	1	1	0	0	0	0
.....TATTCCTCAGAATAAGTCGCTC.....	22	0	1	1.00	1	1	0	0	0	0
.....TTCCTCAGAATAAGTCGCT.....	19	0	1	1.00	1	0	1	0	0	0
.....TATTCCTCAGAATAAGTCGCTT.....	22	1	1	1.00	1	0	0	0	1	0
.....CTGGTGTTAAATCGATTGTGC.....	21	0	1	1.00	1	0	0	0	1	0
.....GTATTCCTCAGAATAAGTCGCTG.....	23	1	1	1.00	1	1	0	0	0	0
.....TATTCCTCAGAATAAGTCGCTCTGC.....	25	1	1	1.00	1	1	0	0	0	0
.....CTGGTGTTAAATCGATTGTGCGGA...	24	0	1	1.00	1	0	0	0	1	0
.....TCTGGTGTTAAATCGATTGTGCGGAC..	26	0	1	1.00	1	0	0	0	0	1
.....AGCGACTTATTCTGAGGC.....	18	0	1	1.00	1	1	0	0	0	0
.....ATTCCTCAGAATAAGTCGCTCTG.....	23	0	1	1.00	1	0	0	0	1	0
.....CAAGCGACTTATTCTGAGGCA.....	21	0	1	1.00	1	0	1	0	0	0
.....TAATAACAGAGGCTGACAAGCGACT.....	25	0	11	0.27	3	0	0	0	3	0
.....CTTCAGTAATAACAGAGG.....	18	0	6	0.17	1	0	0	1	0	0
.....TAATAACAGAGGCTGACAAGCGA.....	23	0	11	0.09	1	0	0	0	1	0

Anti-sense strand reads

CCCTTTTGTACTTTCCAGTCGGGAGAAGTCATTATTGTCTCCGACTGTTCGCTGAATAAGACTCCGTGCGCAGAATCACTCCATATGCATAAGGAGTCTTATTCAGCGAGACACCGATTTTAGCTCGTTTTTAGACCACAATTTAGCTAACACGCCTGAT	Read size	# Mismatch	Hit Count	Total Norm	Total		M045 female body	V117 male body
**********.....((((.((((((((((((((((((((...(((..((.....)).))))...)))))))))))))))))).)))))))).....**********								
.....TTTAGCTCGTTTTTAGACCACAAT.....	24	0	1	1.00	1	1	1	0
.....CATAAGGAGTCTTATTCAGCGAGACAC.....	27	0	1	1.00	1	1	1	0
.....TAAGGAGTCTTATTCAGCGAGA.....	22	0	1	1.00	1	0	1	1
.....CCGATTTTAGCTCGTTTTTAGACCAC.....	26	0	1	1.00	1	1	1	0
.....CTCCGACTGTTCGCTGAATAAGACTCCGT.....	29	0	1	1.00	1	1	1	0
.....AGTCATTATTGTCTCCGACTGTTCGCT.....	27	0	6	0.17	1	1	1	0
.....AAGTCATTATTGTCTCCGACTGTTCGC.....	27	0	6	0.17	1	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004961:5385921-5386080 +	dwi_84	GGGAAAA-CATGAAAG-GTCAGCCCTCTTCAGTAATAACAGAGGCTGACAAGCGACTTATTCTGAGGCACGCGTCTTAGTGAGGTATACGTATTCCTCAGAATAAGTCGCTCTGTGGCTAAAATCGAGCAAAAATCTGGTGTTAAATCGATTGTGCGGACTA------
droVir3	scaffold_13036:950433-950571 -		GGAAAAAAATGAAAG-GAGGAAAAAATCTGCTACAAGGCATGAGAGAGGCGACTAATCGTTCGAACTGGTTCGA----------ATTCCC--------ACGTCTCTGCCAGTAAAATCAGGGATGAATGCGGTGTAAATGCTAGTTTGCAACGG------
droMoj3	scaffold_6473:3194053-3194094 +		CT-----T--------T----------AAGATTAGGGAAAAAGCGGTGTTAAGGCGAGCTTATCAA----------
dp5	Unknown_group_108:16373-16494 +		GCAAAAA-TATGAAAG-AGGGTGTCAGCACACAACAACACCAGGAGACAGACGATTTACCATTAGAACTGCTTGCAA----------ATTCCA--------AGCGTTCAGCAGCAAAAATCAGGGAAGA----------TGCAAGTTTGGCAA----------
droPer2	scaffold_53:58027-58163 +		GCAAAAA-TATGAA-G-GAGGGTGTCAGCACGCATCAACACCAGGAGACAGACGACTTATCATTAGAACTGCTTGCAA----------ATTTCA--------AGCGTTCAGCAGCCAAAATCAGGGAAGAATGCGGTGTAAATGCAAGTTTGGCGACTG------
droAna3	scaffold_13034:719761-719895 +		GAAAAAA-TATAAAAG-GTCGCAAAAGTAATGGCCTTAGCGGCAGAGATAAAGGTGCGATTCTGCGGGAAGCCTGCA----------ATTCTT--------ATGACTCCGTGAGCAAGATAAGGCAAAAAGCAGGTGTTCACGCGAGCAAAACTA----------
droBip1	scf7180000391772:10963-11097 -		GCAAAAA-CATGGAAG-GACGAAGTTCCAGTGCAGTTAACGCCAGCGGACAGCAGAGTTATTTTGAGGCATGCATCCA----------ATTCCC--------ATGACTCTGCTGCAAAAATTAAGCAAAAATCCGGTGTGAAGGCTAGGTTGGCCA----------
droKik1	scf7180000297735:8694-8827 +		GGAAAAA-TATAAAG-GACGAACCTGCAGTGCAATTAAGCCCGGCGACAGCAGAGCTATTTTGAGGCATGCACCA----------ATTCCC--------ATGACTCTGCAGCAAAGATTAGGCAA-AATCTGGTGTGAAGACTAGGTTGGCAC----------
droFic1	scf7180000451884:1466-1600 -		GCAAAAA-CATGAAGG-GCGGCATCACAGTGTACTTAGTAGCGGCGACAAGCGACTTATAATCAGAGAAGCTTGCA----------ATTCGC--------ACGACTCTTTGGCAAAGATAAGACAAAAATGTGACGTCAAAGCAAGTTTGACAA----------
droEle1	scf7180000486474:1651609-1651621 +		AAATTTAA-GATGAA----------
droRho1	scf7180000780091:392101-392159 -		-------T--------T----------CTCTACCGGCAAAATAATAGAAAAACTGGTGTTAAGGCAAGCAAATCGACTGTTTTAA
droTak1	scf7180000414703:1700-1758 +		-------T--------T----------CTCTACCGCCAAAATAATAGAAAAACTGGTGTTAGGGCAAGCAAATCGACTGTTTTAA
dm3	chr3LHet:2480711-2480845 +		GAATGAA-TATGAAAG-GAGGAAAAAATATGTAACAACACCATGAGAGAGGCGTGTTATTCTACGAACTGCCTGCAA----------ATTCTC--------ACGCTTCTGCTGCGAAAAATTAAGCAAAAATGTGGTTTAAATGGTAGTGTGGCCA----------
droSim2	4:147862-147995 +		AAAAAAC-G-TATAGGGGTGGCATAACAGTGTCTTTAAAGCGGCAGATCGCAGTCCTTAGGTCGAATACGTTGCA----------ATTCCC--------ACGACTTCTCCGGCCAAAATTCGAGAAAAAGTGGTGAAAACCCGAGCAAATC-G----------
droSec2	scaffold_52:141893-142027 +		AAAAAAA-GCTATAAGCGGTGGCCATAACAGTGTCTTTAAAGCGGCAGATCGCAGTCCTTAGGTCGAATACGTTGCA----------ATTCCC--------ACGACTTCTCCGGCCAAAATTCGAGAAAAAGTGGTGAAAACCCGAGCAAATC-G----------
droEre2	scaffold_4784:23939126-23939262 +		GGAAAAA-CATGAAAG-GTCGGCCATCATCAGTAATAACACCAGCTGACGAGCGAATCATACTACGACACGCATCTA----------ATTCCC--------ACGACTCAGCCGGCCAAAATAAGCAAAAAACTGGTGTTAAAGCGTGCGTTCGGACT-T----------

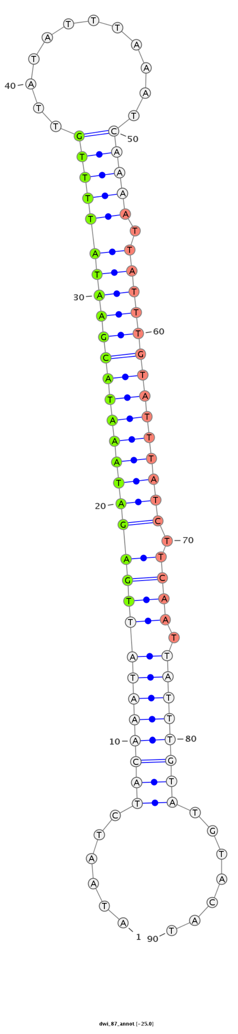
Generated: 09/08/2015 at 07:40 PM

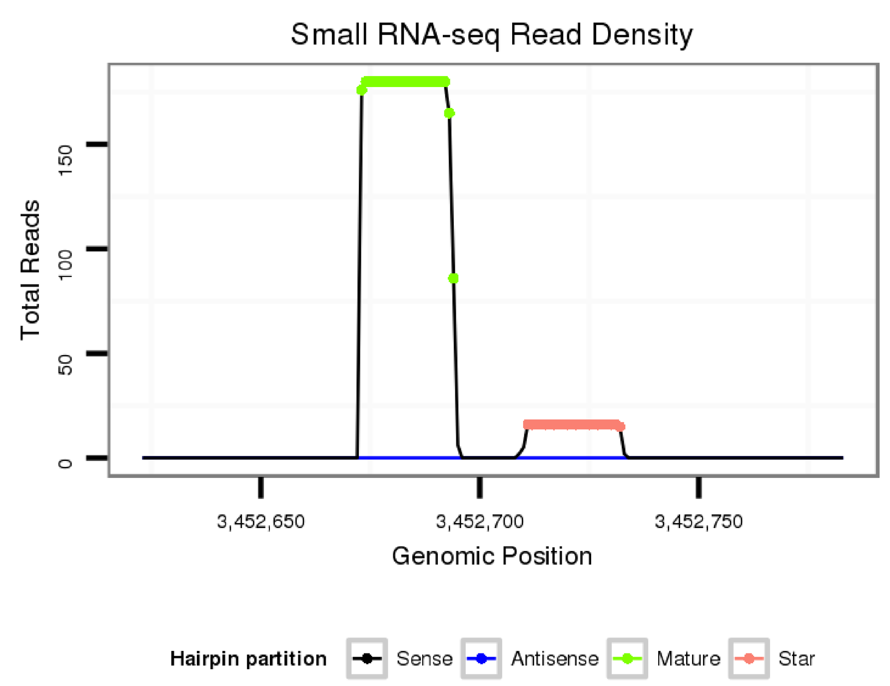
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

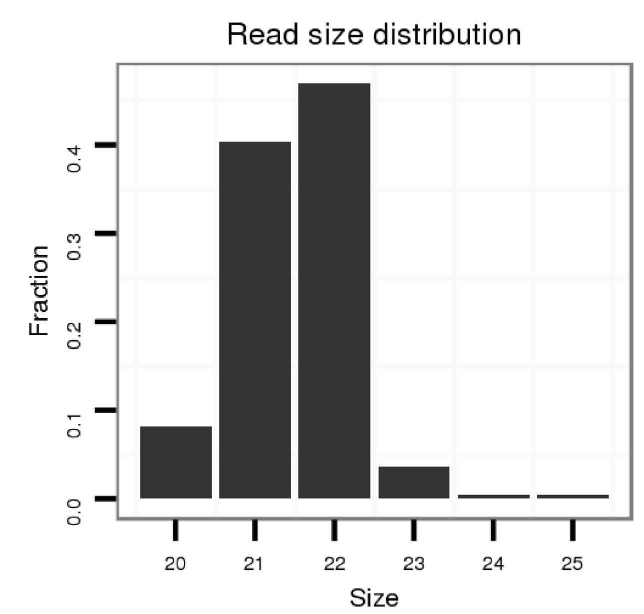
ID: dwi_87	Coordinate: scf2_1100000004513:3452673-3452733 +	Confidence: confident	Class: Testes-restricted	Genomic Locale: intergenic	[View on UCSC Genome Browser {Cornell Mirror}]

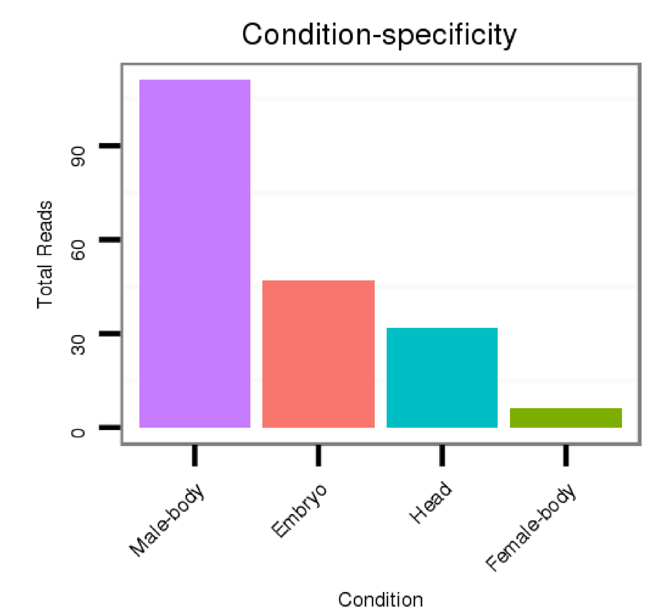
Legend: mature star mismatch in alignment mismatch in read

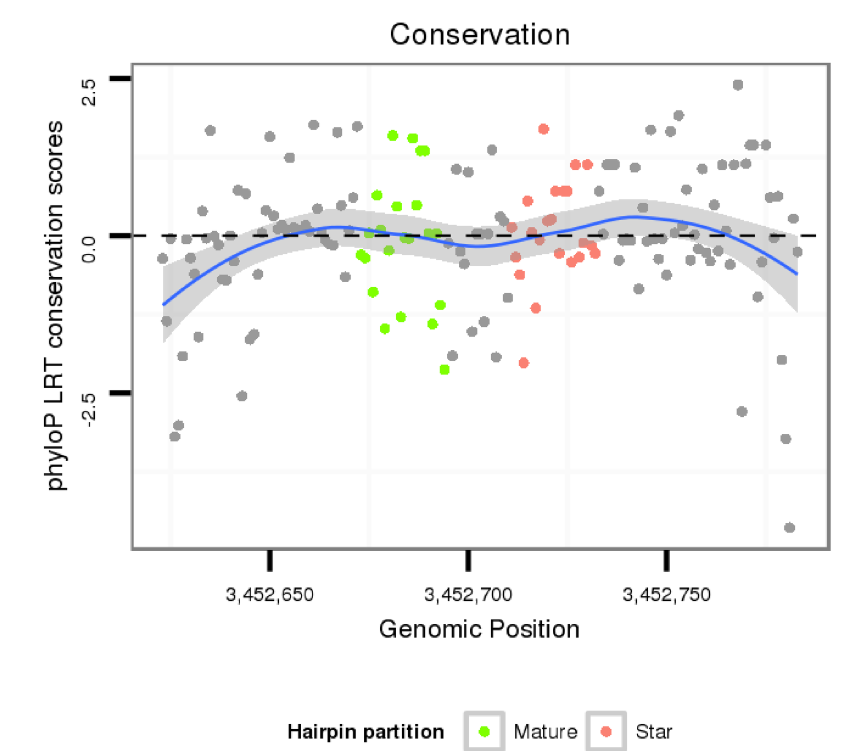
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAAATTAAGTGAAACGACACAACAGAAATATAATAATAATCTACAAATATTGAGATAAATACGAATATTTTGTTATATTTAAATCAAAATTATTTGTATTTATCTTCAATTATTTGTATGTACATCACAAAAAGGAAGAAAAAGAAAAAAAATTAAATTCAA ***********************************......((((((((((((((((((((((((((((((((((...........))))).)))))))))))))))).)))).))))))))).......***********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	V118 embryo	V119 head	M020 head	M045 female body
....TGAGATAAATACGAATATTTTG..	22	0	1	79.00	79	33	35	3	6	2
....TGAGATAAATACGAATATTTT...	21	0	1	78.00	78	58	4	15	0	1
....TGAGATAAATACGAATATTT..	20	0	1	15.00	15	13	0	2	0	0
....ATTATTTGTATTTATCTTCAAT...	22	0	1	10.00	10	2	4	0	4	0
....TGAGATAAATACGAATATTTTGT...	23	0	1	4.00	4	3	1	0	0	0
....GAGATAAATACGAATATTTTGT...	22	0	1	2.00	2	2	0	0	0	0
....TGAGATAAATACGAATATTTAA..	22	2	1	2.00	2	2	0	0	0	0
....AATTATTTGTATTTATCTTCAAT...	23	0	1	2.00	2	0	0	0	2	0
....ATTATTTGTATTTATCTTCAATT..	23	0	1	1.00	1	0	1	0	0	0
....AAATTATTTGTATTTATCTTCAAT...	24	0	1	1.00	1	0	0	0	0	1
....GAGATAAATACGAATATTTT...	20	0	1	1.00	1	0	1	0	0	0
....AAATTATTTGTATTTATCTTCAATT..	25	0	1	1.00	1	0	0	0	0	1
....AATTATTTGTATTTATCTTCAA..	22	0	1	1.00	1	0	0	0	0	1
....ATTATTTGTATTTATCTTCAATG..	23	1	1	1.00	1	0	0	0	1	0
....ATTATTTGTATTTATCTTCAATA..	23	1	1	1.00	1	0	0	1	0	0
....GAGATAAATACGAATATTTTG..	21	0	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

TTTTAATTCACTTTGCTGTGTTGTCTTTATATTATTATTAGATGTTTATAACTCTATTTATGCTTATAAAACAATATAAATTTAGTTTTAATAAACATAAATAGAAGTTAATAAACATACATGTAGTGTTTTTCCTTCTTTTTCTTTTTTTAATTTAAGTT ***********************************......((((((((((((((((((((((((((((((((((...........))))).)))))))))))))))).)))).))))))))).......***********************************	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
droWil2	scf2_1100000004513:3452623-3452783 +	dwi_87	AAAATTAAGTGAA------ACG-ACAC-AACAGAAATATAATAATAATCTACAAATATTGAGATAAATACGAATATTTTGTTATATTTAAATCA---------AAATTATTTGTA---------------------TTTATC-------------------------TTCAATTATTTGTATG--------------------TA--CATCACAAAAAGGAAGAAAAAGAAA-----AAAATTAAATTCA---A
droVir3	scaffold_12472:204596-204750 -		AAATAATACA-AA------------------AGCAATTTGAAAATGAAC---AAGAAAAAGAAAATGAAACAGGAAATATTTTAACAACATAAAATTCATGCAGAAATACGCT---ATTATTATTTATGCAGAAATACAATTATTTATG--------------TGTA------AA------AA-----ATGCA-AAATAAAAAA-----AAAAAAA---A
droMoj3	scaffold_6473:10865511-10865657 -		AATATTATCTATA-----AGCGAT-A-TCAATGAAAT-----------CTATATGCATCTTGTTAA-------------------------TAA---------AGTGTTTAGTTTATAAAAATTAAATAAATGAAATTAATA-------------------------TGAAAATATTTTAGAGTG-----------------CTTA---AAAAAAAAAA-----ATAAAATAAAAAAAAA-----AAAATAA---A
droGri2	scaffold_14592:11514-11672 +		AAATATAAATATA-------AATA-T-AAATATAAATATAAATATAAAGTATAAATATAAATATAAATATAAATA---TAAATATAAATAG----AAATATAAATATAAATATAAATATAAATATAAATATAAGTATGAGTATAAATA------------TAAGTATAAATAT-----AAATATAAATATA---A
dp5	Unknown_singleton_2584:781-845 +		ACAACAAAAA---C-GT----------AAAAAT-----------AATCCTCAACTATCTAGACCAATCTAAA-----------------------------ATC----CTTCACT--ACATATA---A
droPer2	scaffold_0:3771800-3771839 +		TATGTACGA-------------T-A-CCATTAA--AAAAAAAAAAAAA-----AAATTAA---A
droAna3	scaffold_13248:2215584-2215620 +		ATAACACAAA--CAA-----AAAAAAAAAAAAAAA-----GAAAAAA---A
droBip1	scf7180000395994:59986-60044 -		CCTCAAAAATATA-------TATG-T-TGG--CCAA--AAAAAAGAG-----AAAAAAAAAG-----AAAATTGAATGGA---A
droKik1	scf7180000302808:48232-48319 -		TAAACTAAAT---T---TTTTTGT-----------------------------------ATTCATTACA---------------CCTGTATCTTCTATTTGAACCTA---AAAACTAAAA-----AGAAATCAAGACAAAA-----AAATTAAATTT
droEle1	scf7180000488940:865-991 +		AAAAATAAGA---GAAA----C--AC-AATAAAAACACAAAACCAATC----------TAGACCGATAAGAA------------------------AAA----C------A---------------------C-----AGGAAAATTTTTTTACAACACTAACA---------------GACTTA---ACACAAAAATTCACAACAAAAAC-----AAACTTAAACACA---A
droBia1	scf7180000300750:1504-1640 +		ATATAAATAT---AAT--------------------AATATATAAATATTTATATAAATATAAATATGTATAAATATATATATAA---------AAA--AATAGTA--------------------T-----A---TAAATATAAATATAAAT--AAATATAAATATAA---------ATAAATA-----------T--AAATATAAAT-----AAATATATATATA---G
droTak1	scf7180000415846:426388-426421 +		CAAAAAAAAA--ACAAAAAAAAAAAAATG-----CAATAAA---A
droEug1	scf7180000405004:46214-46235 -		AAAAACAAAA---AATT---ATCGTTA---G
dm3	chrUextra:12587316-12587366 -		ATAAAAACGA---TTACTCTATAACGTGCAAATTA---------AAATTTTACT---ATTTATT---T
droSec2	scaffold_0:16592045-16592148 +		ATGCGCACAT---TTTTATGCAT----------------------AA-------ATTTTGACATT---------------------TGTTTGCTCTTTGGTT----CCTC---TTCAC--GTTTTTATG--------------------TCA--CACCGCAAAA-----ATGAAAGAAAAGAAAA-----AAACGAA---A
droYak3	2R:791842-791942 +		ATATTTATTTATA-------CGTA-T-TTATTTATAT---------------TTATTTGTATTTATTTA--TATTTATTTA--TAATTATTTATAA----TTATTTATATTTATTTATAATTATTTATA-------------------------------TTT---A
droEre2	scaffold_4784:14503407-14503515 -		GAAAAATATT---TAA--------------------GATCACCAAACATTTGTATCGAACTAAATATCTTGTGACATTTAAATTA---------TC---ATTCGTA--------------------T---CTCCAAATAAT------------------------------AT-----TAAATGTAATTTATTA-----AAAAAAG---G

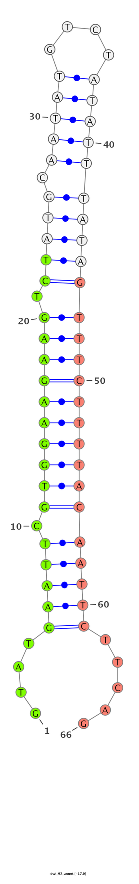
Generated: 09/08/2015 at 07:54 PM

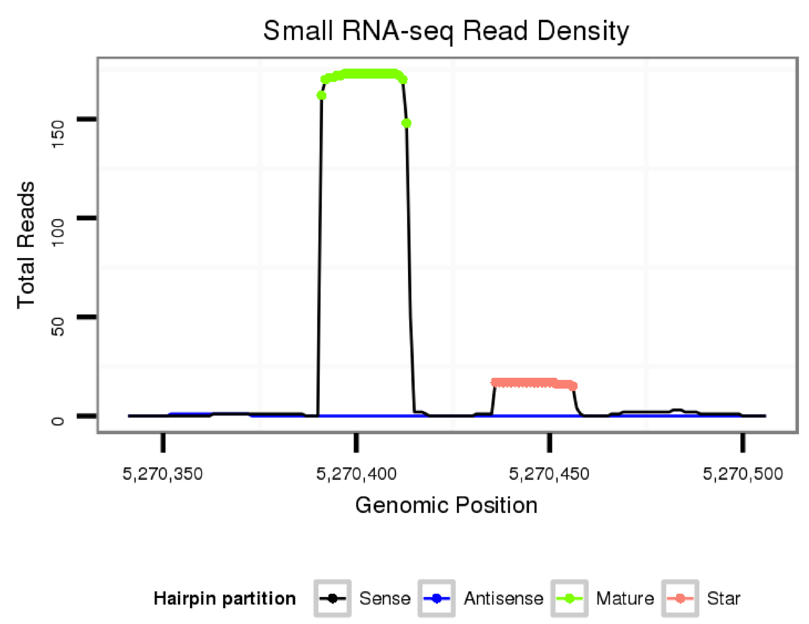
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

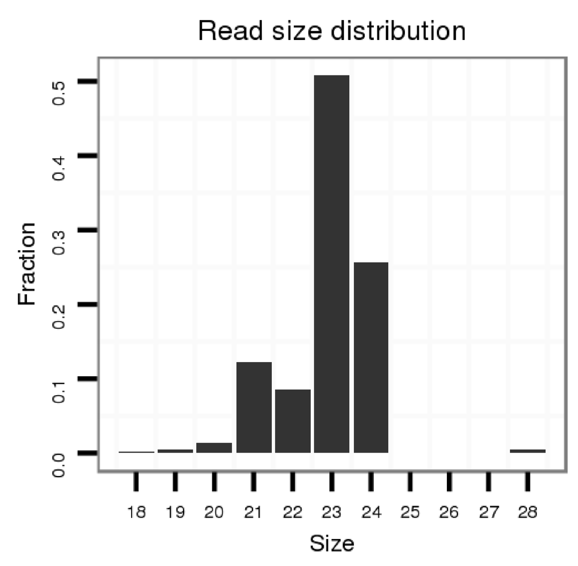
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_92	scf2_1100000004943:5270391-5270456 +	confident	Mirtron	intron	[View on UCSC Genome Browser {Cornell Mirror}]

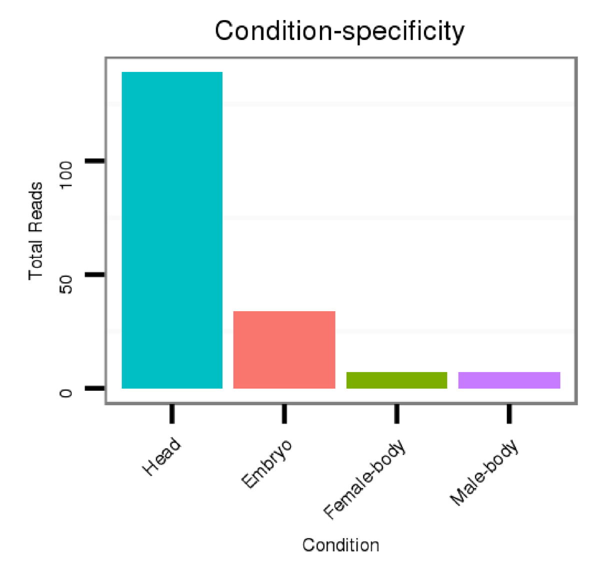
Legend: mature star mismatch in alignment mismatch in read

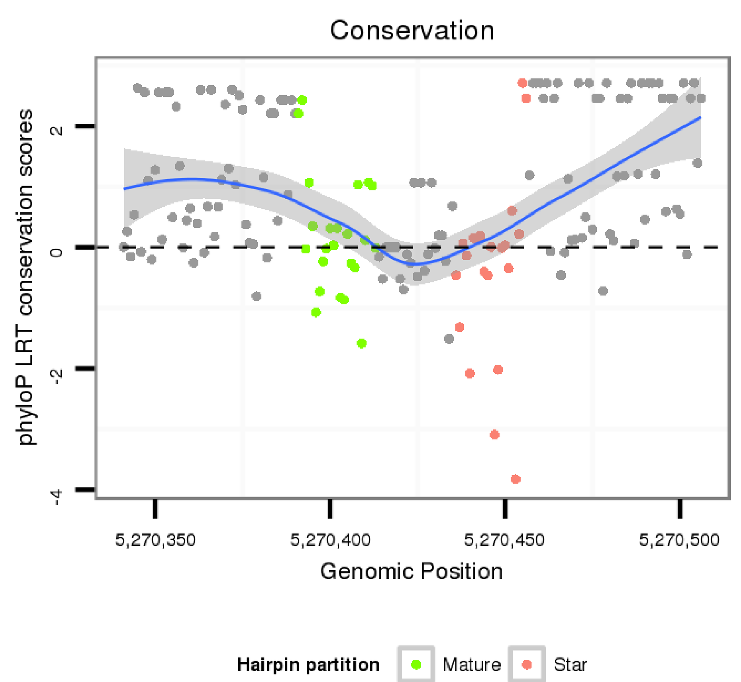
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK13868-in]; CDS [Dwil\GK13868-cds]; CDS [Dwil\GK13868-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GCCGATTCAAAGTTCCATCAATACTTTTCCAATACATCGAGTGCGTTTAGGTATGAATTCGTGGAAGAAGTCTATGCAATATGTCTATATTTATAGTTTCTTTTACAATTCTTCAGATATGTGGTAACAAATTATGGTTTTCGGGAATTATATAGAGGCATTGAAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V118 embryo	M045 female body	V119 head	V117 male body
....(((((.((((((((((.(((((.(((((....))))))))))))))))))))))))).....										
....GTATGAATTCGTGGAAGAAGTCT...	23	0	1	95.00	95	84	6	0	3	2
....GTTTCTTTTACAATTCTTCAGT...	22	1	2	59.00	118	46	47	11	12	2
....GTATGAATTCGTGGAAGAAGTCTA..	24	0	1	48.00	48	19	23	0	4	2
....GTATGAATTCGTGGAAGAAGTC..	22	0	1	15.00	15	14	0	0	1	0
....GTTTCTTTTACAATTCTTCAG..	21	0	1	11.00	11	5	3	3	0	0
....TATGAATTCGTGGAAGAAGTC..	21	0	1	7.00	7	7	0	0	0	0
....GTTTCTTTTACAATTCTTCAGC...	22	1	1	4.00	4	2	2	0	0	0
....GTTTCTTTTACAATTCTTCAGA...	22	0	1	3.00	3	0	0	2	1	0
....GTTTCTTTTACAATTCTTCAGG...	22	1	1	2.00	2	2	0	0	0	0
....GTATGAATTCGTGGAAGAAGTCG...	23	1	1	2.00	2	1	0	0	1	0
....GTATGAATTCGTGGAAGAAGT...	21	0	1	2.00	2	1	1	0	0	0
....GTATGAATTCGTGGAAGAAGTCC...	23	1	1	2.00	2	2	0	0	0	0
....ATTCGTGGAAGAAGTCTATGC...	21	0	1	1.00	1	0	0	0	0	1
....GAATTCGTGGAAGAAGTCT...	19	0	1	1.00	1	0	0	0	0	1
....TTATAGTTTCTTTTACAATTC...	21	0	1	1.00	1	0	0	1	0	0
....ATGAATTCGTGGAAGAAGTCT...	21	0	1	1.00	1	0	0	0	0	1
....GTTTCTTTTACAATTCTTCA...	20	0	1	1.00	1	0	0	1	0	0
....GTATGAATTCGTGGAAGAAG..	20	0	1	1.00	1	0	1	0	0	0
....CGGGAATTATATAGAGGC.......	18	0	1	1.00	1	0	1	0	0	0
....TATGAATTCGTGGAAGAAGTCT...	22	0	1	1.00	1	0	0	1	0	0
....GTATGAATTCGTGGAAGAAGTCTATGCA..	28	0	1	1.00	1	1	0	0	0	0
....GTTTCTTTTACAATTCTTCAGAT..	23	0	1	1.00	1	1	0	0	0	0
....AACAAATTATGGTTTTCGG......................	19	0	1	1.00	1	0	0	1	0	0
....AAATTATGGTTTTCGGGAAT..................	20	0	1	1.00	1	0	0	0	0	1
......................ACTTTTCCAATACATCGAGTGCGT..	24	0	1	1.00	1	0	1	0	0	0
....TCTTTTACAATTCTTCAG..	18	0	2	0.50	1	0	0	1	0	0
....TTTCTTTTACAATTCTTCAG..	20	0	2	0.50	1	0	0	1	0	0

Anti-sense strand reads

CGGCTAAGTTTCAAGGTAGTTATGAAAAGGTTATGTAGCTCACGCAAATCCATACTTAAGCACCTTCTTCAGATACGTTATACAGATATAAATATCAAAGAAAATGTTAAGAAGTCTATACACCATTGTTTAATACCAAAAGCCCTTAATATATCTCCGTAACTTG	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	M045 female body
....(((((.((((((((((.(((((.(((((....))))))))))))))))))))))))).....							
...........CAAGGTAGTTATGAAAAGGTT..	21	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004943:5270341-5270506 +	dwi_92	GCCGATTCAAAGTTCCATCAATACTTTTCCAATACATCGAGTGCGTTTAGGTATGAAT--TCG--------------------------------TGGAA---GAAG---TCTATGCAATATG----TCTATATTTA--T--------AGTTTCT------TTTACAATTCTTCAGATATGTGGTAACAAATTATGGTTTTCGGGAATTATATAGAGGCATTGAAC
droVir3	scaffold_12855:3453583-3453744 +		GCCGACTCGAAGTTCCATCAATATTTCTCCAATACGCAGAATGCGTTTAGGTAAGAGAG--TCACCTAC---GAATTCTCC----CGAGCCTCTGTCAATCAGT---CT------GTTGCACCTTTTCAGATATGTAGTCACCAACTATGGTTTTCGGGAGCTATACAGGGGCATTGAAC
droMoj3	scaffold_6540:7755281-7755437 +		GCCGACTCAAAGTTCCATCGTTATTTCTCCAATACGCCGAACGCGTTTAGGTAAGCGAAAGTA--AAGT-------------------TCTCTTC-----GATTCCGA---GATAAA----TTAT------ATAAATTTTTGTAGATATGTTGTCACGAATTACGGTTTTCGGGAACTATACAGAGGCATTGAAC
droGri2	scaffold_14906:6132961-6133130 +		GCCGACTCGAAATTCCATCAATATTTCTCCAATACGCAAAATGCGTTTAGGTGAGTAGCTGAC--AATA-------------------ATTTTTT-----GACTCTGC--AGAGGACTAAATAGAT--------------------------------------AATTTGT------GTGCTCCTATTTTAGATATGTAGTCAGCAATTATGGATATCGGGAACTATACAGGGGCATTGAGC
dp5	2:980755-980931 +		GCGGACTCGAAATTCCATCAACATTTCTCCAATACCTCAAATGCTTTCAGGTGAGA---TCCGCAGCACTCGCAATATAGAAGCAA---------------------TAATATAGC-----------------AAA--------------TAATGA-----AACGCG---ATATT------TGAATCAATATCCAGATATGTAGTGGCCCATCATGGATACAGGGAGCTCTACAGGGGTATAGAAC
droPer2	scaffold_7:3767047-3767220 +		GCGGACTCGAAATTCCATCAACATTTCTCCAATACCTCAAATGCTTTCAGGTGAGA---TCCGCAGCACTCGCAATATAGAAGCAA------------------------TATAGC-----------------AAA--------------TAATGA-----AACGCG---ATATT------TGAATCCCTATGCAGATATGTAGTGGCCCATCATGGATACAGGGAGCTCTACAGGGGTATAGAAC
droAna3	scaffold_13340:20862628-20862841 +		GCGGACTCCAAGTTCCATAAATACTTCTCCAACACACCCAACGCATTCAGGTGATTTGAAGTAGTGGTGTCAT------------AATAATGGCTAACGACTAAAGCTAACAATGACCAAATAGCAATTTATTCGTTC--AATTAGAAA---------GCG---CTTTATCAAGTTCTTTATTTTTCCAGGTATGTAGTGGCAAACCATGGATACCGAGAGCTCTACAGGGGATTAGAAC
droBip1	scf7180000396413:1542789-1542969 -		GCGGATTCCAAGTTCCATCAACATTTCTCCAACACAACCAACGCATTCAGGTAACCAG---TAAAGCTAACAAAGACTGAGCAACGATTTATTGGTTC-----C--ACTATGATATAATCATGGC-T------TTTATTCCTTTCCAGGTATGTGGTGGCAAACCATGGCTACCGGGAGCTCTACAGGGGATTAGAAC
droKik1	scf7180000302261:315302-315468 -		GCGGACTCCAAGTTTCACCAGCACTTTTCCAACACACCGAATGCATTCAGGTGAGTGTT--TGCCT---TA---CTT--------------------------------TTTAGCTTATGA--------------------A--------------TGTGAAAG-----TTAATACTTAAT------CTTATCATCTGTTAGGTATGTGGTAACCCATCATGGTTACCGGGAACTATACAGGGGAATAGAAC
droFic1	scf7180000454073:3469521-3469775 -		GCCGACTCCAAGTTCCACCAGCACTTCACCAACACACCCAACGCATTCAGGTGAGCAGGGGAAATGGAATCCCGTGAGACCACTCAACCTTAGC-------TAAAGCAAA---------------TGTTTATTCATCCAATTTCCAAGCAAATTATAATCGCTTGGTTCAAGAGGCGCCCCCTCG---AAATTCCCA----ACACACTC-------TTA--A--------C-GTTGC------TATTTTGTCCCCCAGGTATGTGGTGGCCAACCACGGCTATCGGGAGCTCTACAGGGGACTTGAAC
droEle1	scf7180000491280:2152216-2152295 +		TA---TCTAAACTTG---TAC------TTTCTTATCTCGCAGGTATGTGGTGGCCCACCATGGCTTTCGGGAGCTCTACAGGGGACTTGAAC
droRho1	scf7180000765878:252-335 -		ATA----------------CCCACATTTACAA--TAC------TTTATCATCCCGCAGGTATGTGGTGGCCCACCATGGCTATCGGGAGCTCTACAGGGGACTTGAAC
droBia1	scf7180000302113:1521245-1521296 -		GCGGACTCCAAGTTCCACCAGCACTTCTCCAACACACCGAATGCATTCAGGT--
droTak1	scf7180000415765:279482-279581 +		AAGAAT----------ATAACCAACTCACCCACAC---TTG--C--------A-TTTAC------TTAATTATCCCCCAGGTATGTGGTGGCCCACCATGGCTATCGGGAGCTCTACAGGGGACTCGAAC
droEug1	scf7180000409555:354388-354466 +		TCATAATTTTATTTACTT---TACTTTCTCAGGTATGTGGTAACCCACTATGGCTATCGGGAGCTCTACAGGGGACTTGAAC
dm3	chr3R:25873316-25873478 +		GCGGACTCCAAGTTCCACCAGCACTTCTCCAACACACAAAACGCATTCAGGTGAGCTGA---CGGATCTTTAAGTTTGCTAATGGGATCTTCTTATGGCTT------TTAATCATTCCACAGGTATGTGGTTTCCCACCACGGCTACCGGGAGCTCTACAGGGGACTCGAAC
droSim2	3r:25219647-25219852 +		GCGGACTCCAAGTTCCATCAGCACTTCTCCAACACACAAAACGCATTCAGGTGAGCAGG--TGACC---GAAG---T--------------------------------TTATGTCTGTGAGAGATGCGGATAGATAGCTGCCGGGTCTTTAACTTTGCGAACGTCATTTCCTTATGGCTT------TTTACCATTCCCCAGGTATGTGGTATCCCACCACGGGTACCGGGAGCTCTACAGGGGACTCGAAC
droSec2	scaffold_4:4719417-4719622 +		GCGGACTCCAAGTTCCATCAGCACTTCTCCAACACACAAAACGCATTCAGGTGAGCAGG--TGACC---GATG---T--------------------------------TTATGTCTCTGAGAGATGCGAAAAGATAGCTGAGGGATCTTTAACTTTGTGAACGTCATCTTCTTATGGCTT------TTTACCATTCCCCAGGTATGTGGTATCCCACCACGGGTACCGGGAGCTCTACAGGGGACTCGAAC
droYak3	3R:26796382-26796547 +		GCGGACTCCAAGTTCCATCAGCACTTCTCCAACACACCAAACGCATTCAGGTGAGCAGGGCAA--A--------------------CGTATGTTTGTGGT-----------------AAA--------------TAGAAA-----AGTTCTTATGTCTT------TTTATGCTTCCGCAGGTATGTGGTATCCCACCACGGCTACCGGGAGCTCTACAGGGGACTTGAAC
droEre2	scaffold_4820:2133997-2134201 -		GCGGACTCCAAGTTCCATCAGCACTTCTCCAACACACCAAACGCATTCAGGTGAGCAGAACAA---AGGCGACTATAGGTCACCATACGTATGTTTGTGATAGA------------------CGGATCTTTCACTTTGAGAAATACAATTTCTTATGGCAT------TTTATCATTCCGCAGGTATGTGGTATCCCACCACGGCTACCGGGAGCTCTACAGGGGACTTGAAC

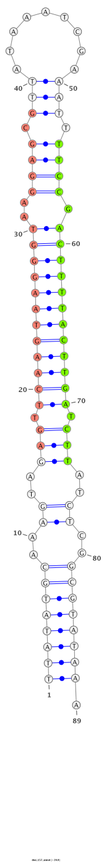
Generated: 09/08/2015 at 10:34 PM

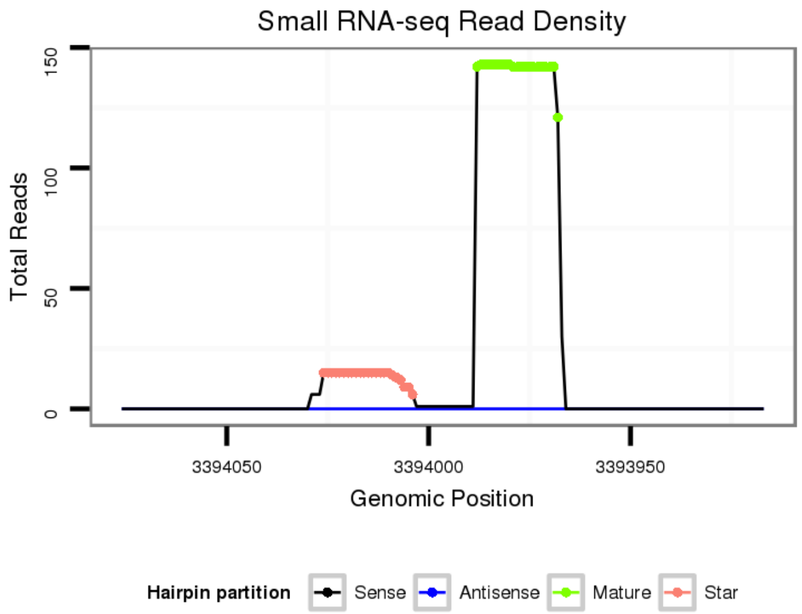
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

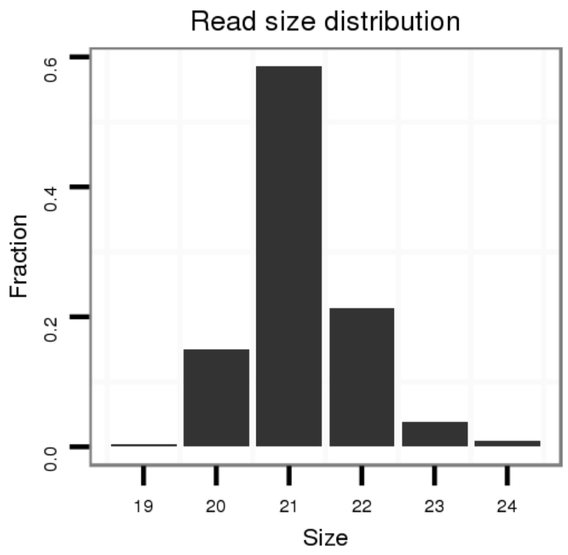
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_157	**scf2_1100000004511:3393967-3394026 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

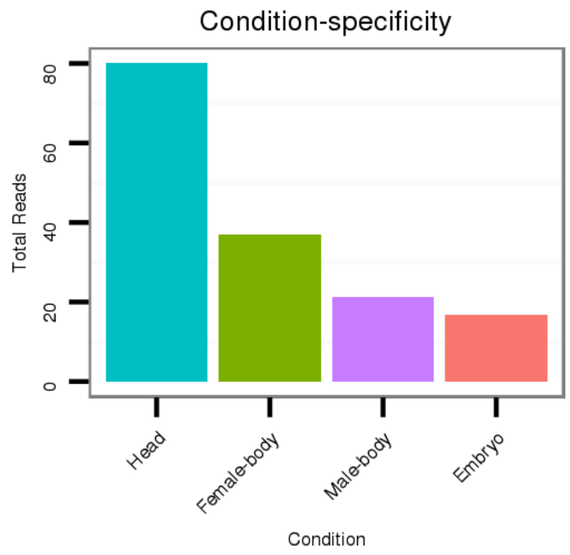
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

mature	star
1. dwi_194 scf2_1100000004511:3392895-3392915 - 2. dwi_72 scf2_1100000004511:3393111-3393131 - 3. dwi_157 scf2_1100000004511:3393968-3393988 -	1. dwi_72 scf2_1100000004511:3393147-3393169 - 2. dwi_192 scf2_1100000004511:3393720-3393742 - 3. dwi_157 scf2_1100000004511:3394004-3394026 - 4. dwi_190 scf2_1100000004511:3394936-3394958 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTAAGTGATCATCGCAGGATCATAAAAATCATATCTTATATGCAAAGTAGAGTTCAAGTAAGGGTAAGGAGCGTTATAAATCGAAATTTTCCGACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTAAGAGAAAAACTAAGTGATCGTCGCAGG **********(((((((..((..(((.(((((((((((..((((.(((.........))).))))).))))))))))).)))..))..)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	M045 female body	V117 male body	V118 embryo	V119 head
..........TTCCGACTTTTACTTGATCTT..........	21	0	3	90.00	270	165	62	24	11	8
..........TTCCGACTTTTACTTGATCTTA..........	22	0	3	30.00	90	5	35	15	35	0
..........TTCCGACTTTTACTTGATCT..........	20	0	3	21.00	63	55	3	4	0	1
..........AGTTCAAGTAAGGGTAAGGAGCG..........	23	0	4	6.00	24	0	3	15	6	0
..........TTCCGACTTTTACTTGATCTTAA..........	23	1	3	4.67	14	2	10	0	1	1
..........TAGAGTTCAAGTAAGGGTAAGGA..........	23	0	4	3.50	14	0	0	5	9	0
..........AGTTCAAGTAAGGGTAAGGAGC..........	22	0	4	3.00	12	0	2	9	0	1
..........TAGAGTTCAAGTAAGGGTAAGG..........	22	0	4	1.75	7	0	0	6	1	0
..........TAGAGTTCAAGTAAGGGTAAG..........	21	0	4	1.75	7	0	0	7	0	0
..........TCCGACTTTTACTTGATCTT..........	20	0	3	1.67	5	0	5	0	0	0
..........TTATAAATCGAAATTTTCCGACTT..........	24	0	2	1.50	3	3	0	0	0	0
..........TAGAGTTCAAGTAAGGGTAA..........	20	0	4	1.00	4	0	0	3	1	0
..........TTCCGACTTTTACTTGATCTTC..........	22	1	3	0.67	2	1	1	0	0	0
..........AGTTCAAGTAAGGGTAAGGA..........	20	0	4	0.50	2	0	0	2	0	0
..........AGTTCAAGTAAGGGTAAGGAG..........	21	0	4	0.50	2	0	1	1	0	0
..........TTCCGACTTTTACTTGATCTTT..........	22	1	3	0.33	1	0	0	0	1	0
..........TCCGACTTTTACTTGATCTTAA..........	22	1	3	0.33	1	0	1	0	0	0
..........TTCCGACTTTTACTTGATCTC..........	21	1	3	0.33	1	1	0	0	0	0
..........TCCGACTTTTACTTGATCTTA..........	21	0	3	0.33	1	0	1	0	0	0
..........TTCCGACTTTTACTTGATC..........	19	0	3	0.33	1	0	0	0	0	1
..........TTCCGACTTTTACTTGATCC..........	20	1	3	0.33	1	1	0	0	0	0
..........CGACTTTTACTTGATCTTATCTA..........	23	1	3	0.33	1	0	0	0	1	0
..........TTCCGACTTTTACTTGATCG..........	20	1	3	0.33	1	1	0	0	0	0
..........TAGAGTTCAAGTAAGGGTAAGGAA..........	24	1	4	0.25	1	0	0	0	1	0
..........AGTTCAAGTAAGGGTAAGG..........	19	0	4	0.25	1	0	0	1	0	0
..........AGAGTTCAAGTAAGGGTAAG..........	20	0	4	0.25	1	0	0	1	0	0
..........TAGAGTTCAAGTAAGGGTAAA..........	21	1	9	0.11	1	0	0	1	0	0

Anti-sense strand reads

GATTCACTAGTAGCGTCCTAGTATTTTTAGTATAGAATATACGTTTCATCTCAAGTTCATTCCCATTCCTCGCAATATTTAGCTTTAAAAGGCTGAAAATGAACTAGAATAGAGCCGCATATTTTTTGAGAATTCTCTTTTTGATTCACTAGCAGCGTCC **********(((((((..((..(((.(((((((((((..((((.(((.........))).))))).))))))))))).)))..))..)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V119 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3393917-3394076 -	dwi_157	CTAAGTGATCATCGCAGGATCATAAAAATCATATCTTATATGCAAAGTAGAGTTCAAGTAAGGGTAAGGAGCGTTATAAATCGAAATTTTCCGACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTAAGAGAAAAACTAAGTGATCGTCGCAGG

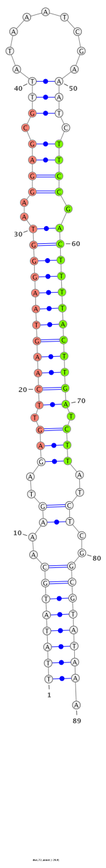
Generated: 09/08/2015 at 08:00 PM

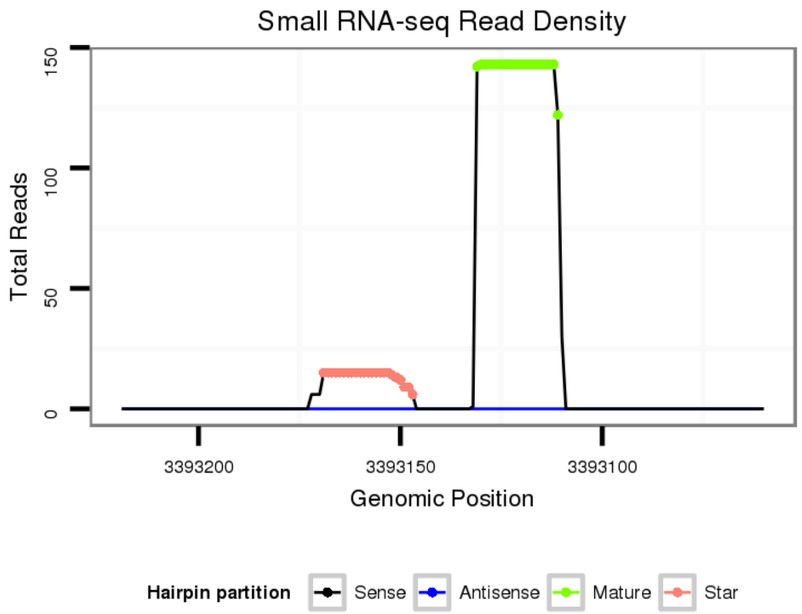
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

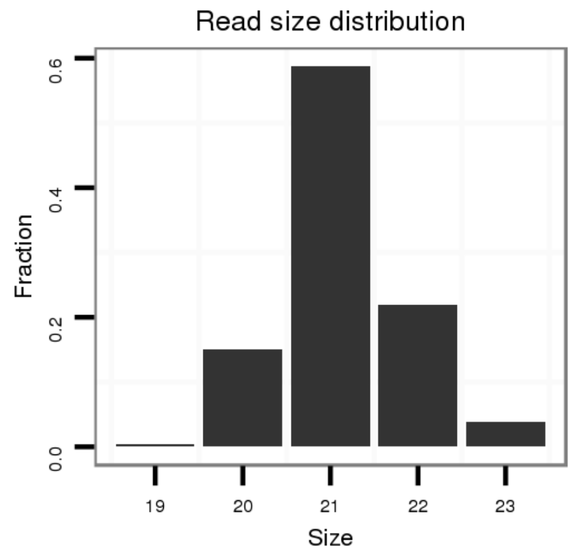
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_72	**scf2_1100000004511:3393110-3393169 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

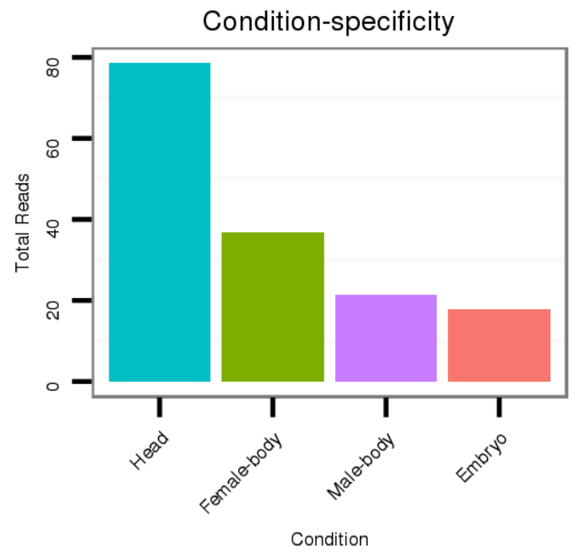
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

mature	star
1. dwi_194 scf2_1100000004511:3392895-3392915 - 2. dwi_72 scf2_1100000004511:3393111-3393131 - 3. dwi_157 scf2_1100000004511:3393968-3393988 -	1. dwi_72 scf2_1100000004511:3393147-3393169 - 2. dwi_192 scf2_1100000004511:3393720-3393742 - 3. dwi_157 scf2_1100000004511:3394004-3394026 - 4. dwi_190 scf2_1100000004511:3394936-3394958 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTAAGTGATCGTCGCAGGATCATAAAAATCATATCTTATATGCAAAGTAGAGTTCAAGTAAGGGTAAGGAGCGTTATAAATCGAAATCTTCCGACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCATAAAAAAAATACAAATCAACATTTTTCTA **********(((((((..((..(((.(((((((((((..((((.(((.........))).))))).)))))))))))).)))..))..)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	M045 female body	V117 male body	V118 embryo	V119 head
.....TTCCGACTTTTACTTGATCTT.....	21	0	3	90.00	270	165	62	24	11	8
.....TTCCGACTTTTACTTGATCTTA.....	22	0	3	30.00	90	5	35	15	35	0
.....TTCCGACTTTTACTTGATCT.....	20	0	3	21.00	63	55	3	4	0	1
.....AGTTCAAGTAAGGGTAAGGAGCG.....	23	0	4	6.00	24	0	3	15	6	0
.....TTCCGACTTTTACTTGATCTTAA.....	23	1	3	4.67	14	2	10	0	1	1
.....TAGAGTTCAAGTAAGGGTAAGGA.....	23	0	4	3.50	14	0	0	5	9	0
.....AGTTCAAGTAAGGGTAAGGAGC.....	22	0	4	3.00	12	0	2	9	0	1
.....TAGAGTTCAAGTAAGGGTAAG.....	21	0	4	1.75	7	0	0	7	0	0
.....TAGAGTTCAAGTAAGGGTAAGG.....	22	0	4	1.75	7	0	0	6	1	0
.....TCCGACTTTTACTTGATCTT.....	20	0	3	1.67	5	0	5	0	0	0
.....CTTCCGACTTTTACTTGATCTT.....	22	0	1	1.00	1	0	0	0	1	0
.....TAGAGTTCAAGTAAGGGTAA.....	20	0	4	1.00	4	0	0	3	1	0
.....TTCCGACTTTTACTTGATCTTC.....	22	1	3	0.67	2	1	1	0	0	0
.....AGTTCAAGTAAGGGTAAGGA.....	20	0	4	0.50	2	0	0	2	0	0
.....AGTTCAAGTAAGGGTAAGGAG.....	21	0	4	0.50	2	0	1	1	0	0
.....CGACTTTTACTTGATCTTATCTA.....	23	1	3	0.33	1	0	0	0	1	0
.....TTCCGACTTTTACTTGATCTTT.....	22	1	3	0.33	1	0	0	0	1	0
.....TTCCGACTTTTACTTGATC.....	19	0	3	0.33	1	0	0	0	0	1
.....TTCCGACTTTTACTTGATCTC.....	21	1	3	0.33	1	1	0	0	0	0
.....TCCGACTTTTACTTGATCTTA.....	21	0	3	0.33	1	0	1	0	0	0
.....TTCCGACTTTTACTTGATCC.....	20	1	3	0.33	1	1	0	0	0	0
.....TTCCGACTTTTACTTGATCG.....	20	1	3	0.33	1	1	0	0	0	0
.....TCCGACTTTTACTTGATCTTAA.....	22	1	3	0.33	1	0	1	0	0	0
.....AGTTCAAGTAAGGGTAAGG.....	19	0	4	0.25	1	0	0	1	0	0
.....TAGAGTTCAAGTAAGGGTAAGGAA.....	24	1	4	0.25	1	0	0	0	1	0
.....AGAGTTCAAGTAAGGGTAAG.....	20	0	4	0.25	1	0	0	1	0	0
.....TAGAGTTCAAGTAAGGGTAAA.....	21	1	9	0.11	1	0	0	1	0	0

Anti-sense strand reads

GATTCACTAGCAGCGTCCTAGTATTTTTAGTATAGAATATACGTTTCATCTCAAGTTCATTCCCATTCCTCGCAATATTTAGCTTTAGAAGGCTGAAAATGAACTAGAATAGAGCCGCATATTTTTTGAGTATTTTTTTTATGTTTAGTTGTAAAAAGAT **********(((((((..((..(((.(((((((((((..((((.(((.........))).))))).)))))))))))).)))..))..)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	V118 embryo
Show Alignment With Reads							

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3393060-3393219 -	dwi_72	CTAAGTGATCGTCGCAGGATCATAAAAATCATATCTTATATGCAAAGTAGAGTTCAAGTAAGGGTAAGGAGCGTTATAAATCGAAATCTTCCGACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCATAAAAAAAATACAAATCAACATTTTTCTA

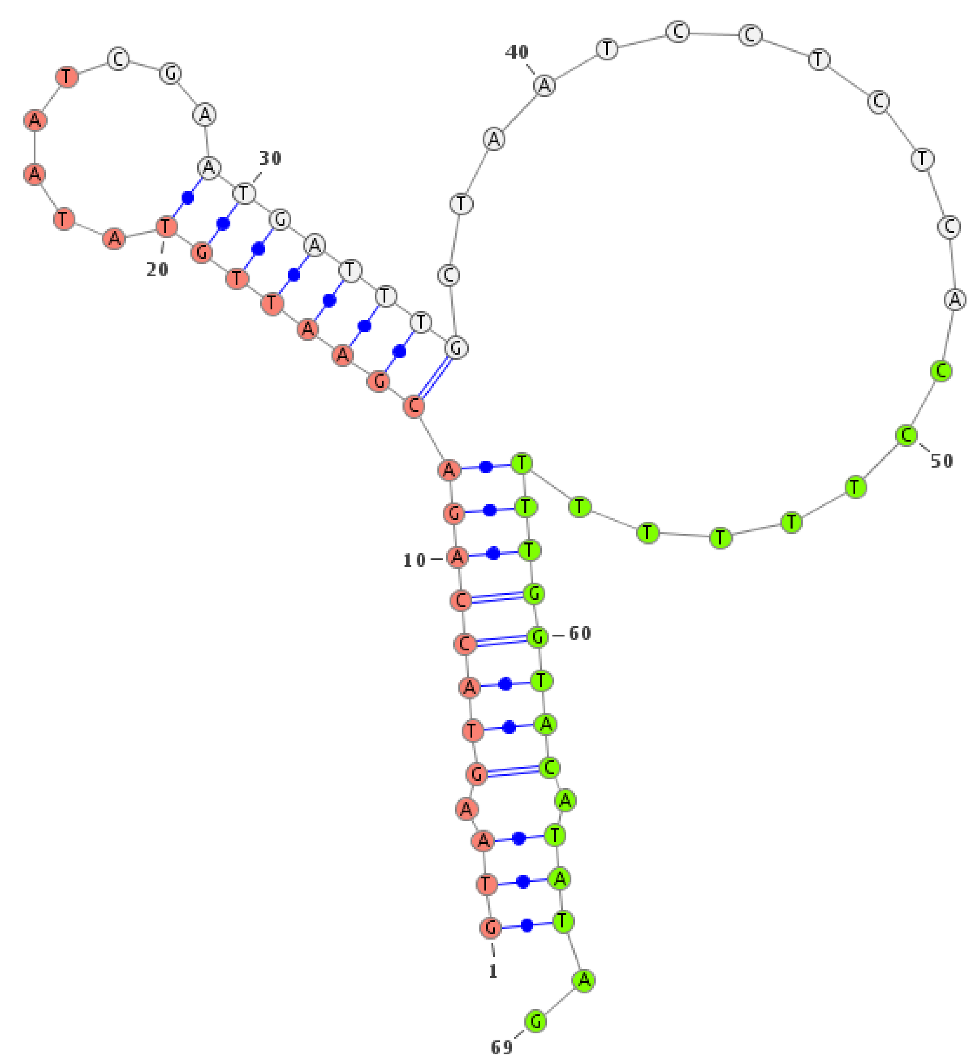
Generated: 09/08/2015 at 08:01 PM

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

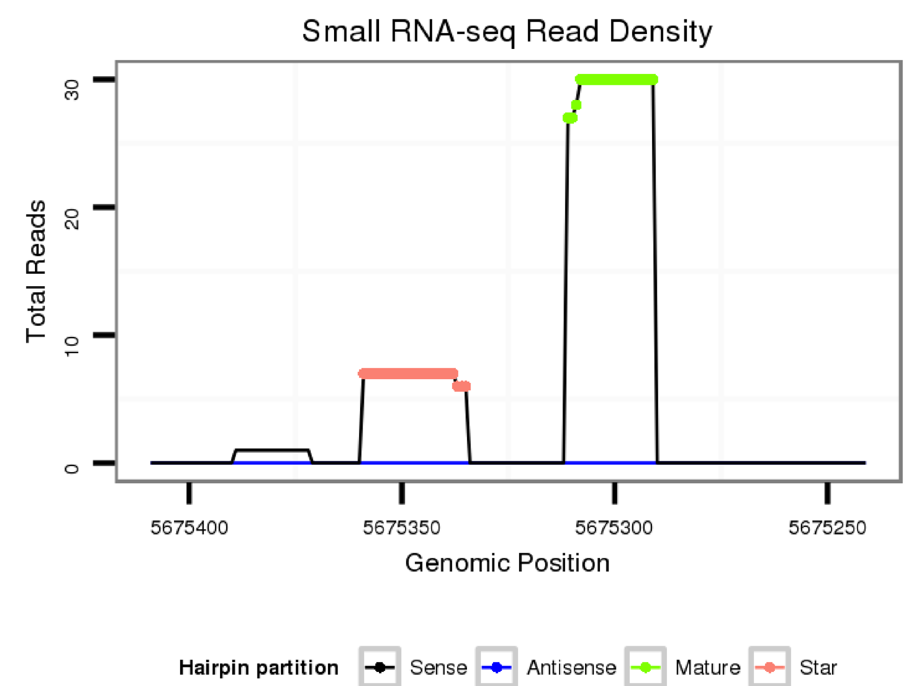
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_2068	**scf2_1100000004762:5675291-5675359 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

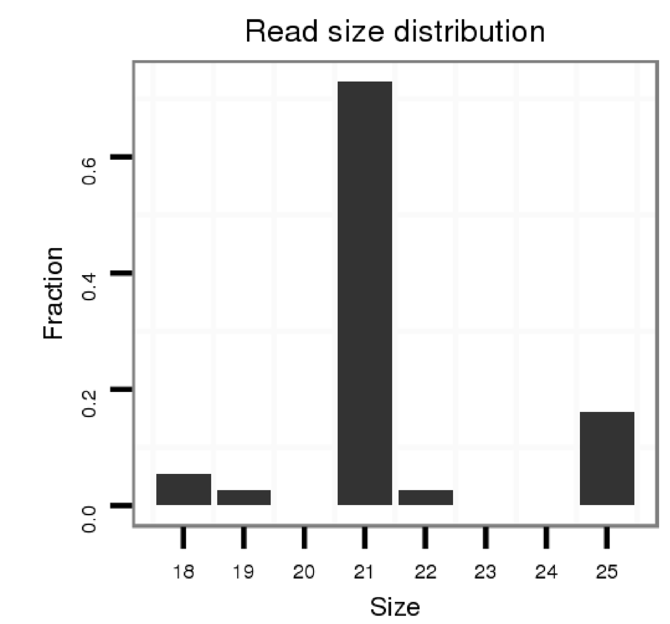
Legend: mature star mismatch in alignment mismatch in read

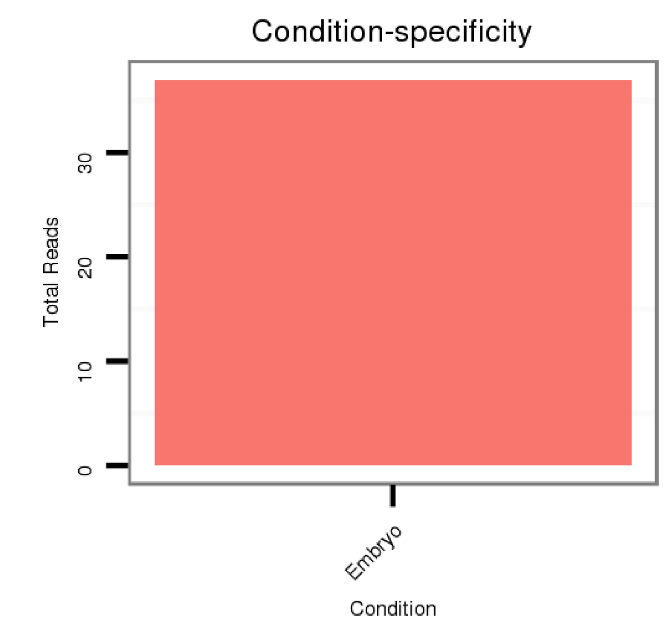
Predicted structure

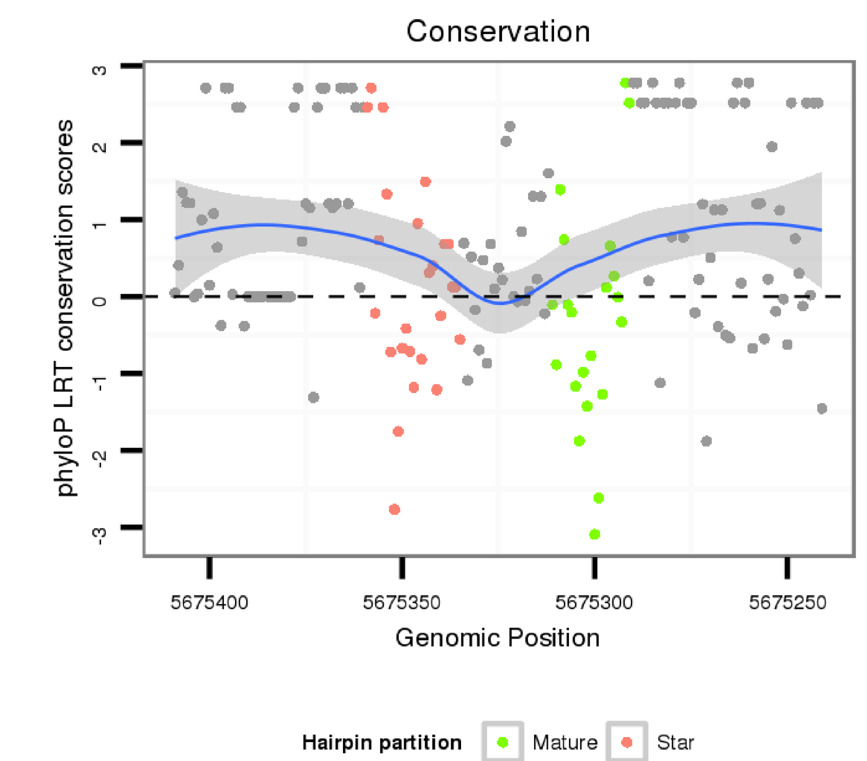


dwi_2068_annot [-10.8]









Show Alternate Folds

Flybase annnotation

intron [Dwil\GK25299-in]; CDS [Dwil\GK25299-cds]; CDS [Dwil\GK25299-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GCAGCAGCTAATTAATGGCAAAGAAACCGCTGATAATGATAATAAATCGGGTAAGTACCAGACGAATTGTATAATCGAATGATTTGCTAATCCTCTCACCTTTTTTTTGGTACATATAGAAGCCACAGCTGAAGCCAATGGTCAGGAGGAGTCTTCAGTTGATCCACCA **(((.((((((((((((((((........))))))))..................)))))))).)))..**	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	M045 female body	M020 head
....CCTTTTTTTTGGTACATATAG..	21	0	1	27.00	27	27	0	0
....GTAAGTACCAGACGAATTGTATAAT..	25	0	1	6.00	6	6	0	0
....TTTTTTTGGTACATATAG..	18	0	1	2.00	2	2	0	0
....................AAGAAACCGCTGATAATG...	18	0	1	1.00	1	1	0	0
....TTTTTTTTGGTACATATAG..	19	0	1	1.00	1	1	0	0
....GTAAGTACCAGACGAATTGTAT...	22	0	1	1.00	1	1	0	0

Anti-sense strand reads

CGTCGTCGATTAATTACCGTTTCTTTGGCGACTATTACTATTATTTAGCCCATTCATGGTCTGCTTAACATATTAGCTTACTAAACGATTAGGAGAGTGGAAAAAAAAACCATGTATATCTTCGGTGTCGACTTCGGTTACCAGTCCTCCTCAGAAGTCAACTAGGTGGT **(((.((((((((((((((((........))))))))..................)))))))).)))..**	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004762:5675241-5675409 -	dwi_2068	GCAGCAGCTAATTAATGGCAAAGAAACCGCTGATAATGATAATAAATCGGGTAAGTACCA-----------------GA-------------------------CG---AATTGTAT--AATC---------------GAATGATTTGCTAATCC--TCTCACCTTTTT-----------TTT---GGTACATATAGAAGCCACAGCTGAAGCCAATGGTCAGGAGGAGTCTTCA---GTTGATCCACCA
droVir3	scaffold_13049:8430554-8430705 +		GAAGCCGCTGACCAACGGC-----------GATGCGGATGCCAAGTCCGGTAAGTTGTTG---AGACAG-----CACTGCAT---AAAAA--------------CCCGATAGCT----- -- -------AACATTCACGCTTTACCTC---TAAATATATAGAAGCCACAGCTGAGGCGGCGCCCGGCGAGGACGC---A------GATCCGCCG
droMoj3	scaffold_6680:12085318-12085457 +		GAAGCAGCTGACCAACGGC-----------GATGCGGATGCCAAGTCGGGTAAGTAGAG-----------------AG--CGGCTGGACC--------TGTC---CCA----CAATTGCT----- -- ---AATGAAC-----------TGT---ATTCCAAATAGAAGCCACAGCTGAAGCAGCGGCTGCTGAGGATGC---A------GATCCGCCA
droGri2	scaffold_15110:7462090-7462231 +		GAAGCAACTAAACAATGGC-----------GATGCGGATGCCAAGTCGGGTAAGTTTGG-----------------AAG--AAACATACT-GAAAACTGATGCAATAGCT----- -- -------AATCCC-----------GA---TTCCCAAACAGAAGCCACCGCTGAAGCTGCCGCTGTCGAGGATGC---T------GATCCGCCG
dp5	XR_group8:4848100-4848249 -		GGCGC---TCGTAAATGGA-----------GACGCGGATGCCAAGTCGGGTATGTCATA-----------------G-------------A---TTTTCCT-GTTCATTTGTACGAGAACT----- -- -------AACCTGA---------GATTTTCATTTGCACAGAAGCCACTGCTGAAGCTGCCGCAGCGGAGGACGCAGCAGCCGTGGATCCGCCA
droAna3	scaffold_13337:13842479-13842620 -		ACAGC---TGGTTAATGGC-----------GATGCAGATGCCAAGTCGGGTAAGTTTCC-----------------AGAAAA----CCGGAAA--TATC--CTA-----------GTTC--TCTTACCAATCTGT---------GTC-----CTTTTTAGAAGCTACAGCCGAAGCTGCTCCCGCAGAAGATGCTGCC------GAGGCGCCC
droBip1	scf7180000395832:781674-781817 -		GCAGC---TGGTCAATGGC-----------GATGCTGATGCCAAGTCGGGTAAGTTTCC-----------------TAAAT----CCAGAGA---TGATTCTA-----------GTTC--TCTTACTAATCAT---------TGT---CCTTCTTTTAGAAGCTACAGCCGAAGCTGCTCCCGCAGAAGACGGTGCT------GAGGCGCCT
droKik1	scf7180000302577:1135253-1135442 +		ACAGT---TGGTTAATGGA-----------GATGCCGATGCCAAGTCAGGTGAGTTGAC-----------------TG--------GGTTTACTAAATATGGA-----------------------------------T---TTTGAGACCTTAGTCA---------TATT----------------------------------TT----TTAATTCCT-AAAAACGCAAT-TTG-----------AACT----- -- -------AATTTATAATC----TCTA---TATATTTACAGAAGCCACCGCTGAAGCCACCCCAGCTGAAGATGCCTCG---GAGGCACCGCCC
droFic1	scf7180000453839:2160743-2160951 +		ACAAC---TGGTCAATGGA-----------GATGCCGATGCCAAGTCGGGTGAGTAATTAAAT--------AATTCCTGAAATTATACAAGAAATGTTTAGGT---------AAA---AGGGA--------ATTC--------CTTTCATTCCT----------------TGTTCTATGATTTTAATATTTAGTAAATGTATT-TAA------------AACT----- -- -------AATTCAT---------ATT---TTAATTTGCAGAAGCGACAGCTGAAGCTGCTCCCGCTGATGATGC---C------GAAGCTCCT
droEle1	scf7180000491255:3194932-3195171 +		ACAGC---TGGTCAACGGA-----------GATGCTGATGCCAAGTCGGGTGAGTGCGTTTTTTAAGCTATAACTTTTG-------------------G---AAAGG----------GTTCAAAAATAA------------GT--------ATAAA---ACATA------AATTA---CG-----TCTTTCCTTAAAGATAAAGTACTATTATTCTATCCTTATAA------GATTATATGCCATGAATTAAACTATACCT----- -- -------ATGTCTT---------CTT---TTCATTTGTAGAAGCCACAGCTGAAGCTACACCCGCTGATGAAGCTTCC------GATCCACCG
droRho1	scf7180000778301:63788-63836 +		---AGAAGCCACAGCTGAAGCTACCCCCGCTGATGATGCATCC------GATCCACCT
droBia1	scf7180000302428:3345137-3345344 -		GCAGC---TGGTGAATGGA-----------GATGCCGATGCCAAGTCGGGTTAGTACATTGATT------C------T---------TT--ATTA-CTATTTACAAAAGGTGGAAATATTTTACTCATTTATACAGAATGTTTCGTACCA---TTTGAGATA-------ATAC--------CCTA--CAGT-GCG-----------AACT----- -- -------AATTCGT---------TTC---TCCATTTACAGAAGCCACAGCTGAAGCTACGCCTGGCGATGATGCCTCC------GATGCACCA
droTak1	scf7180000415352:603486-603629 -		GCAGC---TGGTGAACGGC-----------GATGCCGATGCCAAGTCGGGTTGGTATTTTTATA------A------------------A---------TT--TTAA-TTA---TAAT----CAAAAACT----- -- -------AATTTGA---------TGC---TCTCTTTATAGAAGCCACCGCAGAGGCTACGCCCGGCGATGATGCCTCC---GATGCTCCGCCA
droEug1	scf7180000409711:572916-573061 -		GCAGC---TGGTCAACGGT-----------GATGCCGATGCCAAGTCTGGTTAGTAAATA-----------------TGA---GATTATCTCTCTGGGATTAAGCTATAACT----- -- -------AATTTAT---------ATT---ATTGTTTACAGAAGCAACTGCTGAAGCTACTCCCGGTGATGATGCCTCC------GATGCACCA
dm3	chr3L:16767432-16767576 +		GCAGC---TGGTCAACGGT-----------GACGCGGATGCCAAGTCTGGTAAGTTAAA-----------------TCA---AAATAAGTTTTGTAAATCAAA------------C--TCTAAAAAATTTGC---------TTC---CATTTTTGCAGAAGCCACAGCTGAAGCAACGCCCGCTGAAGATGCCTCC------GATGCACCA
droSim2	3l:16358414-16358558 +		GCAGC---TGGTCAACGGT-----------GACGCGGATGCCAAGTCTGGTAAGTTAAA-----------------TAA---AAATACATTTTCTAAATCAAA------------C--TCTAAAAAATTCGC---------TTC---CATTTTTGCAGAAGCCACTGCTGAAGCTACGCCCGCTGAAGATGCCTCC------GATGCACCA
droSec2	scaffold_0:8839113-8839257		GCAGC---TGGTCAACGGT-----------GACGCGGATGCCAAGTCTGGTAAGTTAAA-----------------TAA---AAATACATTTTCTAAATCAAA------------C--TCTAAAAAATTCGC---------TTC---CACTTTTGCAGAAGCCACAGCTGAAGCTACGCCCGCTGAAGATGCCTCC------GATGCACCA
droYak3	3L:17300601-17300799 -		GCAGC---TGGTCAACGGA-----------GACGCAGATGCCAAGTCTGGTAAGCACATTTAATA----TTAT-------------AGAATACGCAAACG--TATTT---CG------T-ATTTCT----------------TGTTCTATCAAGTCA-----TA--GAACAGATTTCATAAAAAAAA------------TTTTCTAAAAAATCCTT---------TAT---CGTTTTTGCAGAAGCCACAGCTGAAGCTACGCCCGCTGAAGACGCCTCC------GATGCACCA
droEre2	scaffold_4784:17066243-17066449 -		GCAGC---TGGTCAACGGA-----------GACGCAGATGCCAAGTCTGGTGAGCACATTCAATA----TAATTCCCGT-----------------AG---AATGG---TAAAAACTATAGT----------------------------A---ATTGAGCGACTATC---TATACTATCAAGCCA-----TA--AAATAAATTCCATAATTCAAA-----------T--TTTAAAAAATC-C---------TA-----CCTTTTGCAGAAGCCACCGCTGAAGCTACGCCCGCTGAAGATGCCTCC------GATGCACCA

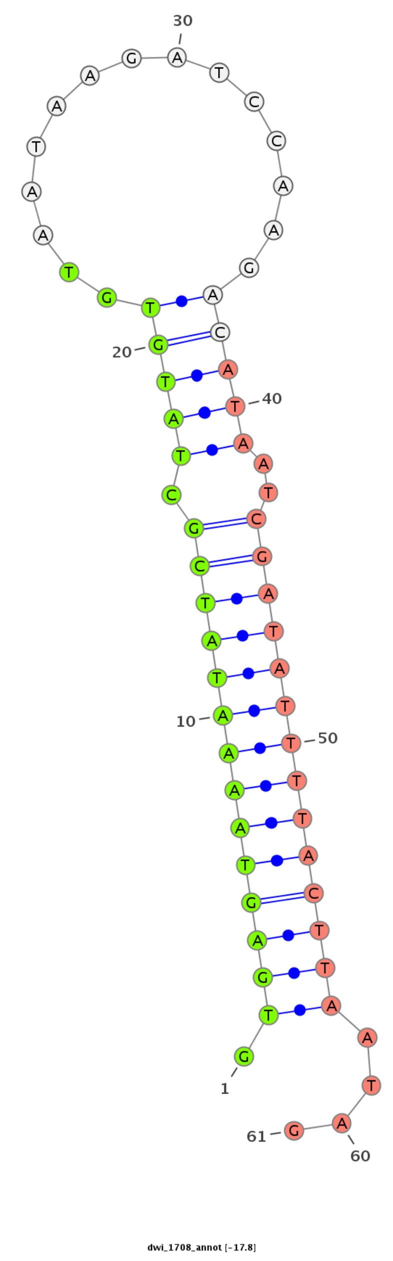
Generated: 09/08/2015 at 10:36 PM

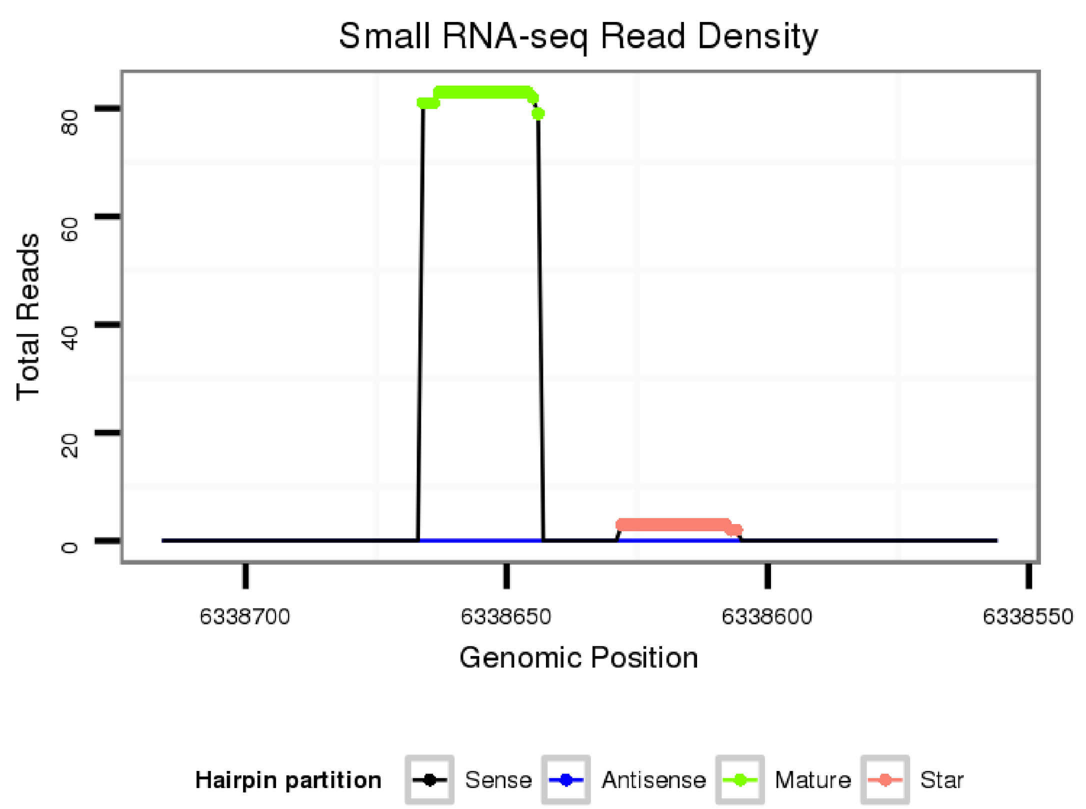
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	0
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

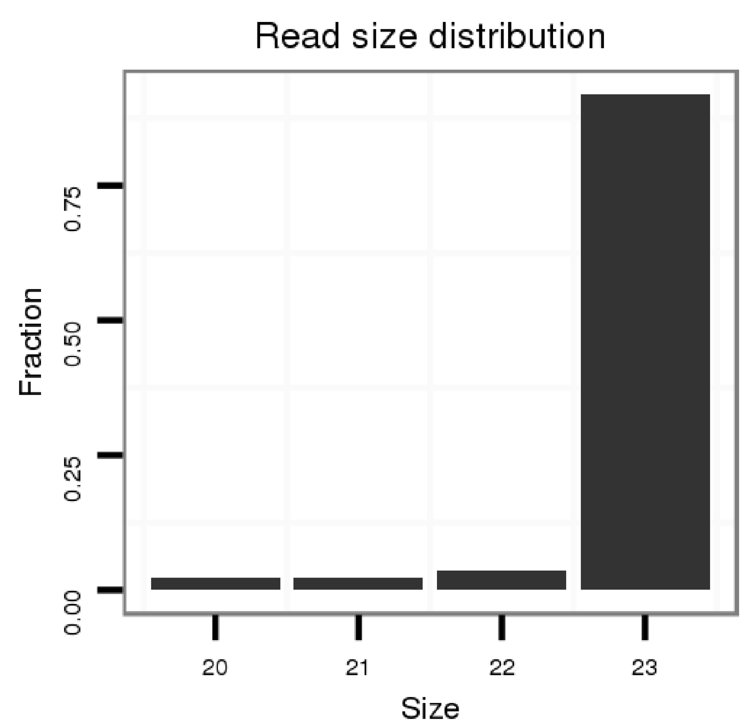
ID: dwi_1708	Coordinate: scf2_1100000004585:6338606-6338666 -	Confidence: confident	Class: Mirtron	Genomic Locale: intron	[View on UCSC Genome Browser {Cornell Mirror}]

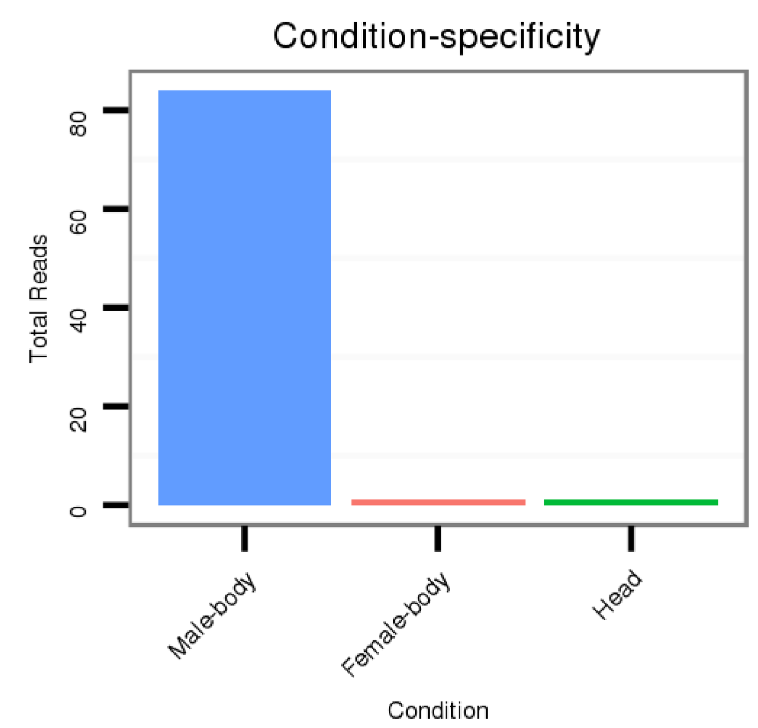
Legend: mature star mismatch in alignment mismatch in read

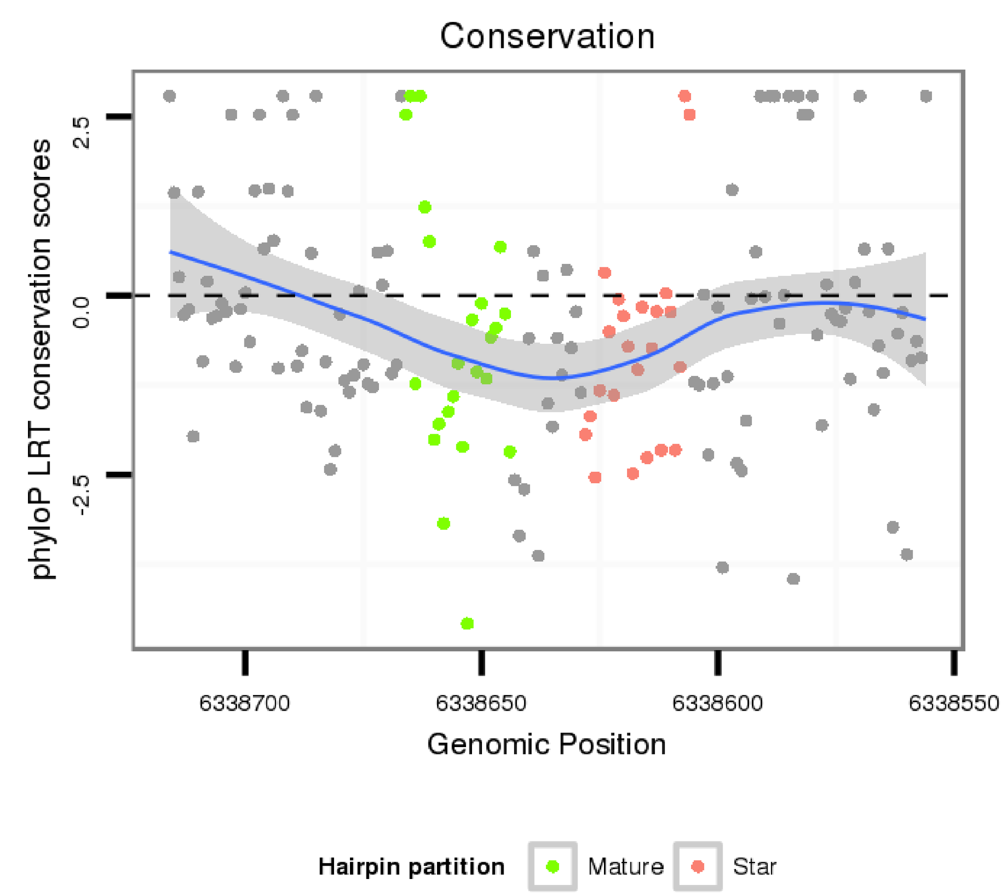
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK24266-in]; CDS [Dwil\GK24266-cds]; CDS [Dwil\GK24266-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAACGTTACCAGAGTTTTAGTAATATGCCCATGCTCAGAATGCGTCCAAAGTGAGTAAAATATCGCTATGTGTAATAAGATCCAAGACATAATCGATATTTTACTTAATAGTTATGATCTGAGAGATTATGTTTGGTGTAACTATGAGATCACGCCACCAA **.((((((((((((((.(((((...............)))))..))))))))))))))....**	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	V118 embryo	M045 female body	M020 head
....GTGAGTAAAATATCGCTATGTGT...	23	0	1	77.00	77	77	0	0	0
....GTGAGTAAAATATCGCTATGTG..	22	0	1	3.00	3	1	0	1	1
....GTGAGTAAAATATCGCTATGTGTC..	24	1	1	2.00	2	2	0	0	0
....AGTAAAATATCGCTATGTGT...	20	0	1	2.00	2	2	0	0	0
....ATAATCGATATTTTACTTAATAG..	23	0	1	2.00	2	2	0	0	0
....GTGAGTAAAATATCGCTATGT..	21	0	1	1.00	1	1	0	0	0
....ATAATCGATATTTTACTTAAT..	21	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

TTTGCAATGGTCTCAAAATCATTATACGGGTACGAGTCTTACGCAGGTTTCACTCATTTTATAGCGATACACATTATTCTAGGTTCTGTATTAGCTATAAAATGAATTATCAATACTAGACTCTCTAATACAAACCACATTGATACTCTAGTGCGGTGGTT **.((((((((((((((.(((((...............)))))..))))))))))))))....**	Read size	# Mismatch	Hit Count	Total Norm	Total	V119 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004585:6338556-6338716 -	dwi_1708	AAACGTTACCAGAGTTTTAGTAATATGCCCATGCTCAGAATGCGTCCAAAGTGAGTAAAATATCG--------C------------------------------TATGTGTAATAAGATCCAAGAC-------ATAA----TC--GA-------TAT------TT-TAC--TTAATAGTTATGATCTGAGAGATTATGTTTGGTGTAACTATGAGATCACGCCACCAA
droVir3	scaffold_12822:2358905-2359062 -		AAGCGGATGACCGGCCTGAGCAACATGCCCGTTAAGGAGATCAAGCCACAGTAAGATCAGTTCAG--------C------------------------------TGT---TAAGCGATAGATAGACATTTAATG--------------------TGA------TT-CCA--CTTGCAGCGAGAATATTAAGGATTATATTTGGTGCGAGTTCAAGGAGTCGGTGCCCA
droMoj3	scaffold_6496:21902978-21903136 +		AAGAACTACACCGGATTGAGCAATACGCCCGTCAGTAAATGCGTGGATCAGTAAGTTTCTGACCG--------GC-----------------------------TCA---AAAATGCTTCGGGGCT------------------TGAACA--AGTGG------CT-TTC--ATTTCAGTGGCCGCCTTCAGGACTATGTGTGGTGTCAGCATGAGCCGCTGCTCAGCA
droGri2	scaffold_14624:3277978-3278138 -		AAGCGTTTCACCGGCCTGAGCAATATGCCCGTTAAGGAGATCACGCCCAAGTAAGTCAAAGTTGG--------C------------------------------CACTTATATAT---ATATATATATA----TATG----TA--TA-------TAT------AT-AAA--TTTGTAGTGAGAAATAGCGGACTACATTTGGTGCGAGTTCGAGGAGTCTGTGCCGA
dp5	4_group4:4697619-4697787 -		AAGCGCTTCCAGAGCTTCAGCACAATGAAAGTGGTATCAGTGTTGGCCCAGTAAGTAAACCAAAT--------AT-----------------------------------TCGATAATCCAAAGACTCCTACTA---------CTATAAGTAT---TATTTTCA-CAT--CCCACAGCAAGGAAATGAAGGACTACGTGTGGTCGGTTCACGAGACGACGCCACTGA
droPer2	scaffold_49:436639-436807 +		AAGCGCTTCCAGAGCTTCAGCACCATGAAAGTGGTATCAGTGTTGGCCCAGTAAGTAAACCAAAT--------AT-----------------------------------TCGATAATCCAAAGACTCCTACTA---------CTATAAGTAT---TATTTTCA-CAT--CCCACAGCAAGGAAATGAAGGACTACGTGTGGTCGGTTCACGAGACGACGCCACTGA
droAna3	scaffold_12916:501391-501564 +		AAACGCTACCAAAGTTTTAGCAACATGAAAGTCCTGAAGGTCCTGCCCAAGTAAATATGTGGTTA----------------TAGGGC-C---------------------TCCCAATTCTACAGTC-------ATATTATA--ATCTGTCTTT---GGTTTTTT-CTT--GTTCAGCCACCAGTTGGTGGATTATGTTTGGTCCGTTCATGAGACGTCCCCCCAA
droBip1	scf7180000396554:1790722-1790893 -		AAACGCTTCCAGAGCTTCAGCAACATGAAGGTCCAGAAAGTCCTGCCCAAGTGAGTTCATTTTCAAGGTCTCTTCAAA---TGCTTC-ACCTC-----------------AGAGTACTCTATATT---------------------------TGGTT------TTCTTT--TTTTTAGTCACCAGTTTGAGGACTATGTCTGGTCTGTTCACGAGACATCGCCACCAA
droKik1	scf7180000302468:952080-952255 +		AAGCGCTTCCAGAGCTTCAGCAATATGAGGGTCCTAGCGATTCTGCCCAAGTGAGTAATCGAAAT--------AACG---------G-A-AT-TCGAATGTATTTGT---TTTTGATTCCGGTGAT-------CCC---------------T----TATTGTCCCTTT--CGATCAGCCCCGATCTGCCGGACTATGTGTGGTCACTACATGAGGTGACTCCCTCGA
droFic1	scf7180000453776:369775-369950 -		AAGAACTACACGGGTCTTAGCAATATGCCGGTAAAGGAAATAAAGCCACAGTAAGTTCCCTTAAA--------AA-------ACTCA-G---------------------ATTACAATAAAAAAT-TATTATA---------TTTAATGTAA----TATTTTTT-CTACCCTGCAGTGAAATCCATCCCCACTACGTATGGTGCGAGTTCGAGGAATCAGTGCCGA
droEle1	scf7180000491028:128477-128632 +		AGGCGTTTCCAGAGCTACAGCAATATGCATGTTAGAGCTGTGCTGCCCAAGTTAGTTATGCAGTT--------CC-----------------------------------TCTTTAGTTCTTAATT-------ATT---------TTATT----TTT------TT-TTT--TGACTAGCCTTGAACTTCAGGACTATGTTTGGTCGGTGCATGAAGTGACCCCCTCA
droRho1	scf7180000769671:1121-1279 +		AGGCGATTCCAAAGCTACAGCAACATGAATGTCCGTGCTGTGCTGCCCAAGTTAGTAAAGCATCC--------CC-----------------------------CA----CTTGTACTCT-TAGTC-CC----TAAT----AA--TT-------TAA------CC-GGT--TTAATAGCCATGAACTGCAGGACTACGTGTGGTCCGTGCATGAGGTTACTCCCTTGA
droBia1	scf7180000302408:1436129-1436290 +		AAGCGGTTCCAGAGCTACAGCAACATGAATGTCCGAGCAGTGTTGCCCAAGTGAGTGGGATAACT--------AACCC--------------------------------TATTTGATCCATAGGCGTTAACCACTC----TT--G-----------------TG-CTT--TGGATAGCCATGATATTCCGGACTACGTGTGGTCTGTGCATGAGGTGACTCCCTTGA
droTak1	scf7180000415765:1141498-1141657 +		AAGAAGTACACGGGTCTCAGCAATATGCCCGTCAAGGAAACAAAGCCACAGTAAGTTAAATATAT--------AT-------GATTT-GATAT-----------------AAGATATGATATAAAT-------G--------------------AAC------TTATCT--CTTTCAGTGAGACCCTCGCGGACTACATTTGGTGCGAGTTCCAGGAGTCCGTGCCTA
droEug1	scf7180000409787:498665-498830 +		AAGAAGTACACCGGACTTAGCAATATGCCCGTGAAGGAAACGAAACCACAGTAAGGAATATATTA--------AA--C---TGATCA-AT--------------------ATGATATTCCCCAATT------------------TGTACA--ACAAC------TTTTCC--CTTTCAGTGAAACCCTTGCCGACTACATATGGTGCGAGTTCCAGGAGTCCGTACCAA
dm3	chr2R:19233195-19233363 -		AAAAAATACATGGGATTGAGTGGCATGCCTGTTCTCAGGTGTCAGGATCAGTAAGTAGCCCTA-T--------ATTGTGAAGGATTAGG----------------------ATTGAAGTTCATGAAA-------TGC---------TCGCT----TAA------AT-TTT--ATTCCAGTGATAGTCTTACAAATTATGTATGGTGCGATCACGACACTCTTCTAAGGA
droSim2	2L:15456948-15457107 -		AAGCGCTTTCAGAGCTACGGCAATATGAAGGTCCAAGCAGTGCTGCCCAAGTGAGTTTGATCCGT--------T-------TAGTTT-G---------------------TCCGTAATCTATAGAC-------GCAT----TT--GT-------T--------AT-TTT--TTTCTAGCCATGAAATACAGGACTATGTGTGGTCCGTGCACGAGGTAACGCCCACGA
droSec2	scaffold_5:4610559-4610718 -		AAGCGCTTTCAGAGCTACGGCAATATGAAGGTCCAAGCAGTGCTGCCCAAGTGAGTTTGATCCGT--------T-------TGGTTT-G---------------------TCCGTAACCTATAGAC-------GCAT----TT--GT-------T--------AT-TTT--TTTCTAGCCATGAAATACAGGACTATGTGTGGTCCGTGCACGAGGTAACGCCCACGA
droYak3	2L:19465528-19465682 +		AAGCGCTTTCAGAGCTACAGCAATATGAATATCCGAGCTGTGCAGCCCAAGTGAGTTTGATCCAT--------A-------TAGTTT-G---------------------TTAGTAATTAATAAAC-------G--------------------CTT------TT-CTT--TTTCTAGCCGTGAAATAGAGGACTATGTGTGGTCTGTGCATGAGGTTACGCCTGCGA
droEre2	scaffold_4929:7577715-7577878 -		AAGCGCTTCCAGAGCTACAGCAATATGCATATCCAAGCTGTGCAGCCCAAGTGAGTTTGATCCGT--------GTGGA---TGGCTT-G---------------------CCCGTAATCCCTAAAC-------GCCA----TT--GT-------T--------AC-CTT--TTTCTAGCCGCGAGATACAGGACTATGTATGGTCCGTGCATGAGGTTACGCCCTTGA

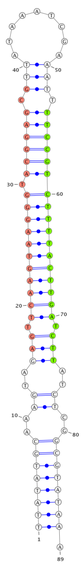
Generated: 09/08/2015 at 06:59 PM

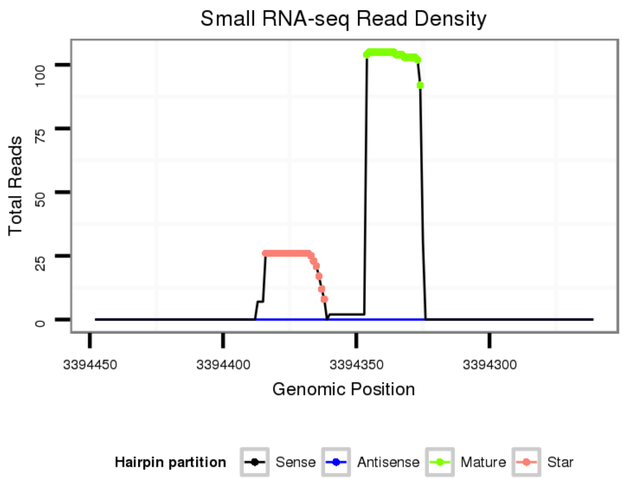
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

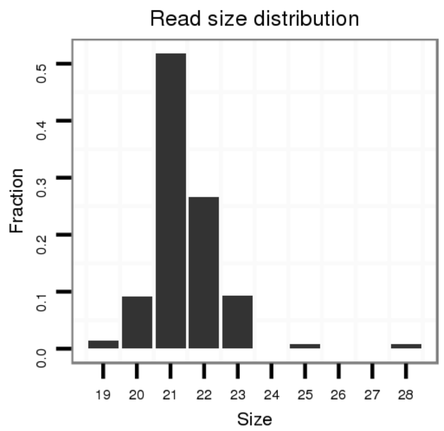
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_191	**scf2_1100000004511:3394311-3394398 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

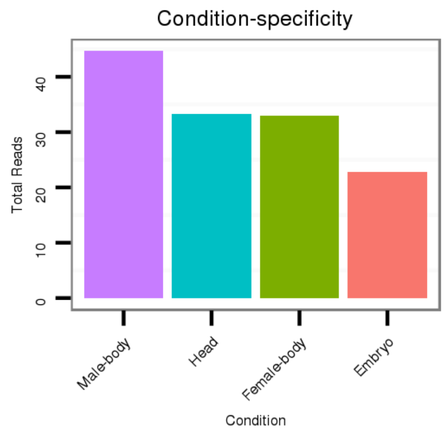
Legend: mature star mismatch in alignment mismatch in read

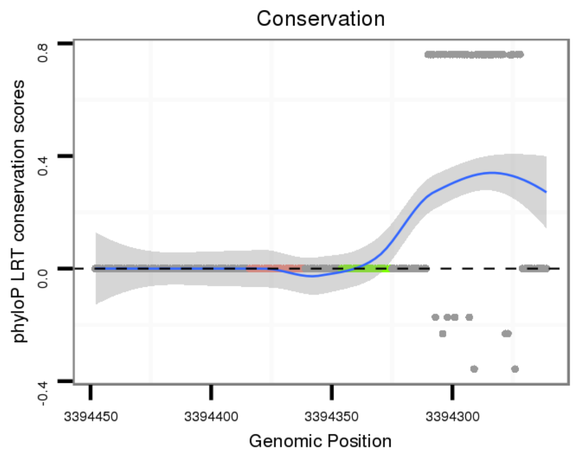
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

mature	star
	1. dwi_197 scf2_1100000004511:3392357-3392379 - 2. dwi_191 scf2_1100000004511:3394362-3394384 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TCTTAAGAGAAAAACTAAGTGATCGTCGCAGGATCATAAAAATCATATCTTATATGCAAAGTAGAGTTCAAGTAAGGGTACGGAGCGTTATAAATCGAAATTTTCCGTCTTTTACTTGATCTTATCTCGGCGTATAAAAAACTTATAAAAAAAATACAAATCAACTTTTTTTCTAATCATTCCATTTG **********(((((((..((..(((.(((((((((((.(((((((.(((.........))).)))))))))))))))))).)))..))..)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	M045 female body	M020 head	V118 embryo	V119 head
.....TTCCGTCTTTTACTTGATCTT.....	21	0	1	61.00	61	15	22	20	3	1
.....TTCCGTCTTTTACTTGATCTTA.....	22	0	1	30.00	30	5	6	3	15	1
.....TTCCGTCTTTTACTTGATCT.....	20	0	1	10.00	10	0	1	5	2	2
.....AGTTCAAGTAAGGGTACGGAGCG.....	23	0	2	8.50	17	14	0	0	3	0
.....AGTTCAAGTAAGGGTACGGAG.....	21	0	3	5.33	16	11	4	0	0	1
.....AGTTCAAGTAAGGGTACGGAGC.....	22	0	2	4.00	8	8	0	0	0	0
.....TAGAGTTCAAGTAAGGGTACGGA.....	23	0	3	3.67	11	7	0	0	4	0
.....TTCCGTCTTTTACTTGATCTTAA.....	23	1	1	3.00	3	0	1	0	2	0
.....TAGAGTTCAAGTAAGGGTACG.....	21	0	3	2.00	6	5	1	0	0	0
.....TAGAGTTCAAGTAAGGGTACGG.....	22	0	3	1.67	5	4	1	0	0	0
.....AGTTCAAGTAAGGGTACGGAGT.....	22	1	3	1.67	5	5	0	0	0	0
.....AGTTCAAGTAAGGGTACGGA.....	20	0	3	1.33	4	4	0	0	0	0
.....TATAAATCGAAATTTTCCGTCTTTT.....	25	0	1	1.00	1	0	1	0	0	0
.....TCCGTCTTTTACTTGATCTTA.....	21	0	1	1.00	1	0	1	0	0	0
.....TTCCGTCTTTTACTTGATC.....	19	0	1	1.00	1	0	0	1	0	0
.....TATAAATCGAAATTTTCCGTCTTTTACT.....	28	0	1	1.00	1	1	0	0	0	0
.....TAGAGTTCAAGTAAGGGTAC.....	20	0	3	1.00	3	3	0	0	0	0
.....AGTTCAAGTAAGGGTACGG.....	19	0	3	1.00	3	3	0	0	0	0
.....AGTTCAAGTAAGGGTACGGT.....	20	1	3	0.67	2	1	1	0	0	0
.....TAGAGTTCAAGTAAGGGTACGGAA.....	24	1	3	0.67	2	1	0	0	1	0
.....AGTTCAAGTAAGGGTACGGAGA.....	22	1	3	0.33	1	1	0	0	0	0
.....TAGAGTTCAAGTAAGGGTACGGAT.....	24	1	3	0.33	1	1	0	0	0	0
.....TAGAGTTCAAGTAAGGGTACGGAAA.....	25	2	3	0.33	1	1	0	0	0	0
.....AGAGTTCAAGTAAGGGTACGGAG.....	23	0	3	0.33	1	1	0	0	0	0
.....TAGAGTTCAAGTAAGGGTACGA.....	22	1	3	0.33	1	1	0	0	0	0

Anti-sense strand reads

AGAATTCTCTTTTTGATTCACTAGCAGCGTCCTAGTATTTTTAGTATAGAATATACGTTTCATCTCAAGTTCATTCCCATGCCTCGCAATATTTAGCTTTAAAAGGCAGAAAATGAACTAGAATAGAGCCGCATATTTTTTGAATATTTTTTTTATGTTTAGTTGAAAAAAAGATTAGTAAGGTAAAC **********(((((((((..((..(((.((((((((((.(((((((.(((.........))).)))))))))))))))))).)))..))..)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head
.....TCTCAAGTTCATTCCCATGC.....	20	0	3	0.33	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3394261-3394448 -	dwi_191	TCTTAAGAGAAAAACTAAGTGATCGTCGCAGGATCATAAAAATCATATCTTATATGCAAAGTAGAGTTCAAGTAAGGGTACGGAGCGTTATAAATCGAAATTTTCCGTCTTTTACTTGATCTTATCTCGGCGTATAAAAAACTTATAAAAAAAATACAAATCAACTTTTTTTCTAATCATTCCATTTG
droEre2	scaffold_4784:8804544-8804582 -		----------AAATTTTTGAAGAAAATGCCAATCAACTTTTTAACTCAT----------

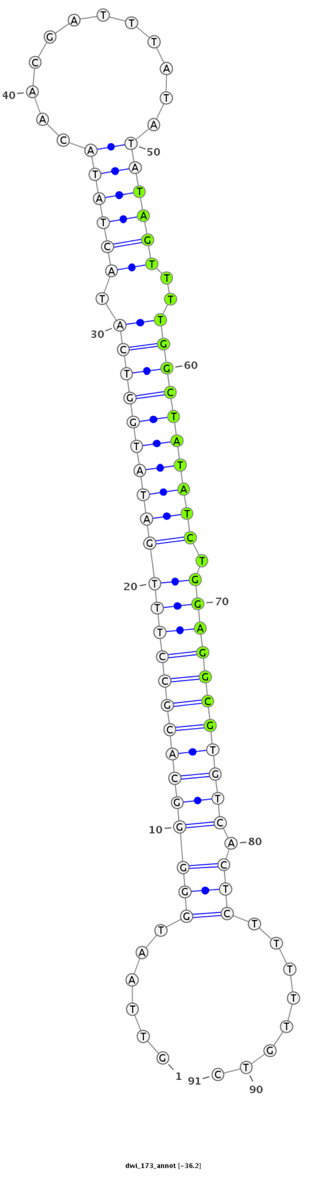
Generated: 09/08/2015 at 07:57 PM

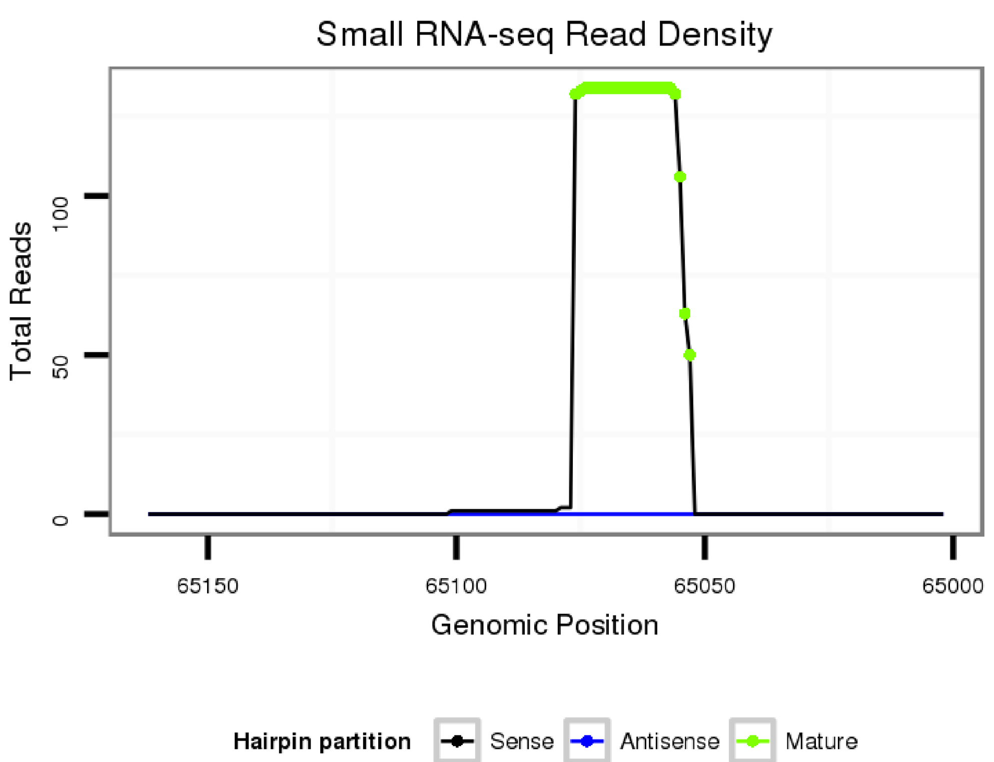
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

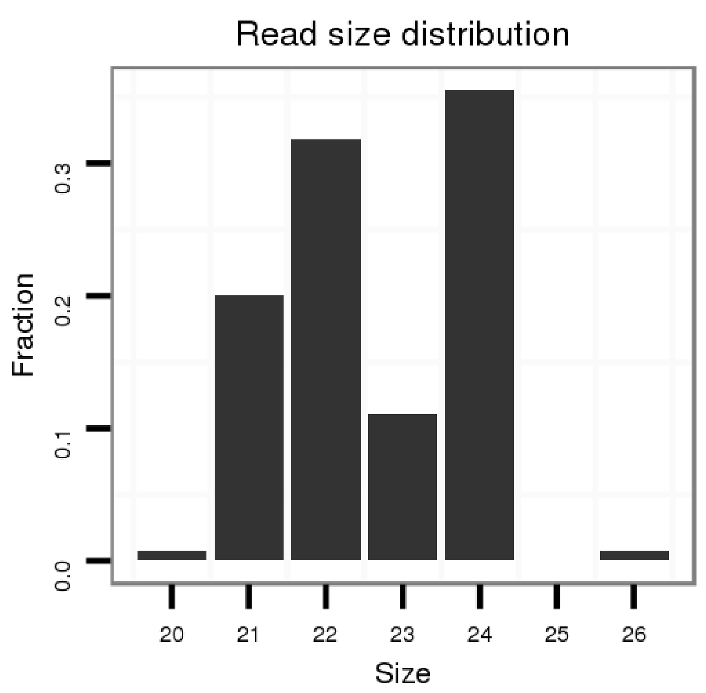
ID: dwi_173	Coordinate: scf2_1100000004512:65052-65112 -	Confidence: confident-exception	Class: Canonical miRNA	Genomic Locale: intron	[View on UCSC Genome Browser {Cornell Mirror}]

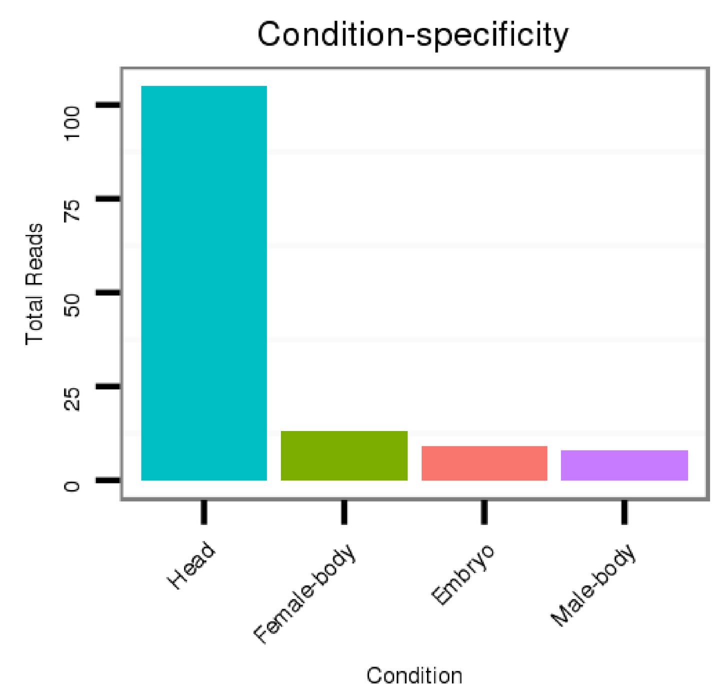
Legend: mature star mismatch in alignment mismatch in read

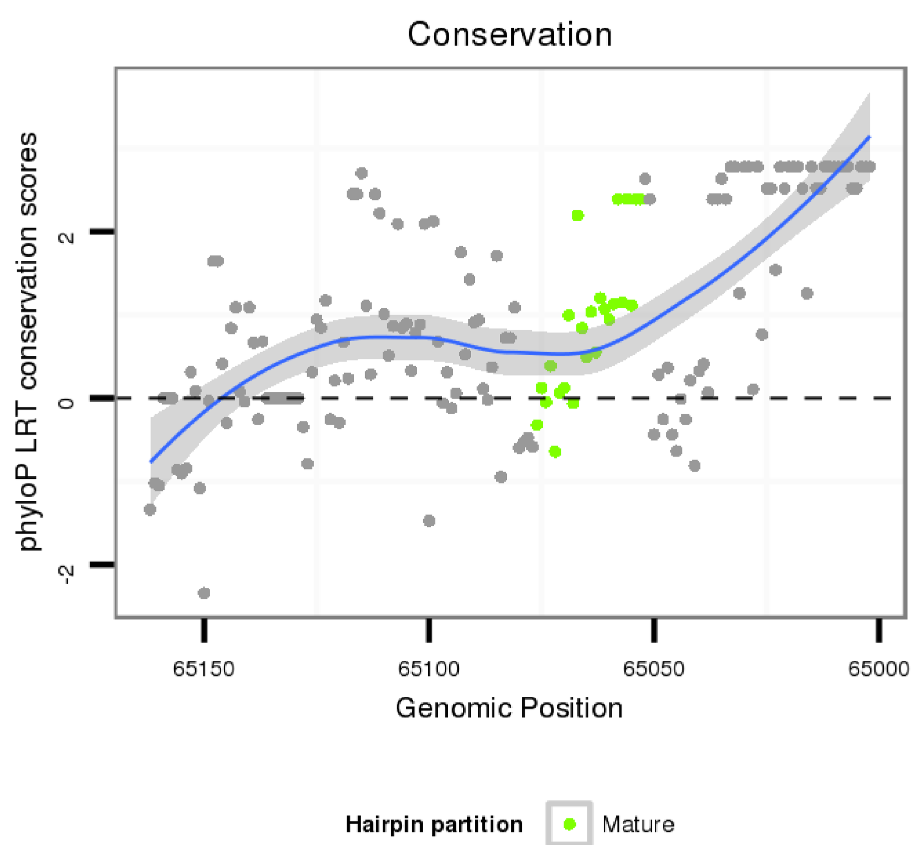
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK19565-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTCCAATTCCTTTGATATATATACCACAAAAAATAGTTAATGGGGGCACGCCTTTGATATGGTCATACTATACAACGATTTATATATAGTTTTGGCTATATCTGGAGGCGTGTCACTCTTTTTGTCCACTACATTTGCGCTCTATGTTCGTATTATCCAAA **********************************......((((((((((((((((((((((.((((((...........))))))..))))))))))).))))))))))).))).......**********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V119 head	M045 female body	V118 embryo	V117 male body
....TAGTTTTGGCTATATCTGGAGGCG...	24	0	1	48.00	48	28	8	5	6	1
....TAGTTTTGGCTATATCTGGAGG...	22	0	1	42.00	42	11	20	4	3	4
....TAGTTTTGGCTATATCTGGAG..	21	0	1	26.00	26	5	16	3	0	2
....TAGTTTTGGCTATATCTGGAGGC..	23	0	1	13.00	13	11	1	0	0	1
....TAGTTTTGGCTATATCTGGAGGCT...	24	1	1	4.00	4	4	0	0	0	0
....TAGTTTTGGCTATATCTGGG...	20	1	1	1.00	1	1	0	0	0	0
....GTCATACTATACAACGATTTATATAT..	26	0	1	1.00	1	1	0	0	0	0
....ATATAGTTTTGGCTATATCTGGA...	23	0	1	1.00	1	0	0	1	0	0
....TAGTTTTGGCTATATCTGGA...	20	0	1	1.00	1	1	0	0	0	0
....AGTTTTGGCTATATCTGGAGGCG...	23	0	1	1.00	1	0	1	0	0	0
....GTTTTGGCTATATCTGGAGGCG...	22	0	1	1.00	1	0	1	0	0	0
....AGTTTTGGCTATATCTGGAGG...	21	0	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

AAGGTTAAGGAAACTATATATATGGTGTTTTTTATCAATTACCCCCGTGCGGAAACTATACCAGTATGATATGTTGCTAAATATATATCAAAACCGATATAGACCTCCGCACAGTGAGAAAAACAGGTGATGTAAACGCGAGATACAAGCATAATAGGTTT **********************************......((((((((((((((((((((((.((((((...........))))))..))))))))))).))))))))))).))).......**********************************	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
droWil2	scf2_1100000004512:65002-65162 -	dwi_173	TTCCAATTCCTTT--GATATA-------------------------TATA--------------CCACAAAAAAATAGTT-AATGG----GG--GCACGC-------CTTTGATATGGT-CA---TAC--TATACAA-CGATTTATA----TATAGTTTTGGCTATATCTGGAGGCGTGTCACTCTTTTTGTCCACTACATT----TGCGCTCTATGTTCGTATTATCCAAA
droVir3	scaffold_12875:3297446-3297564 +		AAA---AA-----------AAACAAAATA-------------------------AAAC--------------------T-TTGA----AT-AAT--GCACGC-------CCTTGCACCAGG-------T---GGTATAGCCTGGAGTTAGGGGCGTGCC------CGTTGCCACTACATA--TCTACGCTCTATGCTCGTATTATCCAAA
droMoj3	scaffold_6496:21844576-21844652 -		TTA--T-AAT--GCACGC-------CCGT--------AC-AG--------------------------------------CCTGTAGCTTGGGGCCTTTACACA---TATATC----TACGCTCTATGCTCGTATTATCCAAA
droGri2	scaffold_15112:2846723-2846891 -		TTT---TTTTTTA--AATGACAATT-------T------------------------TAACTTGTTGAACTA-------------TA-A----AA-AATGCGCACGC-------CCTTG----GGCAC-AGGTGAAATTAATAATAAAAAAAAAGAAGAAAATATAAAACCTGA-----------------------------------AGCTCTGGGGGCGTGCCACT---T-CTGCCACTACATA--TCTACGCTCTATGCTCGTATTATCCAAA
dp5	3:2990783-2990922 -		ATT---G-----------AAATTGAATGAA------------------------TAAC---------------------CACT-----AAGGCCA--GCAGCCACTACACCCTCGATTCGGG-CA---CTC-----------------------T---ATAGGTGACTGGGTCGGGGTCGTGGTCGGCCCCTTGCCACTACATAAACATACGCTCTATGCTCGTATTATCCAAA
droAna3	scaffold_13266:10936814-10936955 +		TTT---C---TGGAAAATGGAAATTAAATGATATACCATCTATGTATGTATGTAACCTA----------------CT-A----CT-GAA--GCACCC--ACT----CCCGATCCCATCTGGATCGGGGGCGTGTGCCA------TCCCCACTACATA----TTCGCTCTATGCTCGTATTATCCAAA
droBip1	scf7180000396547:1527940-1528056 -		TAT---AC-CATC--TATGTA-------------------------TGTATGTAACCTA----------------CT-A----CT-GAA--GCACCC--ACT----CCCGATCCCATCTGGATCGGGGGCGTGTGCCA------TCCCCACTACATA----TTCGCTCTATGCTCGTATTATCCAAA
droKik1	scf7180000302366:421684-421816 -		TCG---C---CG-------ATATT-----------------------TGAA--GAAC-------------------CCCT-G----AT-GAT--GCACTC-------CCCCGATTCGGTAC--CATT-----------ACTTAGA-----GAAGCTGCTGCCCGGATCGGGGGCGTGCGCTG-C-C-CCTCCACTACATG----TACG-TCTATGCTCGTATTATCCAAA
droFic1	scf7180000454066:3354699-3354807 +		AT---CC----AT--GCACTC-------CCTCGATTCGGGCC---ATGTATAT-----ATAA----TGATT---ATGATTGCCCGGATCGGGGGCGTGAC------C-CCGCCACTACATG----TACG-TCTATGCTCGTATTATCCAAA
droEle1	scf7180000491186:173126-173263 +		TCT---T---TGA--AATGGAAATGGAATAGTT--TAAACCC----AT--GCACTC-------CCTCGATTCGGAGC---ATGTACATA--T-ATAG----AGATT---ATGATTGCCCGGATCGGGGGCGTGTC--------CCGCCACTACATG----TACG-TCTATGCTCGTATTATCCAAA
droRho1	scf7180000779777:17699-17838 -		CAA---TCGCTTG--AATGGAAATGGAATAGTT--TAAATCC----AT--GCACTC-------CCTCGATTCGGCGC---ATGTATAT-----ATAT----AGATT---ATGATTGCCCGGATCGGGGGCGTGTC------C-CCGCCACTACATG----TACG-TCTATGCTCGTATTATCCAAA
droBia1	scf7180000301754:4635025-4635074 +		--GGGGCGTGTC------C-CCGCCACTACATG----TACG-TCTATGCTCGTATTATCCAAA
droTak1	scf7180000415238:254216-254330 +		TTT--TGAACCCAT-GAT--GCACTC-------CCTCGATTCGGCGC---AT-------------ATAT----CGATTGTAATGGTTGCCCGGATCGGGGGCGTGTC------C-CCGCCACTACATG----TACG-TCTATGCTCGTATTATCCAAA
droEug1	scf7180000409672:7351748-7351861 +		ATA---T---CCAT-GAT--GCACTC-------CCTCGATTCGGCGC---ATGTATAT-----ATAA----TGATT---ATGGTTGCCCGGATCGGGGGCGTGTC------C-CCGCCACTACATG----TACG-TCTATGCTCGTATTATCCAAA
dm3	chr2R:17541004-17541146 +		CAA---TTACTTC--AATGGAAATGGATTAATT--TAAACCA----AT--GCACTC-------CCTCGATTCGGCGC---ATGTATATACAT-ATAT----AGATT---ATGGTTGCCCGGATCGGGGGCGTGAC--------CCGCCACTACATG----TACG-TCTATGCTCGTATTATCCAAA
droSim2	2r:18095789-18095931 +		CAA---TCACTTC--AATGGAAATGGATTAATT--TAAACCA----AT--GCACTC-------CCTCGATTCGGCGC---ATGTATATACAT-ATAT----AGATT---ATGGTTGCCCGGATCGGGGGCGTGAC--------CCGCCACTACATG----TACG-TCTATGCTCGTATTATCCAAA
droSec2	scaffold_9:867012-867124 +		AA--CCA----AT--GCACTC-------CCTCGATTCGGCGC---ATGTATATACAT-ATAT----AGATT---ATGGTTGCCCGGATCGGGGGCGTGAC--------CCGCCACTACATG----TACG-TCTATGCTCGTATTATCCAAA
droYak3	2R:11630969-11631080 -		C---CA----AT--GCACTC-------CCTCGATTCGGCGC---ATGTATATACATACTAT----AGCTG---ATGGTAGCCCGGATCGGGGGCGTGAC--------CCGCCACTACATG----TACG-TCTATGCTCGTATTATCCAAA
droEre2	scaffold_4845:11690033-11690143 +		C---CA----AT--GCACTC-------CCTCGATTCGGCGC---TTGTATATACAT-ATAT----AGATT---ATGGTTGCCCGGATCGGGGGCGTGAC--------CCGCCACTACATG----TACG-TCTATGCTCGTATTATCCAAA

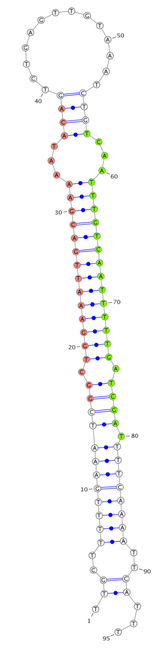
Generated: 09/08/2015 at 07:44 PM

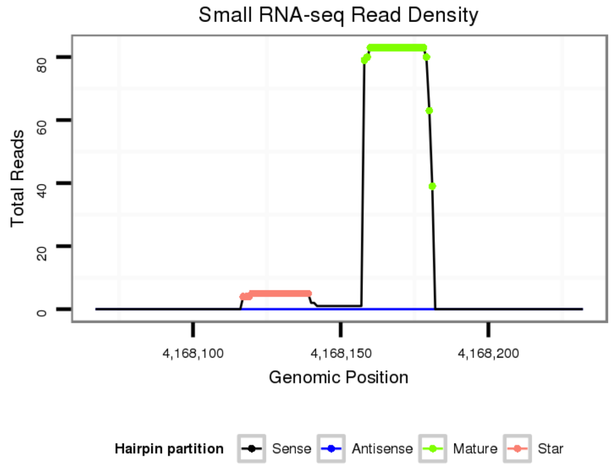
	PASS/FAIL
crit.star	0
crit.loop	1
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

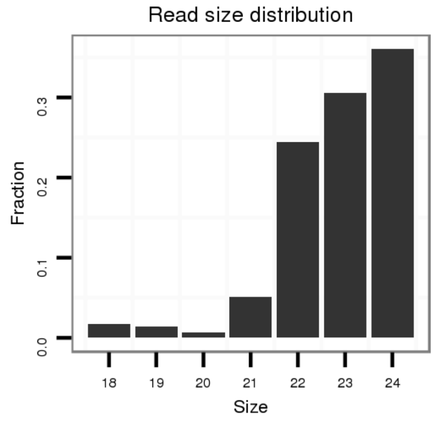
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_78	**scf2_1100000004909:4168117-4168182 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

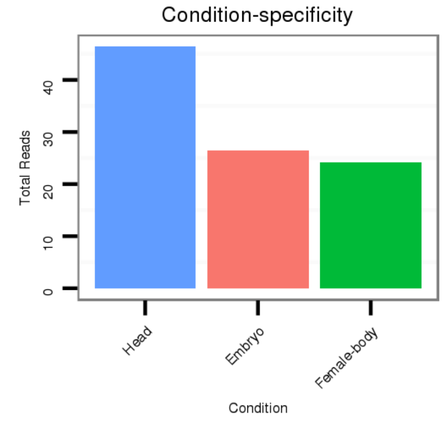
Legend: mature star mismatch in alignment mismatch in read

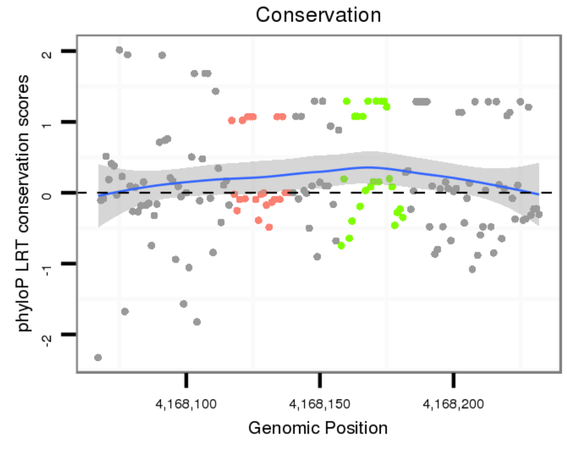
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dwi_79 scf2_1100000004909:4166676-4166699 + 2. dwi_80 scf2_1100000004909:4167417-4167440 + 3. dwi_78 scf2_1100000004909:4168158-4168181 +	1. dwi_79 scf2_1100000004909:4166635-4166657 + 2. dwi_80 scf2_1100000004909:4167376-4167398 + 3. dwi_78 scf2_1100000004909:4168117-4168139 +

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTTTTTTTTTTTTAAGTCGTCTTGAAATTAATTAATTTGCTTTTTGAAATCGGCTGGAAATTGACGAAAATACAGTCTGAGTTGTAAATCTGTCAATTTGTCAATTTTTGATCGATTTTCAAAAATTCATTTCCACCAAGAAGTAAAATTTTGACCATTTTCGCATAA **********.((..(((((((((((.(((((((((((((...((((.............))))...))))))))))))))).))))).))))))..))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V118 embryo	M045 female body	V119 head	V117 male body
.....TCAATTTGTCAATTTTTGATCGAT.....	24	0	3	35.00	105	39	33	10	23	0
.....TCAATTTGTCAATTTTTGATCGA.....	23	0	3	24.00	72	24	22	13	13	0
.....TCAATTTGTCAATTTTTGATCG.....	22	0	3	17.33	52	13	3	30	6	0
.....TCAATTTGTCAATTTTTGATCGT.....	23	1	3	8.67	26	26	0	0	0	0
.....GGCTGGAAATTGACGAAAATACA.....	23	0	3	4.33	13	0	11	1	1	0
.....AATTTGTCAATTTTTGATCGAT.....	22	0	3	3.67	11	6	0	2	3	0
.....TCAATTTGTCAATTTTTGATC.....	21	0	3	3.33	10	0	0	5	5	0
.....TCAATTTGTCAATTTTTGATCGG.....	23	1	3	1.67	5	5	0	0	0	0
.....TGGAAATTGACGAAAATACAGT.....	22	0	5	1.40	7	0	4	1	2	0
.....CAATTTGTCAATTTTTGATCGAT.....	23	0	3	1.33	4	2	0	2	0	0
.....GTCTGAGTTGTAAATCTG.....	18	0	3	1.33	4	0	4	0	0	0
.....GCTGGAAATTGACGAAAATACA.....	22	0	3	0.67	2	0	2	0	0	0
.....AATTTGTCAATTTTTGATCGA.....	21	0	3	0.67	2	1	1	0	0	0
.....TCAATTTGTCAATTTTTGA.....	19	0	3	0.67	2	0	0	2	0	0
.....TCAATTTGTCAATTTTTGATCGAC.....	24	1	3	0.67	2	2	0	0	0	0
.....TGTCAATTTGTCAATTTTTGA.....	21	0	3	0.67	2	0	0	1	1	0
.....CAATTTGTCAATTTTTGATCG.....	21	0	3	0.33	1	0	0	1	0	0
.....GGCTGGAAATTGACGAAAATAC.....	22	0	3	0.33	1	0	1	0	0	0
.....GTCAATTTGTCAATTTTTG.....	19	0	3	0.33	1	0	0	1	0	0
.....TGTCAATTTGTCAATTTTTGAT.....	22	0	3	0.33	1	0	0	1	0	0
.....CAATTTGTCAATTTTTGATC.....	20	0	3	0.33	1	0	0	1	0	0
.....TCAATTTGTCAATTTTTGAT.....	20	0	3	0.33	1	0	0	0	1	0
.....TTTGTCAATTTTTGATCG.....	18	0	3	0.33	1	0	0	1	0	0
.....TTGTCAATTTTTGATCGAT.....	19	0	3	0.33	1	0	0	1	0	0
.....TGTCAATTTGTCAATTTTTGATT.....	23	1	3	0.33	1	0	0	0	1	0

Anti-sense strand reads

AAAAAAAAAAAATTCAGCAGAACTTTAATTAATTAAACGAAAAACTTTAGCCGACCTTTAACTGCTTTTATGTCAGACTCAACATTTAGACAGTTAAACAGTTAAAAACTAGCTAAAAGTTTTAAGTAAAGGTGGTTCTTCATTTTAAAACTGGTAAAAGCGTATT **********.((..(((((((((((.(((((((((((((...((((.............))))...))))))))))))))).))))).))))))..))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo
..AAAAAAAAATTCAGCAG.....	18	0	4	0.25	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004909:4168067-4168232 +	dwi_78	TTTTTTTTTTTTAAGTCGT----------C----------TTGAAATTAAT----------TAATTTGCTTTTGAAATCGGCTGGAAATTGACGAAAATACAGTCTGAGTTGTAAATCTGTCAATTTGTCAATTTTTGATCGATTTCAAAATTCATTTCCACCAAGAAGTAAAATTTTGAC--CA----TTTTC-GCATAA
droVir3	scaffold_13047:4120085-4120158 -		GTTTTTTTTTTAAACTGA----------C----------GCGAAATTGTT----------AATTTGATTTCCGGACAAGACGAAAACGAACTGAGT----------|--|----|-----|--TCTG
droMoj3	scaffold_6473:1094620-1094806 -		TTTTTTTTTTTTAAGAATTTTGCTTGTTCATACTTTAAAATAATAATTTTAATTGAAAACAATCGAACTTTCATAAAATCGAAATTAGT----------TTTCTTCAGTTTCGAG----------TTCCAAATCAGCCAG------AAATATTGATCGCCTAAAAAATTCGGGTTCTTCAACTGATTTAATTGTGCCTTCA----ACTTT-ACATAA
droGri2	scaffold_14853:5408044-5408105 -		AGACT----------GT----------C----------CGAAATAAAG----------|----------TTTGACATGTATTTGGACATGTTTTCAGTTTTGACTAATTT----------|--|----|-----|-----T
dp5	XL_group1e:8978021-8978040 -		TTTTTTTTTTGTCAGGCGT----------C----------|----------|----------|----------|--|----|-----|------
droAna3	scaffold_13266:4483924-4483970 -		TTTGTTTTTTCTAAGTTGC----------C----------TCACAATTAAT----------TTTTGTGATTTTGGAA----------|----------|--|----|-----|------
droBip1	scf7180000396371:1369506-1369593 -		GTTTTTGATAA-AGATTGT----------T----------CGAAAATTGAACTACAAATCTTTTAAAGTCTTCCTTTCAGAGATCGGGTGAAAATTGCGAAAAT----------|----------|--|----|-----|--ATAG
droKik1	scf7180000302388:754227-754238 -		TTTTTTTTTTTT-------|----------|----------|----------|----------|--|----|-----|------
droFic1	scf7180000453839:1551741-1551783 -		CGATTTTTTTGTGCGTTGA----------T----------CTTAACTTATT----------TAATTTTCTTTT----------|----------|--|----|-----|------
droEle1	scf7180000491080:3252710-3252741 -		GTATC----------|----------|----------|--AAAACCAGT----------TCATTTGCTTTTTGAAAT----------|----------|--|----|-----|------
droBia1	scf7180000301703:425003-425087 -		AAATAATA----------|----------|----------|----------|----------TTTATGTTTTAAA-----TAATTTGTTAATTTTTGTTCGTTTTCAAAAATGTATTGCCT------AGTTTCTTGGTG--|--|----|-CTTTTCCATTG
droTak1	scf7180000413955:48624-48653 -		TGTTTTAGTAATATGTTTT----------C----------CTGAAATTAA----------|----------|--|----|-----|------
droYak3	X:4745943-4746009 -		TTTTAATT----------|----------|----------|----------|----------AGTCGTCAAAATTGCATTGGCGTAAGAAGTGAAATTTTTGTT--CAAGATTTCTGACGTATG

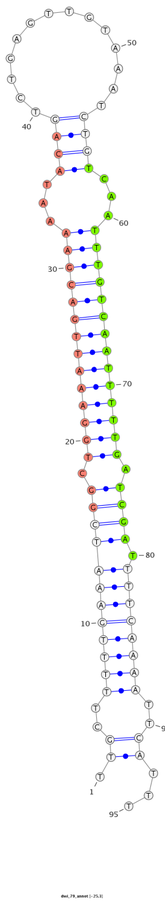
Generated: 09/08/2015 at 07:46 PM

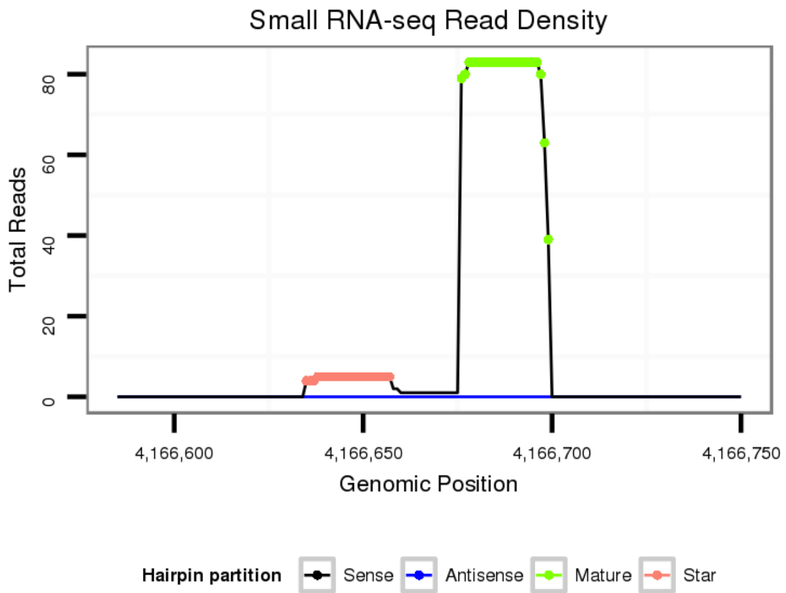
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

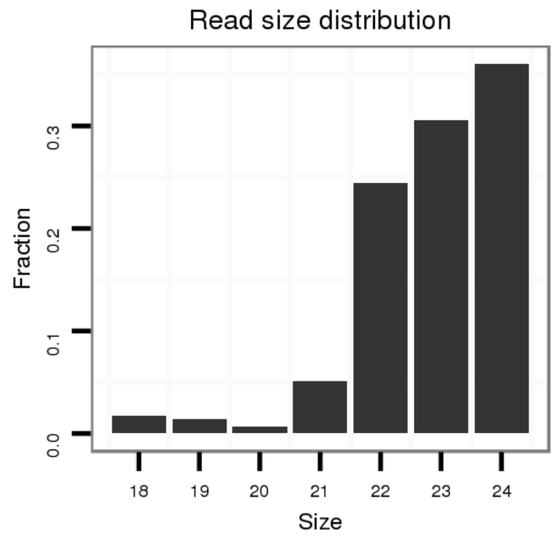
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_79	**scf2_1100000004909:4166635-4166700 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

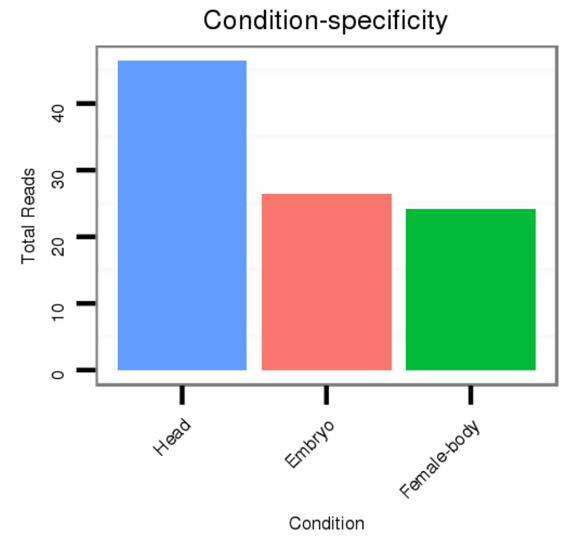
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dwi_79 scf2_1100000004909:4166676-4166699 + 2. dwi_80 scf2_1100000004909:4167417-4167440 + 3. dwi_78 scf2_1100000004909:4168158-4168181 +	1. dwi_79 scf2_1100000004909:4166635-4166657 + 2. dwi_80 scf2_1100000004909:4167376-4167398 + 3. dwi_78 scf2_1100000004909:4168117-4168139 +

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTTTTTTTTTTTAAGTCGTCTTGAAATTAATTAATTTGCTTTTTGAAATCGGCTGGAAATTGACGAAAATACAGTCTGAGTTGTAAATCTGTCAATTTGTCAATTTTTGATCGATTTTCAAAATTCATTTCCACCAAGAAGTAAAATTTTGACCATTTTCGCATAA **********.((..((((((((((((.((((((((((((((...((((.............))))))...))))))))))))))).)))))).)))))))..))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V118 embryo	M045 female body	V119 head	V117 male body
.....TCAATTTGTCAATTTTTGATCGAT.....	24	0	3	35.00	105	39	33	10	23	0
.....TCAATTTGTCAATTTTTGATCGA.....	23	0	3	24.00	72	24	22	13	13	0
.....TCAATTTGTCAATTTTTGATCG.....	22	0	3	17.33	52	13	3	30	6	0
.....TCAATTTGTCAATTTTTGATCGT.....	23	1	3	8.67	26	26	0	0	0	0
.....GGCTGGAAATTGACGAAAATACA.....	23	0	3	4.33	13	0	11	1	1	0
.....AATTTGTCAATTTTTGATCGAT.....	22	0	3	3.67	11	6	0	2	3	0
.....TCAATTTGTCAATTTTTGATC.....	21	0	3	3.33	10	0	0	5	5	0
.....TCAATTTGTCAATTTTTGATCGG.....	23	1	3	1.67	5	5	0	0	0	0
.....TGGAAATTGACGAAAATACAGT.....	22	0	5	1.40	7	0	4	1	2	0
.....GTCTGAGTTGTAAATCTG.....	18	0	3	1.33	4	0	4	0	0	0
.....CAATTTGTCAATTTTTGATCGAT.....	23	0	3	1.33	4	2	0	2	0	0
.....AATTTGTCAATTTTTGATCGA.....	21	0	3	0.67	2	1	1	0	0	0
.....TCAATTTGTCAATTTTTGA.....	19	0	3	0.67	2	0	0	2	0	0
.....TCAATTTGTCAATTTTTGATCGAC.....	24	1	3	0.67	2	2	0	0	0	0
.....TGTCAATTTGTCAATTTTTGA.....	21	0	3	0.67	2	0	0	1	1	0
.....GCTGGAAATTGACGAAAATACA.....	22	0	3	0.67	2	0	2	0	0	0
.....TGTCAATTTGTCAATTTTTGATT.....	23	1	3	0.33	1	0	0	0	1	0
.....CAATTTGTCAATTTTTGATC.....	20	0	3	0.33	1	0	0	1	0	0
.....GTCAATTTGTCAATTTTTG.....	19	0	3	0.33	1	0	0	1	0	0
.....TGTCAATTTGTCAATTTTTGAT.....	22	0	3	0.33	1	0	0	1	0	0
.....TTTGTCAATTTTTGATCG.....	18	0	3	0.33	1	0	0	1	0	0
.....CAATTTGTCAATTTTTGATCG.....	21	0	3	0.33	1	0	0	1	0	0
.....TCAATTTGTCAATTTTTGAT.....	20	0	3	0.33	1	0	0	0	1	0
.....GGCTGGAAATTGACGAAAATAC.....	22	0	3	0.33	1	0	1	0	0	0
.....TTGTCAATTTTTGATCGAT.....	19	0	3	0.33	1	0	0	1	0	0

Anti-sense strand reads

AAAAAAAAAAAATTCAGCAGAACTTTAATTAATTAAACGAAAAACTTTAGCCGACCTTTAACTGCTTTTATGTCAGACTCAACATTTAGACAGTTAAACAGTTAAAAACTAGCTAAAAGTTTTAAGTAAAGGTGGTTCTTCATTTTAAAACTGGTAAAAGCGTATT **********.((..((((((((((((.((((((((((((((...((((.............))))))...))))))))))))))).)))))).)))))))..))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo
..AAAAAAAAAATTCAGCAG.....	18	0	4	0.25	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004909:4166585-4166750 +	dwi_79	TTTTTTTTTTTTAAGTCGTCTTGAAATTAATTAATTTGCTTTTTGAAATCGGCTGGAAATTGACGAAAATACAGTCTGAGTTGTAAATCTGTCAATTTGTCAATTTTTGATCGATTTTCAAAATTCATTTCCACCAAGAAGTAAAATTTTGACCATTTTCGCATAA

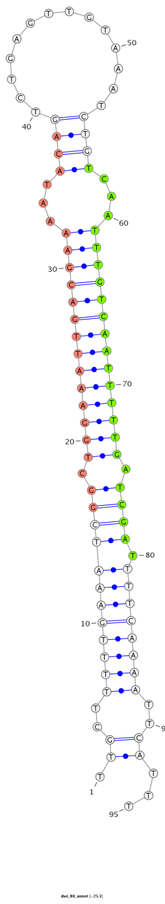
Generated: 09/08/2015 at 07:46 PM

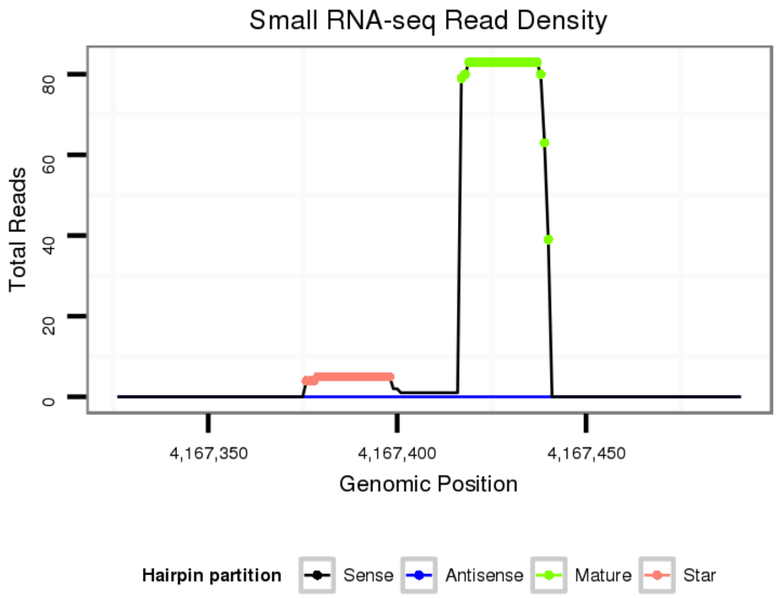
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

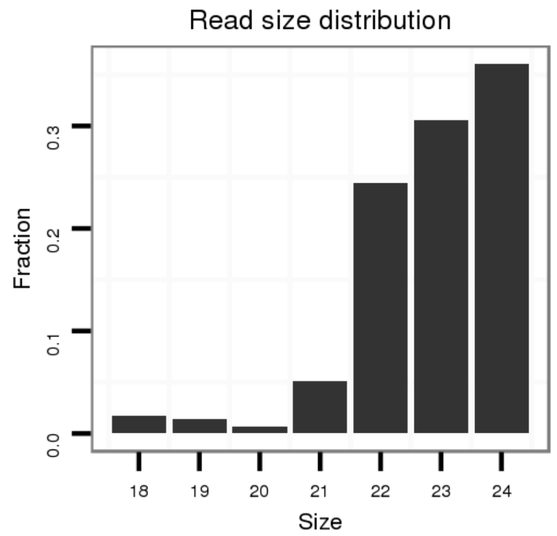
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_80	**scf2_1100000004909:4167376-4167441 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

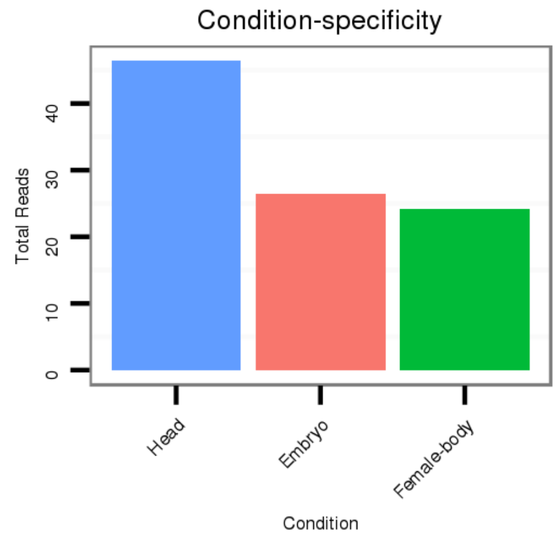
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dwi_79 scf2_1100000004909:4166676-4166699 + 2. dwi_80 scf2_1100000004909:4167417-4167440 + 3. dwi_78 scf2_1100000004909:4168158-4168181 +	1. dwi_79 scf2_1100000004909:4166635-4166657 + 2. dwi_80 scf2_1100000004909:4167376-4167398 + 3. dwi_78 scf2_1100000004909:4168117-4168139 +

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTTTTTTTTTTTAAGTCGTCTTGAAATTAATTAATTTGCTTTTTGAAATCGGCTGGAAATTGACGAAAATACAGTCTGAGTTGTAAATCTGTCAATTTGTCAATTTTTGATCGATTTTCAAAATTCATTTCCACCAAGAAGTAAAATTTTGACCATTTTCGCATAA **********.((..(((((((((((.(((((((((((((...((((.............))))...)))))))))))))).)))).)))))))..))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V118 embryo	M045 female body	V119 head	V117 male body
.....TCAATTTGTCAATTTTTGATCGAT.....	24	0	3	35.00	105	39	33	10	23	0
.....TCAATTTGTCAATTTTTGATCGA.....	23	0	3	24.00	72	24	22	13	13	0
.....TCAATTTGTCAATTTTTGATCG.....	22	0	3	17.33	52	13	3	30	6	0
.....TCAATTTGTCAATTTTTGATCGT.....	23	1	3	8.67	26	26	0	0	0	0
.....GGCTGGAAATTGACGAAAATACA.....	23	0	3	4.33	13	0	11	1	1	0
.....AATTTGTCAATTTTTGATCGAT.....	22	0	3	3.67	11	6	0	2	3	0
.....TCAATTTGTCAATTTTTGATC.....	21	0	3	3.33	10	0	0	5	5	0
.....TCAATTTGTCAATTTTTGATCGG.....	23	1	3	1.67	5	5	0	0	0	0
.....TGGAAATTGACGAAAATACAGT.....	22	0	5	1.40	7	0	4	1	2	0
.....CAATTTGTCAATTTTTGATCGAT.....	23	0	3	1.33	4	2	0	2	0	0
.....GTCTGAGTTGTAAATCTG.....	18	0	3	1.33	4	0	4	0	0	0
.....TCAATTTGTCAATTTTTGA.....	19	0	3	0.67	2	0	0	2	0	0
.....TGTCAATTTGTCAATTTTTGA.....	21	0	3	0.67	2	0	0	1	1	0
.....TCAATTTGTCAATTTTTGATCGAC.....	24	1	3	0.67	2	2	0	0	0	0
.....GCTGGAAATTGACGAAAATACA.....	22	0	3	0.67	2	0	2	0	0	0
.....AATTTGTCAATTTTTGATCGA.....	21	0	3	0.67	2	1	1	0	0	0
.....CAATTTGTCAATTTTTGATCG.....	21	0	3	0.33	1	0	0	1	0	0
.....TTGTCAATTTTTGATCGAT.....	19	0	3	0.33	1	0	0	1	0	0
.....TCAATTTGTCAATTTTTGAT.....	20	0	3	0.33	1	0	0	0	1	0
.....TTTGTCAATTTTTGATCG.....	18	0	3	0.33	1	0	0	1	0	0
.....GGCTGGAAATTGACGAAAATAC.....	22	0	3	0.33	1	0	1	0	0	0
.....TGTCAATTTGTCAATTTTTGATT.....	23	1	3	0.33	1	0	0	0	1	0
.....TGTCAATTTGTCAATTTTTGAT.....	22	0	3	0.33	1	0	0	1	0	0
.....GTCAATTTGTCAATTTTTG.....	19	0	3	0.33	1	0	0	1	0	0
.....CAATTTGTCAATTTTTGATC.....	20	0	3	0.33	1	0	0	1	0	0

Anti-sense strand reads

AAAAAAAAAAAATTCAGCAGAACTTTAATTAATTAAACGAAAAACTTTAGCCGACCTTTAACTGCTTTTATGTCAGACTCAACATTTAGACAGTTAAACAGTTAAAAACTAGCTAAAAGTTTTAAGTAAAGGTGGTTCTTCATTTTAAAACTGGTAAAAGCGTATT **********.((..(((((((((((.(((((((((((((...((((.............))))...)))))))))))))).)))).)))))))..))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo
..AAAAAAAAAATTCAGCAG.....	18	0	4	0.25	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004909:4167326-4167491 +	dwi_80	TTTTTTTTTTTTAAGTCGTCTTGAAATTAATTAATTTGCTTTTTGAAATCGGCTGGAAATTGACGAAAATACAGTCTGAGTTGTAAATCTGTCAATTTGTCAATTTTTGATCGATTTTCAAAATTCATTTCCACCAAGAAGTAAAATTTTGACCATTTTCGCATAA

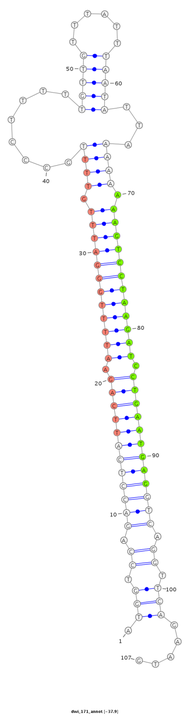
Generated: 09/08/2015 at 07:47 PM

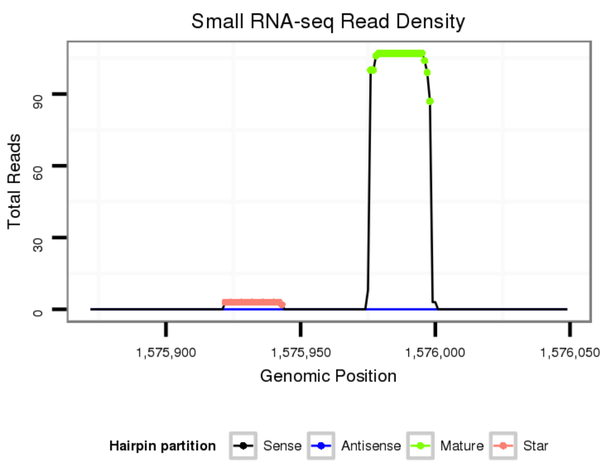
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

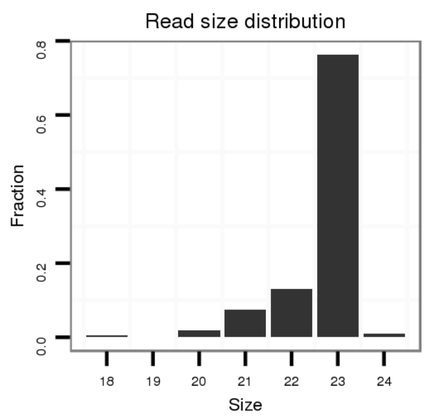
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_171	**scf2_1100000004909:1575922-1575999 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

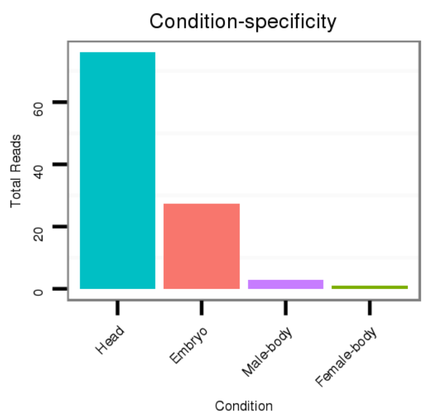
Legend: mature star mismatch in alignment mismatch in read

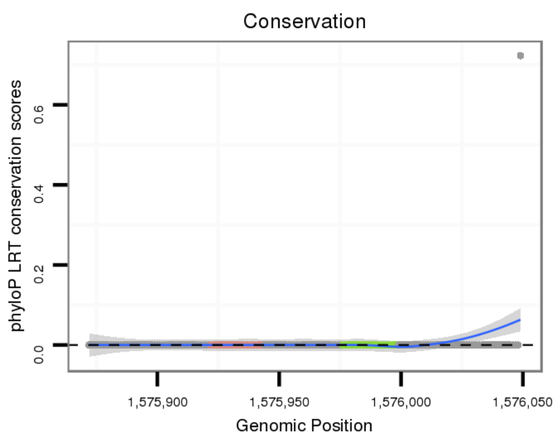
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK25487-in]

Repeatable elements

Name	Class	Family	Strand
AT_rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGAAGTCTAAAATTAAAGTTTAAGCACAAACGTAGATGGTCCAGACCTCATTCAGAATTTTGGGATTTGTTTTGCCCTTTTTGTTGTTTATTTAATATTAAAAAAAAGTCCTAAGATCCTGAATGAGGTCAGGTTCAGAATGGCTACTATCATTCTAGGTCGATTGCACTTATTTCAT **********.(((.((.(((((((((((.(((((((((((.((((.....((((.....))))))...))))).)))))))))))).)))))))))).)).)))********** **Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V119 head**	**M020 head**	**V118 embryo**	**V117 male body**	**M045 female body**
..........AAAGTCCTAAGATCCTGAATGAG..........	23	0	1	80.00	80	37	19	21	2	1
..........AAAGTCCTAAGATCCTGAATGA..........	22	0	1	9.00	9	5	3	1	0	0
..........AGTCCTAAGATCCTGAATGAGT..........	22	1	1	3.00	3	1	1	1	0	0
..........AGTCCTAAGATCCTGAATGAG..........	21	0	1	3.00	3	1	2	0	0	0
..........AAAAGTCCTAAGATCCTGAATG..........	22	0	1	3.00	3	1	2	0	0	0
..........AAAAGTCCTAAGATCCTGAAT..........	21	0	1	2.00	2	0	2	0	0	0
..........AAAGTCCTAAGATCCTGAATG..........	21	0	1	2.00	2	1	1	0	0	0
..........TTCAGAATTTTGGGATTTGTTT..........	22	0	1	2.00	2	0	0	2	0	0
..........AAAAGTCCTAAGATCCTGAATGA..........	23	0	1	2.00	2	0	0	2	0	0
..........AGTCCTAAGATCCTGAATGAGGT..........	23	0	1	2.00	2	0	2	0	0	0
..........AAAGTCCTAAGATCCTGAATGAA..........	23	1	1	1.00	1	1	0	0	0	0
..........TTCAGAATTTTGGGATTTGTT..........	21	0	1	1.00	1	0	0	0	1	0
..........AAAGTCCTAAGATCCTGAATGAGT..........	24	1	1	1.00	1	1	0	0	0	0
..........GTCCTAAGATCCTGAATGAGGT..........	22	0	1	1.00	1	0	0	1	0	0
..........AGTCCTAAGATCCTGAATGAGA..........	22	1	1	1.00	1	1	0	0	0	0
..........AGTCCTAAGATCCTGAATGA..........	20	0	1	1.00	1	1	0	0	0	0
..........AGTCCTAAGATCCTGAATGAGGG..........	23	1	1	1.00	1	0	1	0	0	0
..........AAAGTCCTAAGATCCTGAAT..........	20	0	1	1.00	1	0	1	0	0	0
..........AAAGTCCTAAGATCCTGAATGAGA..........	24	1	1	1.00	1	1	0	0	0	0
..........AAAAGTCCTAAGATCCTGAATGAG..........	24	0	1	1.00	1	0	0	1	0	0
..........AAAGTCCTAAGATCCTGAATGG..........	22	1	1	1.00	1	0	1	0	0	0
..........CTTTTTGTTGTTTATTTA..........	18	0	2	0.50	1	0	0	1	0	0

Anti-sense strand reads

ACTTCAGATTTTAATTTCAAATTCGTGTTTGCATCTACCAGGTCTGGAGTAAGTCTTAAAACCCTAAACAAAACGGGAAAAACAACAAATAAATTATAATTTTTTTTCAGGATTCTAGGACTTACTCCAGTCCAAGTCTTACCGATGATAGTAAGATCCAGCTAACGTGAATAAAGTA **********.(((.((.(((((((((((.(((((((((((.((((.....((((.....))))))...))))).)))))))))))).)))))))))).)).)))********** **Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M020 head**	**V117 male body**	**V119 head**
..........AGTCCTAAGATCCTGAATGAGA..........	22	1	1	1.00	1	1	0	0	0
..........AGTCCTAAGATCCTGAATGA..........	20	0	1	1.00	1	1	0	0	0
..........AGTCCTAAGATCCTGAATGAGGG..........	23	1	1	1.00	1	0	1	0	0
..........AAAGTCCTAAGATCCTGAAT..........	20	0	1	1.00	1	0	1	0	0
..........AAAGTCCTAAGATCCTGAATGAGA..........	24	1	1	1.00	1	1	0	0	0
..........AAAAGTCCTAAGATCCTGAATGAG..........	24	0	1	1.00	1	0	0	1	0	0
..........AAAGTCCTAAGATCCTGAATGG..........	22	1	1	1.00	1	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004909:1575872-1576049 +	dwi_171	TGAAGTCTAAAATTAAAGTTTAAGCACAAACGTAGATGGTCCAGACCTCATTCAGAATTTTGGGATTTGTTTTGCCCTTTTTGTTGTTTATTTAATATTAAAAAAAAGTCCTAAGATCCTGAATGAGGTCAGGTTCAGAATGGCTACTATCATTCTAGGTCGATTGCACTTATTTCAT
droKik1	scf7180000299665:440-440 -		----------T

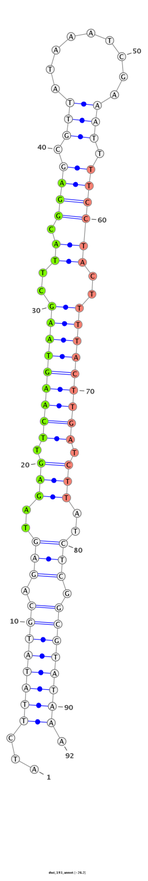
Generated: 09/08/2015 at 07:41 PM

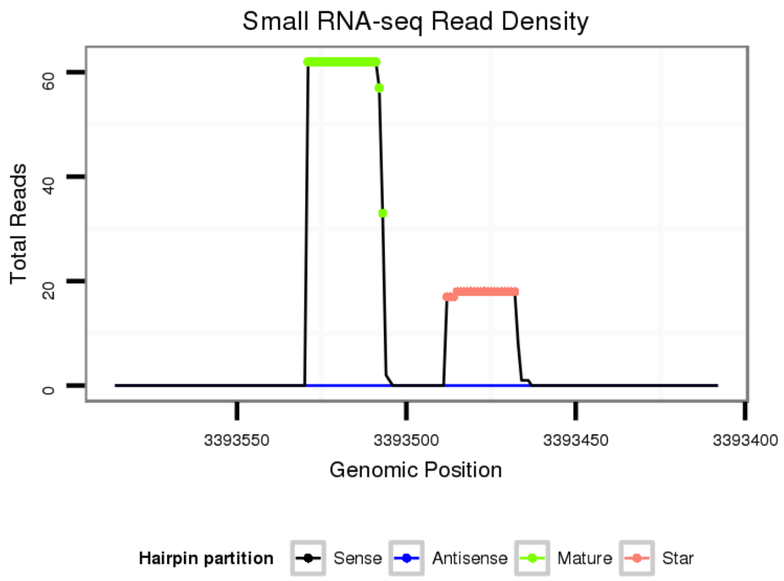
+PASSTAR	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

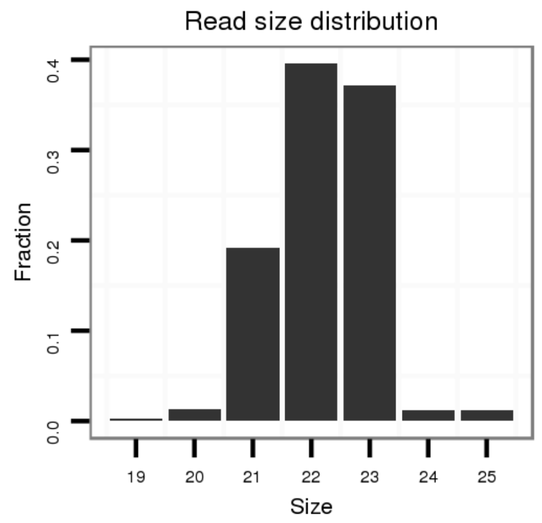
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_193	**scf2_1100000004511:3393458-3393536 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

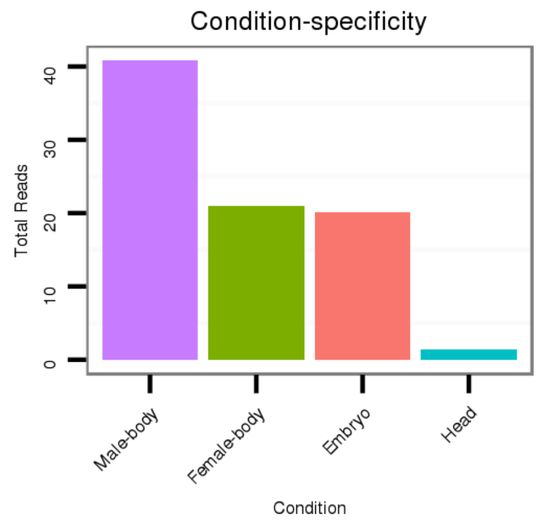
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

mature	star
	1. dwi_197 scf2_1100000004511:3392321-3392341 - 2. dwi_196 scf2_1100000004511:3392537-3392557 - 3. dwi_195 scf2_1100000004511:3392679-3392699 - 4. dwi_61 scf2_1100000004511:3393253-3393273 - 5. dwi_193 scf2_1100000004511:3393468-3393488 - 6. dwi_63 scf2_1100000004511:3393826-3393846 - 7. dwi_64 scf2_1100000004511:3394110-3394130 - 8. dwi_65 scf2_1100000004511:3394468-3394488 - 9. dwi_89 scf2_1100000004511:3394684-3394704 - 10. dwi_190 scf2_1100000004511:3394900-3394920 - 11. dwi_189 scf2_1100000004511:3395101-3395121 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CAGAGAAAAACTTAGTGATAGTCGCAGGATCATAAAAATCACATCTTATATGCAGAGTAGAGTTCAAGTAAGCTTACGGAGCGTTATAAATCGAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAATAAATCTTAAAAAAATACAAATCAACATTTTTTCTAATCATTCCA	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	V118 embryo	M045 female body	V119 head	M020 head
**********...(((((((((.(((..(((.((((((((((..((.((((.(((.........))).)))))).))))))))).)))..))).)))))))).**********										
.....TAGAGTTCAAGTAAGCTTACGGA.....	23	0	1	31.00	31	19	12	0	0	0
.....TAGAGTTCAAGTAAGCTTACGG.....	22	0	1	24.00	24	17	2	5	0	0
.....TAGAGTTCAAGTAAGCTTACGGAA.....	24	1	1	14.00	14	8	6	0	0	0
.....TTCCTACTTTTACTTGATCTT.....	21	0	11	10.73	118	5	8	94	8	3
.....TTCCTACTTTTACTTGATCTTA.....	22	0	11	7.73	85	2	43	40	0	0
.....TAGAGTTCAAGTAAGCTTACG.....	21	0	1	5.00	5	3	0	2	0	0
.....TAGAGTTCAAGTAAGCTTACGGAT.....	24	1	1	3.00	3	3	0	0	0	0
.....TAGAGTTCAAGTAAGCTTACGGAAA.....	25	2	1	2.00	2	1	1	0	0	0
.....CTACTTTTACTTGATCTTATCT.....	22	0	11	1.27	14	2	2	6	1	3
.....TAGAGTTCAAGTAAGCTTACGGAAT.....	25	2	1	1.00	1	1	0	0	0	0
.....TAGAGTTCAAGTAAGCTTACGGAGC.....	25	0	1	1.00	1	0	1	0	0	0
.....TAGAGTTCAAGTAAGCTTACGGAG.....	24	0	1	1.00	1	1	0	0	0	0
.....TAGAGTTCAAGTAAGCTTACGGAAG.....	25	2	1	1.00	1	1	0	0	0	0
.....TTCCTACTTTTACTTGATCT.....	20	0	11	0.73	8	0	1	7	0	0
.....TTCCTACTTTTACTTGATCTTAA.....	23	1	11	0.64	7	1	0	6	0	0
.....TCCTACTTTTACTTGATCTT.....	20	0	11	0.27	3	0	0	3	0	0
.....TTCCTACTTTTACTTGATCTTAAA.....	24	2	11	0.18	2	0	0	2	0	0
.....TTCCTACTTTTACTTGATCTC.....	21	1	11	0.18	2	0	0	0	0	2
.....CCTACTTTTACTTGATCTT.....	19	0	11	0.18	2	0	1	1	0	0
.....TCCTACTTTTACTTGATCTTA.....	21	0	11	0.18	2	0	0	2	0	0
.....TTTTCCTACTTTTACTTGATCC.....	22	1	11	0.09	1	0	0	1	0	0
.....TCCTACTTTTACTTGATCT.....	19	0	11	0.09	1	0	0	1	0	0
.....CCTACTTTTACTTGATCTTA.....	20	0	11	0.09	1	0	1	0	0	0
.....CCTACTTTTACTTGATCTTATCTA.....	24	1	11	0.09	1	0	0	1	0	0
.....CTACTTTTACTTGATCTTATCC.....	22	1	11	0.09	1	1	0	0	0	0
.....CTACTTTTACTTGATCTTATC.....	21	0	11	0.09	1	0	1	0	0	0
.....CTACTTTTACTTGATCTTATCTA.....	23	1	11	0.09	1	0	0	1	0	0
.....TCCTACTTTTACTTGATCTTAA.....	22	1	11	0.09	1	0	0	1	0	0
.....TTCCTACTTTTACTTGATCTTT.....	22	1	11	0.09	1	0	0	1	0	0

Anti-sense strand reads

GTCTCTTTTTGAATCACTATCAGCGTCCTAGTATTTTTAGTGTAGAATATACGTCTCATCTCAAGTTCATTCGAATGCCTCGCAATATTTAGCTTTAAAAGGATGAAAATGAACTAGAATAGAGCCGCATATTTATTTAGAATTTTTTTATGTTTAGTTGTAAAAAAGATTAGTAAGGT	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo
**********...(((((((((.(((..(((.((((((((((..((.((((.(((.........))).)))))).))))))))).)))..))).)))))))).**********						
.....TTAGCTTTAAAAGGATGAAAA.....	21	0	7	0.14	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3393408-3393586 -	dwi_193	CAGAGAAAAACTTAGTGATAGTCGCAGGATCATAAAAATCACATCTTATATGCAGAGTAGAGTTCAAGTAAGCTTACGGAGCGTTATAAATCGAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAATAAATCTTAAAAAAATACAAATCAACATTTTTTCTAATCATTCCA

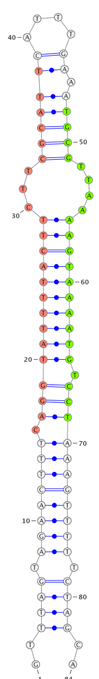
Generated: 09/08/2015 at 08:05 PM

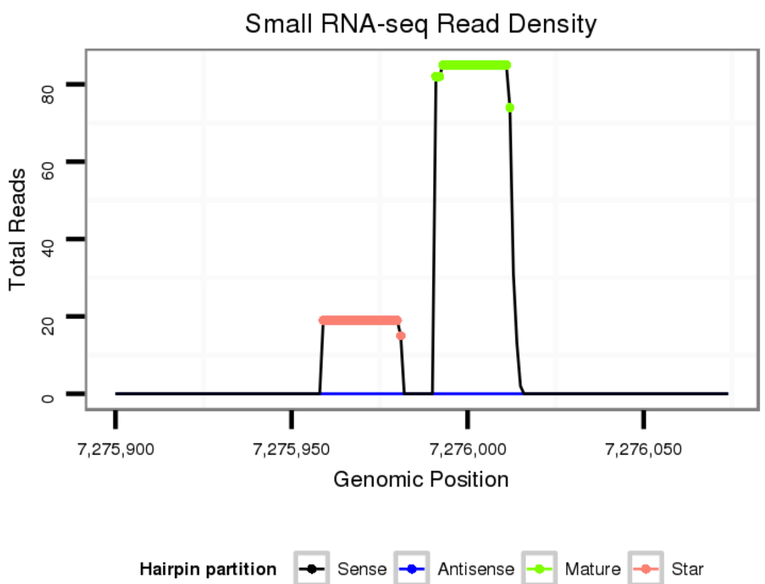
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

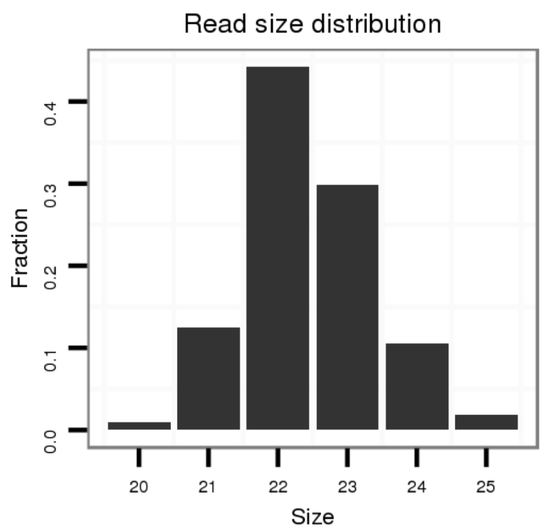
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_200	**scf2_1100000004902:7275950-7276024 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

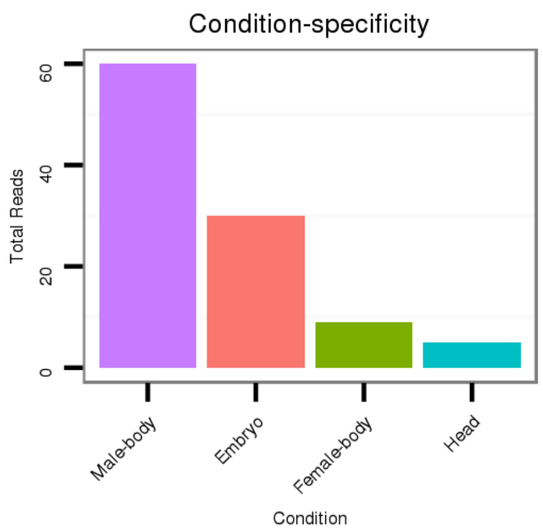
Legend: mature star **mismatch in alignment** mismatch in read

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

GTGCAACAAACATAAGATAAATAATAATTAAATAAATCAACCAAGTTTAGTAGAACTTTCAGGTATTTTACTTCTTCGCATTCATTTGAAATGCGTTAAAAGTAAAATGTCCTAAAGTTTTTCTAGCATCACTTCATGTCTTAAAGTAATAATAACTTAACTCTAAAAAGTCTTG	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	V118 embryo	M045 female body	V119 head	M020 head
**********..((((.(((((((((.(((((((((((((...(((((((....)).)))))....))))))))))).))))))))))).))))..**********										
.....TGCGTTAAAAGTAAAATGTCCT.....	22	0	1	42.00	42	35	4	3	0	0
.....TGCGTTAAAAGTAAAATGTCCTA.....	23	0	1	16.00	16	6	8	1	1	0
.....CAGGTATTTTACTTCTTCGCATT.....	23	0	1	15.00	15	2	9	1	1	2
.....TGCGTTAAAAGTAAAATGTCCTAA.....	24	0	1	11.00	11	2	6	2	1	0
.....TGCGTTAAAAGTAAAATGTCC.....	21	0	1	11.00	11	9	2	0	0	0
.....CAGGTATTTTACTTCTTCGCAT.....	22	0	1	4.00	4	2	0	2	0	0
.....CGTTAAAAGTAAAATGTCCTA.....	21	0	1	2.00	2	2	0	0	0	0
.....TGCGTTAAAAGTAAAATGTCCTAAA.....	25	0	1	2.00	2	1	1	0	0	0
.....CGTTAAAAGTAAAATGTCCT.....	20	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

CACGTTGTTTGTATTCTATTTATTATTAATTTATTTAGTTGGTTCAAATCATCTTGAAAGTCCATAAAATGAAGAAGCGTAAGTAAACTTTACGCAATTTTCATTTTACAGGATTTCAAAAAGATCGTAGTGAAGTACAGAATTTCATTATTATTGAATTGAGATTTTTCAGAAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	V118 embryo	V117 male body	V119 head
**********..((((.(((((((((.(((((((((((((...(((((((....)).)))))....))))))))))).))))))))))).))))..**********									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004902:7275900-7276074 +	dwi_200	GTGCAACAAACATAAGATAAATAATAATTAAATAAATCAACCAAGTTTAGTAGAACTTTCAGGTATTTTACTTCTTCGCATTCATTTGAAATGCGTTAAAAGTAAAATGTCCTAAAGTTTTTCTAGCATCACTTCATGTCTTAAAGTAATAATAACTTAACTCTAAAAAGTCTTG

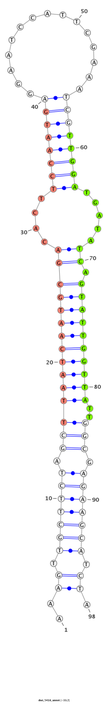
Generated: 09/08/2015 at 07:41 PM

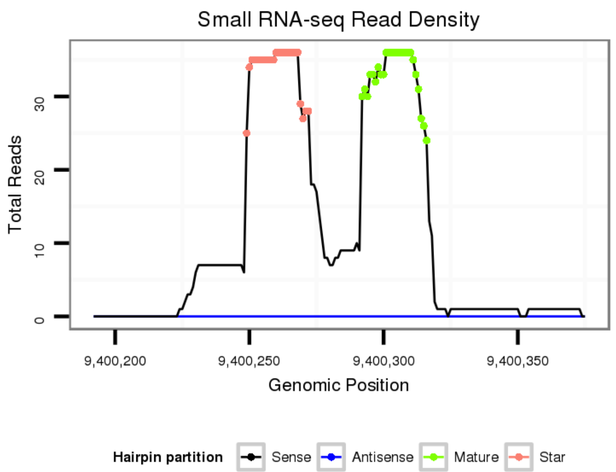
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

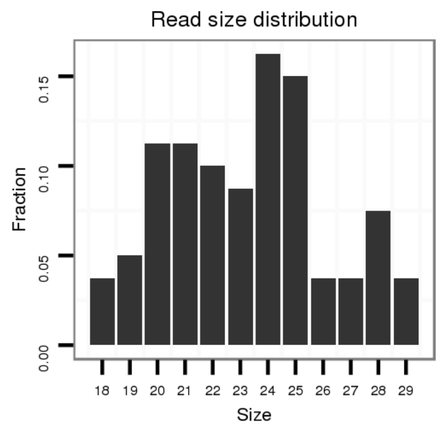
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_5416	**scf2_1100000004902:9400242-9400325 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

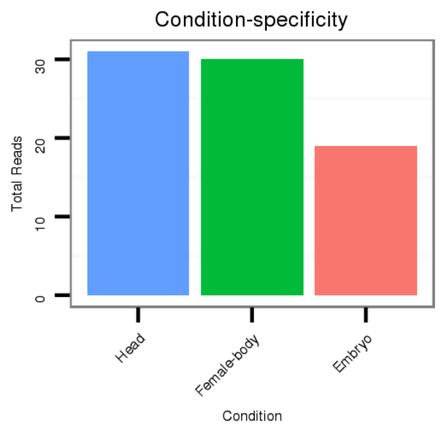
Legend: mature star mismatch in alignment mismatch in read

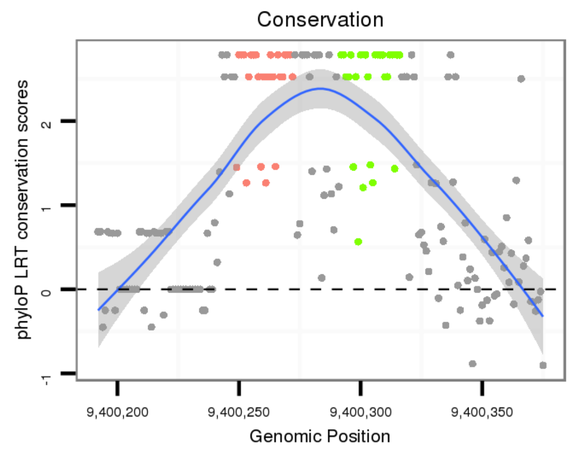
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTAAACGGCTCTTCATTAAGGCTAGCGTTTTTTCATGTTGTTAAAGTTGCTTCTAGCTTAATCAATGCGACACTTCCAATGAGGAATCCATTCGAAATCGTTGGATGATATCAGTATTGGTTATTGGCGAGAAGCATCTAAAAGCAGCTTTAAGTTAACAAACAATTAGATTGTTAAGCATTAT **********..((.(((((((.(((((((((((((((....(((((((.............)))))))).....)).)))))))))..)))).)))))))..)).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	V119 head	V118 embryo	M020 head	V117 male body
.....TTGGATGATATCAGTATTGGTTATT.....	25	0	1	11.00	11	1	4	6	0	0
.....TTAATCAATGCGACACTTCC.....	20	0	1	7.00	7	3	1	3	0	0
.....TTAATCAATGCGACACTTCCAATG.....	24	0	1	6.00	6	3	1	0	2	0
.....TAATCAATGCGACACTTCCAATG.....	23	0	1	6.00	6	0	2	2	2	0
.....TTGGATGATATCAGTATTGGTT.....	22	0	1	4.00	4	0	4	0	0	0
.....TTAATCAATGCGACACTTCCAATGAGGA.....	28	0	1	3.00	3	1	0	2	0	0
.....GATGATATCAGTATTGGTTATTGG.....	24	0	1	3.00	3	3	0	0	0	0
.....TTAATCAATGCGACACTTCCAATGAGGAA.....	29	0	1	3.00	3	2	0	1	0	0
.....TTGGATGATATCAGTATTGGT.....	21	0	1	2.00	2	0	2	0	0	0
.....TTAATCAATGCGACACTTCCA.....	21	0	1	2.00	2	0	1	1	0	0
.....TGTTAAAGTTGCTTCTAGC.....	19	0	1	2.00	2	0	1	1	0	0
.....AGGAATCCATTCGAAATCGTTGGA.....	24	0	1	2.00	2	1	0	0	1	0
.....TTAATCAATGCGACACTTCCAATGAGG.....	27	0	1	2.00	2	2	0	0	0	0
.....ATCAGTATTGGTTATTGG.....	18	0	1	2.00	2	0	0	0	2	0
.....GATATCAGTATTGGTTATTGG.....	21	0	1	2.00	2	2	0	0	0	0
.....TTGGATGATATCAGTATTGGTTAT.....	24	0	1	2.00	2	1	0	1	0	0
.....TGATATCAGTATTGGTTATTG.....	21	0	1	1.00	1	0	0	0	1	0
.....GTTAAAGTTGCTTCTAGC.....	18	0	1	1.00	1	0	0	1	0	0
.....TAATCAATGCGACACTTCC.....	19	0	1	1.00	1	1	0	0	0	0
.....TATCAGTATTGGTTATTGG.....	19	0	1	1.00	1	1	0	0	0	0
.....TAATCAATGCGACACTTCCAATGAGG.....	26	0	1	1.00	1	1	0	0	0	0
.....CGTTGGATGATATCAGTATTG.....	21	0	1	1.00	1	0	0	1	0	0
.....TTGTTAAAGTTGCTTCTAGC.....	20	0	1	1.00	1	0	0	1	0	0
.....TGATATCAGTATTGGTTATTGGCGAGA.....	27	0	1	1.00	1	1	0	0	0	0
.....TTGGATGATATCAGTATTGG.....	20	0	1	1.00	1	1	0	0	0	0
.....TCATGTTGTTAAAGTTGCTTCTAG.....	24	0	1	1.00	1	0	1	0	0	0
.....TTGGATGATATCAGTATTGGTTA.....	23	0	1	1.00	1	0	1	0	0	0
.....ATCAGTATTGGTTATTGGC.....	19	0	1	1.00	1	0	1	0	0	0
.....AATCAATGCGACACTTCCA.....	19	0	1	1.00	1	1	0	0	0	0
.....TGATATCAGTATTGGTTATTGG.....	22	0	1	1.00	1	1	0	0	0	0
.....TGAGGAATCCATTCGAAATCGTTGGA.....	26	0	1	1.00	1	1	0	0	0	0
.....GACACTTCCAATGAGGAATC.....	20	0	1	1.00	1	0	0	1	0	0
.....TGAGGAATCCATTCGAAATCGTTGGATG.....	28	0	1	1.00	1	0	0	0	1	0
.....TTCGAAATCGTTGGATGA.....	18	0	1	1.00	1	0	0	0	1	0
.....TTAATCAATGCGACACTTCCAATGAG.....	26	0	1	1.00	1	1	0	0	0	0
.....ATGTTGTTAAAGTTGCTTCTAGC.....	23	0	1	1.00	1	0	1	0	0	0
.....CAATTAGATTGTTAAGCATT..	20	0	1	1.00	1	0	0	0	0	1
.....AATGAGGAATCCATTCGAAATCGTTGGA.....	28	0	1	1.00	1	1	0	0	0	0
.....TTAATCAATGCGACACTTCCAA.....	22	0	1	1.00	1	0	0	1	0	0
.....CGAAATCGTTGGATGATATCAGTATTGG.....	28	0	1	1.00	1	1	0	0	0	0
.....TGGATGATATCAGTATTGGTTATTG.....	25	0	1	1.00	1	0	1	0	0	0
.....TAATCAATGCGACACTTCCAAT.....	22	0	1	1.00	1	0	1	0	0	0
.....GAGGAATCCATTCGAAATCGTT.....	22	0	1	1.00	1	0	0	0	1	0
.....TTAATCAATGCGACACTTCCAAC.....	23	1	1	1.00	1	0	0	0	1	0
.....GCATCTAAAAGCAGCTTTAAGTTAAC.....	26	0	1	1.00	1	1	0	0	0	0
.....ATGAGGAATCCATTCGAAATC.....	21	0	1	1.00	1	0	1	0	0	0
.....TGTTGTTAAAGTTGCTTCTAGC.....	22	0	1	1.00	1	0	0	1	0	0
.....TTCGAAATCGTTGGATGG.....	18	1	3	0.33	1	0	0	0	1	0

Anti-sense strand reads

AATTTGCCGAGAAGTAATTCCGATCGCAAAAAAGTACAACAATTTCAACGAAGATCGAATTAGTTACGCTGTGAAGGTTACTCCTTAGGTAAGCTTTAGCAACCTACTATAGTCATAACCAATAACCGCTCTTCGTAGATTTTCGTCGAAATTCAATTGTTTGTTAATCTAACAATTCGTAATA **********..((.(((((((.(((((((((((((((....(((((((.............)))))))).....)).)))))))))..)))).)))))))..)).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	V117 male body	V118 embryo
Show Alignment With Reads								

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004902:9400192-9400375 +	dwi_5416	TTAAACGGCTCTTCATTAAGGCTAGCGTTTTTTCATGTTGTTAAAGTTGCTTCTAGCTTAATCAATGCGACACTTCCAATGAGGAATCCATTCGAAATCGTTGGATGATATCAGTATTGGTTATTGGCGAGAAGCATCTAAAAGCAGCTTTAAGT----------TAACAAAC----------AATT-AGATTGTTAAGC----------ATTAT
droVir3	scaffold_13047:9559462-9559617 -	dvi_24635	TTCGACGAC--------AAAGCGAGCGATT----------GGG--TTTCTAGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTCGAAATCGTTGGATGTTCTCAGTATTGGTTATTGGCCAGAAGAACCCAAACACAGCTATAAGA---------.....AAC----------..CAAAAAT-A-.....AAATAAACA--ACAA
droMoj3	scaffold_6540:7667621-7667779 -	dmo_270	----------TTCTAGCTTAACCAATGTGGCACCTCCAATGAAAAATCAATTCGAAATCGTTGGATGTTCTCAATATTGGTTATTGGCCAGAAGAGCTCAAACACAGCTATAAG---------.....AAAC----------GAAACCATCAAATATATGATATAA--ACTCTGAAATTA-AATAGCATAGATTTT
droGri2	scaffold_14906:2448916-2449060 -	dgr_463	----------TTCTAGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTGCAATCGTTGGATGTTCTCAGTATTGGTTATTGGCCAGATGAATCAAACACAGCAATAATT---------.....AAAA-------CCAAATACA--ACAACAAAAAACTC---.....TAA-AATAT--AGTAT
dp5	2:16675565-16675695 -		----------GTCTCTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTTGGACGTTCTCAGTATTGGTTATTGGCAAGAAGAGCCCACAGGCAGCTATAAGAGTTACAATTG--------.....----.----------.....TAAAGATAGA-TTAG
droPer2	scaffold_0:3721655-3721785 +		----------GTCTCTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTTGGACGTTCTCAGTATTGGTTATTGGCAAGAAGAGCCCACAGGCAGCTATAAGAGTTACAATTG--------.....----.----------.....TAAAGATAGA-TTAG
droAna3	scaffold_12911:3664272-3664396 -	dan_200	----------TTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGTCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGGCCCGAGACAACTGTTGTC---------C---ACCC----------ACTCT-----AGTCC--.....GTTCT
droBip1	scf7180000396640:523316-523439 -		----------TCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGTCCTTGGATGCTCTCAGTATTGGTTTTGGCGAGATTGGGCCCGGGGCAACTGTTGTC---------T---ACCC----------AGTCT-----AGTCC--.....ATTCT
droKik1	scf7180000302810:681879-682036 +		----------GCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGGAATCAATTGCAAGTCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGGCCCCAGGCAGCTATAGT---------....TGT----------TGTTCCGCTTAGTCCGAGTAATTT--TCCCCCAATTTA-GTTGTCGCA-CCAC
droFic1	scf7180000454114:125813-125969 +		----------GCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGGCCCGAGGCAGCGGTATT---------....GGGCACTAG------ACCCTATAGTTCCGATCAGTCCGAATTTG----------AACCCAACA-CCCC
droEle1	scf7180000491194:1479880-1480041 +		----------GCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGACGTTGGATGCTCTCAGTATTGGTTATTGGCAAGATTGGGCCCGAGACAGCAGTATTC---------T---AGGCACTTGGATACCAATCCAATAGTTCCGATCAGTCCGACTTTAA----------TAC--CCTCC
droRho1	scf7180000779322:264808-264944 -		----------GCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATAGGCCCTAGGCAGCAATATTT---------....AGGCACTGG------TACCCATAGTTCCGATCAGTCC--.....-----
droBia1	scf7180000302035:101942-102072 +		----------GCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCTGTATTGGTTATTGGCGAGATTGGGCCCGAGGCAGCGTCACTAG-------GT-CTAGGC----------AGTTCCGATCAGTCC--.....-----
droTak1	scf7180000415712:510704-510851 +		----------GCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGTTTGGCCCCGAGGCAGCATAACT---------....ATAT-------CTAGATCCG--GGTTCCGATCAGTCCGAGTTAAA----------.....C--CCCCT
droEug1	scf7180000409488:463405-463556 -		----------GCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGGCCCGAGACAGCATTTCT---------....AAGC----------AGTTTCGTTCAGTCCGAGTTAAAACTCCCCTCGATTTA-GACA------.....
dm3	chr3R:27444094-27444225 +		----------GCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGGCCCGGGACAGCATTACT---------....AGAC----------AGTTCCGATCAGTCCGCACTA----------.....----A
droSim2	3r:26724067-26724198 +		----------GCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGGCCCGGGACAGCATTACT---------....AGAC----------AGTTCCGATCAGTCCGCACTA----------.....----A
droSec2	scaffold_2807:1136-1267 +		----------GCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGGCCCGGGACAGCATTACT---------....AGAC----------AGTTCCGATCAGTCCGCACTA----------.....----A
droYak3	3R:28380208-28380332 +		----------GCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGGCCCGGGACAGCATTACC---------....AGAC----------CGTTCCGATTAGTCC--.....-----
droEre2	scaffold_4820:530482-530613 -		----------GCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGGCCCGGGGCAGCATAACT---------....AGAC----------AGTTCCGATCAGTCCGCACTA----------.....----A

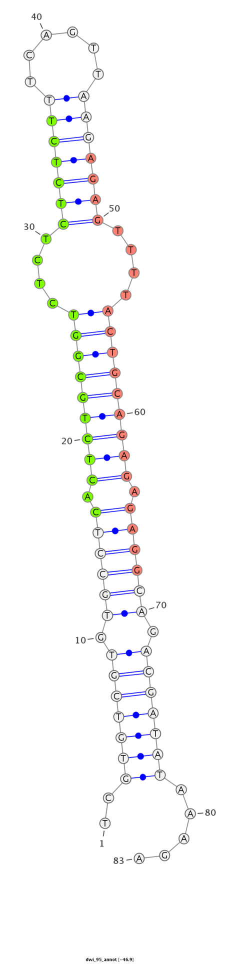
Generated: 09/08/2015 at 07:49 PM

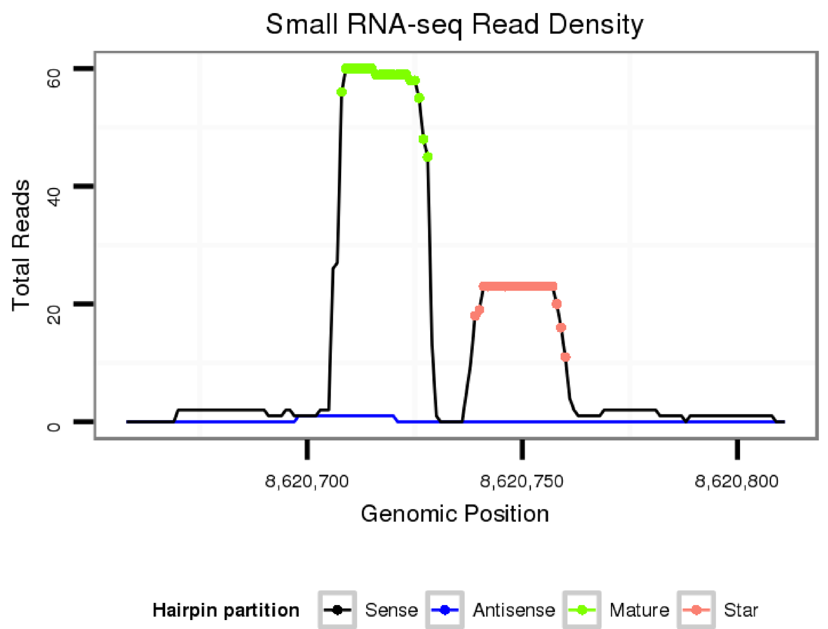
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	7
rescue.candidate	5

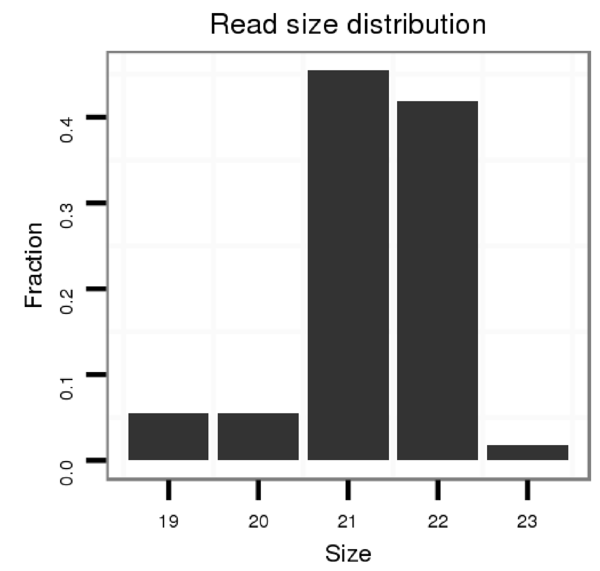
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_95	**scf2_1100000004511:8620708-8620761 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

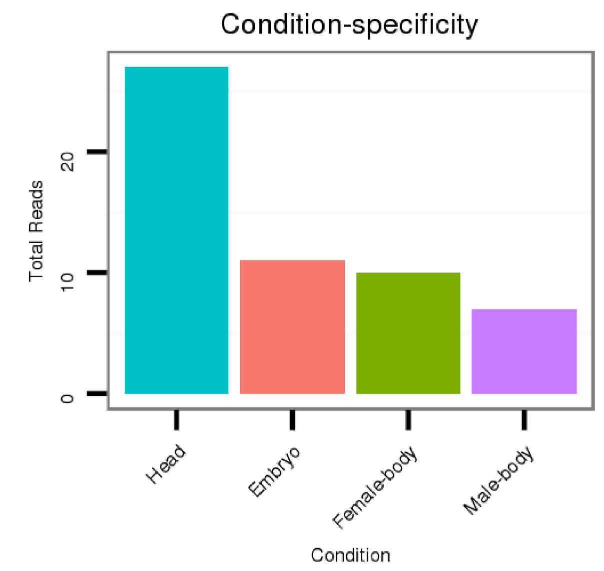
Legend: mature star mismatch in alignment mismatch in read

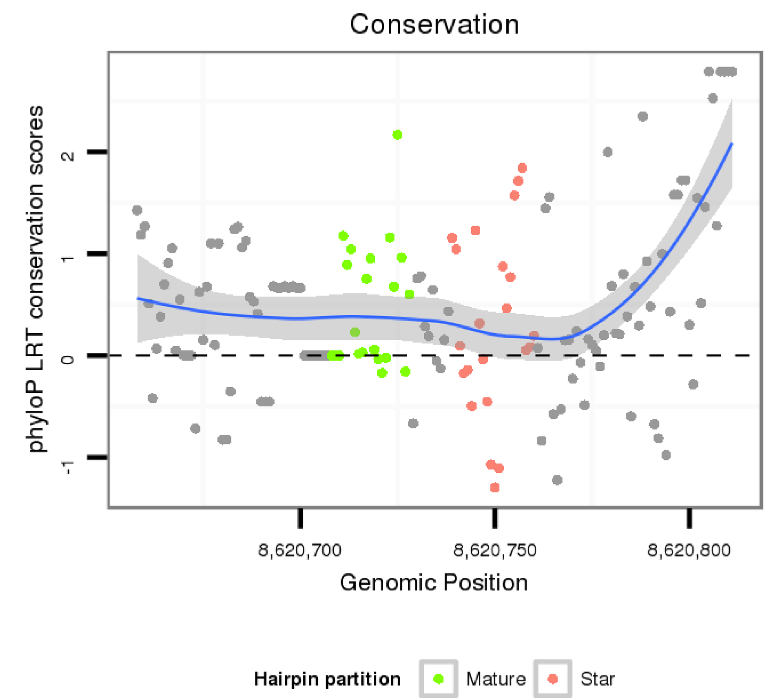
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TGACTGAACGGACGGGTGTCCGGTTCACAGAGTTTTCGTGTCGTGTGCCTCACTCTGCGGTCTCTCTCTCTTTCAGTTAAGAGAGTTTTACTGCAGAGAGAGGCAGACGATATAAAGAGAAAGAGCGTGCAAAACCTACGTAATGAAACGTAAA	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	M045 female body	V118 embryo	V119 head	V117 male body
**********************************..(((((((.((((((.(((((((((....(((((((......)))))))....))))))))).)))))).))))))).....*************************************										
....CACTCTGCGGTCTCTCTCTCT...	21	0	1	19.00	19	10	3	3	0	3
....CTCACTCTGCGGTCTCTCTCTCT...	23	0	1	12.00	12	7	3	2	0	0
....CACTCTGCGGTCTCTCTCTCTT..	22	0	1	9.00	9	2	5	1	1	0
....AGAGTTTTACTGCAGAGAGAGG...	22	0	1	6.00	6	0	0	0	5	1
....CTCACTCTGCGGTCTCTCTCT...	21	0	1	6.00	6	2	2	1	1	0
....CACTCTGCGGTCTCTCTCTCC...	21	1	1	4.00	4	4	0	0	0	0
....GAGAGTTTTACTGCAGAGAGAG..	22	0	1	4.00	4	0	0	3	0	1
....CTCACTCTGCGGTCTCTCTCTT..	22	1	1	3.00	3	1	2	0	0	0
....AGAGAGTTTTACTGCAGAGAG..	21	0	1	3.00	3	0	0	3	0	0
....CTCACTCTGCGGTCTCTCTCTC..	22	0	1	3.00	3	1	1	0	1	0
....AGTTTTACTGCAGAGAGAG..	19	0	1	2.00	2	0	0	0	2	0
....CTCACTCTGCGGTCTCTCTC..	20	0	1	2.00	2	0	1	0	1	0
....ACTCTGCGGTCTCTCTCTCTT..	21	0	1	2.00	2	0	1	0	1	0
....AGAGAGTTTTACTGCAGAGAGA...	22	0	1	2.00	2	0	1	0	0	1
....GCAGACGATATAAAGAGAAAGA..............................	22	0	1	1.00	1	0	0	0	0	1
....CTCACTCTGCGGTCTCTCTCTCTT..	24	0	1	1.00	1	0	1	0	0	0
.....................................GTGTCGTGTGCCTCACTCTGC..	21	0	1	1.00	1	0	1	0	0	0
....AAACCTACGTAATGAAACGT...	20	0	1	1.00	1	0	0	0	0	1
....CACTCTGCGGTCTCTCTCTCG...	21	1	1	1.00	1	1	0	0	0	0
....AGAGTTTTACTGCAGAGAGA...	20	0	1	1.00	1	0	0	0	1	0
....TGCCTCACTCTGCGGTCTCTC..	21	0	1	1.00	1	0	1	0	0	0
....ACTCTGCGGTCTCTCTCTCTTT...	22	0	1	1.00	1	0	0	0	1	0
....TCACTCTGCGGTCTCTCTC..	19	0	1	1.00	1	0	1	0	0	0
....CACTCTGCGGTCTCTCTCTCTTG...	23	1	1	1.00	1	0	1	0	0	0
....AGAGTTTTACTGCAGAGAGAGGC..	23	0	1	1.00	1	0	0	0	1	0
....GAGAGTTTTACTGCAGAGAGAGTT..	24	2	1	1.00	1	0	1	0	0	0
....ACTCTGCGGTCTCTCTCTCT...	20	0	1	1.00	1	1	0	0	0	0
....GAGAGTTTTACTGCAGAGAGAGT...	23	1	1	1.00	1	0	0	1	0	0
....CACTCTGCGGTCTCTCTCT...	19	0	1	1.00	1	1	0	0	0	0
............CGGGTGTCCGGTTCACAGAGT...	21	0	1	1.00	1	0	0	0	0	1
....CTCACTCTGCGGTCTCTCC...	19	1	1	1.00	1	0	0	0	1	0
....AGTTTTACTGCAGAGAGAGG...	20	0	1	1.00	1	0	0	0	0	1
....AGAGTTTTACTGCAGAGAGAGGT..	23	1	1	1.00	1	0	0	1	0	0
....ATAAAGAGAAAGAGCGTGC........................	19	0	1	1.00	1	0	0	1	0	0
....CTCACTCTGCGGTCTCTCTCTCTG..	24	1	1	1.00	1	0	1	0	0	0
............CGGGTGTCCGGTTCACAGAGTTTTCGT...	27	0	1	1.00	1	0	0	1	0	0
....AGAGTTTTACTGCAGAGAGAGT...	22	1	1	1.00	1	0	0	0	0	1
....GAGTTTTACTGCAGAGAGAGGC..	22	0	1	1.00	1	1	0	0	0	0
....GAGAGTTTTACTGCAGAGAGA...	21	0	1	1.00	1	0	0	1	0	0
....CTCACTCTGCGGTCTCTCTCC...	21	1	1	1.00	1	1	0	0	0	0
....AGTTTTACTGCAGAGAGAGGCA...	22	0	1	1.00	1	0	0	0	1	0
....CTCACTCTGCGGTCTCTCTCTCC...	23	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

ACTGACTTGCCTGCCCACAGGCCAAGTGTCTCAAAAGCACAGCACACGGAGTGAGACGCCAGAGAGAGAGAAAGTCAATTCTCTCAAAATGACGTCTCTCTCCGTCTGCTATATTTCTCTTTCTCGCACGTTTTGGATGCATTACTTTGCATTT	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	M020 head	M045 female body
**********************************..(((((((.((((((.(((((((((....(((((((......)))))))....))))))))).)))))).))))))).....*************************************								
....AGCACACGGAGTGAGACGCCAGA...	23	0	1	1.00	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:8620658-8620811 +	dwi_95	TGACTGAACG-G------ACGGGTGTCCGGTT-------CACAGAG--------TTTTCGTGTCGTGTGCCTCACTCT--GCGGTCT--------CTCTC------TCTTTCAGTTAAGAGAGTTTTAC---T---G-------C----AGAGA---GAG--------GCAGACGATATAAAGA--GAAAGAGCGTGC----AAAACCTA---CGTAAT------------GAAACGTAAA
droVir3	scaffold_13049:22853408-22853518 +		TGACATT-CG-G------G----TATCCGGCT-------CGTGCGC-----------------------------TCTTCGTACTCG-CTTTG--TGCTC--------TCTTTGCGTGT------------------------------AGAGAG--TCGCATAAGAGAACTTGTGTGT------------AGCGTAACG-G------TGTGCAACGTAAA
droMoj3	scaffold_6680:17469614-17469740 +		TC-------G-G------G----TGTCCGAAC-------CGTGTGC-----------------------------TCT-----------------TG-------------CTTGCTCTGTGCATCTGAG---A---G-------A-----GA---GCGAGAGAGAGAGAGAGG-------------------------A----AGACGCGCGAGAGAGTTGCTTAAGAGAGGTTT-TTGT------------CACGTAACG-G------AGTGCAACGTAAA
droGri2	scaffold_15110:18127538-18127661 +		TGACATT-------------------------------CGTGTGTTCATCGTCGGGTCGTGTCG----------------------------GGTTCTCTTTTTA--CACTTACTCT-------T-GA---CGCGCTCTTAGCG-GAAAGAGAG--TCTCTTAAGAGAATATACGCGTAACGAA-------------T--G------GCTGCGACGTAAA
dp5	XR_group6:11798026-11798151 +		TGACGGAGCG-A------G----TGTCTGCACTCTTTTTCG--AG--------TGTTC--------GTTTCCCAAAGAGAGTCGC------------------CTTAAGAGAG-------------------------TC--------------------------------------AGCGACAAGAGAGTGA--GAGAGAGTAGCG----AGAGCCTA---CGTAGTGGG------CCTGCAACGTAAA
droPer2	scaffold_20:1719312-1719434 +		TGACGGAGCG-A------G----TGTCTGCACTCTTTTTCG--TG--------TGTTC--------GTTTCCCAAAGAGCGCCTTAA---------------------GAGAG-------------------------TC--------------------------------------AGCGACAAGAGAGTGA--GAGAGAGTAGCG----AGAGCCTA---CGTAGTGGG------CCTGCAACGTAAA
droAna3	scaffold_13337:19376485-19376619 +		GGCTGTCGC--------------TGT-------------CGCGTGC-----------------------------TCA--ACGCTCT--------TTCA---------TCTTTGCGCTTATAT-TTTGT---T---T-------TTA--AGAGAGCG------------TC-TCCGTGATTC--------------------------------------AGCGAGAAG----------------------------CGCGATAACG----------------------------AGTTAACCTACGTAGCCGACCGTCCTCCGCAACGTAAA
droBip1	scf7180000396360:570259-570409 +		TGACTGAGAGTCTCGGGGA---CTGT-------------CGCGTGC-----------------------------TTA--GCGCTCT--------TTCA---------TCTTTGC-----GCTTATTTG---T---T-------TTTTAAGAGAGCGAGAGAGAGAGAGCCATCC---AT--CCAGCG----AGACGCGATAACG----------------------------AGTTAACCTACGTAGTAGC-CGTCCTCCGCAACGTAAA
droKik1	scf7180000302391:602951-603100 +		TGATGGAGCGAC------A----GGG-------------AGCGTAC-----------------------------TCT--TAGCTCGGCATGGGATTCTC--------TTTCTATCGAGAGAGCG-----------A-------TCTTAAGAGAG-------------------------TGATCTAAAATAAGAGAGTTACCATGAGAG---------------------TGCAA--ATGAACACAACGAGCGAGTAACCCTA---CGTAG--------------TAACGTAAA
droFic1	scf7180000454113:2427375-2427473 +		TGACGGAG-G-A------A---TGGT-------------CGCGTGC-----------------------------TCT--GCACTCC--------CGCTC--------TCTTTGCTAAGAGAACTT-GATGAA---G-------AAG----A---GAG---------------GGAGAGCG----AGAGAGCAAC-----------------G----------------------------AG---------------------------TAACGTAAA
droEle1	scf7180000491193:4161765-4161869 -		TGACGGAGCG-A------A----TGT-------------CGCGTGC-----------------------------G-----CGC-----------TGCTC--------TTTTTGCTAAGAGAACCTTGA---A---T-------A-----AA---GAG---------------GGAGAGTAA--GAGAGAGCAGCG----AGAGGCTAGAGCG----------------------------AG---------------------------TAACGTAAA
droRho1	scf7180000773422:45749-45854 +		TGACGGAGCG-A------A----TAA-------------CGCGTGC-----------------------------G-----CGC-----------TGCTC--------TCTTTGCTAAGAGAACCTTGA---A---T-------AAA----A---GAC---------------GGAGAGTAA--AAGAGAGCAGCG----AGAGGCTAAAGCG----------------------------AG---------------------------TAACATAAA
droBia1	scf7180000302193:5791902-5792026 +		TGACGGAGCCTA------A----TGT-------------CGCGTGC-----------------------------TCT--GCACTCG--------TGCGC------TCTCTTCGCTAAGAGAGCCTTGC---T---G-------CAGTGCGG---GCGC---------GGAGGAGCTCAAGA--GAGAGCGCGGCG----AGAGGCGAGAGCG----------------------------AG---------------------------TAACGTAAA
droTak1	scf7180000415254:687935-688042 +		TGACAGAGCG-A------A----TGT-------------CGCGTGC-----------------------------TCT--GCACTCG--------CGCTC--------TCTTCGCTAAGAGAACCTTGA---A---T-------ACG--TGAGAGCGG--GAGAGAGCAACG----AGAGGCGAGAGCG----------------------------AG---------------------------TAACGTAAA
droEug1	scf7180000409466:5057747-5057862 +		TGACGGAGCG-A------A----TGT-------------CGCGTGC-----------------------------TCT--GCACTCG--------TGCTC------TTTCTTTGCTAAGAGAACCTTGA---A---A-------T-----AA---GATA-------------AAGAGAGCGGGA-GAAGAGCAACG----AGTGACAAGAACG----------------------------AG---------------------------TAACGTAAA
dm3	chr3L:19890665-19890781 -		TGACAA--CG-A------A----TGT-------------CGCGTGC-----------------------------TCT--GCACTAG--------TGCTC--------TCTTTGCTAAGAGAACCTTGA---A---T-------TT-TGAAT---GAGT-------------AAGGGAGCGGGAGAGAGAGCAACG----AGAGCCAAGAGCG----------------------------AG---------------------------TAACGTAAA
droSim2	3l:19484575-19484691 -		TGACAA--CG-A------A----TGT-------------CGCGTGC-----------------------------TCT--GCACTCG--------CGCTC--------TCTTTGCTAAGAGAAACTTGA---G---T-------TTTTGAAA---GAGT-------------TAGGGAACGGGA-AGAGAGCAACG----AGAGCCAAGAGCG----------------------------AG---------------------------TAACGTAAA
droSec2	scaffold_29:535924-536040 -		TGACAA--CG-A------A----TTT-------------CGCGTGC-----------------------------TCT--GCACTCG--------CGCTC--------TCTTTGCTAAGAGAAACTTGA---G---T-------TTTTGAAA---GAGT-------------AAGGGAGCGGGA-AGAGAGCAACG----AGAGCCAAGAGCG----------------------------AG---------------------------TAACGTAAA
droYak3	3L:20686595-20686702 +		TG-----------------------T-------------CGCGTGC-----------------------------TCT--GTACTCG--------CGCTC--------TTTTTGCTAAGAGAACCTTGA---G---T-------TTAAGAAA---GAGT-------------AATGAAGCGGGAGTGAGAGCAACG----AGATGAAAGAGCG----------------------------AG---------------------------TAACGTAAA
droEre2	scaffold_4784:19628792-19628903 -		TGACAG--CG-A------A----TGT-------------CGCGTGC-----------------------------TCT--GCACCCG--------CGCTC--------TCTTTGCTAAGAGAACCTTGA---G---T-------TTG----A---GAGT-------------GTTGGAGCGG--GTGAGAGCAACG----AGAGGCAAGAGCG----------------------------AG---------------------------TAACGTAAA

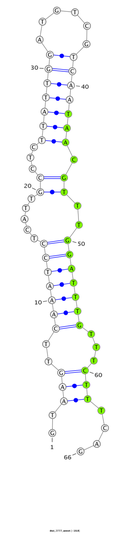
Generated: 09/08/2015 at 07:41 PM

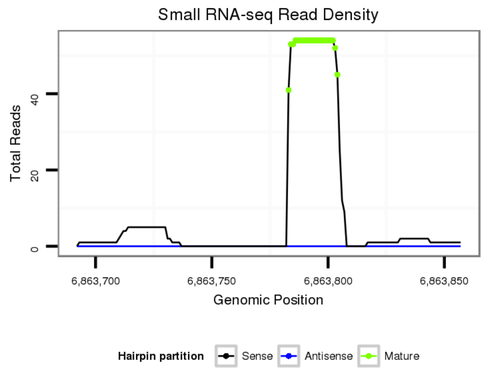
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

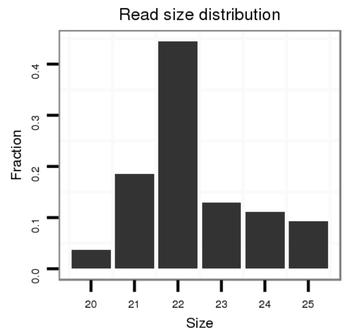
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_2777	**scf2_1100000004909:6863742-6863807 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

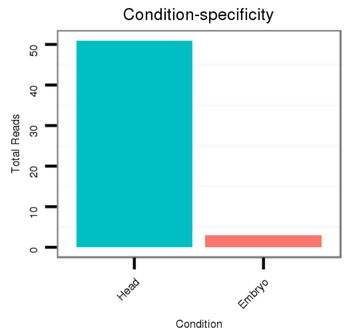
Legend: mature star mismatch in alignment mismatch in read

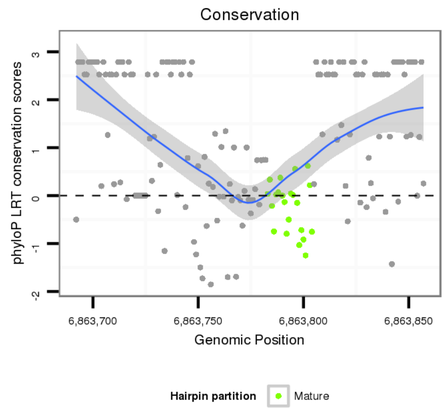
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK25732-in]; CDS [Dwil\GK25732-cds]; CDS [Dwil\GK25732-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CATACCAAAAACATGCCCAGAAACCTGGGGTTGGGGAGCCCTAATGAAAAGTAAGTTCAAATCCTCATTGCCTCTTATTGGATGTCGTCAATAACGTTTGGATTTGTTTCTTTCAGGACTGCTGGCAAATTGATCCGCACACACGACCAGGATTTAAGGAGATACTC	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V118 embryo	V119 head	V117 male body	M045 female body
**********..(((..(((((((.....((...(((((((.....)))))))..))..)))))))...)))....**********											
.....TAACGTTTGGATTTGTTTCTTT.....	22	0	1	17.00	17	16	1	0	0	0
.....TAACGTTTGGATTTGTTTCTT.....	21	0	1	7.00	7	6	0	1	0	0
.....TAACGTTTGGATTTGTTTCTTTC.....	23	0	1	7.00	7	7	0	0	0	0
.....AACGTTTGGATTTGTTTCTTTC.....	22	0	1	6.00	6	5	0	1	0	0
.....TAACGTTTGGATTTGTTTCTTTCAG.....	25	0	1	5.00	5	5	0	0	0	0
.....AACGTTTGGATTTGTTTCTTTCAG.....	24	0	1	3.00	3	1	1	1	0	0
.....AACGTTTGGATTTGTTTCTTT.....	21	0	1	3.00	3	1	0	2	0	0
.....TAACGTTTGGATTTGTTTCTTTCA.....	24	0	1	3.00	3	3	0	0	0	0
.....TAACGTTTGGATTTGTTTCT.....	20	0	1	2.00	2	2	0	0	0	0
.....CGTTTGGATTTGTTTCTTTCAGA.....	23	1	1	2.00	2	1	1	0	0	0
.....ACACGACCAGGATTTAAGGAGATACTC	27	0	1	1.00	1	0	1	0	0	0
.....AGAAACCTGGGGTTGGGGAGC.....	21	0	1	1.00	1	0	0	0	1	0
.....AAATTGATCCGCACACACGACCAGGAT.....	27	0	1	1.00	1	0	1	0	0	0
.....CGTTTGGATTTGTTTCTTTCAGA.....	23	1	1	1.00	1	0	1	0	0	0
.....CGTTTGGATTTGTTTCTTTCAGC.....	23	1	1	1.00	1	1	0	0	0	0
.....ACGTTTGGATTTGTTTCTTTCAGA.....	24	1	1	1.00	1	0	1	0	0	0
.....AAACCTGGGGTTGGGGAGC.....	19	0	1	1.00	1	0	1	0	0	0
.....ACCTGGGGTTGGGGAGCCC.....	19	0	1	1.00	1	0	1	0	0	0
.....TTTGGATTTGTTTCTTTCAGA.....	21	1	1	1.00	1	0	1	0	0	0
.....GAAACCTGGGGTTGGGGAGC.....	20	0	1	1.00	1	0	0	0	1	0
.ATACCAAAAACATGCCCAGA.....	20	0	1	1.00	1	0	0	0	0	1
.....CGTTTGGATTTGTTTCTTTCAG.....	22	0	1	1.00	1	0	1	0	0	0
.....AACCTGGGGTTGGGGAGCCCTAAT.....	24	0	1	1.00	1	0	1	0	0	0
.....TAACGTTTGGATTTGTTTCTTTCG.....	24	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

GTATGGTTTTTGTACGGGTCTTTGGACCCCAACCCCTCGGGATTACTTTTCATTCAAGTTTAGGAGTAACGGAGAATAACCTACAGCAGTTATTGCAAACCTAAACAAAGAAAGTCCGACGACCGTTTAACTAGGCGTGTGTGCTGGTCCTAAATTCCTCTATGAG	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
droWil2	scf2_1100000004909:6863692-6863857 +	dwi_2777	CATACCAAAAACATGCCCAGAAACCTGGGGTTGGGGAGCCCTAATGAAAAGTAAGTTCA-AA--TC----------CTCATTGCCT--------CTTATTGGATGTCGTCAA----------TAACGTTTGGAT----------TT----------GTT-----TCTTTCAGGCTGCTGGCAAATTGATCCGCACACACGACCAGGATTTAAGGAGATACTC
droVir3	scaffold_12970:8386548-8386713 -		GATACCAAAAACGTGCCCGGAAACCTGG------GGTGCTTTAATGAAAAGTAGTGAA-AT--TC----------ATAAGTGTCTACGTATA--------C----------AAATATGTA----------AATCAAAATATTAACGTT-TAG----------TC----------ACG-----CATTGCAGGCTGCTGGCAAACGCATCCGCATAGACGGCCGCAGTTTAAGAAGATTATT
droMoj3	scaffold_6482:886335-886485 +		GATACCAAAAACGTGCCCGGAAACGTGG------GCGCTCTTATGAAGCAGTGAGTCGCA-AT--TGCGA----------ATTATCAACAGAAG----------AT----------C----------CGATGCTAATAC-----TC----------TTA----------ATC-----CTTGCAGGCTGCTGGCAAACGCATCCGCACACACGCCAGATTTCAAGAAGATCATC
droGri2	scaffold_14853:8224667-8224887 +		GATACCAAAAACGTGCCCGGAAACGTGG------GCAGCCCTCATGAAAAGTGAGTGCA-AA--TG------AG----------TAGAAAGAGCAACAAGTTGCAAACACAT----------CCA--------T--------GACATTTTGGCCTTGGTTAAACTA-----TGGATGGGATTCAT---CT--TGAGATTAACGCACAATATTCACATTTGGTT----------TC-----TCTTGCAGGCTGCTGGCAAATGATCCGCATTTACGACGCAGTTTAAGAAGATTATT
dp5	XL_group1e:4001325-4001499 -		GATACCAAAAACGTGTCCCGAAACCTGG------GGATGTCTTATGAAGCAGTAAGTCTT-C---TC----------CGCAT-----C----CCCCCCATGCA-GATGCA-----TGTTTGTGATTGATTCCCCTCATAT----------ATATATA--TA----------AGC----------CTC-----TATTTCAGGCTGCTGGCAAACGCGATCCGCACAAACGACCGGGATTCAAGGAATACTC
droPer2	scaffold_17:936288-936464 -		GATACCAAAAACGTGCCCGAAACCTGG------GGATGTCTTATGAAGCAGTAAGTCTT-C---TC----------CGCAT-----C----CCCCCCATACA-GATGCA-----TGTTTGTGATTGATTCCCCTCATAT----------ATATATATTA----------AGC----------CTC-----TATTTCAGGCTGCTGGCAAACGCGATCCGCACAAACGACCGGGATTCAAGGAATACTC
droAna3	scaffold_13417:406515-406665 -		GATACCAAAAACGTGCCCGGAAACCTGG------GGAGCTCTTGATGAAGCAGTGAGTTC-TTGAAAG----------CCCCC----------GATTTCCCTTCAAA----------AAATATTAATAA------TTGTGC----------TCT-----CTCGATAGGCTGCTGGCAAACGCGATCCAGATAAGCGACCGGATTTAAGGAGATACTC
droBip1	scf7180000396573:71097-71251 +		GATACCAAAAACGTGCCCGGAAACCTGG------GGAGCTCTTGATGAAGCAGTGAGTCG-TAT--TCT----------CC----------AAAGATTTC----------TCTTTCAGTTT--TTAT------TCAAAAA-TT--T----------TCT-----CCGGCAGGCTGCTGGCAAACGCGATCCACACAAGCGACCGGGTTTCAAGGAGATACTC
droKik1	scf7180000302698:1007559-1007738 -		CATACCAAAAACATGCCCGGAAACCTGG------GGAGCCCTCATGAAAAGTGAGTTC-TCC--TG------GT----------CTT----------GCTCCTGCTCTTCCT--------C----------GTTCCT---CC--TTCTCCTGCTTCTTTATAT----------TAATT----------GTTTTTTGTTTA-----ATCTTTAGGCTGCTGGCAGACGATCCACACAAGCGACCGGGTTTCAAGGAGATACTC
droFic1	scf7180000454077:1923029-1923178 +		GATACCAAAAACGTGCCCAGAAACCTGG------GGAGCCCTCATGAAAAGTGGGTAG-TAC--TC----------CAGAAATTATGACTGTTG----------TTATATGTTTTAATCG----------C----------C----------C----------C----------ATT-----TCCCGCAGGCTGCTGGCAAACGCGATCCACACAACGACCGGGTTTCAAGGAGATACTC
droEle1	scf7180000491006:1584453-1584613 -		CATACCAAAAACGTGCCCAGACACCTGG------GGTGCATCATGAAAAGTAAGTAGA-T---TC----------CTCAGAGCCT--------T----------C----------TTTTT----------GAATTTCTAAGA-TACCGAT-----GATAA-GCTG----------AGA-----ACCACAGGCTGCTGGCAAACGCGATCCGCATAAGCGACCGGCTTCAAGGAGATCCTC
droRho1	scf7180000779580:12225-12371 +		GATACCAAAAACGTGCCCAGAAACCTGG------GGAGCCCTCATGAAAAGTGAGTTG-TTT--TC----------C----------C----------T----------C----------CTTTT----------GCATTTCCA------AATT----------C----GACTAATCAAAA-----ACCACAGGCTGCTGGCAAACGCGATCCGCACAAACGACCGGCTTCAAGGAGATACTC
droBia1	scf7180000302421:2002640-2002795 -		CATACCAAAAACGTGCCCAGACACCTGG------GGAGCCCTCATGAAAAGTGAGTAA-TGC--TC----------C----------C----------C----------C----------C----------C----------ASCCAA--TGTTTGAGTTTCCC----CA--TGTGACTCTCGGCACA----------C----------C----------C----------AAA---CCAATCCACAGGCTGCTGGCAAACGCGATCCACACAAGCGACCGGGTTTCAAGGAGATACTC
droTak1	scf7180000415141:148105-148254 -		CATACCAAAAACGTGCCCAGAAACCTGG------GGAGCCTTGATGAAAAGTGGGTAA-TAT--TC----------C----------C----------C----------ATCCA----------T--------GCAAGTTTG--C----------C----------C----------C----------C----------C----CGAAA-TCTAATT----------C----C--------ACAAACCCCCTTTACAGGCTGCTGGCAAACGCGATCCCCACAAGCGACCGGGTTTCAAGGAGATACTC
droEug1	scf7180000409064:147899-148054 -		TATACCAAAAACGTGCCCAGACACCTGG------GGAGCTCTAATGAAAAGTGAGTAA-CTT-TATACC----------C----------C----------C----------C----------C----------C----------C----------ATACATTTA----------AATTTCGATTTC-TTA-A-TATAATC----------C----C--------AGA-----ACCATAGGTGCTGGCAAATGAAATCCACATGACGGACCGGGTTTCAAGGAGATACTT
dm3	chrX:8068982-8069145 -		CATACCAAAAACGTGCCCGAGACGTGG------GGAGCCCTCATGAAGAGTAAGTGAACGCAAAGACAATGATCCCTATACATATTATTGTA----------C----------C----------ATATTTCATTATGTCC----------C----------C----------C----------C----------C----------AAA-----TCCGCAGGCTGCTGGCAAACGCGATCCGCACAAGCGACCGGCTTCAAGGAGATCCTC
droSim2	x:7642015-7642176 -		CATACCAAAAACGTGCCCGAGACGTGG------GGAGCCCTCATGAAGAGTAAGTGGACGCAAAGCGA---TGAGCATGTACATATTATTGTA----------C----------C----------ATATATCCTTATGTCG----------C----------C----------C----------C----------C----------AAA-----TCCGCAGGCTGCTGGCAAACGCGATCCGCACAAGCGACCGGCTTCAAGGAGATCCTC
droSec2	scaffold_44:155239-155400 -		CATACCAAAAACGTGCCCGAGACGTGG------GGAGCCCTCATGAAGAGTAAGTGGACGCAATGCGA---TGAGCGTGTACATATTATTGTA----------C----------C----------ATATATCATTATGTCG----------C----------C----------C----------C----------C----------AAA-----TCCGCAGGCTGCTGGCAAACGCGATCCGCACAAGCGACCGGCTTCAAGGAGATCCTC
droYak3	v2_chrX_random_017:1769-1922 -		CATACCAAAAACGTGCCCAGACACCTGG------GGAGCCCTAATGAAAAGTAAGTGA-TGCAAGGCGG---TGAAAATGAAC---TATGA----------C----------C----------C----------C----------C----------C----------C----------AATTTTATTAT------C----------C----------C----------ATT-----TCCCGCAGGCTGCTGGCAAACGCGATCCGCACAAGCGACCGGCTTCAAGGAGATCCTC
droEre2	scaffold_4690:10440303-10440456 -		CATACCAAAAACGTGCCCAGACACCTGG------GGAGCCCTCATGAAAAGTAAGTGA-TGCAAGCAA---TGGACTTGAAG----TA----------C----------C----------C----------C----------C----------C----------C----------TTT----------GAATGTCTTAT------C----------ACG----------AAA-----TCCGCAGGCTGCTGGCAAACGTGATCCGCACAAGCGACCGGCTTCAAGGAGATCCTC

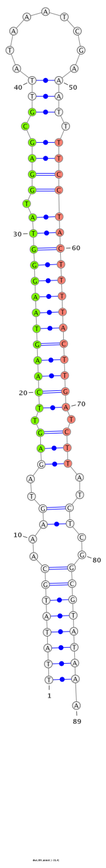
Generated: 08/18/2015 at 04:02 PM

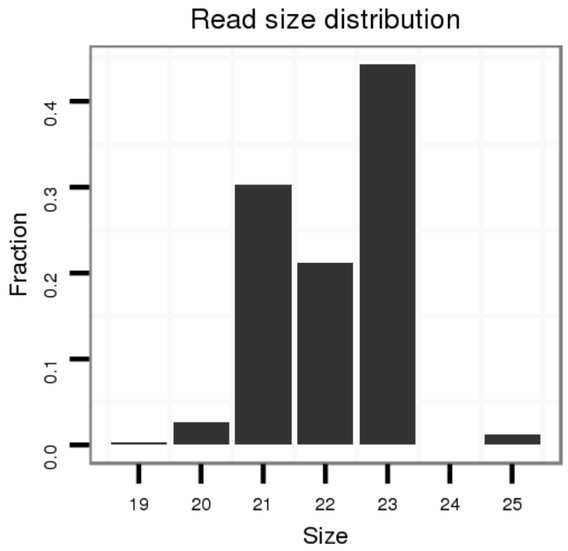
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

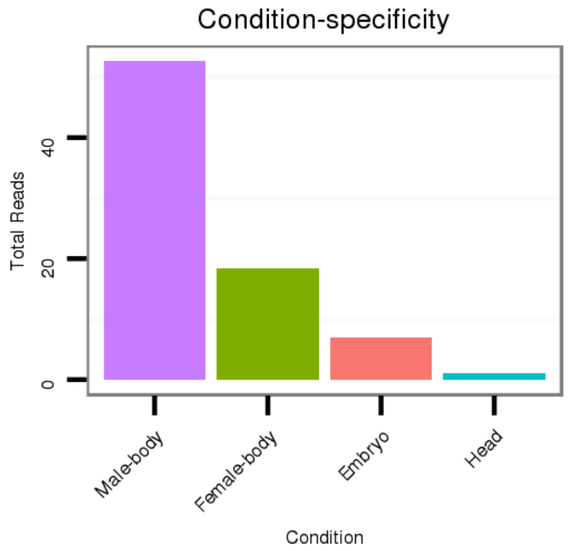
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_89	**scf2_1100000004511:3394682-3394742 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

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

Predicted structure







No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

mature	star
	1. dwi_197 scf2_1100000004511:3392321-3392341 - 2. dwi_196 scf2_1100000004511:3392537-3392557 - 3. dwi_195 scf2_1100000004511:3392679-3392699 - 4. dwi_61 scf2_1100000004511:3393253-3393273 - 5. dwi_193 scf2_1100000004511:3393468-3393488 - 6. dwi_63 scf2_1100000004511:3393826-3393846 - 7. dwi_64 scf2_1100000004511:3394110-3394130 - 8. dwi_65 scf2_1100000004511:3394468-3394488 - 9. dwi_89 scf2_1100000004511:3394684-3394704 - 10. dwi_190 scf2_1100000004511:3394900-3394920 - 11. dwi_189 scf2_1100000004511:3395101-3395121 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTTAGTGATCGTCGCAGGATCATAAAAATCATATCTTATATGCAAAGTAGAGTTCAAGTAAGGGTATGGAGCGTTATAAATCGAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTAAAAGAAACTCAAATCAACATTTTTCTAA
**********************************(((((((..((..(((.((((((((((((((.((((.(((.........))).)))))))))))))))))).)))..))..)))))))).**********************************

Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	M045 female body	V118 embryo	V119 head	M020 head
23	0	1	35.00	35	34	0	1	0	0
21	0	1	13.00	13	11	2	0	0	0
21	0	11	10.73	118	5	94	8	8	3
22	0	1	9.00	9	7	1	1	0	0
22	0	11	7.73	85	2	40	43	0	0
21	0	1	4.00	4	4	0	0	0	0
23	0	1	2.00	2	0	0	2	0	0
22	0	11	1.27	14	2	6	2	1	3
22	1	1	1.00	1	1	0	0	0	0
23	1	1	1.00	1	1	0	0	0	0
25	0	1	1.00	1	0	1	0	0	0
22	0	1	1.00	1	1	0	0	0	0
24	2	1	1.00	1	1	0	0	0	0
20	0	1	1.00	1	0	1	0	0	0
20	0	11	0.73	8	0	7	1	0	0
23	1	11	0.64	7	1	6	0	0	0
20	0	11	0.27	3	0	3	0	0	0
24	2	11	0.18	2	0	2	0	0	0
21	1	11	0.18	2	0	0	0	0	2
21	0	11	0.18	2	0	2	0	0	0
19	0	11	0.18	2	0	1	1	0	0
23	1	11	0.09	1	0	1	0	0	0
19	0	11	0.09	1	0	1	0	0	0
20	0	11	0.09	1	0	0	1	0	0
22	1	11	0.09	1	0	1	0	0	0
24	1	11	0.09	1	0	1	0	0	0
21	0	11	0.09	1	0	0	1	0	0
22	1	11	0.09	1	0	1	0	0	0
22	1	11	0.09	1	0	1	0	0	0

Anti-sense strand reads

GAATCACTAGCAGCGTCCTAGTATTTTTAGTATAGAATATACGTTTCATCTCAAGTTCATTCCCATACCTCGCAATATTTAGCTTTAAAAGGATGAAAATGAACTAGAATAGAGCCGCATATTTTTTGAGAATTTTCTTTGAGTTTAGTTGTAAAAAGATT
**********************************(((((((..((..(((.((((((((((((((.((((.(((.........))).)))))))))))))))))).)))..))..)))))))).**********************************

Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	V117 male body	V119 head
21	0	7	0.14	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3394632-3394792 -	dwi_89	CTTAGTGATCGTCGCAGGATCATAAAAATCATATCTTATATGCAAAGTAGAGTTCAAGTAAGGGTATGGAGCGTTATAAATCGAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTAAAAGAAACTCAAATCAACATTTTTCTAA

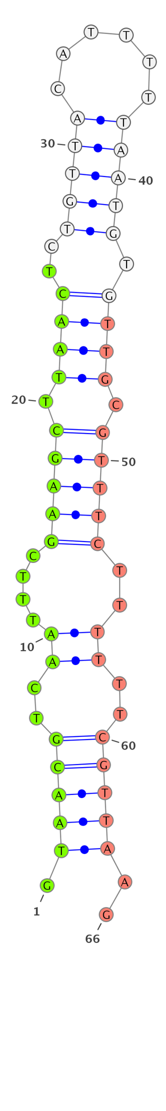
Generated: 09/08/2015 at 07:58 PM

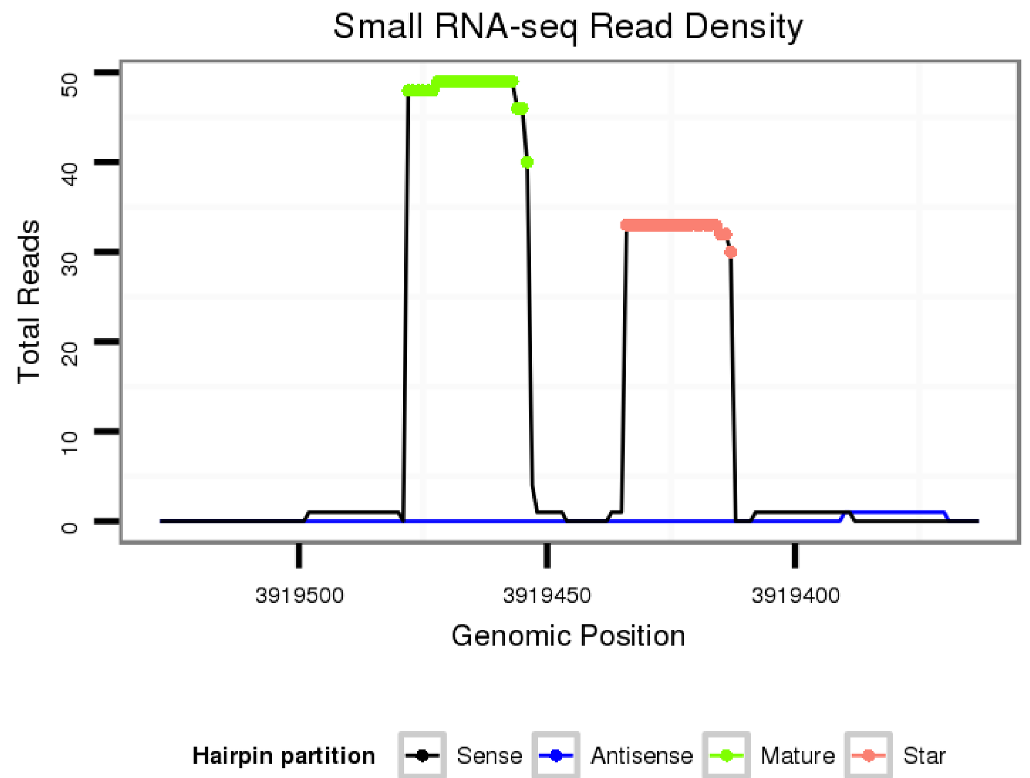
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

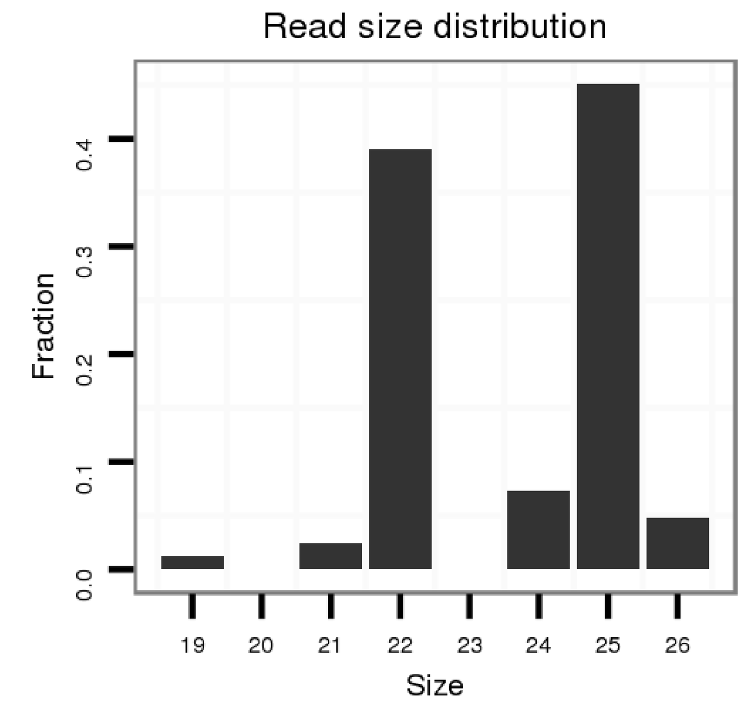
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_3741	**scf2_1100000004954:3919413-3919478 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

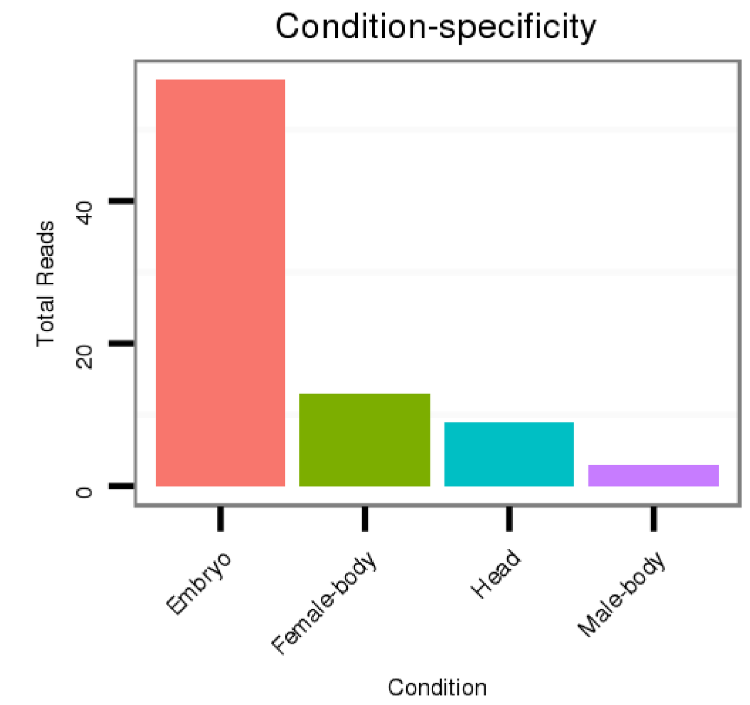
Legend: mature star mismatch in alignment mismatch in read

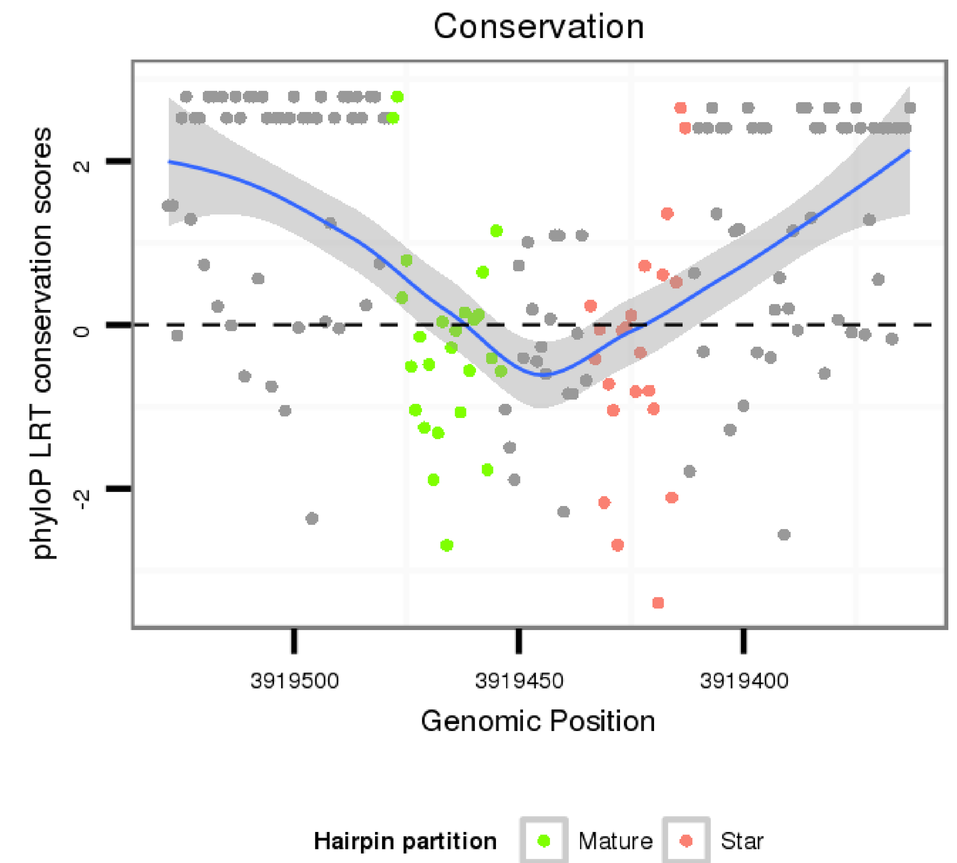
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK22951-in]; CDS [Dwil\GK22951-cds]; CDS [Dwil\GK22951-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGTCAGGGATTCACCACCAAATCAGGTCATGGGCATCGCATGAGCTATGGGTAACGTCAATTTCGAAGCTTAACTCTGTTACATTTTTAATGTGTTGCGTTTCTTTTTTCGTTAAGCACTGATCCGGCCACGGGAGTGACGTTTCCGAAACCTTCCTCGCCCCGCA **.(((((..((....(((((.((((..(((((......))))).)))).)))))..))..)))))..**	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	M045 female body	M020 head	V117 male body	V119 head
....GTAACGTCAATTTCGAAGCTTAACT...	25	0	1	36.00	36	25	6	5	0	0
....TTGCGTTTCTTTTTTCGTTAAG..	22	0	1	29.00	29	22	3	3	1	0
....GTAACGTCAATTTCGAAGCTTAAC..	24	0	1	6.00	6	2	2	0	2	0
....GTAACGTCAATTTCGAAGCTTA..	22	0	1	3.00	3	2	0	0	0	1
....GTAACGTCAATTTCGAAGCTTAACTC..	26	0	1	3.00	3	3	0	0	0	0
....TTGCGTTTCTTTTTTCGTTAA...	21	0	1	2.00	2	1	1	0	0	0
....TTGCGTTTCTTTTTTCGTTAAGA...	23	1	1	2.00	2	1	0	0	1	0
....GATCCGGCCACGGGAGTGAC..........................	20	0	1	1.00	1	0	0	0	1	0
....TCAATTTCGAAGCTTAACTCTGTTAC..	26	0	1	1.00	1	1	0	0	0	0
....GTAACGTCAATTTCGAAGCTTAACC...	25	1	1	1.00	1	0	0	1	0	0
..............................GGGCATCGCATGAGCTATG...	19	0	1	1.00	1	0	0	0	1	0
....TTGCGTTTCTTTTTTCGTT...	19	0	1	1.00	1	0	1	0	0	0
....GTAACGTCAATTTCGAAGCTTAACA...	25	1	1	1.00	1	1	0	0	0	0
....GTGTTGCGTTTCTTTTTTCGTTAAG..	25	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

ACAGTCCCTAAGTGGTGGTTTAGTCCAGTACCCGTAGCGTACTCGATACCCATTGCAGTTAAAGCTTCGAATTGAGACAATGTAAAAATTACACAACGCAAAGAAAAAAGCAATTCGTGACTAGGCCGGTGCCCTCACTGCAAAGGCTTTGGAAGGAGCGGGGCGT **.(((((..((....(((((.((((..(((((......))))).)))).)))))..))..)))))..**	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	V117 male body
....TGCAAAGGCTTTGGAAGGAGC.......	21	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004954:3919363-3919528 -	dwi_3741	TGTCAGGGATTCACCACCAAATCAGGTCATGGGCATCGCATGAGCTATGGGTAACGTCA-ATTTCGAAGCTTAAC-TCTGTTACATTTTTAATGTGTTGCG-------TTTCT---TTTTTCGTTAAGCACTGATCCGGCCACGGGAGTGACGTTTCCGAAACCTTCCTCGCCCCGCA
droVir3	scaffold_12823:558415-558567 +		AACCAGGGATTCACCACCAAATCTGGACATGGACATCGCATGAGCTATGGGTAAGTAAC------AGTTACTTGCTCCTG---TT-----C-----------TAGCTTTAACTGTCTTTCAATTACAGCTCCGATCCAGCAACGGGCGCTACATTTCCCAAGCCCTCGTCGCCGCGCA
droMoj3	scaffold_6496:3428316-3428468 -		AATCAGGGCTTCACCACCAAGTCGGGGCATGGACATCGCATGAGCTATGGGTGAGTGGC------AAGACCTTGC-TTGA---TT-----A--------CAACTCTAACG--TTTTCATCATTTTCAGCTCCGATCCAACGACGGGCACGACATTCCCGAAACCTTCCGCGCCGCGCA
droGri2	scaffold_15245:9071667-9071720 -		AATCAGGGATTCACCACCAAATCGGGGCATGGCCATCGCATGAGCTACGGGTAA--
dp5	3:16434167-16434322 -		AACCAGGGATTCACAACCAAATCCGGTCACGGCCATCGTATGAGCTATGGGTGAGCGCAATCTATC-C---CTA-TCAAT---GG-----G--------CTATT-TAATGTACTCCAATGCATTGCAGATCTGATCCAGCGACGGGGGCCACTTTTCCAAAACCATCTTCTCCGCGCA
droPer2	scaffold_4:328096-328251 +		AACCAGGGATTCACAACCAAATCCGGTCACGGCCATCGTATGAGCTATGGGTGAGCACAAACTATC-C---CTG-TCAAT---GG-----G--------CTATT-TAATGTATTCCAATGCATTGCAGATCTGATCCAGCAACGGGGGCCACTTTTCCAAAACCATCTTCTCCGCGCA
droAna3	scaffold_13266:10562891-10563049 +		AACCAGGGATTCACTACAAAGTCGGGACATGGTCACAGGATGAGTTATGGGTATGATAA-TACCC--A---TGA---------AA-CCTTAAATTGTAGCTTACTAACTTAAC---GCTTATTTTCAGAGCCGATCCTGCCACAGGCGCTCCCTTTCCCAAGCCCTCCTCGCCACGCA
droBip1	scf7180000396428:984873-985031 +		AACCAGGGATTCACTACCAAGTCTGGGCATGGCCATAGGATGAGTTATGGGTATGCTAA-ACCCTAT-----G---------AAA-CCTTGTGTTATAGTTTACTGAGGTAAT---GCTTACTTGCAGGGCCGATCCAGCCACAGGTGCTCCCTTTCCCAAGCCTTCCTCGCCACGCA
droKik1	scf7180000302385:378698-378863 -		AACCAGGGCTTCACCACGAAGTCGGGGCACGGCCACCGCATGAGTTATGGGTAACT----ATCACAGAGCCTTAC-TTAATGATAAGCTTGTGGTATTAACTCC----TCA---TCCTTTATTTGCAGCTCCGATCCGGTAACGGGAACCCCCTTTCCCAAACCCTCCTCGCCACGCA
droFic1	scf7180000453948:1825246-1825401 +		AATCAGGGATTTACCACGAAGTCGGGGCACGGTCATCGCATGAGCTATGGGTAAAC-GT-TGTTTGTA---TCA-CCAGA---TA-----A--------CTCCCCAATATAATGCATATTCTTTACAGCTCGGATCCCGCGACAGGAACGAACTTTCCCAAGCCCTCCTCACCACGCA
droEle1	scf7180000491214:629510-629666 +		AATCAGGGATTCACCACAAAGTCAGGTCACGGGCATCGCATGAGTTACGGGTGAGTTGA-TCATCAGA---TCA-TCAGT---TA-----A--------ACGTTCTAATTTATTTGTTTTTAAAACAGTTCCGATCCTGCGACGGGAGCTACCTTTCCCAAGCCCTCCTCACCGCGCA
droRho1	scf7180000777956:170461-170616 +		AATCAGGGATTCACTACAAAGTCGGGTCACGGACATCGCATGAGCTACGGGTAAG-TGA-GCTCCAGA---TCA-ACAGT---TT-----A--------TTCTTACTAACAGTGTATATCCCATCCAGTTCCGACCCTGCGACGGGAGCCACCTTTCCCAAGCCCTCCTCACCGCGCA
droBia1	scf7180000301754:2952350-2952506 +		AATCAGGGATTTACCACAAAGTCGGGCCACGGTCATCGAATGAGTTATGGGTAATGTGT-GGTCTTAA---TTA-TTCGC---TT-----G--------GTCCTGTACATAATATAAATACATTCTAGATCTGATCCTGCAACTGGAGCTACTTTTCCGAAGCCCTCCTCACCACGCA
droTak1	scf7180000415313:67859-68015 +		AATCAGGGATTTACCACCAAGTCGGGCCACGGTCACCGCATGAGTTATGGGTATAGTGG-GCTGCAGA---TTA-TTAAC---TT-----A--------TTCTTATAATCAATGTACATCCCTTACAGTTCCGATCCCGCAACCGGGGCCACTTTTCCCAAGCCCTCCTCACCACGCA
droEug1	scf7180000409672:1481956-1482112 +		AATCAGGGATTCACCACAAAGTCGGGTCACGGTCACCGCATGAGTTATGGGTAAAGTAC-ACTCCAGA---TCT-TCGTT---TT-----G--------TTCTTATAATGATATAATATTATTTCCAGTTCCGATCCGGCAACCGGAGCCACTTTTCCTAAGCCCTCCTCACCACGCA
dm3	chr2R:13623732-13623886 -		AACCAAGGATTCACCACGAAGTCGGGTCATGGCCATCGAATGAGTTATGGGTAAAGTAA-ACTAC--A---TAG-TCGGC---TT-----G--------CAATTATAATAAATTTCTAAAAATTCCAGATCTGATCCTGCAACCGGAGTACCTTTTCCCAAGCCCTCTTCACCGCGCA
droSim2	2r:14315687-14315843 -		AACCAAGGATTCACCACGAAGTCGGGTCACGGCCATCGAATGAGTTATGGGTAAAGTAA-ACTACACA---TGA-TCGTC---TT-----G--------CAATTATAATACATTTCTAAACATTCCAGATCTGATCCTGCAACCGGAGTCCCTTTTCCCAAGCCCTCTTCACCACGCA
droSec2	scaffold_1:11122254-11122412 -		AACCAAGGATTCACCACGAAGTCAGGTCACGGCCATCGAATGAGTTATGGGTAAAGTAA-ACTACACA---TAA-TCGGC---TA-----A-----ACATTCAT-TCATACATTTCTAAACATTCCAGATCTGATCCTGCAACCGGAGTCCCTTTTCCCAAGCCCTCTTCACCACGCA
droYak3	2R:15557735-15557890 +		AACCAAGGATTTACCACGAAGTCGGGTCACGGTCATCGAATGAGTTATGGGTAAAGTGA-ACTACAGA---CAA-TTGGT---TT-----G--------CAATTGTAAACAA-TTATATACATTCCAGCTCTGATCCTGCAACTGGAGTCCCTTTTCCCAAGCCCTCATCACCACGCA
droEre2	scaffold_4845:7852616-7852772 -		AACCAAGGATTCACTACGAAGTCGGGTCATGGCCATCGAATGAGTTATGGGTAAAGTAA-ATTGCAGA---TTG-CCGGC---TT-----T--------CAATTATAAACAATTTATAAACTTTCCAGTTCTGATCCTGCAACCGGAGTACCTTTTCCCAAGCCCTCTTCACCACGCA

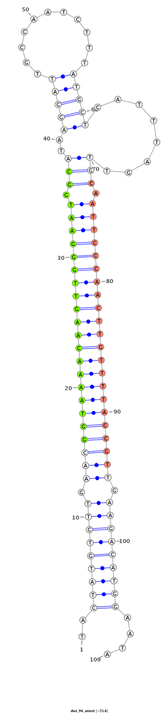
Generated: 09/08/2015 at 07:00 PM

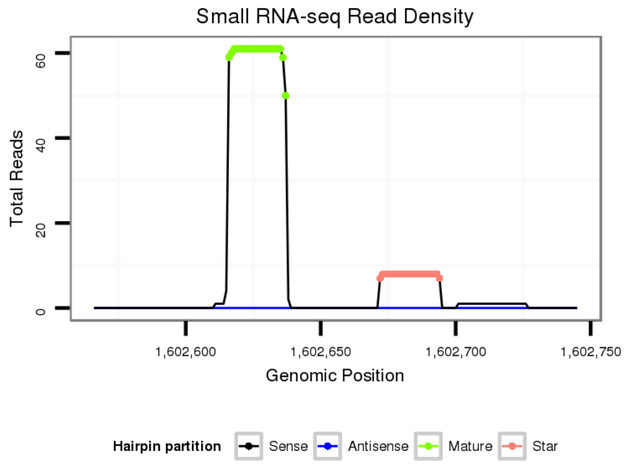
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

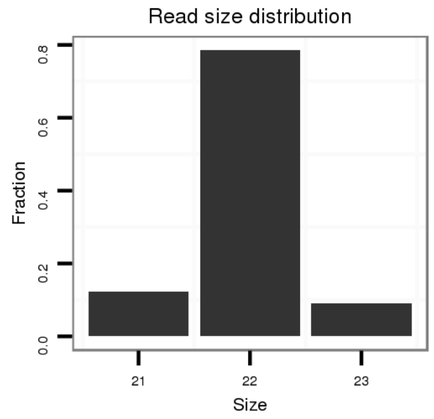
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_96	**scf2_1100000004961:1602616-1602695 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

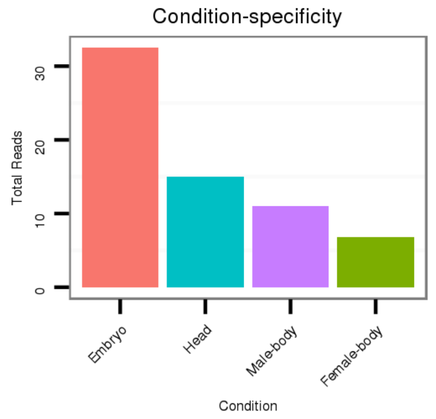
Legend: mature star mismatch in alignment mismatch in read

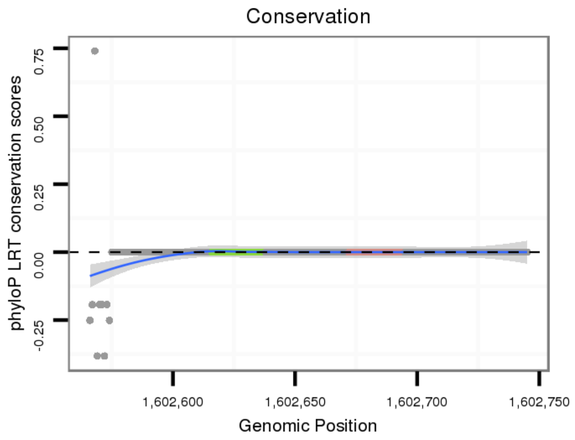
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK23434-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TCACCAGCTAAAAAACTTCAGAATTGCAACGGCACTACTATGTCTTGAACGGTAAAACAAGTTGGGAATGGCATAAGCATTGCCAATCTTTATGCTCATTTAGTTGCAATTCCCAACTTGTTTTACCGTTGAAGACATGGAATAGCCTTTGCAATGCTGTAGTTATTTTGCATAGTCTAC	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	V119 head	V117 male body	M045 female body
**********..(((((((((.(((((((((((((((((((((((.(((..(((((.....)))))).....))).)))))))))))))))))))).)))))))))....**********									
.....GGTAAAACAAGTTGGGAATGGC.....	22	0	1	48.00	48	20	14	11	3
.....GGTAAAACAAGTTGGGAATGG.....	21	0	1	7.00	7	7	0	0	0
.....CAATTCCCAACTTGTTTTACCGT.....	23	0	1	6.00	6	4	0	0	2
.....CGGTAAAACAAGTTGGGAATG.....	21	0	1	2.00	2	2	0	0	0
.....CATGGAATAGCCTTTGCAATGCTGTA.....	26	0	1	1.00	1	0	0	1	0
.....GGTAAAACAAGTTGGGAATGGT.....	22	1	1	1.00	1	1	0	0	0
.....TGAACGGTAAAACAAGTTGGGAATGG.....	26	0	1	1.00	1	0	0	1	0
.....CGGTAAAACAAGTTGGGAATGG.....	22	0	1	1.00	1	0	1	0	0
.....TAAAACAAGTTGGGAATGGCA.....	21	0	1	1.00	1	0	1	0	0
.....CAATTCCCAACTTGTTTTACCG.....	22	0	1	1.00	1	0	0	0	1
.....GTAAAACAAGTTGGGAATGGCA.....	22	0	1	1.00	1	1	0	0	0
.....AATTCCCAACTTGTTTTACCGT.....	22	0	2	1.00	2	1	0	0	1
.....ATTCCCAACTTGTTTTACCGTT.....	22	0	3	0.33	1	0	0	0	1

Anti-sense strand reads

AGTGGTCGATTTTTTGAAGTCTTAACGTTGCCGTGATGATACAGAACTTGCCATTTTGTTCAACCCTTACCGTATTCGTAACGGTTAGAAATACGAGTAAATCAACGTTAAGGGTTGAACAAAATGGCAACTTCTGTACCTTATCGGAAACGTTACGACATCAATAAAACGTATCAGATG	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	V117 male body	V118 embryo
**********..(((((((((.(((((((((((((((((((((((.(((..(((((.....)))))).....))).)))))))))))))))))))).)))))))))....**********								
.....TTGCCATTTTGTTCAACCCTTA.....	22	0	3	0.33	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004961:1602566-1602745 +	dwi_96	TCACCAGCTAAAAAACTTCAGAATTGCAACGGCACTACTATGTCTTGAACGGTAAAACAAGTTGGGAATGGCATAAGCATTGCCAATCTTTATGCTCATTTAGTTGCAATTCCCAACTTGTTTTACCGTTGAAGACATGGAATAGCCTTTGCAATGCTGTAGTTATTTTGCATAGTCTAC
droBip1	scf7180000396655:3526-3534 +		ATAATGTTA----------

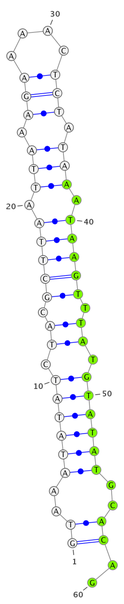
Generated: 08/08/2015 at 07:41 PM

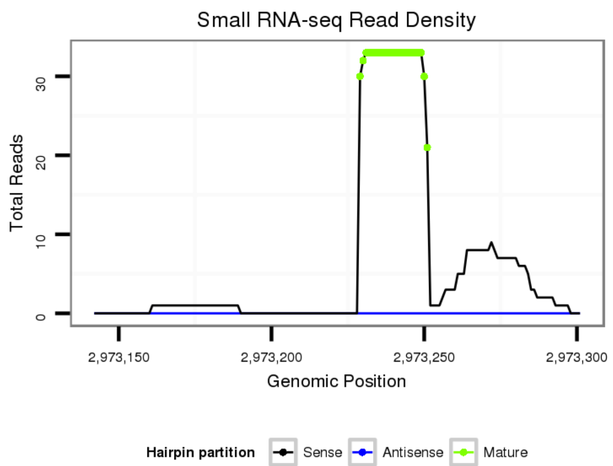
PASS/FAIL	
criteria	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

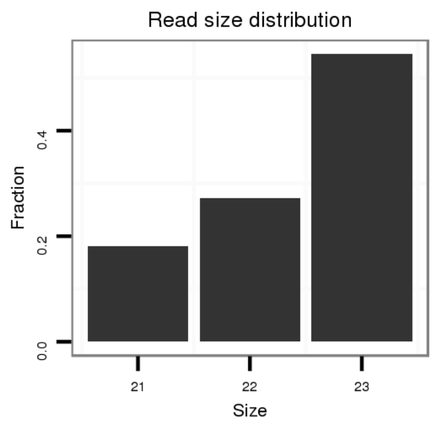
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_2460	**scf2_1100000004902:2973192-2973251 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

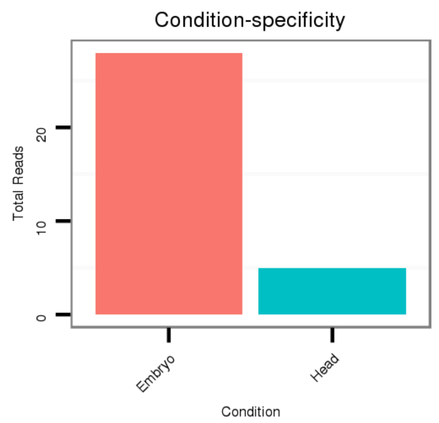
Legend: mature star mismatch in alignment mismatch in read

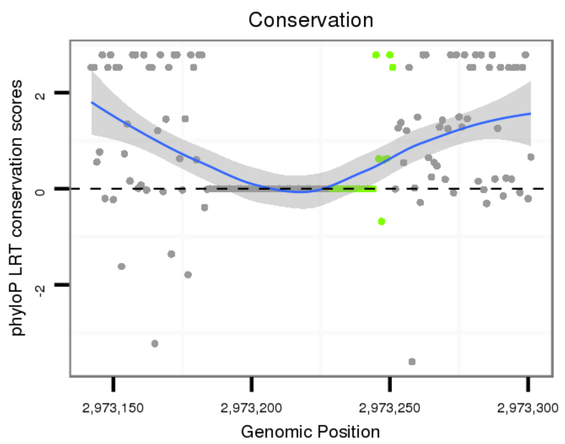
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK11725-in]; CDS [Dwil\GK11725-cds]; CDS [Dwil\GK11725-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CGCAATGAAGCAATTTTCTTAGGAAACACCTATAATACATATCTCGCTAGGTAAATATATCTACGCTTAATTAAAGAAAACTCTATAAATAAGTTTATGTATATGCACAGCCTCAGGAACTACAAGGAGCTGTACATGGAGTATCATGGACGCGGCGAGC **((..((((((.((.((((((.(((.(((.....))).).))).))))))..)).)))))))..))..**	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	V117 male body	V119 head	M045 female body	M020 head
..AATAAGTTTATGTATATGCACAG..	23	0	1	18.00	18	16	0	2	0	0
..AATAAGTTTATGTATATGCACA..	22	0	1	8.00	8	8	0	0	0	0
..AATAAGTTTATGTATATGCAC..	21	0	1	4.00	4	2	0	2	0	0
..AATAAGTTTATGTATATGCACAA..	23	1	1	2.00	2	2	0	0	0	0
..AATAAGTTTATGTATATGCACAGT..	24	1	1	2.00	2	1	0	0	1	0
..CAAGGAGCTGTACATGGAGTA..	21	0	1	1.00	1	0	1	0	0	0
..GGAACTACAAGGAGCTGTACATGGAGTA..	28	0	1	1.00	1	0	1	0	0	0
..AGCCTCAGGAACTACAAGGAGCT..	23	0	1	1.00	1	0	1	0	0	0
..AGGAACTACAAGGAGCTG..	18	0	1	1.00	1	1	0	0	0	0
..TAAGTTTATGTATATGCACAGT..	22	1	1	1.00	1	1	0	0	0	0
..CAAGGAGCTGTACATGGAGT..	20	0	1	1.00	1	1	0	0	0	0
..CTACAAGGAGCTGTACATGG..	20	0	1	1.00	1	0	1	0	0	0
..TAGGAAACACCTATAATACATATCTCGCT..	29	0	1	1.00	1	0	0	0	1	0
..TGTACATGGAGTATCATGGACGCGGC..	26	0	1	1.00	1	0	0	0	1	0
..CAAGGAGCTGTACATGGAGTATCATGGAC..	29	0	1	1.00	1	0	1	0	0	0
..ATAAGTTTATGTATATGCACAG..	22	0	1	1.00	1	1	0	0	0	0
..TAAGTTTATGTATATGCACAG..	21	0	1	1.00	1	1	0	0	0	0
..CTACAAGGAGCTGTACATGGAGTATC..	26	0	1	1.00	1	0	0	0	1	0
..ATAAGTTTATGTATATGCACA..	21	0	1	1.00	1	0	0	1	0	0
..AATACATATCTCGCTAGCCT..	20	3	8	0.13	1	1	0	0	0	0

Anti-sense strand reads

GCGTTACTTCGTTAAAAGAATCCTTTGTGGATATTATGTATAGAGCGATCCATTTATATAGATGCGAATTAATTTCTTTTGAGATATTTATTCAAATACATATACGTGTCGGAGTCCTTGATGTTCCTCGACATGTACCTCATAGTACCTGCGCCGCTCG **((..((((((.((.((((((.(((.(((.....))).).))).))))))..)).)))))))..))..**	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	M045 female body
..ATAAGTTTATGTATATGCACAG..	22	0	1	1.00	1	1	0	0	0	0
..TAAGTTTATGTATATGCACAG..	21	0	1	1.00	1	1	0	0	0	0
..CTACAAGGAGCTGTACATGGAGTATC..	26	0	1	1.00	1	0	0	0	1	0
..ATAAGTTTATGTATATGCACA..	21	0	1	1.00	1	0	0	1	0	0
..AATACATATCTCGCTAGCCT..	20	3	8	0.13	1	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004902:2973142-2973301 +	dwi_2460	CGCAATGAAGCAATTTTCTTAGGAAACACCTATAATACATATCTCGCTAGGTAAATATATCTACGCTTAATTAAAGAAAACTCTATAAATAAGTTTATGTATATGCACAGCCTCAGGAACTACAAGGAGCTGTACATGGAGTATCATGGACGCGGCGAGC
droVir3	scaffold_13047:644077-644176 -		CGCAACGAGGCATCTTCTGGGTCAAGATATTGACTACGC----------TGAGTAGTCTGCGTAAATACAACGCTCTATACAGGATTATCATAGCGGTGGCGAAG
droMoj3	scaffold_6540:4631796-4631895 -		CGCGACGAGCAATCTTCTTGGGCCAACCTATTTAACTATC----------TGAGCAGCCTGCGCAAATACAACGAGCTATACAGGAGTATCATGGTAGTGGCGAGC
droGri2	scaffold_14906:3679322-3679421 -		CGCAACGAGCAATCTTCTTGGGCCAAGATATTTAACTATC----------TTAGCAGTTTGCGCAAATACAACGAACTCTACAAGGAGTACCATGGTCGTGGGGAAC
dp5	2:3195080-3195179 +		CGCAACGAGGCAGTCTTCTTAGGCCAAGATATTCAACTACT----------TGAGTAGTCTGCGCAACTATAACGAGCTGTACAAGGAGTACCATGGACGTGGAGAGC
droPer2	scaffold_7:1146628-1146727 -		CGCAACGAGGCAGTCTTCTTAGGCCAAGATATTCAACTACT----------TGAGTAGTCTGCGCAACTATAACGAGCTGTACAAGGAGTACCATGGACGTGGAGAGC
droAna3	scaffold_13340:4820633-4820732 +		CGGGACGAGGCACTCTTCTTGGGTCAGGCCTACCTAACTACGC----------TGAGCAGTGAACGAAAGTACACGGAGCTGTACAAGGAGTACCATGGGAGGGGCGAGC
droBip1	scf7180000396359:369022-369121 -		CGGGACGAGGCCTCTTCTTGGGTCAGGCCTACCTTACTACGC----------TGAGCAGCCAACGCAAGTACACGGAGCTGTACAAGGAGTACCACGGGAGGGGCGAGC
droKik1	scf7180000302388:1863468-1863567 +		CGCAACGAGCAATCTTCTTCGGGCAGAGTACCTCACTACGC----------TGAGCAGCCAGGGAAACTACACGGAGCTGTACAAGGAGTTCCATGGGAGGGGAGAGC
droFic1	scf7180000454106:1964577-1964676 +		CGCAATGAAGCAACCTTCCTGGGACAGAGATACTTGACTATC----------TGTCCAGCCAGCGAAAGTACTTGGAGCTCTACAAGGAATTTCACGGCGAGGCGAGA
droEle1	scf7180000491194:390181-390280 -		CGCAATGAGGCGACTTTCCTGGGACAAACCTACTTGACTATT----------TGTCCAGCCAGGGCCAGTATTTGGAGATCTACAAGGAGTTTCAGGGAGGGCGAAA
droRho1	scf7180000779488:441653-441752 -		CGCAACGAGGCGACTTTCCTGGGACAGACCTACTTAACTACGC----------TGTCCAGCCAGGGCAAGTACTTGGAGATCTACAAGGAGTATCAGGGAGGGGAGAGC
droBia1	scf7180000302402:7959755-7959854 -		CGCAACGAAGCCACCTTCCTGGGGCAGACCTACTTGACTACGT----------TGGCCAGCCGAGGGCAGTACCTGGAGCTCTACAAGGAGTTCCACGGGAGGGGCGAGA
droTak1	scf7180000415818:66530-66629 +		CGCAATGAAGCAACCTTCCTGGGCCAGAGTACTTGACTACT----------TGACCAGCCCAGGGCCAGTACCTGGAGCTCTACAAGGAGTTCCAGGGAGGGCGAGA
droEug1	scf7180000407136:476301-476400 +		CGCAATGAAGCTACTTTCCTGTGGGACAGAGTTACTTGACTTATT----------TGTCCAGCCAGGGGAACTACTTGGAACTCTACAAGGAATTCCATGGGAGGGGCGAAA
dm3	chr3R:5225415-5225514 -		CGCAACGAAGCGACTTTCCTGGGTCAAACCTACCTGACTACGC----------TAGCCAGCCAGGGCCGGTACTTGGAGCTCTACAAGGAATATCACGGAAGGGGCGAGA
droSim2	3r:15800997-15801096 +		CGCAACGAGGCTACTTTCCTGGGTCAAACCTACCTAACTACGC----------TAGCCAGCCAGGGCCAGTACTTGAAGCTCTACAAGGAATACCACGGGAGGGGCGAAA
droSec2	scaffold_0:16670147-16670246 +		CGCAACGAGGCGACTTTTCCTGGGGCAAACCTACCTGACTACGC----------TAGCCAGCCAGGGTCAGTACTTGGAGCTCTTAAGGAATACCACGGGAGGGGCGAGA
droYak3	3R:9272412-9272511 -		CGCAACGAGGCGACTTTCCTGGGCCAAACCTACCTGACTACGC----------TGACCAGCCCAGGGCAAGTACGTGGAGCTGTACAAGGAATTCCACGGGAGGGGCGAGA
droEre2	scaffold_4770:16380556-16380655 +		CGCAACGAGGCGACTTTCCTGTGGCCAAACCTATTGGACTACGC----------TGGCCAGCCAGGGACAGTACGTGGAGCTCTACAAGGAATACCACGGGAGGGGCGAGA

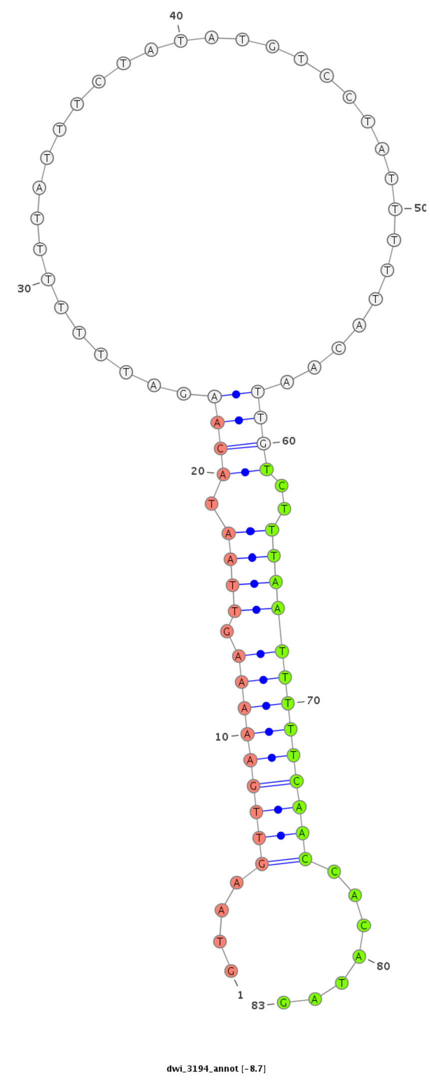
Generated: 09/08/2015 at 10:36 PM

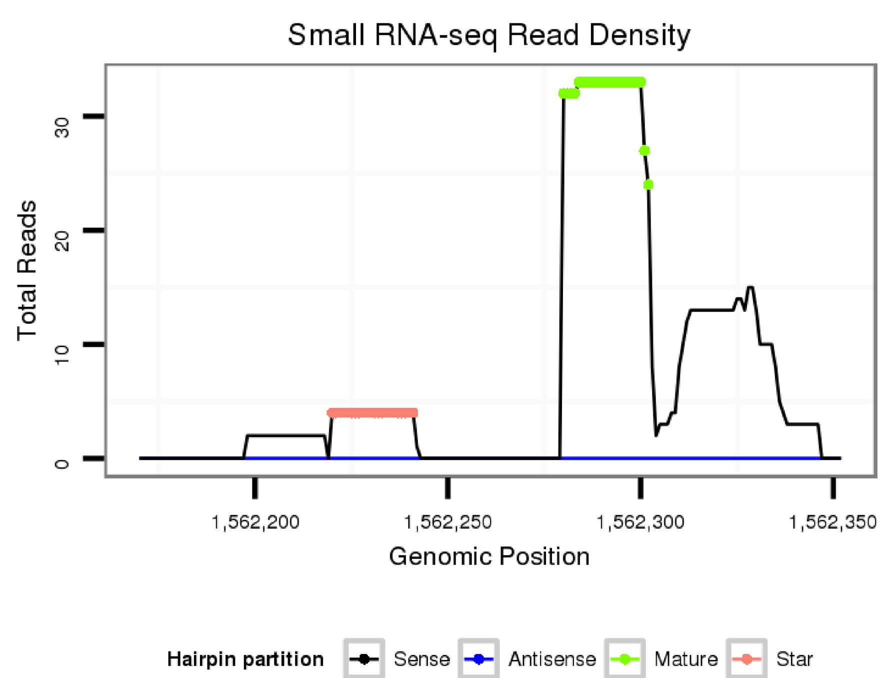
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

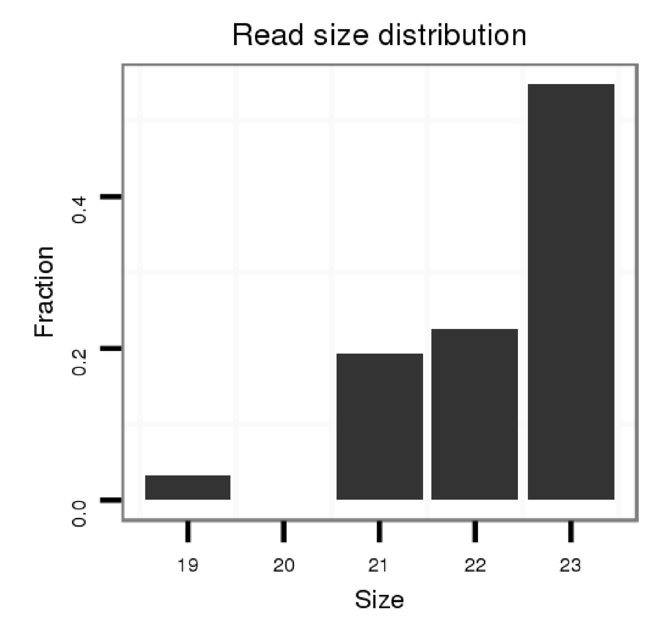
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_3194	**scf2_1100000004943:1562220-1562302 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

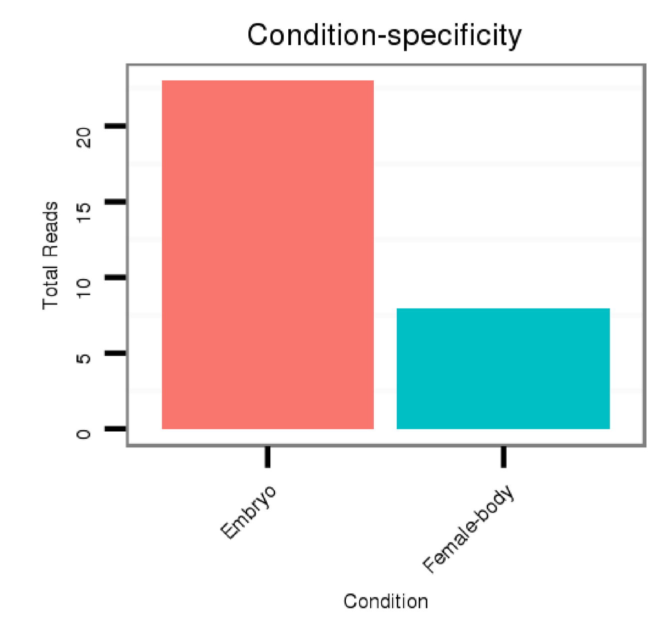
Legend: mature star mismatch in alignment mismatch in read

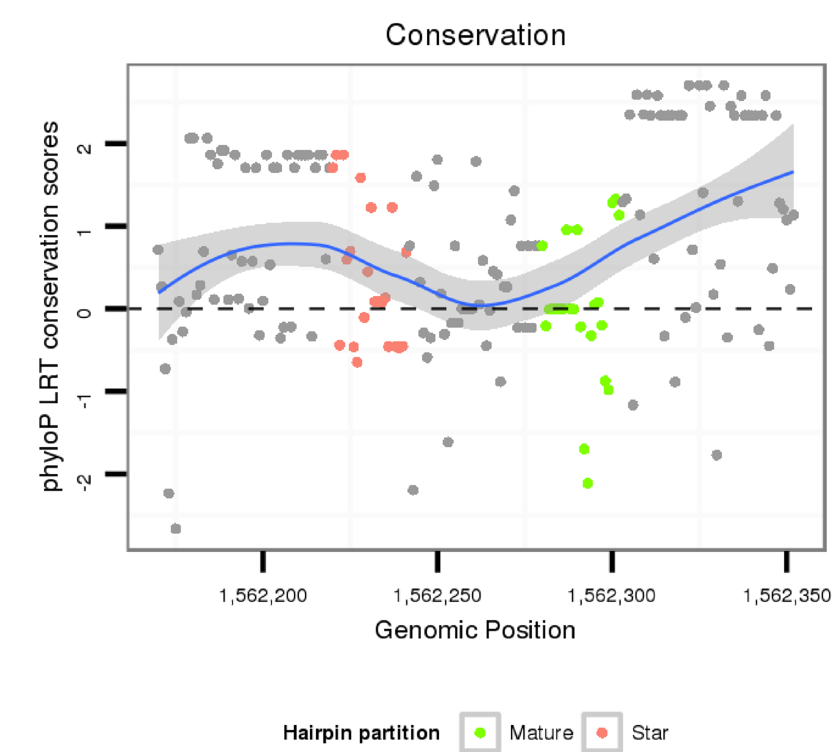
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK13697-in]; CDS [Dwil\GK13697-cds]; CDS [Dwil\GK13697-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTATCAAGCAACTCAAACAATATGGGGCCGCTGGGCCTTCAAAATGATGGGTAAGTTGAAAAAGTTAATACAAGATTTTTTTATTTCTATATGTCCTATTTTTACAATTGTCTTTAATTTTTCAACCACATAGTACGTGGTCAACAGGGCGCAATATTGGAGACGGTTGGCCGGATCCATCAG	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	M045 female body	V117 male body	V119 head	M020 head
....(((((((((.((((.((((..................................))))..))))))))))))).......										
....TCTTTAATTTTTCAACCACATAG..	23	0	1	16.00	16	11	5	0	0	0
....TCTTTAATTTTTCAACCACAT..	21	0	1	6.00	6	4	2	0	0	0
....TCTTTAATTTTTCAACCACATAGT...	24	0	1	6.00	6	5	0	0	1	0
....TCTTTAATTTTTCAACCACATA...	22	0	1	4.00	4	3	1	0	0	0
....TCAACAGGGCGCAATATTGGAGACGG.................	26	0	1	3.00	3	0	3	0	0	0
....GTAAGTTGAAAAAGTTAATACA...	22	0	1	3.00	3	3	0	0	0	0
............................CGCTGGGCCTTCAAAATGATG..	21	0	1	2.00	2	2	0	0	0	0
....GGAGACGGTTGGCCGGATC......	19	0	1	2.00	2	1	0	0	0	1
....TCTTTAATTTTTCAACCACATAAA...	24	2	1	1.00	1	1	0	0	0	0
....CGTGGTCAACAGGGCGCAATAT..........................	22	0	1	1.00	1	0	0	1	0	0
....GTAAGTTGAAAAAGTTAATACAA..	23	0	1	1.00	1	1	0	0	0	0
....AACAGGGCGCAATATTGGA......................	19	0	1	1.00	1	1	0	0	0	0
....AACAGGGCGCAATATTGGAGACG..................	23	0	1	1.00	1	1	0	0	0	0
....TCAACAGGGCGCAATATTGGAGACGGT................	27	0	1	1.00	1	0	1	0	0	0
....GGTCAACAGGGCGCAATATTGGA......................	23	0	1	1.00	1	0	0	1	0	0
....AATATTGGAGACGGTTGGCCGT.........	22	1	1	1.00	1	0	0	1	0	0
....TACGTGGTCAACAGGGCGCAATATTGG.......................	27	0	1	1.00	1	0	1	0	0	0
....CAACAGGGCGCAATATTGGA......................	20	0	1	1.00	1	0	0	1	0	0
....CAACAGGGCGCAATATTGG.......................	19	0	1	1.00	1	1	0	0	0	0
....TCTTTAATTTTTCAACCACATAT..	23	1	1	1.00	1	0	1	0	0	0
....ACAGGGCGCAATATTGGAGACG..................	22	0	1	1.00	1	0	0	0	1	0
....GTACGTGGTCAACAGGGC.................................	18	0	1	1.00	1	1	0	0	0	0
....ATTGGAGACGGTTGGCCGGATC......	22	0	1	1.00	1	0	0	1	0	0
....GCAATATTGGAGACGGTT...............	18	0	1	1.00	1	1	0	0	0	0
....TAATTTTTCAACCACATAG..	19	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

AATAGTTCGTTGAGTTTGTTATACCCCGGCGACCCGGAAGTTTTACTACCCATTCAACTTTTTCAATTATGTTCTAAAAAAATAAAGATATACAGGATAAAAATGTTAACAGAAATTAAAAAGTTGGTGTATCATGCACCAGTTGTCCCGCGTTATAACCTCTGCCAACCGGCCTAGGTAGTC	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	M020 head
....(((((((((.((((.((((..................................))))..))))))))))))).......							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004943:1562170-1562352 +	dwi_3194	TTATCAAGCAACTCAAACAATATGGGGCCGCTGGGCCTTCAAAATGATGGGTAAGTTGAAA---AAG---TTAA--T-ACAAGATTTTTT--------------------TATTTCTATATGTCCTATTTTTACAATTGTCTTTAATTTTTCAACCACATAGTACGTGGTCAACAGGGCGCAATATTGGAGACGGTTGGCCGGATCC---ATCAG
droVir3	scaffold_13052:1266278-1266437 +		TTAACTAGCAACTCAAGCAACATGGGCCCGCTCGGCCTACAAAACGATGGGTCAGTAAACA---AAT---GCTATTATT----------TATAAATAAATAAATTAATTGT---------------------------------------TTTTTTTTGTAGTACTTGGTCAACTGGGCGCAATATTGGAGACGGTTGGCCAGATCCTTCAATTG
droMoj3	scaffold_6498:1174476-1174653 +		TTATCTAGCAACTCAAGCAACATGGGACCATTGGGTCTACAAAATGATGGGTAAATTGAGATGCAATATTATTTAATGAGCCTGTGCGTAATTGACGT--TA---------------TTCTGA-------TTTACCA-----------------------CGCTCTCTATAGTACTTGGTCTACTGGACGCAATATTGGCGATGGTTGGCCAGATCCATCAATTG
droGri2	scaffold_14822:794277-794460 -		TTAGCAAGCAACTCAAACAACATGGGCCCGCTGGGCTTGCAAAATGATGGGTCAGTTG--------------------------TGTGTGATTGTTGTGACAAGG---GCAA--T-GAA-GAACTTTTCTC------TAAAATAGTTGTGA-------TTTTTTGTAT-T----------------------GTATGTAGAACTTGGTCAACGGGTCGTAATATTGAACACGGTTGGCCGGATCCGTCGATTG
dp5	Unknown_group_233:13801-13871 -		TTATTT--TTCCTATCCTAGTACATGGTCAACTGGGCGTAATATTGGTGATGGTTGGCCGGACCCCTCATCTG
droPer2	scaffold_42:458194-458264 +		TTATTT--TTCCTATCCTAGTACATGGTCAACTGGGCGTAATATTGGTGATGGTTGGCCGGACCCCTCATCTG
droAna3	scaffold_13010:222973-223069 -		ATTTTCAAA---CATTTTTTTC---------------TTATTA-------TTATTTAAAT-T----------------------TATTACAGTACATGGTCAACCGGTCGAAGCATTGGAGATGGTTGGCCGGATGCCTCATCTG
droBip1	scf7180000395646:8068-8171 +		AAGCTAAAAAAAAAA---TATTTATTTA--------------TTTG-TC-------TTTTTTACACTT----------------------TATCGCAGTACATGGTCGACAGGTCGAAGCATTGGTGACGGTTGGCCGGATACCTCATCTG
droKik1	scf7180000302673:19923-20158 -		TTGACAAGTAATTCAAGCAATGTTAGCTCTTTGGGCTTACAAAATGATGGGTGAGTGTAAA---AAGTTTTAAACTCCTTTGAATACTTTCTAAATGATACAAATAAAATCGCTGAGCTGAGAATTGAAAAAAGATAAACAAAATAACTGGCTACTACT----------TGT------------TAATTATTA-------TTT---------------------------TCTGTTATTTAGTACTTGGTCAACTGGTCGCAACATTGCAGACGGTTGGCCCGATCCCACATCCG
droFic1	scf7180000454040:274275-274334 +		CG---CCTAGTACTTGGTCAACTGGTCGCAATATTGGGGACGGATGGCCAGACCCCTCATCCG
droEle1	scf7180000491238:566908-566964 +		--ATAGTACATGGTCAACTGGACGTAATATTGGGGACGGTTGGCCAGACCCCTCATCTG
droRho1	scf7180000777693:12472-12555 -		TTTTTGTAA---CA-------------------TT-----------------------------------GA----TCATCGAATTTAATAGTACGTGGTCAACTGGACGCAATATTGGGGACGGTTGGCCAGAGCCCTCATCTG
droBia1	scf7180000301495:565170-565240 -		TTGTCA--TCGATTTTATAGTACATGGTCAACAGGACGCAACATTGGGGATGGTTGGCCAGATCCCTCATCTG
droTak1	scf7180000414052:64053-64113 -		TTAACGAGCAACTCAAGCAACATAAGCTCTTTGGGACTACAAAACGATGGGTAAGTAAAAA--
droEug1	scf7180000408984:519503-519571 +		TTAACAAACAACTCAAGCAACATAAGCTCTTTGGGATTACAAAATGATGGGTAAGT---AACAATGAAAGG----------------------
dm3	chr4:673625-673681 -		--ATAGTACATGGTCAACTGGACGCAGTATTGGTGACGGTTGGCCTGATCCCTCATCTG
droSim2	4:482469-482525 -		--ATAGTACATGGTCAACTGGACGCAGTATTGGTGACGGTTGGCCTGATCCATCATCTG
droSec2	scaffold_30:396267-396357 -		TTGACGGCCAACACAAGCAACATAAGCTCATTGGGTCTTCAAAACGATAGGTAAGAATAAT---T--AGATAGCTT--------------------CACCTT---TATGCTTCTTAGT--T
droYak3	4:729850-729974 -		TTAAGT-----------CAA--TATTCCTTTTT------TGGAATAATTGATT-------TCTCTTACATTTTCTAATGTGA----TCATCGGATTTTATAGTACATGGTCAACTGGACGCAATATTGGAGACGGTTGGCCTGACCCCTCATCTG
droEre2	scaffold_4512:593147-593218 +		TGATTAT---CGAATTTCATAGTACCTGGTCAACTGGTCGCAATATTGGGGACGGTTGGCCTGACCCCTCATCTG

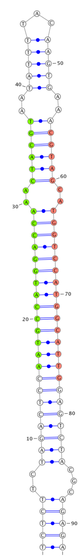
Generated: 09/08/2015 at 10:34 PM

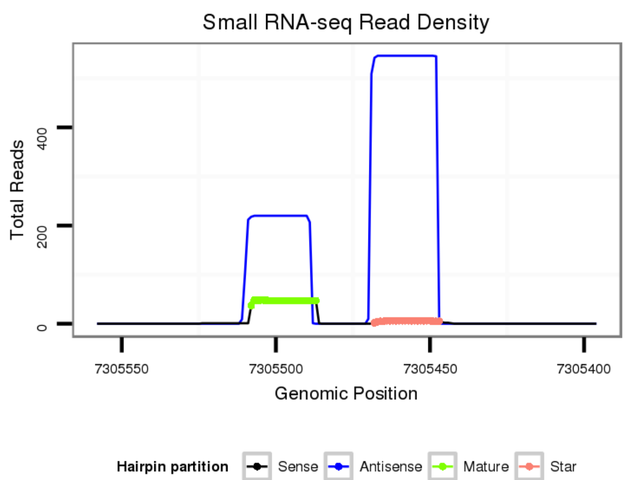
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

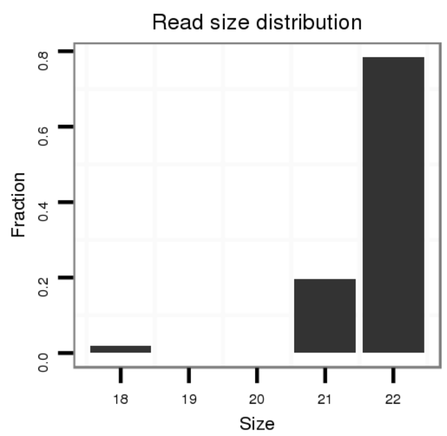
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_98	**scf2_1100000004902:7305446-7305508 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

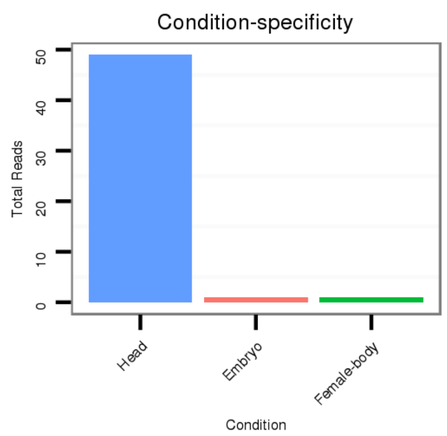
Legend: mature star mismatch in alignment mismatch in read

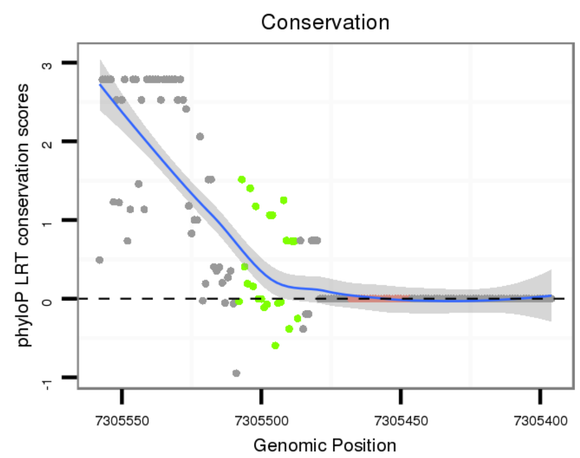
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTTAAGCGGTAAAATGTATTAAGATTAAGTGGCATTCTCTTCTAGACTCCAATGCCATGGACCAAACTACGTAATATTTTACAAGTGAAACGTAGCATGGTCCATGGCATTGGAGTCTACGCAGAGACTAGCTAGCTAGCTAGTGCGACCAAAAAGTGGTTTA	Read size	# Mismatch	Hit Count	Total Norm	Total	V119 head	M020 head	M045 female body	V118 embryo
..AATGCCATGGACCAAACTACGT..	22	0	1	36.00	36	31	3	1	1
..ATGCCATGGACCAAACTACGT..	21	0	1	10.00	10	10	0	0	0
..CGTAGCATGGTCCATGGCATTG..	22	0	1	2.00	2	0	2	0	0
..TAGCATGGTCCATGGCATTGGT..	22	1	1	1.00	1	1	0	0	0
..GTAGCATGGTCCATGGCA..	18	0	1	1.00	1	0	1	0	0
..GCATGGTCCATGGCATTGGAGT..	22	0	1	1.00	1	1	0	0	0
..GTAGCATGGTCCATGGCATTGG..	22	0	1	1.00	1	1	0	0	0
..ATGCCATGGACCAAACTACGTA..	22	0	1	1.00	1	0	1	0	0
..TAGCATGGTCCATGGCATTGGAG..	23	0	1	1.00	1	1	0	0	0
..TTCTCTTCTAGACTCCAATGCC..	22	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

GAATTCGCCATTTTACATAATTCTAATTCACCGTAAGAGAAGATCTGAGGTTACGGTACCTGGTTTGATGCATTATAAAATGTTCACTTTGCATCGTACCAGGTACCGTAACCTCAGATGCGTCTCTGATCGATCGATCGATCACGCTGGTTTTTCACCAAAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	V117 male body	V119 head	M045 female body	M020 head
..TGCATCGTACCAGGTACCGTAA..	22	0	1	498.00	498	324	121	36	17	0
..GTTACGGTACCTGGTTTGATG..	21	0	1	105.00	105	50	45	2	5	3
..GGTTACGGTACCTGGTTTGATG..	22	0	1	92.00	92	65	9	8	10	0
..GCATCGTACCAGGTACCGTAA..	21	0	1	33.00	33	5	13	3	10	2
..TTGCATCGTACCAGGTACCGTAA..	23	0	1	10.00	10	7	1	0	2	0
..AGGTTACGGTACCTGGTTTGAT..	22	0	1	8.00	8	6	0	1	1	0
..TTACGGTACCTGGTTTGATG..	20	0	1	6.00	6	0	0	0	2	4
..GGTTACGGTACCTGGTTTGAT..	21	0	1	3.00	3	0	0	1	2	0
..CGTTACGGTACCTGGTTTGATG..	22	1	1	3.00	3	3	0	0	0	0
..CGCATCGTACCAGGTACCGTAA..	22	1	1	3.00	3	3	0	0	0	0
..CATCGTACCAGGTACCGTAA..	20	0	1	3.00	3	1	2	0	0	0
..TGGTTACGGTACCTGGTTTGATG..	23	1	1	2.00	2	1	1	0	0	0
..GTTACGGTACCTGGTTTGAT..	20	0	1	2.00	2	0	0	0	1	1
..TACGGTACCTGGTTTGATG..	19	0	1	2.00	2	0	0	0	0	2
..GTTACGGTACCTGGTTTGATGC..	22	0	1	1.00	1	0	0	0	0	1
..TTTACGGTACCTGGTTTGATG..	21	1	1	1.00	1	0	0	0	1	0
..CGTTACGGTACCTGGTTTGAT..	21	1	1	1.00	1	0	0	1	0	0
..AGGTTACGGTACCTGGTTTGATG..	23	0	1	1.00	1	1	0	0	0	0
..TGCATCGTACCAGGTACCGTA..	21	0	1	1.00	1	1	0	0	0	0
..CATCGTACCAGGTACCGTAAC..	21	0	1	1.00	1	1	0	0	0	0
..CTGCATCGTACCAGGTACCGTAA..	23	1	1	1.00	1	0	0	1	0	0
..ATGCATCGTACCAGGTACCGTAA..	23	1	1	1.00	1	1	0	0	0	0
..TGTTACGGTACCTGGTTTGATG..	22	1	1	1.00	1	0	0	0	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004902:7305396-7305558 -	dwi_98	CTTAAGCGGTAAAATGTATTAAGATTAAGTGGCA---TTCTCTTCTAGACTCCAATGCCATGGACCAAAC-------TACGTAATATTTTACAAGTGAAACGTAGCATGGTCCATGGCATTGGAGTCTACGCAGAGACTAGCTAGCTAGCTAGTGCGACCAAAAAGTGGTTTA
droVir3	scaffold_12855:6321406-6321442 -		GTTAAACTGTAAAATGTATTAAGATTAAGTGGCA---TTC----------
droMoj3	scaffold_6540:6667618-6667654 -		GTTAAACTGTAAAATGTATTAAGATTAAGTGGCA---TTC----------
droGri2	scaffold_14906:7769571-7769607 +		GTTAAACTGTAAAATGTATTAAGATTAAGTGGCA---TTC----------
dp5	2:26813808-26813846 -		TTTAAGCGGTGGAATGCATTAAGATTAAGTGGCA---CCGC----------
droPer2	scaffold_6:2120586-2120624 -		TTTAAGCGGTGGAATGCATTAAGATTAAGTGGCA---CCGC----------
droAna3	scaffold_13340:3184506-3184593 -		GTTAAGCGGTAGAAAGCATTAAGATTAAGTGGCCAGGTTCGGTTCTCTACCAGATCGA-GACTCCGGAGTTCAGGCTCCGAACCGTTT----------
droBip1	scf7180000396712:1174014-1174044 +		GTTAAGCGGTGGAAAGCATTAAGATTAAGTG----------
droKik1	scf7180000302706:192215-192247 -		GTTAAGCGGTAGAATGCATTAAGATTAAGTGGC----------
droFic1	scf7180000454063:218847-218906 +		GTTAAGCGGTAGAATGCATTAAGATTAAGTGGCCGGGTTCTCTGTTTCTGGCCCAGATCCCA----------
droEle1	scf7180000491104:917526-917556 +		GTTAAGCGGTAGAATGCATTAAGATTAAGTG----------
droRho1	scf7180000779821:25048-25080 +		GTTAAGCGGTAGAATGCATTAAGATTAAGTGGC----------
droBia1	scf7180000302155:1182995-1183053 +		GTTAAGCGGTAGAATGCATTAAGATTAAGTGGCCTGGTTCTCTGTTTCTGGCCGGATCCC----------
droTak1	scf7180000415875:608997-609029 -		GTTAAGCGGTAGAATGCATTAAGATTAAGTGGC----------
droEug1	scf7180000409760:315887-315946 -		GTTAAGCGGTAGAATGCATTAAGATTAAGTGGCCGGGTTCTCTGTTTCTGGCCCAGATCCCA----------
dm3	chr3R:3413439-3413507 -		GTTAAGCGGTAGAATGCATTAAGATTAAGTGGTCGAGTTCTCTGTTTCTGGCCACAACCG-AGCCACCCAGC----------
droSim2	3r:3327921-3327989 -		GTTAAGCGGTAGAATGCATTAAGATTAAGTGGTCGGGTTCTCTGTTTCTGGCCGCAACCG-AGCCACCCAGC----------
droSec2	scaffold_6:3505016-3505084 -		GTTAAGCGGTAGAATGCATTAAGATTAAGTGGTCGGGTTCTCTGTTTCTGGCCGCAACCG-AGCCACCCAGC----------
droYak3	3R:6918757-6918789 +		GTTAAGCGGTAGAATGCATTAAGATTAAGTGGC----------
droEre2	scaffold_4770:3673377-3673409 -		GTTAAGCGGTAGAATGCATTAAGATTAAGTGGC----------

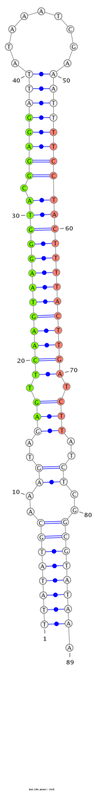
Generated: 09/08/2015 at 07:42 PM

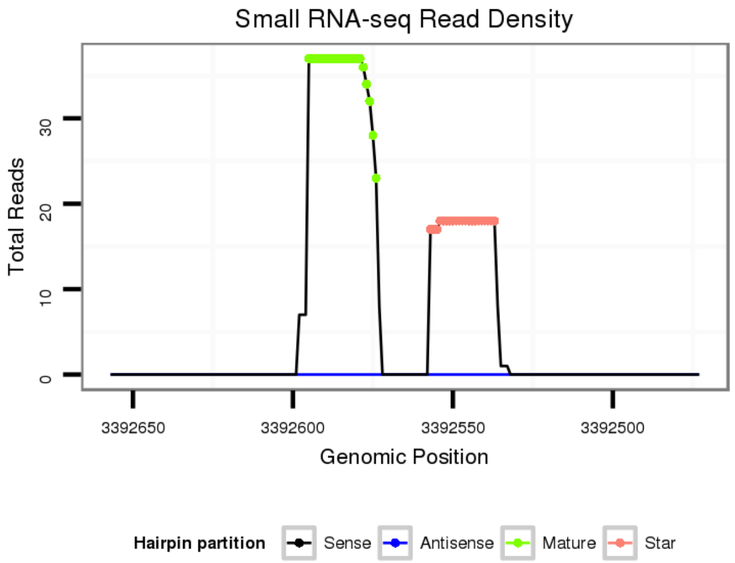
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

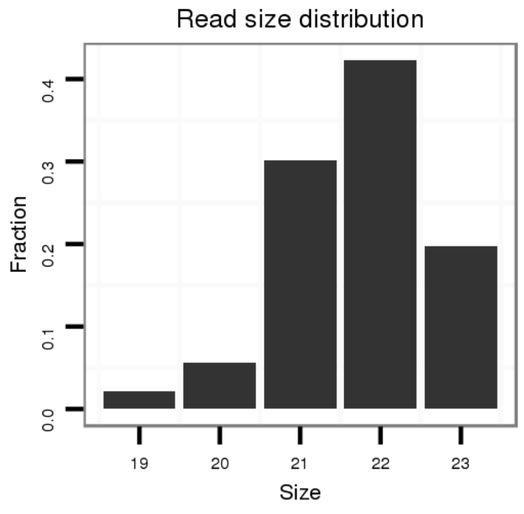
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_196	**scf2_1100000004511:3392523-3392607 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

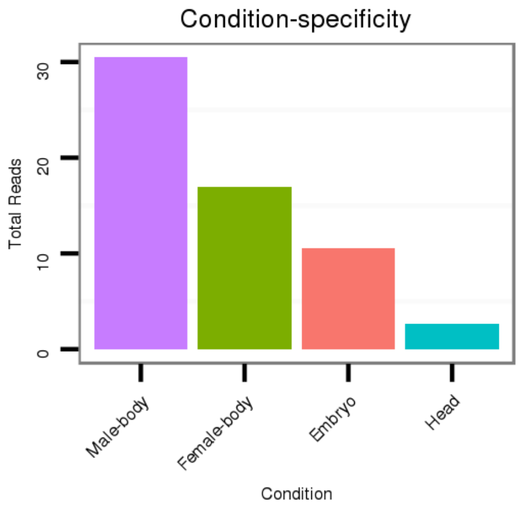
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

mature	star
	1. dwi_197 scf2_1100000004511:3392321-3392341 - 2. dwi_196 scf2_1100000004511:3392537-3392557 - 3. dwi_195 scf2_1100000004511:3392679-3392699 - 4. dwi_61 scf2_1100000004511:3393253-3393273 - 5. dwi_193 scf2_1100000004511:3393468-3393488 - 6. dwi_63 scf2_1100000004511:3393826-3393846 - 7. dwi_64 scf2_1100000004511:3394110-3394130 - 8. dwi_65 scf2_1100000004511:3394468-3394488 - 9. dwi_89 scf2_1100000004511:3394684-3394704 - 10. dwi_190 scf2_1100000004511:3394900-3394920 - 11. dwi_189 scf2_1100000004511:3395101-3395121 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTAAGAGAAAAACTACGTGATCGTCGCAGGATCATAAAAATCATATCTTATATGCAAAGTAGAGTTCAAGTAAGGGTACGGAGGATTATAAATCGAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAAATCTTTAAAAAAATACAAATCAACATTTTTCTAATTTTTCCATTTG **********(((((((..((..(((.(((((((((((((.(((((((.........)))))))))))))))))))).)))..))..)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	M045 female body	V118 embryo	V119 head	M020 head
.....AGTTCAAGTAAGGGTACGGAGG.....	22	0	1	15.00	15	11	1	2	1	0
.....TTCCTACTTTTACTTGATCTT.....	21	0	11	10.73	118	5	94	8	8	3
.....AGTTCAAGTAAGGGTACGGAGGA.....	23	0	1	8.00	8	6	0	2	0	0
.....TTCCTACTTTTACTTGATCTTA.....	22	0	11	7.73	85	2	40	43	0	0
.....AGTTCAAGTAAGGGTACGGAG.....	21	0	3	5.33	16	11	4	0	1	0
.....TAGAGTTCAAGTAAGGGTACGGA.....	23	0	3	3.67	11	7	0	4	0	0
.....TAGAGTTCAAGTAAGGGTACG.....	21	0	3	2.00	6	5	1	0	0	0
.....TAGAGTTCAAGTAAGGGTACGG.....	22	0	3	1.67	5	4	1	0	0	0
.....AGTTCAAGTAAGGGTACGGAGT.....	22	1	3	1.67	5	5	0	0	0	0
.....AGTTCAAGTAAGGGTACGGA.....	20	0	3	1.33	4	4	0	0	0	0
.....CTACTTTTACTTGATCTTATCT.....	22	0	11	1.27	14	2	6	2	1	3
.....AGTTCAAGTAAGGGTACGG.....	19	0	3	1.00	3	3	0	0	0	0
.....TAGAGTTCAAGTAAGGGTAC.....	20	0	3	1.00	3	3	0	0	0	0
.....TTCCTACTTTTACTTGATCT.....	20	0	11	0.73	8	0	7	1	0	0
.....TAGAGTTCAAGTAAGGGTACGGAA.....	24	1	3	0.67	2	1	0	1	0	0
.....AGTTCAAGTAAGGGTACGGT.....	20	1	3	0.67	2	1	1	0	0	0
.....TTCCTACTTTTACTTGATCTTAA.....	23	1	11	0.64	7	1	6	0	0	0
.....TAGAGTTCAAGTAAGGGTACGGAAA.....	25	2	3	0.33	1	1	0	0	0	0
.....TAGAGTTCAAGTAAGGGTACGA.....	22	1	3	0.33	1	1	0	0	0	0
.....TAGAGTTCAAGTAAGGGTACGGAT.....	24	1	3	0.33	1	1	0	0	0	0
.....AGTTCAAGTAAGGGTACGGAGGG.....	23	1	3	0.33	1	1	0	0	0	0
.....AGTTCAAGTAAGGGTACGGAGA.....	22	1	3	0.33	1	1	0	0	0	0
.....AGAGTTCAAGTAAGGGTACGGAG.....	23	0	3	0.33	1	1	0	0	0	0
.....TCCTACTTTTACTTGATCTT.....	20	0	11	0.27	3	0	3	0	0	0
.....TCCTACTTTTACTTGATCTTA.....	21	0	11	0.18	2	0	2	0	0	0
.....CCTACTTTTACTTGATCTT.....	19	0	11	0.18	2	0	1	1	0	0
.....TTCCTACTTTTACTTGATCTC.....	21	1	11	0.18	2	0	0	0	0	2
.....TTCCTACTTTTACTTGATCTTAAA.....	24	2	11	0.18	2	0	2	0	0	0
.....TTCCTACTTTTACTTGATCTTT.....	22	1	11	0.09	1	0	1	0	0	0
.....CCTACTTTTACTTGATCTTATCTA.....	24	1	11	0.09	1	0	1	0	0	0
.....TCCTACTTTTACTTGATCTTAA.....	22	1	11	0.09	1	0	1	0	0	0
.....TTTTCCTACTTTTACTTGATCC.....	22	1	11	0.09	1	0	1	0	0	0
.....CTACTTTTACTTGATCTTATC.....	21	0	11	0.09	1	0	0	1	0	0
.....CCTACTTTTACTTGATCTTA.....	20	0	11	0.09	1	0	0	1	0	0
.....CTACTTTTACTTGATCTTATCTA.....	23	1	11	0.09	1	0	1	0	0	0
.....TCCTACTTTTACTTGATCT.....	19	0	11	0.09	1	0	1	0	0	0
.....CTACTTTTACTTGATCTTATCC.....	22	1	11	0.09	1	1	0	0	0	0

Anti-sense strand reads

AATTCTCTTTTTGATGCACTAGCAGCGTCCTAGTATTTTTAGTATAGAATATACGTTTCATCTCAAGTTCATTCCCATGCCTCCTAATATTTAGCTTTAAAAGGATGAAAATGAACTAGAATAGAGCCGCATATTTTTTTAGAAATTTTTTTATGTTTAGTTGTAAAAAGATTAAAAAGGTAAAC **********(((((((..((..(((.(((((((((((((.(((((((.........)))))))))))))))))))).)))..))..)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V118 embryo
.....TCTCAAGTTCATTCCCATGC.....	20	0	3	0.33	1	1	0
.....TTAGCTTTAAAAGGATGAAAA.....	21	0	7	0.14	1	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3392473-3392657 -	dwi_196	TTAAGAGAAAAACTACGTGATCGTCGCAGGATCATAAAAATCATATCTTATATGCAAAGTAGAGTTCAAGTAAGGGTACGGAGGATTATAAATCGAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAAATCTTTAAAAAAATACAAATCAACATTTTTCTAATTTTTCCATTTG

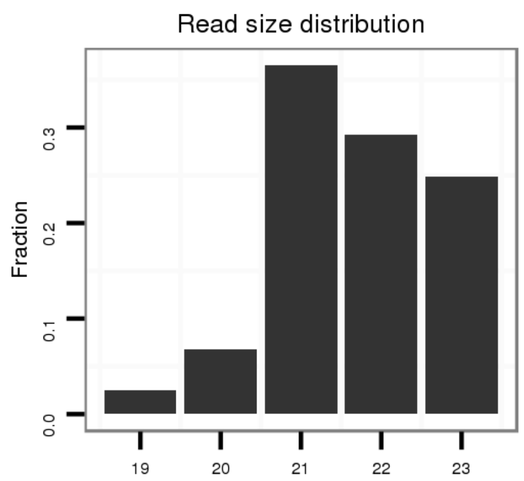
Generated: 09/08/2015 at 07:58 PM

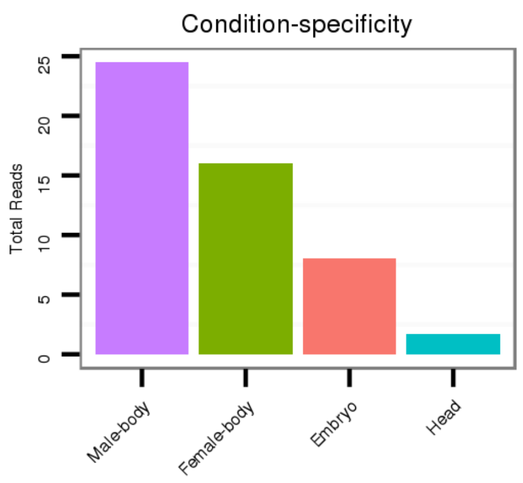
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_197	**scf2_1100000004511:3392307-3392391 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

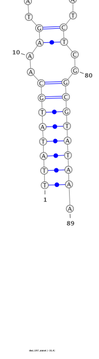
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure





No conservation details.



Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

mature	star
1. dwi_197 scf2_1100000004511:3392321-3392341 - 2. dwi_196 scf2_1100000004511:3392537-3392557 - 3. dwi_195 scf2_1100000004511:3392679-3392699 - 4. dwi_61 scf2_1100000004511:3393253-3393273 - 5. dwi_193 scf2_1100000004511:3393468-3393488 - 6. dwi_63 scf2_1100000004511:3393826-3393846 - 7. dwi_64 scf2_1100000004511:3394110-3394130 - 8. dwi_65 scf2_1100000004511:3394468-3394488 - 9. dwi_89 scf2_1100000004511:3394684-3394704 - 10. dwi_190 scf2_1100000004511:3394900-3394920 - 11. dwi_189 scf2_1100000004511:3395101-3395121 -	1. dwi_197 scf2_1100000004511:3392357-3392379 - 2. dwi_191 scf2_1100000004511:3394362-3394384 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GACAGAGAAAAACTTAGTGATCGTCGCAGGATCATAAAAATCATATCTTATATGCAAAGTAGAGTTCAAGTAAGGGTACGGAGCGTTATAAATCGAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTGAAAAAAATACAAATCAACATTTTTCTAAACATTCCATTTG **********(((((((..((..(((.(((((((((((((.((((.(((.........))).))))))))))))))))).)))..))..)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	M045 female body	V118 embryo	V119 head	M020 head
..........TTCCTACTTTTACTTGATCTT..........	21	0	11	10.73	118	5	94	8	8	3
..........AGTTCAAGTAAGGGTACGGAGCG..........	23	0	2	8.50	17	14	0	3	0	0
..........TTCCTACTTTTACTTGATCTTA..........	22	0	11	7.73	85	2	40	43	0	0
..........AGTTCAAGTAAGGGTACGGAG..........	21	0	3	5.33	16	11	4	0	1	0
..........AGTTCAAGTAAGGGTACGGAGC..........	22	0	2	4.00	8	8	0	0	0	0
..........TAGAGTTCAAGTAAGGGTACGGA..........	23	0	3	3.67	11	7	0	4	0	0
..........TAGAGTTCAAGTAAGGGTACG..........	21	0	3	2.00	6	5	1	0	0	0
..........TAGAGTTCAAGTAAGGGTACGG..........	22	0	3	1.67	5	4	1	0	0	0
..........AGTTCAAGTAAGGGTACGGAGT..........	22	1	3	1.67	5	5	0	0	0	0
..........AGTTCAAGTAAGGGTACGGA..........	20	0	3	1.33	4	4	0	0	0	0
..........CTACTTTTACTTGATCTTATCT..........	22	0	11	1.27	14	2	6	2	1	3
..........TAGAGTTCAAGTAAGGGTAC..........	20	0	3	1.00	3	3	0	0	0	0
..........AGTTCAAGTAAGGGTACGG..........	19	0	3	1.00	3	3	0	0	0	0
..........TTCCTACTTTTACTTGATCT..........	20	0	11	0.73	8	0	7	1	0	0
..........TAGAGTTCAAGTAAGGGTACGGAA..........	24	1	3	0.67	2	1	0	1	0	0
..........AGTTCAAGTAAGGGTACGGT..........	20	1	3	0.67	2	1	1	0	0	0
..........TTCCTACTTTTACTTGATCTTAA..........	23	1	11	0.64	7	1	6	0	0	0
..........TAGAGTTCAAGTAAGGGTACGA..........	22	1	3	0.33	1	1	0	0	0	0
..........TAGAGTTCAAGTAAGGGTACGGAT..........	24	1	3	0.33	1	1	0	0	0	0
..........AGTTCAAGTAAGGGTACGGAGA..........	22	1	3	0.33	1	1	0	0	0	0
..........AGAGTTCAAGTAAGGGTACGGAG..........	23	0	3	0.33	1	1	0	0	0	0
..........TAGAGTTCAAGTAAGGGTACGGAAA..........	25	2	3	0.33	1	1	0	0	0	0
..........TCCTACTTTTACTTGATCTT..........	20	0	11	0.27	3	0	3	0	0	0
..........TCCTACTTTTACTTGATCTTA..........	21	0	11	0.18	2	0	2	0	0	0
..........TTCCTACTTTTACTTGATCTTAAA..........	24	2	11	0.18	2	0	2	0	0	0
..........CCTACTTTTACTTGATCTT..........	19	0	11	0.18	2	0	1	1	0	0
..........TTCCTACTTTTACTTGATCTC..........	21	1	11	0.18	2	0	0	0	0	2
..........TTTTCCTACTTTTACTTGATCC..........	22	1	11	0.09	1	0	1	0	0	0
..........CTACTTTTACTTGATCTTATCTA..........	23	1	11	0.09	1	0	1	0	0	0
..........CCTACTTTTACTTGATCTTA..........	20	0	11	0.09	1	0	0	1	0	0
..........CTACTTTTACTTGATCTTATC..........	21	0	11	0.09	1	0	0	1	0	0
..........CCTACTTTTACTTGATCTTATCTA..........	24	1	11	0.09	1	0	1	0	0	0
..........TTCCTACTTTTACTTGATCTTT..........	22	1	11	0.09	1	0	1	0	0	0
..........TCCTACTTTTACTTGATCT..........	19	0	11	0.09	1	0	1	0	0	0
..........TCCTACTTTTACTTGATCTTAA..........	22	1	11	0.09	1	0	1	0	0	0
..........CTACTTTTACTTGATCTTATCC..........	22	1	11	0.09	1	1	0	0	0	0

Anti-sense strand reads

CTGTCTCTTTTTGAATCACTAGCAGCGTCCTAGTATTTTTAGTATAGAATATACGTTTCATCTCAAGTTCATTCCCATGCCTCGCAATATTTAGCTTTAAAAGGATGAAAATGAACTAGAATAGAGCCGCATATTTTTTGAGAACTTTTTTTATGTTTAGTTGTAAAAAGATTTGTAAGGTAAAC **********(((((((..((..(((.(((((((((((((.((((.(((.........))).))))))))))))))))).)))..))..)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V118 embryo	V117 male body	V119 head
..........TCTCAAGTTCATTCCCATGC..........	20	0	3	0.33	1	1	0	0	0
..........TTAGCTTTAAAAGGATGAAAA..........	21	0	7	0.14	1	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3392257-3392441 -	dwi_197	GACAGAGAAAAACTTAGTGATCGTCGCAGGATCATAAAAATCATATCTTATATGCAAAGTAGAGTTCAAGTAAGGGTACGGAGCGTTATAAATCGAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTGAAAAAAATACAAATCAACATTTTTCTAAACATTCCATTTG

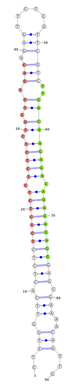
Generated: 09/08/2015 at 08:04 PM

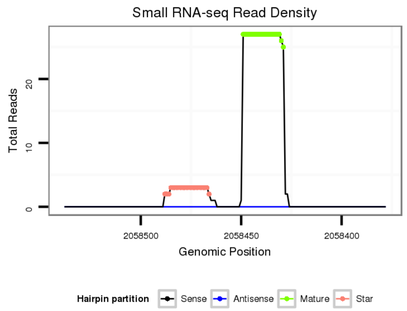
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

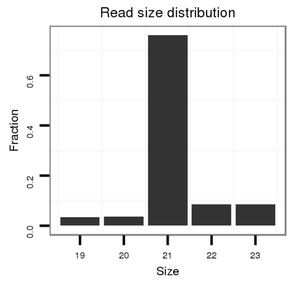
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_160	**scf2_1100000004511:2058428-2058488 -**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

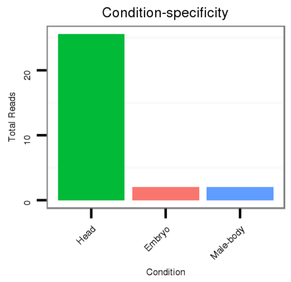
Legend: mature star mismatch in alignment mismatch in read

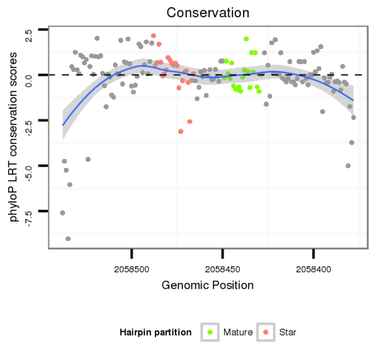
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK17021-in]

Repeatable elements

Name	Class	Family	Strand
(GA)n	Simple_repeat	Simple_repeat	+

mature	star
	1. dwi_160 scf2_1100000004511:2058466-2058488 - 2. scf2_1100000004909:12285884-12285906 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTAAGAGACACTGCTCTCTCTCCGTTACTACTTGTCTCTGGTTCACTCTCTCTCTCTCTCTGCTCTGACAGAGTTCTCGTTCGTCTTGACAAGAGACAGAGAGAGGGAGCGAAAACAGTTGGGGCCACCATCAGCAACATCATCATCATTATCATAC	Read size	# Mismatch	Hit Count	Total Norm	Total	V119 head	M020 head	V118 embryo	V117 male body	M045 female body
**********..(((.(((.(((((((((((((.(((((.((.(((.(((.(((.....)))))).)))))))))).)))))))))))).)))..))))...**********										
.....TTGACAAGAGACAGAGAGAGG.....	21	0	1	22.00	22	18	1	2	1	0
.....TTGACAAGAGACAGAGAGAGGT.....	22	1	1	10.00	10	6	2	2	0	0
.....TTGACAAGAGACAGAGAGAGGGA.....	23	0	1	2.00	2	2	0	0	0	0
.....TCTCTCTCTCTCTGCTCTGAC.....	23	0	2	1.50	3	0	3	0	0	0
.....TCTCTCTCTCTCTGCTCTGA.....	22	0	2	1.50	3	0	3	0	0	0
.....TTGACAAGAGACAGAGAGAG.....	20	0	1	1.00	1	1	0	0	0	0
.....CTCTCTCTCTCTCTGACAGA.....	23	0	1	1.00	1	0	1	0	0	0
.....CTTGACAAGAGACAGAGAGAGG.....	22	0	1	1.00	1	0	0	0	1	0
.....TTGACAAGAGACAGAGAGA.....	19	0	1	1.00	1	0	1	0	0	0
.....TCTCTCTCTCTCTCTGCTCTG.....	21	0	2	0.50	1	0	1	0	0	0
.....AGAGACAGAGAGAGGGAGCGA.....	21	0	4	0.50	2	0	0	2	0	0
.....TTGACAAGAGACAGAGAGAGA.....	21	1	5	0.20	1	1	0	0	0	0
.....ATCAGCAACATCATCATCA.....	19	0	8	0.13	1	0	0	1	0	0
.....TCTCTCTCTCTCTGCTCTGG.....	22	1	9	0.11	1	0	1	0	0	0
.....TCTCTCTCTCTCTGCTCT.....	20	0	10	0.10	1	0	1	0	0	0

Anti-sense strand reads

GATTCTCTGTGACGAGAGAGAGGCAATGATGAACAGAGACCAAGTGAGAGAGAGAGAGAGACGAGACTGTCTCAAGAGCAAGCAGAACTGTTCTCTGTCTCTCCCTCGCTTTTGTCAACCCCGGTGGTAGTCGTTGTAGTAGTAGTAATAGTATG	Read size	# Mismatch	Hit Count	Total Norm	Total	V119 head	M045 female body
**********..(((.(((.(((((((((((((.(((((.((.(((.(((.(((.....)))))).)))))))))).)))))))))))).)))..))))...**********							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:2058378-2058538 -	dwi_160	CTAAGAGACACT-G----C----------TCTCTCTCCGTTACT--------A-------C-------TTG--TCTCTGGTTCACTCTCT--------C--TCTCTCTCTCTG--------CT-CTG-ACA------GAGTTCTCGT----------TCGTCTT--GACAAGAGAC----------AGAGAGAGGGAG----------C--GAAA----------AC-AGTTGGGGCCACCATCAGCAA----------CATCATCATCATTATC----------ATAC
droVir3	scaffold_13049:5773082-5773248 +		CTCAGACACAC-T-ACT---C----------TCTCTCT--------T---T-CGTC-------T-------CTG--TCTCTCTCTCT--------C--TCTCTCTCTCTG---TTGCA--T--TC-GCAGTCGTTCTCTGTGAGCTCTCTTTTCGTTC---A----TTAT---------T----------CGC--TTTGCTGGCA-------T--CGAAATGTGGCGTTAGCTGGCCCCCATGCTATGT--T----------GTGCG----------TC----------TGCG
droMoj3	scaffold_6473:4403702-4403769 -		CTCTC-------T-------T----------TCTCTCT--------T---T-TCTC-------T-------CTT--TCTCTCTCTCT--------C--TCTGCTCTCAGA---ATCCTC---T---T-------T---------T-------T---------T----------T---------T----------T---CGA----------T---------T----------T---------T----------TCGAT----------TGC
droGri2	scaffold_15081:4019172-4019339 -		ACAGATATCTCT-G----C-TTTCTCACTATGCCCCTCTCTCTCT--------T---T-------T-------C--T----T-C----T-TTCTCT--------C--TCTCTACTCTCTCTCTG---TCTGT--T---T---T---------T---------T-------T---------T----------T---------T----------T---GTGTGTGCTCGACAAAACTTTCTTGAA----------AGTGAGTATCGA----------T---------T----------T---------T----------CATATC----------TA----------TAACTA---------CTTGGATAGGTAACTCTCTTAATACTGTTTAAG----------TAG
dp5	XR_group6:10126256-10126330 +		AGCGT---CACTC-AGTTGTC----------T---------T-------T-------CTCTCT--------T---T-TCGCTCTCTCGCT----GTC--T----GC---------T-------CTCTCTCTC----TCTCTCTCT---GC---------T---------T-------T---------T----------T---ATC--T---------T---------T----------T---------T----------T---GCCGCT---------T---------T----------T---------T----------CCATCATCG----------T---------T----------T---------T----------TCT
droPer2	scaffold_2:5828905-5829054 -		TCTCT-------T-------T----------TCTCTCT--------T---T-TCTC-------T-------CTC--TCTCC-----------T---------T----------T---------T----------T---ACTCT---------T---------T----------T---AGCTCTGAGCCCCTT---AT----CTCGCGCGA----------T---------T----------T---------T----------CAC--GTTGACA---GCAGAAGAAT--GA-----ACAACTTGCCCCAAAGTGAGAA----------T---------T----------T---------T----------TTTCGATTGGGCACAATTGAAAGTCTCCCCAAGAGCCGC-CGCAGTC
droAna3	scaffold_13288:958-1016 -		CATCAAGAC---T-------T----------T---------T-------T-------T---T-------T-------T---T---------T---------T----------T---------T----------T---------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---AGCGCA----------T---------T----------T---GGAAA----------T---------T----------T---------T----------AGGACACGACTAGCAATG--TCATTCTGCCACAC
droBip1	scf7180000395898:43574-43598 +		AGTGA-------T-------T----------T---------T-------T-------T---T-------T-------T---T---------T---------T----------T---------T----------T---------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---CGGGAGTGGGAGCGA----------CAGC
droKik1	scf7180000302577:1484600-1484652 -		CTCTC-------T-------T----------TCTCTCT--------T---T-TCTC-------A-------TTT--TCTCCCCGTCTTCTC--------C--TCTCTCTCTCTG---------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------
droFic1	scf7180000454038:245613-245696 +		GTTTT-------T-------T----------T---------T-------T-------T---T-------T-------T---T---------T---------T----------T---------T----------T---------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---AGAGAGTTGTACAACG----------T---------T----------T---------T----------AA-AGAGATTGTACAACG----------T---------T----------T---------T----------AAGCGTTCGATGTTCA
droEle1	scf7180000491201:13506-13591 -		TTCTT-------T-------T----------T---------T-------T-------T---T-------T-------T---T---------T---------T----------T---------T----------T---------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---AGTGTTGT---T---T----CTA----------T---------T----------T---------T----------CTCTATAAAAC---AAAAA----C---CAAA----------T---------T----------T---------T----------AA-A----------T---------T----------T---------T----------A---ACA
droRho1	scf7180000779189:204681-204697 -		ATTGC-------T-------T----------T---------T-------T-------T---T-------T-------T---T---------T---------T----------T---------T----------T---------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------
droBia1	scf7180000302193:26938-27051 +		TGGGAGTCTCT-G-TGTGT----------T---------T-------T-------T---T-------T-------T---T---------T---------T----------T---------T----------T---------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---GAGCGAAGAGAGCCCATGTTGCTGGTGTGCGAGACGGCAGCT----------GCA----------C-GA----------T---------T----------T---------T----------CAA----------CACACACACAACAGC
droTak1	scf7180000415349:70464-70575 +		GCTAGAG-----T-------T----------T---------T-------T-------T---T-------T-------T---T---------T---------T----------T---------T----------T---------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---GCGAGAGAGCAAATGTTGCTGGTGTGCGAGACGGCAGCT----------ACATCAGCA---GCAGCAG-AA----------T---------T----------T---------T----------CAA----------CATCACACACAACAGC
droEug1	scf7180000409182:94674-94839 -		ACCTC-------T-------T----------T---------T-------T-------T---T-------T-------T---T---------T---------T----------T---------T----------T---------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------
dm3	chr3L:11546406-11546537 -		CGGGGA-------T-------T----------T---------T-------T-------T---T-------T-------T---T---------T---------T----------T---------T----------T---------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---G-GGAGAGCAAATGTTGCTGGTGTGCGAGACAGCAGC----------ACATCAGCA---G----------T---------T----------T---------T----------CAA----------CAATACACAACAGC
droSim2	x:9124214-9124261 +		TGCC-------T-------T----------T---------T-------T-------T---T-------T-------T---T---------T---------T----------T---------T----------T---------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---TGTCTG----------T---------T----------T---------T----------
droSec2	scaffold_0:3750451-3750506 -		ATTAC-------T-------T----------T---------T-------T-------T---T-------T-------T---T---------T---------T----------T---------T----------T---------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------
droYak3	3L:11585134-11585230 -		CTCTC-------T-------T----------T---------T-------T-------T---T-------T-------T---T---------T---------T----------T---------T----------T---------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---GGAGCTGCGTTTTCGC----------T---------T----------T---------T----------T---------T----------
droEre2	scaffold_4644:740114-740132 -		ACTT-------T-------T----------T---------T-------T-------T---T-------T-------T---T---------T---------T----------T---------T----------T---------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------T---------T----------

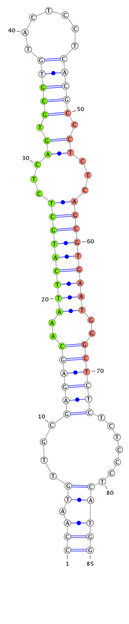
Generated: 09/08/2015 at 07:45 PM

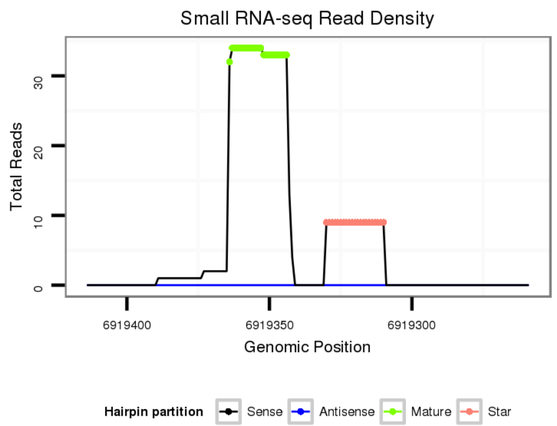
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

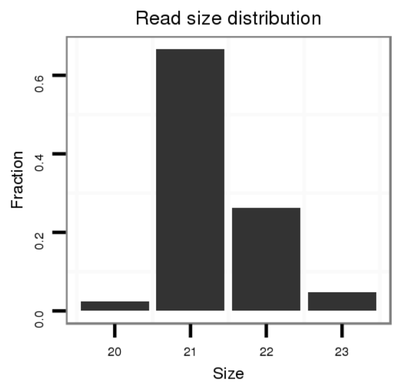
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_103	**scf2_1100000004943:6919309-6919364 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

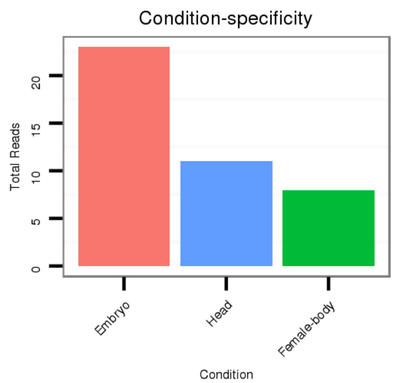
Legend: mature star mismatch in alignment mismatch in read

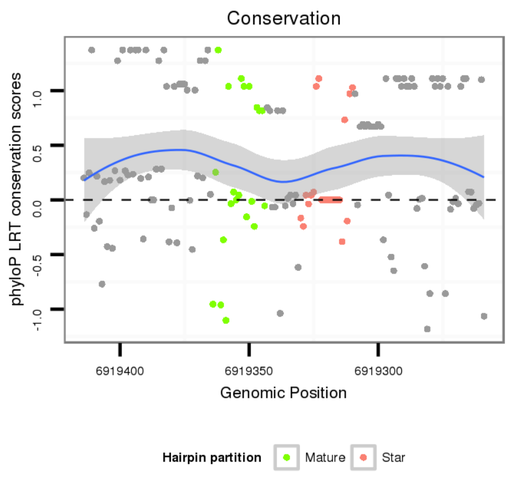
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAAAAACATTTTAGCAACATTTTCTGTACGCACACCCAATGTTGCGAGAGCAAATTCATGCTCTCAGTGCGTGTACTCCTCACGCCCTCTCAGCGTGAATGGGCTCTCTCTCCCTCATGGCATCAGCTGTTTGCTACACTAGGCAACAAGAATTAG **********(((.((....(((((((..((((((((((...((.(((((.......)))))).))...))))))))))..))))))).....)))))**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	V119 head	M045 female body	V117 male body	M020 head
.....CAAATTCATGCTCTCAGTGCG.....	21	0	1	19.00	19	9	4	5	0	1
.....CCCTCTCAGCGTGAATGGGCT.....	21	0	1	9.00	9	5	3	1	0	0
.....CAAATTCATGCTCTCAGTGCGT.....	22	0	1	9.00	9	6	2	1	0	0
.....AAATTCATGCTCTCAGTGCGTG.....	22	0	1	2.00	2	1	0	1	0	0
.....CAAATTCATGCTCTCAGTGCGTG.....	23	0	1	2.00	2	2	0	0	0	0
.....TTGCGAGAGCAAATTCATGCT.....	21	0	1	1.00	1	1	0	0	0	0
.....CCCTCTCAGCGTGAATGGGCG.....	21	1	1	1.00	1	0	0	0	0	1
.....AAATTCATGCTCTCAGTGCG.....	20	0	1	1.00	1	0	1	0	0	0
.....GTACGCACACCCAATGTTGCGAGAGC.....	26	0	1	1.00	1	0	0	0	1	0

Anti-sense strand reads

TTTTTTGTAAAATCGTTGTAAAAGACATGCGTGTGGGTTACAACGCTCTCGTTTAAGTACGAGAGTCACGCACATGAGGAGTGCGGGAGAGTCGCACTTACCCGAGAGAGAGGGAGTACCGTAGTCGACAAACGATGTGATCCGTTGTTCTTAATC **********(((.((....(((((((..((((((((((...((.(((((.......)))))).))...))))))))))..))))))).....)))))**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	V117 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004943:6919259-6919414 -	dwi_103	AAAAAACAT--------TT----TAGCAACATTTTCTGTACGCACACC-----CAATGTTGCGAGAGCAA----------ATTCATGCTCTCAGTGCGTGTACTCCTCACGCCCT-------CTCAGCGTGAATGGGCTCTCTCTCCCTC----------AT--GGCATCAGCTGTTT-----GCTACACTAGGCAACAAGAA----------TTAG
dp5	2:18923446-18923603 +		GGAAAAAAGC--------CT----GAGCAACATTTTGTG--TGTACTACC--TGAAATGTGGAGGAGGCA----------GAGGGCACTGCCAC----------TGGC--GCT--------CCCA----------CTCTCTCTCCCTCTCTTTTCTGCTGCCTCTTTGTTCTT--GCCATCAGCTGTGT-----ATTACACTAGCCACAAAGAAT----------TTAG
droPer2	scaffold_3:1647911-1648063 +		GGAAAAAAGC--------CT----GAGCAACATTTTGTG--TGTACTACC--TGAAATGTGGAGGAGGCA----------GAGGGCACTGCCAC----------TGGC--GCT--------CCCA----------CTCTCTCTCCCTCTCTTTTCTGCTGCCTCTTTGTTCTT--GCCATCAGCTGTGT-----ATTACACTAGCCACAAAGAAT----------TTAG
droAna3	scaffold_13340:23620056-23620254 -		AGAATAATATATGTATAC----TAGAAACACTTAGTA--TGTACGCCTAGTG--------AGAGA--GAGATTAGGGGTAAAAAAAGAGAGATAGGCTTTACAAAAAGACACGTTCTCAGTGCATGCGCTCTATATGATGCTCGATGACTTTCGA----------TGACTCGATGGCGCTGTAAAATCAGCTGGGAAAAACTGGCACACTGGCATACAAAGGC----------CAAC
droBip1	scf7180000396413:18875-19085 -		AGTAATAAGT--------AC----TAGAAATATTTAGTA--TGTACGCCTAGTG--------AGAGAGAGAGATTAGGGC---AAAAAGAGAGATAGGCTTTACAAAGTGTCACGTTCTCGGTGCATGCGCGCTATTAAAGT-------TTCGA--------TGACTCA---------ATTGGCCCTGTAATTATCAGCTGGGA------AAAACACTTGCATACAAAGCAGAAATTTTCCATAATAAAAAGCAATCAAAGAAATTAA
droEre2	scaffold_4820:5964379-5964428 +		AAAAGCTCT--------TTAAAAGGCAGCATTTTATG--TGTA----------AATGCTGAGAGAGTCA----------ATTCATGCTCTCAGTGCGTGTACTCCTCACGCCCT-------CTCAGCGTGAATGGGCTCTCTCTCCCTC----------AT--GGCATCAGCTGTTT-----GCTACACTAGGCAACAAGAA----------TTAG

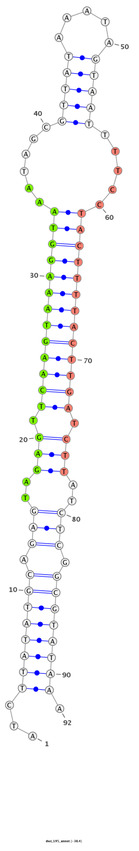
Generated: 09/10/2015 at 07:42 PM

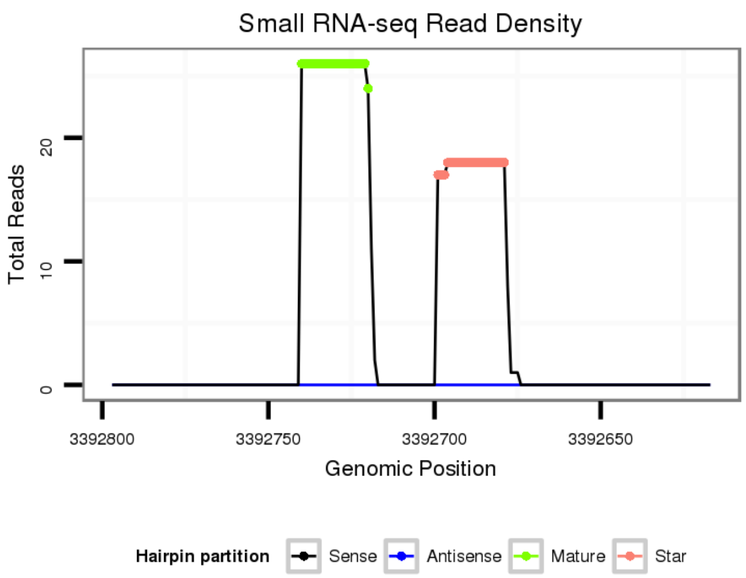
PASS/FAIL	
crit.star	1
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

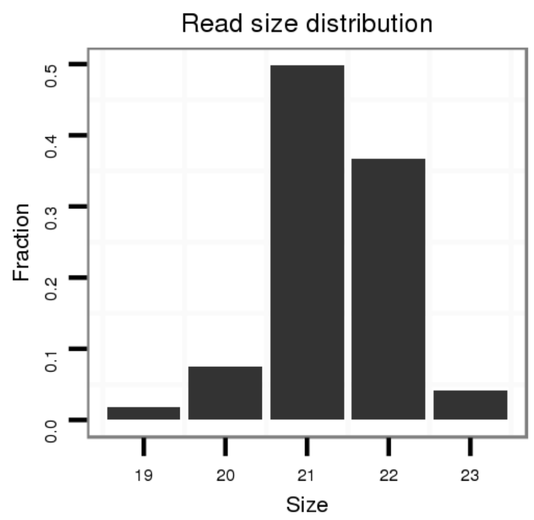
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_195	**scf2_1100000004511:3392667-3392747 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

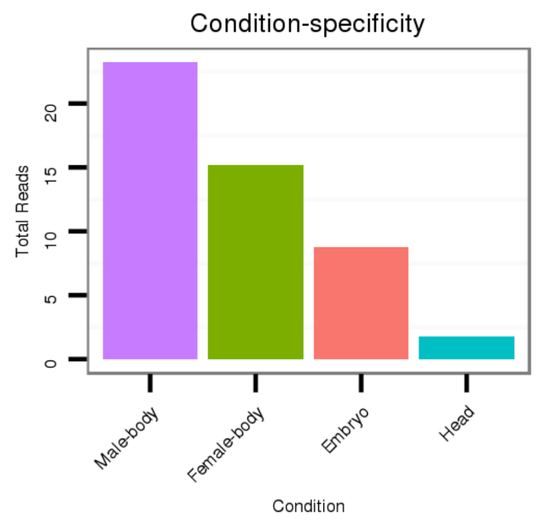
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

mature	star
1. dwi_195 scf2_1100000004511:3392720-3392740 - 2. dwi_61 scf2_1100000004511:3393294-3393314 - 3. dwi_63 scf2_1100000004511:3393867-3393887 - 4. dwi_64 scf2_1100000004511:3394151-3394171 - 5. dwi_65 scf2_1100000004511:3394509-3394529 -	1. dwi_197 scf2_1100000004511:3392321-3392341 - 2. dwi_196 scf2_1100000004511:3392537-3392557 - 3. dwi_195 scf2_1100000004511:3392679-3392699 - 4. dwi_61 scf2_1100000004511:3393253-3393273 - 5. dwi_193 scf2_1100000004511:3393468-3393488 - 6. dwi_63 scf2_1100000004511:3393826-3393846 - 7. dwi_64 scf2_1100000004511:3394110-3394130 - 8. dwi_65 scf2_1100000004511:3394468-3394488 - 9. dwi_89 scf2_1100000004511:3394684-3394704 - 10. dwi_190 scf2_1100000004511:3394900-3394920 - 11. dwi_189 scf2_1100000004511:3395101-3395121 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AGAAAAAAAAACTTAGTGATAGTCGCAGGATCATCAAAATTATATCTTATATGCAGAGTAGAGTTCAAGTAAAGGTAAATAGCGTTATAAATAGTAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTAAGAGAAAAACTACGTGATCGTCGCAGGATCATAAAAAT **********...(((((((((.(((..(((.((((((((((((((.....(((((.....)))))).....))))))))))))))).)))..))))..)))))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	M045 female body	V118 embryo	V119 head	M020 head
.....TAGAGTTCAAGTAAAGGTAAA.....	21	0	5	13.40	67	58	5	3	1	0
.....TTCCTACTTTTACTTGATCTT.....	21	0	11	10.73	118	5	94	8	8	3
.....TAGAGTTCAAGTAAAGGTAAAT.....	22	0	1	9.00	9	7	0	2	0	0
.....TTCCTACTTTTACTTGATCTTA.....	22	0	11	7.73	85	2	40	43	0	0
.....TAGAGTTCAAGTAAAGGTAA.....	20	0	5	2.60	13	11	1	0	1	0
.....TAGAGTTCAAGTAAAGGTAAATA.....	23	0	1	2.00	2	1	0	1	0	0
.....CTACTTTTACTTGATCTTATCT.....	22	0	11	1.27	14	2	6	2	1	3
.....TTCCTACTTTTACTTGATCT.....	20	0	11	0.73	8	0	7	1	0	0
.....TTCCTACTTTTACTTGATCTTAA.....	23	1	11	0.64	7	1	6	0	0	0
.....TAGAGTTCAAGTAAAGGTAAAA.....	22	1	5	0.60	3	3	0	0	0	0
.....TAGAGTTCAAGTAAAGGTA.....	19	0	5	0.60	3	3	0	0	0	0
.....TCCTACTTTTACTTGATCTT.....	20	0	11	0.27	3	0	3	0	0	0
.....CCTACTTTTACTTGATCTT.....	19	0	11	0.18	2	0	1	1	0	0
.....TCCTACTTTTACTTGATCTTA.....	21	0	11	0.18	2	0	2	0	0	0
.....TTCCTACTTTTACTTGATCTTAAA.....	24	2	11	0.18	2	0	2	0	0	0
.....TTCCTACTTTTACTTGATCTC.....	21	1	11	0.18	2	0	0	0	0	2
.....TTCCTACTTTTACTTGATCTTT.....	22	1	11	0.09	1	0	1	0	0	0
.....CTACTTTTACTTGATCTTATCC.....	22	1	11	0.09	1	1	0	0	0	0
.....CCTACTTTTACTTGATCTTATCTA.....	24	1	11	0.09	1	0	1	0	0	0
.....CCTACTTTTACTTGATCTTA.....	20	0	11	0.09	1	0	0	1	0	0
.....TTTTCCTACTTTTACTTGATCC.....	22	1	11	0.09	1	0	1	0	0	0
.....CTACTTTTACTTGATCTTATCTA.....	23	1	11	0.09	1	0	1	0	0	0
.....TCCTACTTTTACTTGATCTTAA.....	22	1	11	0.09	1	0	1	0	0	0
.....CTACTTTTACTTGATCTTATC.....	21	0	11	0.09	1	0	0	1	0	0
.....TCCTACTTTTACTTGATCT.....	19	0	11	0.09	1	0	1	0	0	0

Anti-sense strand reads

TCTTTTTTTTGAATCACTATCAGCGTCCTAGTAGTTTTAATATAGAATATACGTCTCATCTCAAGTTCATTTCCATTTATCGCAATATTTATCATTAAAAGGATGAAAATGAACTAGAATAGAGCCGCATATTTTTTGAGAATTCTCTTTTTGATGCACTAGCAGCGTCCTAGTATTTTTA **********...(((((((((.(((..(((.((((((((((((((.....(((((.....)))))).....))))))))))))))).)))..))))..)))))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo
.....TTCCTACTTTTACTTGATCT.....	19	0	11	0.09	1	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3392617-3392797 -	dwi_195	AGAAAAAAAAACTTAGTGATAGTCGCAGGATCATCAAAATTATATCTTATATGCAGAGTAGAGTTCAAGTAAAGGTAAATAGCGTTATAAATAGTAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTAAGAGAAAAACTACGTGATCGTCGCAGGATCATAAAAAT

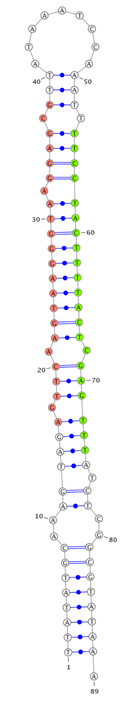
Generated: 09/08/2015 at 08:08 PM

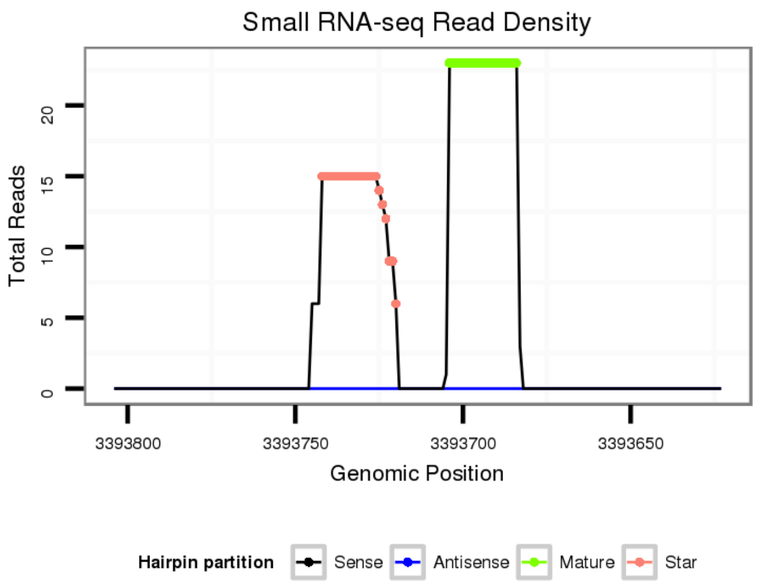
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

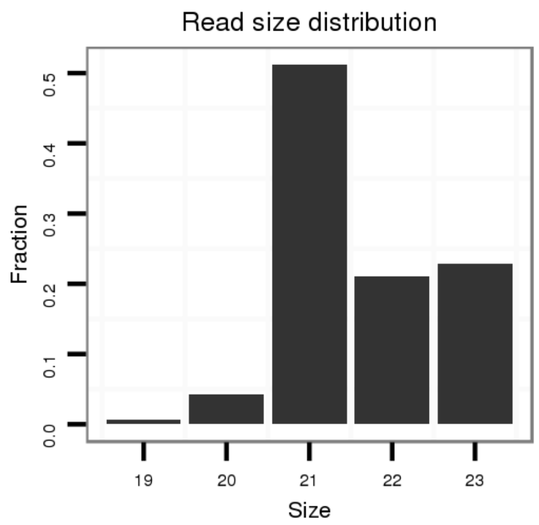
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_192	**scf2_1100000004511:3393673-3393754 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

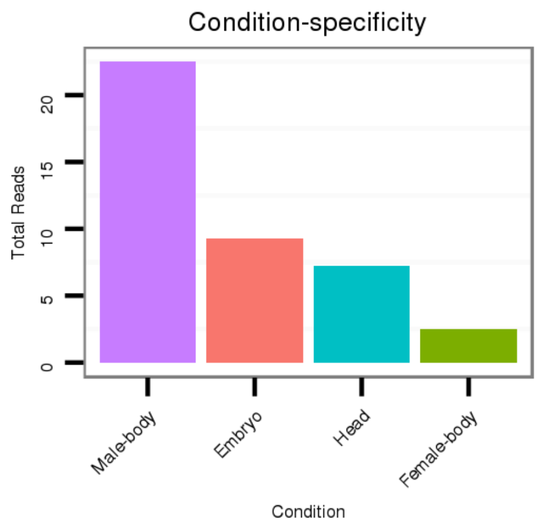
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

mature	star
	1. dwi_72 scf2_1100000004511:3393147-3393169 - 2. dwi_192 scf2_1100000004511:3393720-3393742 - 3. dwi_157 scf2_1100000004511:3394004-3394026 - 4. dwi_190 scf2_1100000004511:3394936-3394958 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTAAGAGAAAAACTAAGTGATCGTCGCAGGATCATAAAAATCATATCTTATATGCAAAGTAGAGTTCAAGTAAGGGTAAGGAGCGTTATAAATCCAAATTTTCCTACTTTTACTCGAGTTTATCTCGGCGTATAAAAAACTCATAAAAAAAATACAAATCAACATTTTTCTAATCATACCAC	Read size	# Mismatch	Hit Count	Total Norm	Total	V117 male body	V118 embryo	V119 head	M045 female body
**********(((((((..(((((((.(((.((((((((((.((((.(((.........))).)))))))))))))).)))))))..))))))))).**********									
.....TTCCTACTTTTACTCGAGTTT.....	21	0	1	19.00	19	9	3	6	1
.....AGTTCAAGTAAGGGTAAGGAGCG.....	23	0	4	6.00	24	15	6	0	3
.....TAGAGTTCAAGTAAGGGTAAGGA.....	23	0	4	3.50	14	5	9	0	0
.....TTCCTACTTTTACTCGAGTTTA.....	22	0	1	3.00	3	1	2	0	0
.....AGTTCAAGTAAGGGTAAGGAGC.....	22	0	4	3.00	12	9	0	1	2
.....TAGAGTTCAAGTAAGGGTAAGG.....	22	0	4	1.75	7	6	1	0	0
.....TAGAGTTCAAGTAAGGGTAAG.....	21	0	4	1.75	7	7	0	0	0
.....TTTCCTACTTTTACTCGAGTTT.....	22	0	1	1.00	1	0	0	1	0
.....TTCCTACTTTTACTCGAGTTTAA.....	23	1	1	1.00	1	0	1	0	0
.....TAGAGTTCAAGTAAGGGTAA.....	20	0	4	1.00	4	3	1	0	0
.....AGTTCAAGTAAGGGTAAGGAG.....	21	0	4	0.50	2	1	0	0	1
.....AGTTCAAGTAAGGGTAAGGA.....	20	0	4	0.50	2	2	0	0	0
.....TAGAGTTCAAGTAAGGGTAAGGAA.....	24	1	4	0.25	1	0	1	0	0
.....AGAGTTCAAGTAAGGGTAAG.....	20	0	4	0.25	1	1	0	0	0
.....AGTTCAAGTAAGGGTAAGG.....	19	0	4	0.25	1	1	0	0	0
.....TAGAGTTCAAGTAAGGGTAAA.....	21	1	9	0.11	1	1	0	0	0

Anti-sense strand reads

AATTCTCTTTTTGATTCACTAGCAGCGTCCTAGTATTTTTAGTATAGAATATACGTTTCATCTCAAGTTCATTCCCATTCCTCGCAATATTTAGGTTTAAAAGGATGAAAATGAGCTCAAATAGAGCCGCATATTTTTTGAGTATTTTTTTTATGTTTAGTTGTAAAAAGATTAGTATGGTG	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo
**********(((((((..(((((((.(((.((((((((((.((((.(((.........))).)))))))))))))).)))))))..))))))))).**********						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3393623-3393804 -	dwi_192	TTAAGAGAAAAACTAAGTGATCGTCGCAGGATCATAAAAATCATATCTTATATGCAAAGTAGAGTTCAAGTAAGGGTAAGGAGCGTTATAAATCCAAATTTTCCTACTTTTACTCGAGTTTATCTCGGCGTATAAAAAACTCATAAAAAAAATACAAATCAACATTTTTCTAATCATACCAC

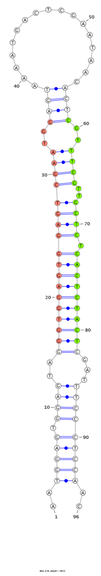
Generated: 09/08/2015 at 08:01 PM

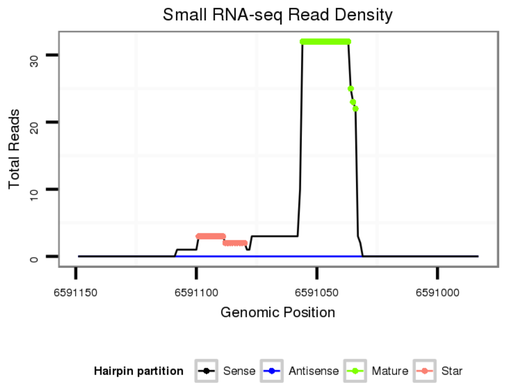
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

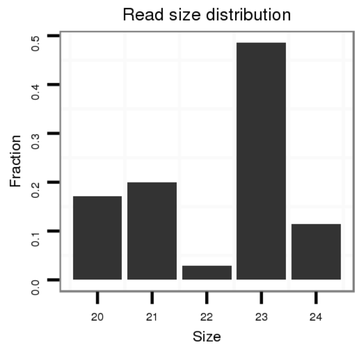
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_134	**scf2_1100000004909:6591033-6591099 -**	**confident-exception**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

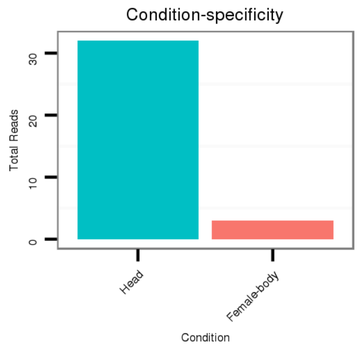
Legend: mature star mismatch in alignment mismatch in read

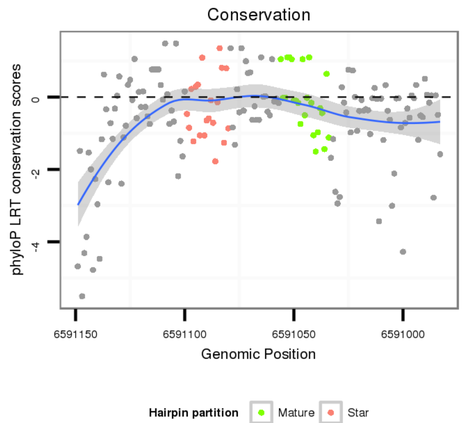
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK25195-in]

Repeatable elements

Name	Class	Family	Strand
GA-rich	Low_complexity	Low_complexity	+
(CACTC)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACCAAAAAGTAAACTAGAGTTTGATGTGGAATTGGAATGGAGTGGAGTAGGGTGGAGTGGAGTCGAATGGAGTAAAATGACTCGAATAACACTCGTTTCGTTGCTCTCACTCTACTCGATTTCCCTCCAACTTCATCTTTTACACACTTCTTCTCTTCCTCTCACCT						M020	M045 female	V119	V118	V117	Read size	# Mismatch	Hit Count	Total Norm	Total	head	body	head	embryo	male body
**********..(((((.((((..(((((((((((((((((((..((((.....................))))..))))..))))).))))))))))...))))))))..**********																				
.....CGTTTCGTTGCTCTCACTCTACT.....												23	0	1	16.00	16	14	1	1	0
.....CGTTTCGTTGCTCTCACTCT.....												20	0	1	5.00	5	4	1	0	0
.....TAAAATGACTCGAATAACACT.....												21	0	1	3.00	3	3	0	0	0
.....TCGTTTCGTTGCTCTCACTCTACT.....												24	0	1	3.00	3	3	0	0	0
.....CGTTTCGTTGCTCTCACTCTA.....												21	0	1	2.00	2	2	0	0	0
.....TCGTTTCGTTGCTCTCACTCT.....												21	0	1	2.00	2	1	0	1	0
.....CGTTTCGTTGCTCTCACTCTACG.....												23	1	1	1.00	1	1	0	0	0
.....GTGGAGTAGGGTGGAGTGGA.....												20	0	1	1.00	1	0	0	1	0
.....CGTTTCGTTGCTCTCACTCTACTC.....												24	0	1	1.00	1	1	0	0	0
.....CGTTTCGTTGCTCTCACTCTACG.....												23	1	1	1.00	1	1	0	0	0
.....GGTGGAGTGGAGTCGAATGG.....												20	0	1	1.00	1	0	0	1	0
.....GGTGGAGTGGAGTCGAATGGAG.....												22	0	1	1.00	1	0	1	0	0
.....CGTTTCGTTGCTCTCACTCTACTCG.....												25	0	1	1.00	1	0	1	0	0
.....TCGTTTCGTTGCTCTCACTCTACTCG.....												26	0	1	1.00	1	0	0	1	0
.....TCGTTTCGTTGCTCTCACTCTAC.....												23	0	1	1.00	1	0	0	1	0

Anti-sense strand reads

TGGTTTTTCATTTGATCTCAAACTACACCTTAACCTTACCTCACCTCATCCCACCTCACCTCAGCTTACCTCATTTTACTGAGCTTATTGTGAGCAAAGCAACGAGAGTGAGATGAGCTAAAGGGAGGTTGAAGTAGAAAATGTGTGAAGAAGAGAAGGAGAGTGGA						V117	Read size	# Mismatch	Hit Count	Total Norm	Total	male body
**********..(((((.((((..(((((((((((((((((((..((((.....................))))..))))..))))).))))))))))...))))))))..**********													

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004909:6590983-6591149 -	dwi_134	ACCAAAA----------AGTAAACTAGAGTTTGATG---TG----GAATTGGAATGGAGTGGA----------GTAGGGTGGAGTGGAGTCGAATGGAGTAAA----------ATGACTCGAATAACACTCGTT--T--CGTTGC-TC----------TCACTCTACT----------CGATTTCCCTCCAACTTCATCTT--------TTACACACTTCTTCTCTTCCTCTCACCT
droVir3	scaffold_12970:8180545-8180694 -		AAATAAA----------AGCAAATAAAATAGA-C---------GAAGAAAAAATACCAGTAAATTCGGGACGAA-ACCCCG----------
droMoj3	scaffold_6496:17884984-17885071 +		TAGTAAA----------ACCTCAATATAATTTATA---------GC----------
droGri2	scaffold_15203:5694230-5694446 +		ATTCAAA----------GATAAACGAAATATTTG---ATTTAAAC---GAAGCATA----------CAAAAGA---GAGCGCAGTGCGACTGTTGCAACAGAGATGAGCGCAATCCTCACAACACCATCCACCCACACACACACACACACACTCACAACAGCAGCGGTGGCACTGCC----------AGATCTCCCGCTCTCTTTATCAAATATACACATACACACTCACTCTCTGCTCTCACTC
dp5	3:2630036-2630184 +		ACACAAA----------CACACACTTTTCTACGATG---TTTCGTTGTAAA-----GAAACCA----------AACTCATGTTAATATCCAAAA---AAACAAAAAAATTCTGTTGGGATATACCA----------
droPer2	scaffold_5:6179053-6179129 -		CTCTCTC----------TATCTCTCCCCTC---TC-ACA----------CTCTCTCTCTCTCTCTCTCTCTC----------TCTCTCTCTCTCTCTCTCTCTC
droAna3	scaffold_13117:3574614-3574629 +		TTTCA---
droKik1	scf7180000302258:79548-79611 +		CTCTCTC----------T----------CTACT----------CTCTCTCTCTCTCTCTCTCTC
droFic1	scf7180000454077:2258726-2258785 -		CTCACAC----------TCATG----------CAGTTCTTCGCCGCCTAC----------CTTCGGCTCTCTCGCTCCTCTCTCTCCT
droEle1	scf7180000491023:1469636-1469707 -		TTTCATA----------GCCCG----------CATGTGCGT----------CGGGGTTTCTCTTTCAGTTTCCT----------TTTTTTATGTTTTTTTTAATTTTATTT
droRho1	scf7180000779914:689665-689712 +		TCAACTC----------C----------CTTGTTCTCTCA----------TCTCTCTCATCTTTTCTTCTCTCTC
droEug1	scf7180000409711:3170051-3170073 +		AACAACA----------ATCGAAAAAGGAATT----------G
dm3	chrUextra:28380908-28381002 -		AATACAA----------TAGAA--TAGAATAGAATAGCCTA---GACTCAGAATAGAATAGA----------CTAGAATAGAATAGAATAGAATGGAATACA----------AAGAAAGAGAATCGAGTA
droSec2	scaffold_11:2464430-2464478		GAACAGG----------ACGCGAAACGA----------GAGGATGGAGTGGAATGAATAGAAGACA----------A
droYak3	X:13093759-13093827 -		TTTGTTG----------CTCTG----------CTCTCTCTCTCTCTCTCTC----------TTTCTCACTCTCTCTCTCTCTC
droEre2	scaffold_4690:11952249-11952372 +		GTGGGTGTGAGTGAGGAGCAATTAAATGCAAATTTCTCC----------TTCAGCATCCCGGT--CATTGC-C----------TCTGTCCCCTTTCTCTTCTCTCTCTCTCTCTCTC

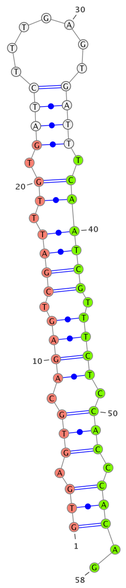
Generated: 09/08/2015 at 07:47 PM

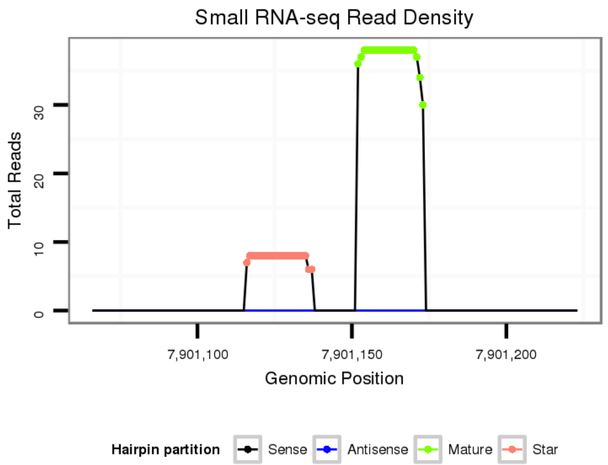
PASS/FAIL	
crit.star	0
crit.loop	1
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

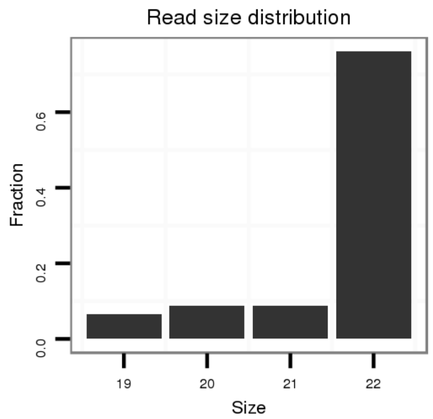
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_644	**scf2_1100000004511:7901116-7901173 +**	**confident**	**Mirtron**	**5pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

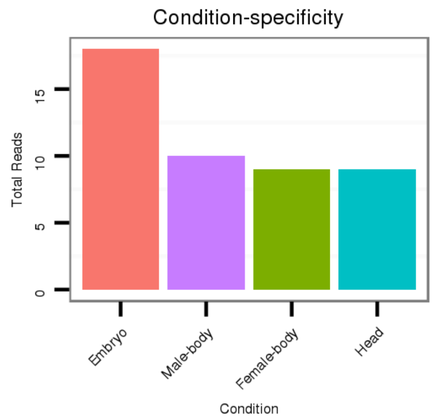
Legend: mature star mismatch in alignment mismatch in read

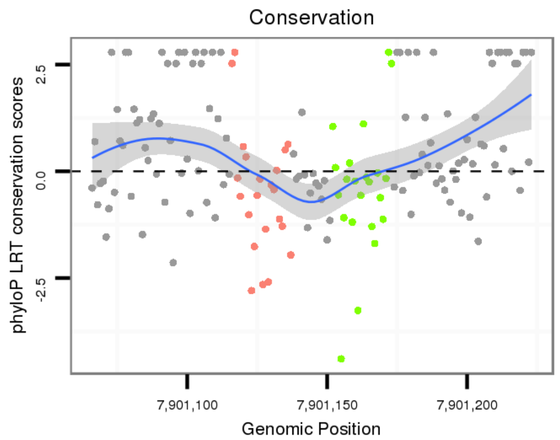
Predicted structure











Show Alternate Folds

Flybase annnotation

utr5 [utr5_minus_6091]; intron [Dwil\GK17463-in]; CDS [Dwil\GK17463-cds]; CDS [Dwil\GK17463-cds]; utr5 [utr5_minus_6092]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GAAGAGTTGAAAAAGCCTCTAGTCGAACCGGACTATGAGGATATCGAGAGGTGAGTGCAGAGTCGATTTGTGATCTTTGAGTGATTTCAATCGTTTCTCCACCCACAGCAATTTGTTGCAGCATTCGAGCAGCTTAATGCCAAGTAATATACGTTACT	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	V117 male body	M045 female body	M020 head	V119 head
**********(((.(((.((((.((((.((.((((.....)))).)))))).)))).))).))..**********										
.....TCAATCGTTTCTCCACCCACAG.....	22	0	1	29.00	29	15	1	6	5	2
.....GTGAGTGCAGAGTCGATTTGTG.....	22	0	1	6.00	6	0	6	0	0	0
.....TCAATCGTTTCTCCACCCACA.....	21	0	1	4.00	4	2	0	0	0	2
.....TCAATCGTTTCTCCACCCAC.....	20	0	1	2.00	2	0	0	2	0	0
.....GTGAGTGCAGAGTCGATTTGTGAA.....	24	1	1	2.00	2	0	2	0	0	0
.....AATCGTTTCTCCACCCACAG.....	20	0	1	1.00	1	1	0	0	0	0
.....CAATCGTTTCTCCACCCAC.....	19	0	1	1.00	1	0	0	1	0	0
.....GTGAGTGCAGAGTCGATTTG.....	20	0	1	1.00	1	0	1	0	0	0
.....TCAATCGTTTCTCCACCCA.....	19	0	1	1.00	1	0	1	0	0	0
.....TGAGTGCAGAGTCGATTTG.....	19	0	1	1.00	1	0	1	0	0	0
.....TCAATCGTTTCTCCACCCACAGT.....	23	1	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

CTTCTCAACTTTTTCGGAGATCAGCTTGGCCTGATACTCCTATAGCTCTCCACTCACGTCTCAGCTAAACACTAGAAACTCACTAAAGTTAGCAAAGAGGTGGGTGTCGTTAAACAACGTCGTAAGCTCGTCGAATTACGGTTCATTATATGCAATGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	M020 head	V117 male body	V119 head	V118 embryo
**********(((.(((.((((.((((.((.((((.....)))).)))))).)))).))).))..**********										
.....GTGAGTGCAGAGTCGATTTG.....	20	0	1	1.00	1	0	1	0	0	0
.....TGAGTGCAGAGTCGATTTG.....	19	0	1	1.00	1	0	1	0	0	0
.....TCAATCGTTTCTCCACCCACAGT.....	23	1	1	1.00	1	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:7901066-7901223 +	dwi_644	G----------AAGA---GTTGAAAAAGCCTCTAGTCGAACCGGACTATGAGGATATCGAGAGGTGAG-TGCAGA----------G---T---C--------GA----------TT--------TG--TGAT--CTT---T-----GAG---TGATTTCAATCGTTTC--------TCCACCCACAGCAATTTGTTGCAGCATTCGAGCAGCTTAATGCCAAGTAATATACGTTACT
droVir3	scaffold_13049:6593580-6593731 -		G----------CCGATGCCGTTGTCAAGTGGCCAACGCATCACGACTTCGATGACATTAAGGGGTAAG-TGGT--------CG---GC---A-------GTG---------------CAGGAA-TTG---C----T-----TTT-------GTAAACCATA-------TATCCACAGCAACCTGCTGGAGGACACCGACTCGGATACGTTCAGTAACATTCGGTATT
droMoj3	scaffold_6680:4912871-4913017 -		G----------AGGA---GCTGATCAAATGGCCAACGCATCATGACTTTGACGATATCAAGAGGTAAG-GGAT--------CT---AG---T---C--------------------TCAGCTACATT---T----T-----T-----TCT-------GCTAAATAAA-------TCGGTGTAGCAATCTCTTAGAGCACGTCGATTCGGATACCTCAGAACATTCGTTACT
droGri2	scaffold_15110:6181154-6181311 +		G-----AAACGG-CAAC---GATCACCAAATGGCCAACGGATCACGATTCGATGATATAAACAGGTACG-TTGT--------CT---AT---AACAA----------------TTTATGGATTTA---T----T-----T-----GTT--------CACATCGTA-------TGTCATTAGCAATCTGTTGGAGGATGTGGATGCGAATGCATTCAGTAACATTCGATATT
dp5	XR_group8:8656417-8656579 +		C----------AGAG---TCTGAACAAGTGGAGTGTGGACCAAGACTATGACGACATTGAGAAGTATC-TGTC--------CC---CGATCAGAGCCACTAGCCC----------------CAACC----T-----T-----T-------TCTAACCAAACCAGAGTTCCGCCCCAGGAACCTGCTGCAGAACCCCAACTCGTACACGCCGAGCAACATCCGCTATT
droPer2	scaffold_50:542654-542816 -		C----------AGAG---CCTGAACAAGTGGAGTGTGGACCAAGACTATGACGACATTGAGAAGTATC-TGTC--------CC---CGATCAGAGCCACTAGCCT----------------CAACC----T-----T-----T-------TCTAACCAAACCAGAGTTCTGCCCCAGGAACCTGCTGCAGAACCCCAACTCGTACACGCCGAGCAACATCCGCTATT
droAna3	scaffold_13337:7745234-7745402 +		G-----A-AGCCCAGAA---TCTCAACAAATGGCCAGTGGATCGTGATTATGATGATATAGAGAAGTAGG-TTCAGGTGCTATGTCTCTT--AA---T---T----------A-ACAAGAGTT-----TATAA---T--T-----T-----TATA------CT-CTCAT-------GTTTTTTTAGGAACCTCTTAACCAATGTGAACTCTTTCACTCCAAGCAACATCCGTTATT
droBip1	scf7180000395543:409884-410054 +		G-----GACACTCACCA---TCTCAACAAATGGGCAGTAGATCGTGATTATGATGATATTGAGAAGTAAG-TGCAAGACTTCTTTCTCCT--GA---T---T----------A-AAGAGAATTAATA--------TA--AGAT--TT----T-----T-----------CTTAT-------TGTTTCTTTAGAAACCTCTTAACCAATGTGACCTCTTTCACTCCAGCAACATCCGTTATT
droKik1	scf7180000302486:1388038-1388202 -		G------ATACCCAAAC---GATGAACAAGTGGGCAGTGGACCACGATTTCGATGACGTCGAAAAGTGAG-TGTT--------CG---TG---T---G-------CTTAAG---------AATTATCCT-TTG--TAATC-T----T-----T-----TTC-------ATATGACATA-------TCTCGTCAGAAATCTGCTGCACAAACGCTACGTCAATGGCTCCAAGCAACATCCGCTATT
droFic1	scf7180000451564:200208-200373 +		C----------AAAA---TATGAACAAGTGGTCGTGGATCAGGATACGATGACATCGAGAGGTGGG-CTAC--------CA---AA---A---GGAAATAGTTTT---------A---T--------ATGTA---TTTCTTAATATTT---ATT-------GTTTATTATA-------TCCCTAGAAATCTCCTTACCAACGTAAACATTTACCCAGAGCAACATCCGCTACT
droEle1	scf7180000490564:135321-135482 -		G-----GACAACCAAAT---CCTGAACAAATGGTCGTGGATCACGATATGATGACATCGAGAAGTAAG-TACAA----------A---T---TGAATTGAA---------T---TCT--GATTTA---TTT----T-----T-----CTT-------AGT-ATTGA-------TTCCGCTAGCAACCTCCTAACCAACGTGAGTTCGTTCGCCTCCAGCAACATCCGCTACT
droRho1	scf7180000766314:147922-148085 -		G-----GACAGCCAAAA---CATGAACAAGTGGACGGTGGACCATGATTACGACGACATCGAGAAGTAAGATGGT--------ATATAT---TGGATACATCT---------T---------GATTTAACT----T-----T-----TTT-------ACT-TGCAAA-------TACCCCTAGCAAATCTTTTAACAAATGGGACTCGTTCGCCTCCAGCAACATCCGCTACT
droBia1	scf7180000300910:2304207-2304373 +		G-----GACACCCAGGA---CCTGAACAAATGGTCGTGGATCAAGACTACGATGACATAGAAAAGTGAG-TGGT--------AC---AC---T---T-------AAA---T---------GAG---------TA---TTTC---TTT---T-----GTC---TATACTTAACTACCCAT-------CCATTTTCAGAAACCTCCTGACCAATGTGAGCTCCTTCGCCCCCAGCAACATCCGCTACT
droTak1	scf7180000415356:302897-303063 +		GAACAGGACAGCCAGCA---CCTAAACAAATGGGCAGTGGACCATGATTACGATGATATCGAAAGTGAG-TACC--------CT---GA---T---T-------A---A---------AAA---------TA---TTTC--CTT---G-----ATC---TATCTTTAATTACCG-A-------T-ACCCTAGAAACCTCCTGACCAATGTGAGTTCGTTCGCCCCAAGCAACATTCGCTACT
droEug1	scf7180000409467:113582-113734 -		C----------AAAA---TCTTAATAAATGGTCGTGGATCAGGATTATGATGATATTGAGAAGTGAG-CTGAAA----------G---T---GATATTGATTTTAAG---------T---------T---T----T-----T-----A---AGAGATTATTTA-CCAT-------TATTCCTAGAAATCTCCTGACCAACGTCAACGCCTTTGCCCCAAGCAATATCCGCTACT
dm3	chr3L:8904439-8904596 -		C----------AAAA---TCTGAACAAGTGGACGGTTGATCATGATTTTGATGACATCGAAAGTGAG-TATT--------AA---AC---T---T-------ATT---------AAAGTATTCTTCGATGTTA---T----T-----T-----CTC-------TAGAACCGAA-------CATCCCTAGCAATCTACTGACCAACGTCGAACACTTCGCCCCAAGTAATATTCGATACT
droSim2	3L:8688446-8688601 -		G-----GACACCCAAAG---TCTGAACAAGTGGACGGTAGATCATGATTTTGATGATATCGAGAAGTGAG-TATATA----------T---T---A---------T---------AACATAGATCTG---T----T-----T-----CTC-------ACGAACCGAA-------TACCCCTAGCAATCTCCTGACCAACGTCGAACACTTCGCCTCCAAGTAATATTCGATACT
droSec2	scaffold_0:1174973-1175127 -		G------ACACCCAAAG---TCTGAACAAGTGGACGGTGGATCATGATTTTGATGATATCGAGAAGTGAG-TATATA----------T---T---A---------T---------TACATCGATCTG---T----T-----T-----CTC-------AGGAACCGAA-------TACCCCTAGCAATCTCCTGACCAACGTCGAACACTTCGCCCCAAGTAATATTCGATACT
droYak3	3L:3009660-3009810 +		C----------AAAA---TCTGAACAAGTGGACGGTGGACCATGACTATGATGACATCGAGCGGTATA-TATAT----------T---A---A---C---------T---------TATTCAGCGATGTT---T----T-----T-----CTT-------ATAAACGAAA-------TACCTCTAGAAATCTGCTGACCAACGTCGAACACTTTGCGCCAAGTAATATTCGCTACT
droEre2	scaffold_4784:5139175-5139332 +		G-----GACCCCCAGCA---TCTGAACAAGTGGACGGTGGACCATGACTACGATGACATCGATAGGTAGG-TATATG----------A---C---A---------T---------TAGTTATAGATGTT---T----T-----T-----CTC-------TTAAACCGAG-------CATCCATAGAAATCTGCTGACCAACGTCGAGCAACTTTGCCCCAAGTAATATTCGCCTACT

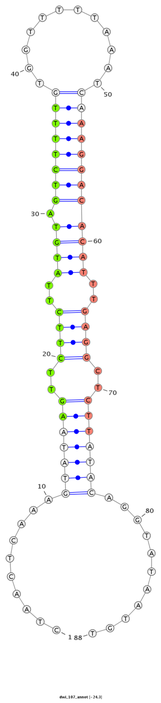
Generated: 09/08/2015 at 10:35 PM

	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

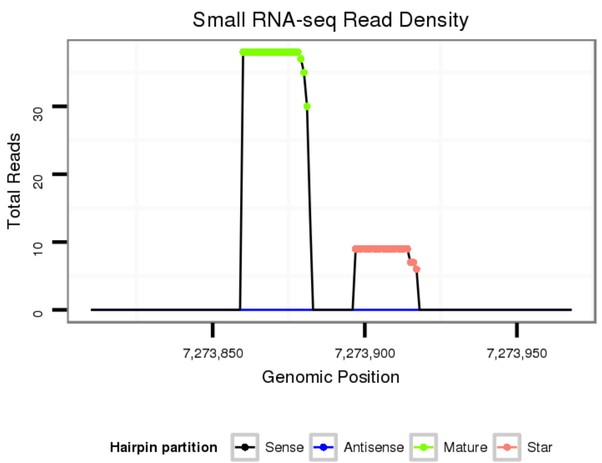
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_107	**scf2_1100000004902:7273860-7273918 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

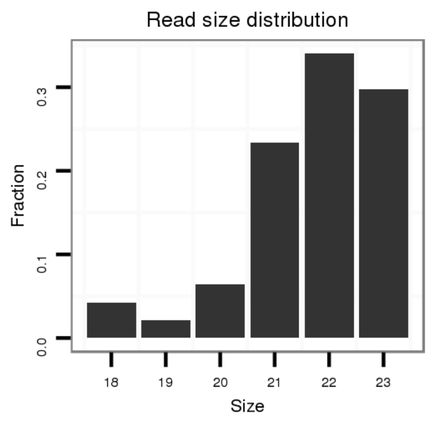
Legend: mature star **mismatch in alignment** mismatch in read

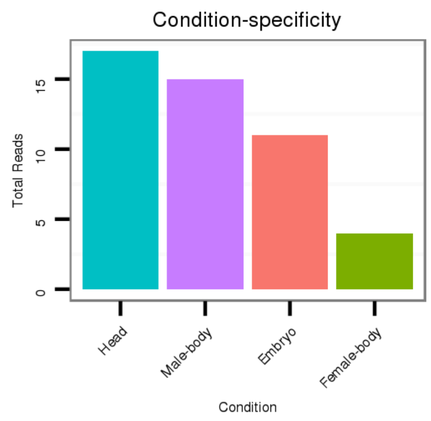
Predicted structure

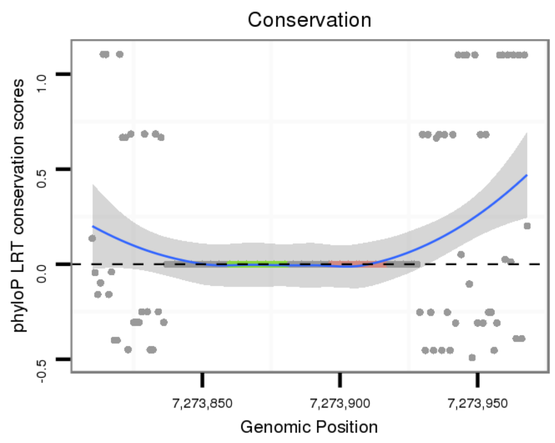


Show Alternate Folds









Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTAATTACAATGGATTAAATCTTTCGAAATAGTTACTAACTCAAAGTATAAGTTCTTCTTATGTAGTCTTTTGTGGTTTTTAAATCAAAGGACACATTTGAGGCTCTTATACAGGTATAATGTTTCTGTTCTATGTTTTAATTACAATTAATTACAGAT	Read size	# Mismatch	Hit Count	Total Norm	Total	M020 head	V117 male body	V118 embryo	M045 female body	V119 head
..... AGTTCTTCTTATGTAGTCTTTT	22	0	1	16.00	16	2	9	3	2	0
..... AGTTCTTCTTATGTAGTCTTTTG	23	0	1	14.00	14	1	2	8	0	3
..... AAGGACACATTTGAGGCTCTT	21	0	1	6.00	6	5	1	0	0	0
..... AGTTCTTCTTATGTAGTCTTT	21	0	1	5.00	5	1	2	0	2	0
..... AAGGACACATTTGAGGCT	18	0	1	2.00	2	2	0	0	0	0
..... AGTTCTTCTTATGTAGTCTT	20	0	1	2.00	2	1	1	0	0	0
..... AGTTCTTCTTATGTAGTCTTTCC	23	2	1	1.00	1	1	0	0	0	0
..... AAGGACACATTTGAGGCTCT	20	0	1	1.00	1	1	0	0	0	0
..... AGTTCTTCTTATGTAGTCT	19	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

GATTAATGTTACCTAATTTAGAAAGCTTTATCAATGATTGAGTTTCATATTCAAGAAGAATACATCAGAAAACACCAAAAATTTAGTTTCCTGTGTAAACTCCGAGAATATGTCCATATTACAAAGACAAGATACAAAATTAATGTTAATTAATGTCTA	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
droWil2	scf2_1100000004902:7273810-7273968 +	dwi_107	CT--AATTACAATGGATTAAATCTTTCGAAATAGTTACTAACTCAAAGTATAAGTTCTTCTTATGTAGTCTTTTGTGGTTTTTAAATCAAAGGACACATTTGAGGCTCTTATACAGGTATAATGTTTCTGTTCTATGTTTTAATTACAATT-AATTACAGAT
droVir3	scaffold_13047:3233409-3233436 +		TA--TGTTTCCCTGGCTATTGTTGGTTGT----------T	
droGri2	scaffold_14853:5075805-5075846 -		TA------------GTTTCGCTTTCATTTGTTCCATTAATGCAT-AATTAAATAT
dm3	chr3R:10784360-10784391 +		TTTTAATTAAAAT----------TATTTAA--------TAAGTAAAAATAC

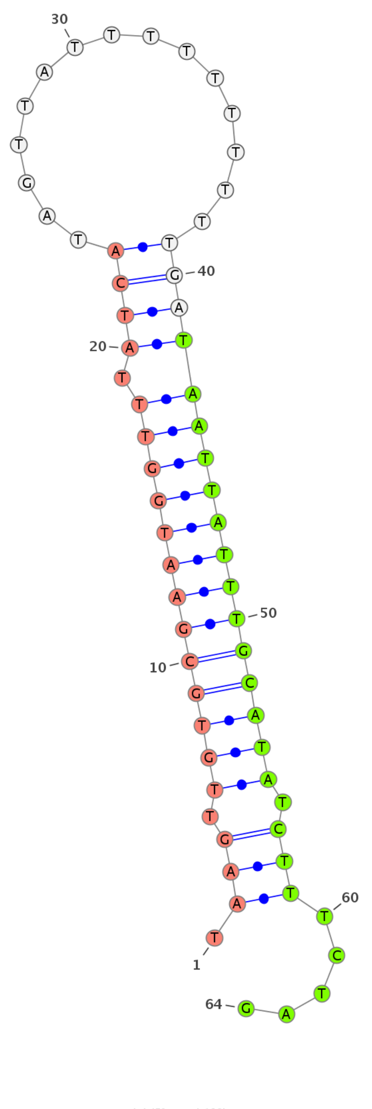
Generated: 06 Nov 2015 at 07:42 PM

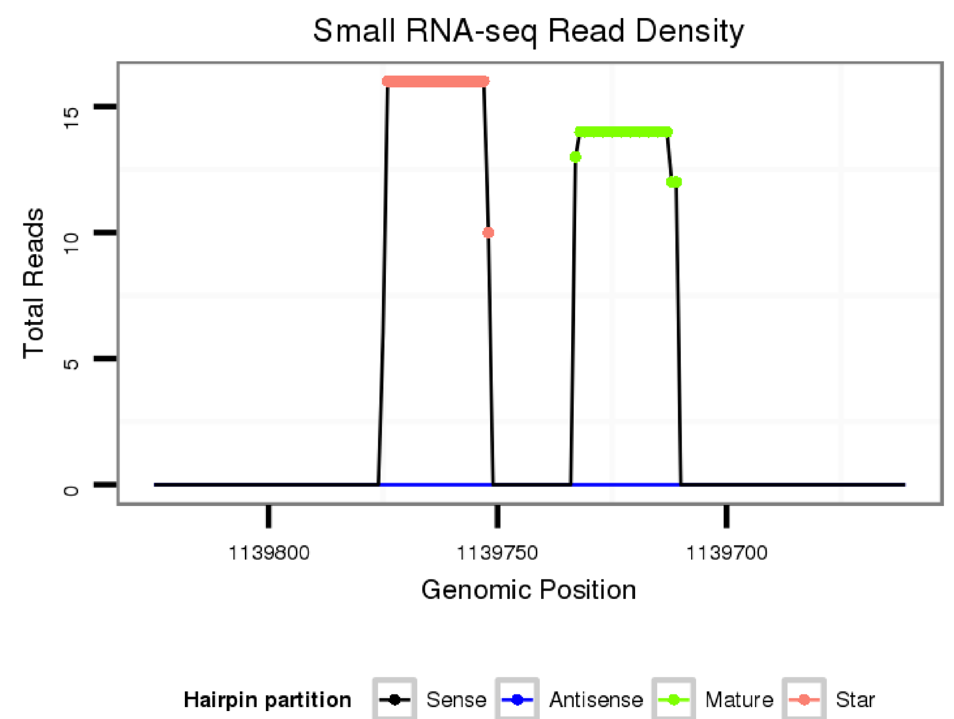
PASS/FAIL	
crit.seq	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

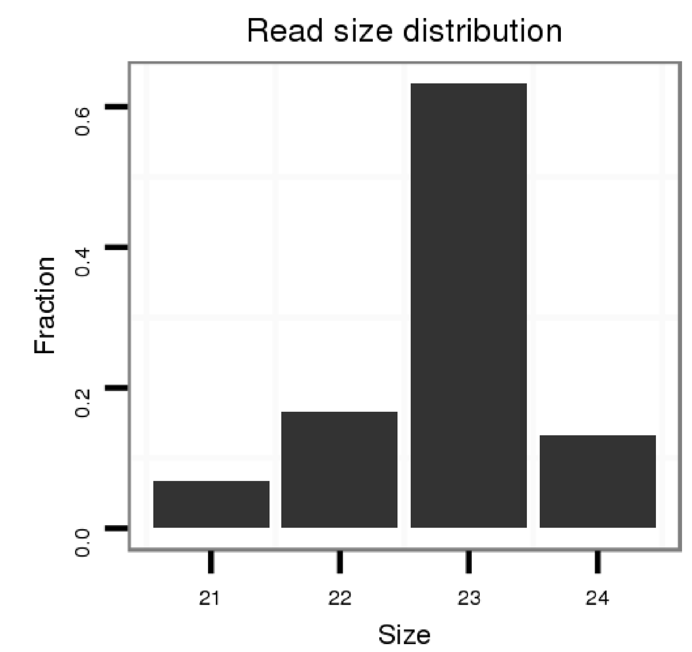
ID: dwi_479	Coordinate: scf2_1100000004511:1139711-1139775 -	Confidence: confident	Class: Mirtron	Genomic Locale: intron	[View on UCSC Genome Browser {Cornell Mirror}]

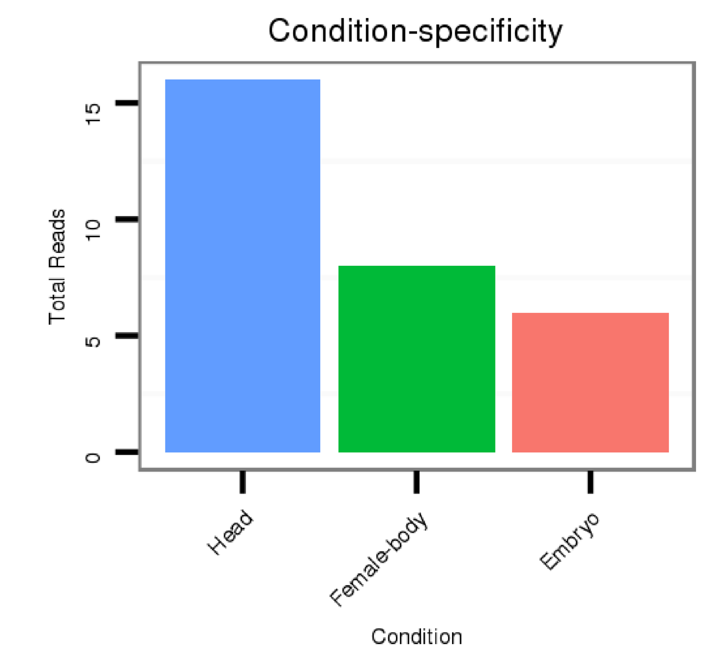
Legend: mature star mismatch in alignment mismatch in read

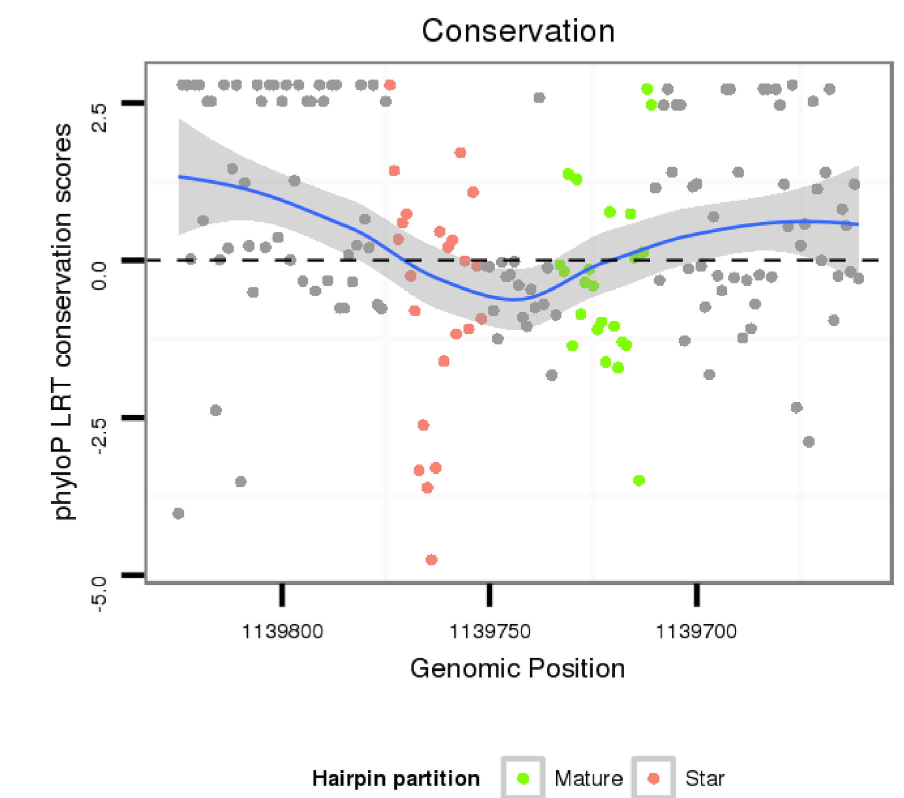
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK17051-in]; CDS [Dwil\GK17051-cds]; CDS [Dwil\GK17051-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTTCAAGCCGTTGGTGGCGTCAAATGTTTTACGTTCGATAAAGTTACTTAGTAAGTTGTGCGAATGGTTTATCATAGTTATTTTTTTTTTGATAATTATTTGCATATCTTTCTAGCTGATGGTTGCATTAGTTTCAACGACAATTGCCTCAGGGCCATTAACGAC **.(((.((((((((((((.((((..............)))))))))))))))))).))).....**	Read size	# Mismatch	Hit Count	Total Norm	Total	V119 head	M045 female body	V118 embryo
....TAATTATTTGCATATCTTTCTAG...	23	0	1	11.00	11	1	5	5
....TAAGTTGTGCGAATGGTTTATCA...	23	0	1	6.00	6	5	0	1
....TAAGTTGTGCGAATGGTTTATC..	22	0	1	4.00	4	4	0	0
....GTAAGTTGTGCGAATGGTTTATCA...	24	0	1	4.00	4	4	0	0
....GTAAGTTGTGCGAATGGTTTATC..	23	0	1	2.00	2	1	1	0
....TAATTATTTGCATATCTTTCT...	21	0	1	2.00	2	1	1	0
....AATTATTTGCATATCTTTCTAG...	22	0	1	1.00	1	0	1	0
....TAAGTTGTGCGAATGGTTTATCC...	23	1	1	1.00	1	1	0	0
....TAATTATTTGCATATCTTTCTC..	22	1	2	0.50	1	0	1	0

Anti-sense strand reads

AAAGTTCGGCAACCACCGCAGTTTACAAAATGCAAGCTATTTCAATGAATCATTCAACACGCTTACCAAATAGTATCAATAAAAAAAAAACTATTAATAAACGTATAGAAAGATCGACTACCAACGTAATCAAAGTTGCTGTTAACGGAGTCCCGGTAATTGCTG **.(((.((((((((((((.((((..............)))))))))))))))))).))).....**	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	M045 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:1139661-1139825 -	dwi_479	TTTCAAGCCGTTGGTGGCGTCAAATGTTTTACGTTCGATAAAGTTACTTAGTAAGTTGTGCGA----ATGGT-----T---------------T-----------AT--CATAGTT--ATTTT-TT-------------------TTTT-----------G-----AT------------------------------A--A-TTATT--T-G-CA-TATCTTTCTAGCTGATGGTTGCATTAGTTTCAACGACAATTGCCTCAGGGCCATTAACGAC
droVir3	scaffold_13049:24300301-24300463 -		TTTCAAGCCGCTGATCGTTTCCAATGTGCTACGTTCGATAAAACTGCTGTGTAAGTTCTCAAAACCAAGGGA-----–-CCCTTTAA-------–-----------–---–-------–---TGTCA-------------------AT-T-----------A-----CT------------------------------–AA–-ATGCT--A--TAG-TATTATTATAGCTGATGGTTGCAATACTTTTACTAAGAACTGTGTGGTTGGTATTAAGCCCG
droMoj3	scaffold_6680:18930309-18930467 -		CTTCAAGCCGTTGATAGCGTCCAACGTTCTGCGCTCGATACAGCTGCTAAGTATTTTAAGATC---------CCAGTTTCCATTGAA-------–-----------–---–-------–------–C-------------------ATTA-----------G-----–------------------------------ACTAAGT--GCTTG--AC-TCATTTCTCAGCTGATGGCTGCAACGCGTTCAACCAGAACTGCGTTGTTGGCATGAAGCCCG
droGri2	scaffold_15110:9452853-9453013 +		ATTCAAGCCTCTGATCTTGTCCAATGTTCTACGTTCGATAAAACTGCTGAGTAAGTTGAGATT---------CGAGTTCAGATATGCATGACAGACTT----------–---–---AATC--–-----–--------------------–---–-----------–-----–------------------------CTTA---–-–------–-TG--TA-TGTGATGCAGCTGATGGATGCAACTCTTTTGCCAAGAACTGCGTTGATGGCATTAAGGCA
dp5	XL_group1a:381244-381404 +		GTTCAAGCCCCTAATAGTGTCAAATGTGCTACGCTCTATTCGCCTGCTTTGTAAGTAGAAGA----------–-----–------------TCTTTTT----------–---CCA--ATATTCTGC-TA-------------------ATGC-----------G-----–------------------------------AGTACG--ATGT--C--CA-TCCATTTCAGCTGACGGCAGTCGCACCTTCACCGCCAATTGCGTGAACGGCATCCAGGCC
droPer2	scaffold_26:283968-284131 -		GTTCAAGCCCCTAATAGTGTCAAATGTGCTACGCTCTATTCGCCTGCTTTGTAAGTAGAAGGA----G---A-----–------------TCTTTTT----------–---CCA--ATATTCTGC-TA-------------------ATGC-----------G-----–------------------------------AGTACG--ATGT--C--CA-TCCATTTCAGCTGACGGCAGTCGCACCTTCACCGCCAATTGCGTGAACGGCATCCAGGCC
droAna3	scaffold_13117:4333180-4333340 +		TTTCAAGCCCCTCATTGTCTCCAATGTCCTGCGATCCATAAGATTGCTTTGTGAGTTTCGGTT---------TAGTTTTTAAGAGAAAGTTTACCTT----------–---TTA--AT--–-----–--------------------–---–-----------–-----–------------------------GTTT---–-–------–-CG--AA-CCTGTTCCAGCCGATGGCTCCATGACATTTAGCAAGAATTGCGTGGAGGGCATTCAGGCC
droBip1	scf7180000396383:75005-75157 -		GTTCAAGCCTCTGATTGTCTCCAATGTCCTGCGTTCCATCCGGCTGCTCTGTAGGTCTTTGTA---------A-TC-–-----CTTAT-------–-----------–---TGTGGC--–-----–C-------------------ATT-–C---------–---TG--------------------ATT--GTAC---–-–------–-G---–-A-TCCCTTCCAGCTGATGGCAGCCGCACCTTCACCGCCAACTGCGTCAACGGCATCCAGGCC
droKik1	scf7180000302272:864032-864187 -		CTTTAAGCCTCTGATCGTGTCCAATGTGCTGCGTTCCATCAAGCTGCTGAGTAATTATTTT-----------A-----–-----------T---–-----------–--CCTTTTA--TT---–ATT-–-------------------TCGTT-T-----------A-----CCT------------------------ATA--–---CAT--C-C-CT-TTTCTCCGCAGCGGATGGATGCCGCAGCTTCAATTTGAACTGCGTCAAGGGCATCAAGCCC
droFic1	scf7180000454072:838566-838724 -		GTTCAAACCGCTGATAGTTTCCAATGTGCTGCGCTCAATTAGGCTGCTGGGTAAGCTCGAAAT---------A-----–-----------A---–-----------–--CCAACTAAGCC--–-----–-------------------ATC--G---------–---TGAA----------------------AAGTAAGG--–---AA--A-C-TC-CTTCCTTTCAGCGGATGGCAGCATGAGCTTCAGCAAGAATTGCGTGGAAGGACTGCAGGCC
droEle1	scf7180000491044:468016-468194 +		GTTCAAACCTCTGATTGTGTCCAATGTGCTGCGCTCCATTCGGCTGTTGTGTAAGTTCATGGC----AAAGA-----T---------T------–---AAAGCGGTTCGTAAACGGTGCAGCTGCTGTAGGAACAGCTTTAAAGTGTTTTAAGCT----AA--–-----–--ATG--------GCTGCATCGTT-TAC-AACCAGTTT-----AAATTACTTA---------------------–---–------–-–-–---–--TTAACGGT----TGCCA
droRho1	scf7180000776942:153319-153566 +		GTTCAAACCTTTGATTGTGTCCAATGTGCTGCGCTCCATTCGGCTGTTGTGTAAGTTTAACGA----ATAGT-----T---------------T-----------A--AGCGATGCAGTGGCAGCGGAAAAAGCTTTTATGCATTTTTA-----------–---AGAAACAGCGACTGCCGCTGCATCGCT-TAC-AATTAGTTC-----CAAGTATTTATTTATTGACAGTC---AAGTAATAA------A--A--CC-TTTTCTTTCAGCTGATGGCAGCAGGACTTTTACTGCCAACTGCGTGAACGGAATCCAGGCT
droBia1	scf7180000301760:2823736-2823896 -		GTTCAAGCCCCTCATCGTGTCCAACGTGCTGCGCTCCATTCGGCTGTTGTGTAAGCTTGGGAGGCGAAGGGC-----T---------------T-----------AT--C---AAGAGG-------------------CT-T-----------C-----CAA------------------------GTA---–---ACT--A--TCT-TCCCTTTGCAGCTGATGGCAGCCGGACCTTCACTGCCAACTGCGTGAATGGCATCCAGGCC
droTak1	scf7180000413955:28976-29134 +		CTTTAAGCCTTTGATTGTGTCCAATGTGCTGCGCTCCATTCGGCTGTTGTGTAAGCTTGGCTT---------TAG--–-----------–-----------–--CCT---GT-----–-----–--CTA--------TCTGTATCGGT-TAT-A--------–---------T-------------------ATT--ATAT---–-–------–-T---–-A-TATTTTCAGCTGATGGCAGCCGTACCTTCACTGCCAACTGCGTGAACGGCATCCAGGCC
droEug1	scf7180000409711:3340506-3340669 -		CTTTAAGCCACTGATAGCCTCCAATGTGCTGCGCTCTATCAAGTTGCTCAGTAAGTCCATTCTAAACATGAA------–-TTTTTTAC-------–-------TGATCTCT--–-----–-A-------------------ATCG-----------G-----–------------------------------TTTAACT-----–-–--GT-TCGATTTCTAGGCGATGGATGCACTAGTTTTAACTGCAATTGCGTTAAGGGCATCAAGGCC
dm3	chr3L:11457078-11457232 -		TTTCAAGCCACTGATCGCATCCAATGTGCTCCGCTCCATCAAGCTGCTGGGTAAGTTTCTATA---------TAAA-–-------ATTATT---–--G---------–--–-----AA-------------------ATA--TA--------TATTTT---------------------AT--AAGA---–-–------–-T---–-G-AATTTCCTAGCTGATGGGTGCATCAGCTTCAACTGCAACTGCGTCAAGGGCATTAAGCCC
droSim2	3L:11187136-11187291 -		TTTCAAGCCACTGATTGCATCCAATGTGCTCCGTTCCATCAAGCTGCTGGGTAGGTTTTATA---------TAAA-–-------ATAATG---–--G---------–--–-----AA-------------------ATA--TA--------TAGTTT---------------------AAT--GGGC---–-–------–-T---–-G-TATTTTCTAGCTGATGGGTGCATCAGCTTCAATTGCAACTGCGTCAAAGGCATTAAACCC
droSec2	scaffold_0:3665304-3665459		TTTCAAGCCACTGATTGCATCTAATGTGCTCCGTTCCATCAAACTGCTGGGTAAGTTTCTAAA---------TAAA-–-------ATAATG---–--G---------–--–-----AA-------------------ATA--TA--------TAGTTT---------------------ATT--GCGG---–-–------–-T---–-G-TATTTTCTAGCTGATGGGTGCATCAGCTTCAACTGCAACTGCGTCAAAGGCATTAAGCCT
droYak3	3L:11496162-11496312 -		ATTCAAGCCACTGATAGCCTCCAATGTGCTACGCTCTATTAAGCTATTGGGTAAGTGTTTTTA---------TTAA-–----GGAAAAATG---–--A---------–--–-----AA-------------------AT–-------------–-----–------------------------------–---–-A--ATTT--ATAT-TTAATTTATAGCGGATGGTTGCATCAGCTTCAACTGCAACTGCGTCAAGGGCATCAAGCCC
droEre2	scaffold_4784:11467112-11467264 -		CTTTAAGCCGCTGATCGCCTCCAACGTGCTTCGCTCCATCAAGCTGTTGGGTAAGTGTTACAT---------T-AA-–----GTAAGAATG---–--G---------–--–-----TA-------------------ATA--T---------–---TT--------------------AAT--GGGC---–-–------–-T---–-G-TACTTCGTAGCGGATGGCTGCATCAGCTTCAACTGCAACTGCGTCAAGGGCATTCGGCCC

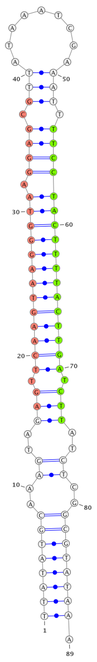
Generated: 09/08/2015 at 10:35 PM

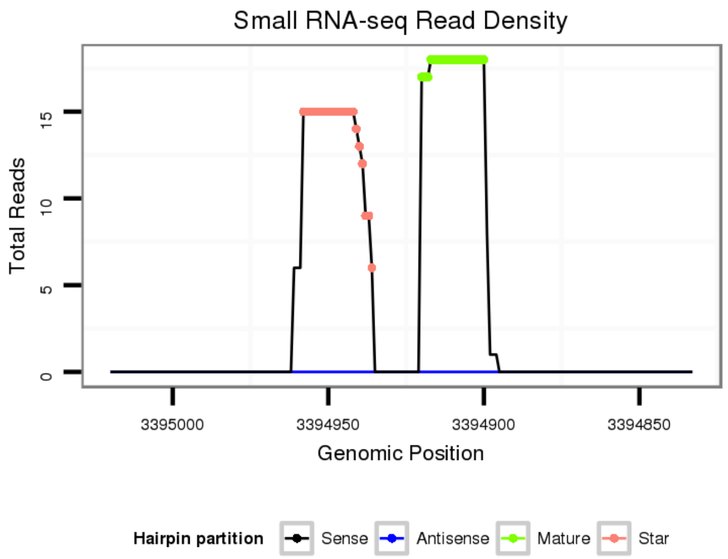
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

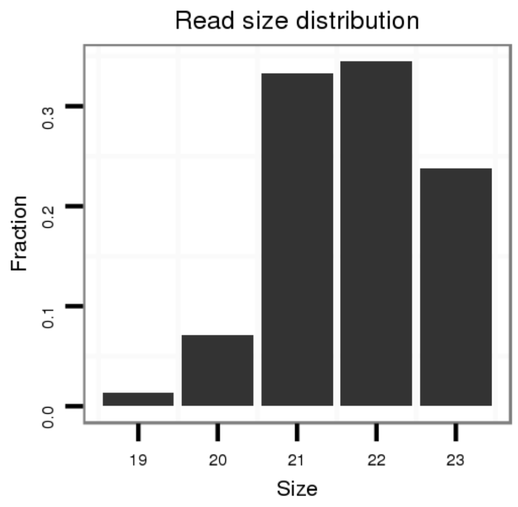
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_190	**scf2_1100000004511:3394883-3394970 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

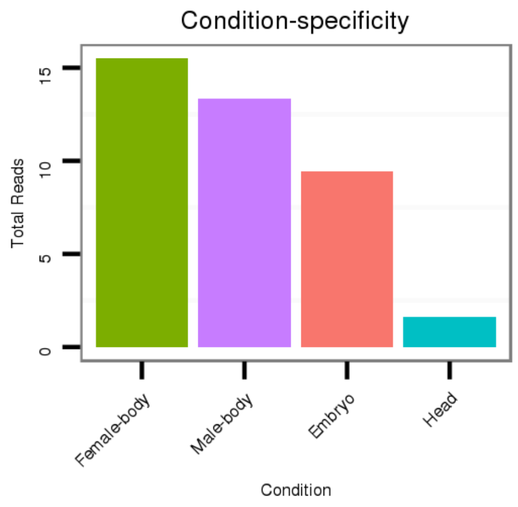
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dwil\GK17265-in]

No Repeatable elements found

mature	star
1. dwi_197 scf2_1100000004511:3392321-3392341 - 2. dwi_196 scf2_1100000004511:3392537-3392557 - 3. dwi_195 scf2_1100000004511:3392679-3392699 - 4. dwi_61 scf2_1100000004511:3393253-3393273 - 5. dwi_193 scf2_1100000004511:3393468-3393488 - 6. dwi_63 scf2_1100000004511:3393826-3393846 - 7. dwi_64 scf2_1100000004511:3394110-3394130 - 8. dwi_65 scf2_1100000004511:3394468-3394488 - 9. dwi_89 scf2_1100000004511:3394684-3394704 - 10. dwi_190 scf2_1100000004511:3394900-3394920 - 11. dwi_189 scf2_1100000004511:3395101-3395121 -	1. dwi_72 scf2_1100000004511:3393147-3393169 - 2. dwi_192 scf2_1100000004511:3393720-3393742 - 3. dwi_157 scf2_1100000004511:3394004-3394026 - 4. dwi_190 scf2_1100000004511:3394936-3394958 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AGAAACAATTGGCAGAGTGATCGTCACTGGATCATAAAAATCATATCTTATATGCAAAGTAGAGTTCAAGTAAGGGTAAGGAGCGTTATAAATCGAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTGAAAAAAATACAAATCAACATTTTTCTAAACATTCCATTTGCTT **********(((((((..((..(((.(((((((((((((.((((.(((.........))).))))))))))))))))).)))..))..)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	V117 male body	V118 embryo	V119 head	M020 head
TTCCTACTTTTACTTGATCTT	21	0	11	10.73	118	94	5	8	8	3
TTCCTACTTTTACTTGATCTTA	22	0	11	7.73	85	40	2	43	0	0
AGTTCAAGTAAGGGTAAGGAGCG	23	0	4	6.00	24	3	15	6	0	0
TAGAGTTCAAGTAAGGGTAAGGA	23	0	4	3.50	14	0	5	9	0	0
AGTTCAAGTAAGGGTAAGGAGC	22	0	4	3.00	12	2	9	0	1	0
TAGAGTTCAAGTAAGGGTAAG	21	0	4	1.75	7	0	7	0	0	0
TAGAGTTCAAGTAAGGGTAAGG	22	0	4	1.75	7	0	6	1	0	0
CTACTTTTACTTGATCTTATCT	22	0	11	1.27	14	6	2	2	1	3
TAGAGTTCAAGTAAGGGTAA	20	0	4	1.00	4	0	3	1	0	0
TTCCTACTTTTACTTGATCT	20	0	11	0.73	8	7	0	1	0	0
TTCCTACTTTTACTTGATCTTAA	23	1	11	0.64	7	6	1	0	0	0
AGTTCAAGTAAGGGTAAGGAG	21	0	4	0.50	2	1	1	0	0	0
AGTTCAAGTAAGGGTAAGGA	20	0	4	0.50	2	0	2	0	0	0
TCCTACTTTTACTTGATCTT	20	0	11	0.27	3	3	0	0	0	0
TAGAGTTCAAGTAAGGGTAAGGAA	24	1	4	0.25	1	0	0	1	0	0
AGTTCAAGTAAGGGTAAGG	19	0	4	0.25	1	0	1	0	0	0
AGAGTTCAAGTAAGGGTAAG	20	0	4	0.25	1	0	1	0	0	0
TTCCTACTTTTACTTGATCTTAAA	24	2	11	0.18	2	2	0	0	0	0
TTCCTACTTTTACTTGATCTC	21	1	11	0.18	2	0	0	0	0	2
TCCTACTTTTACTTGATCTTA	21	0	11	0.18	2	2	0	0	0	0
CCTACTTTTACTTGATCTT	19	0	11	0.18	2	1	0	1	0	0
TAGAGTTCAAGTAAGGGTAAA	21	1	9	0.11	1	0	1	0	0	0
TTCCTACTTTTACTTGATCTTT	22	1	11	0.09	1	1	0	0	0	0
CTACTTTTACTTGATCTTATCC	22	1	11	0.09	1	0	1	0	0	0
TCCTACTTTTACTTGATCT	19	0	11	0.09	1	1	0	0	0	0
CCTACTTTTACTTGATCTTA	20	0	11	0.09	1	0	0	1	0	0
TTTTCCTACTTTTACTTGATCC	22	1	11	0.09	1	1	0	0	0	0
CTACTTTTACTTGATCTTATCTA	23	1	11	0.09	1	1	0	0	0	0
CTACTTTTACTTGATCTTATC	21	0	11	0.09	1	0	0	1	0	0
TCCTACTTTTACTTGATCTTAA	22	1	11	0.09	1	1	0	0	0	0
CCTACTTTTACTTGATCTTATCTA	24	1	11	0.09	1	1	0	0	0	0

Anti-sense strand reads

TCTTTGTTAACCGTCTCACTAGCAGTGACCTAGTATTTTTAGTATAGAATATACGTTTCATCTCAAGTTCATTCCCATTCCTCGCAATATTTAGCTTTAAAAGGATGAAAATGAACTAGAATAGAGCCGCATATTTTTTGAGAACTTTTTTTATGTTTAGTTGTAAAAAGATTTGTAAGGTAAACGAA **********(((((((..((..(((.(((((((((((((.((((.(((.........))).))))))))))))))))).)))..))..)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo
TTAGCTTTAAAAGGATGAAAA	21	0	7	0.14	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004511:3394833-3395020 -	dwi_190	AGAAACAATTGGCAGAGTGATCGTCACTGGATCATAAAAATCATATCTTATATGCAAAGTAGAGTTCAAGTAAGGGTAAGGAGCGTTATAAATCGAAATTTTCCTACTTTTACTTGATCTTATCTCGGCGTATAAAAAACTCTTGAAAAAAATACAAATCAACATTTTTCTAAACATTCCATTTGCTT

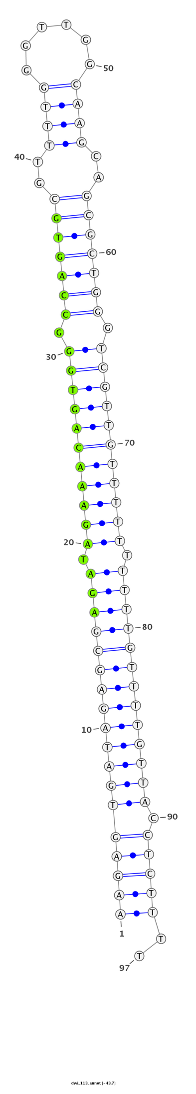
Generated: 09/08/2015 at 08:05 PM

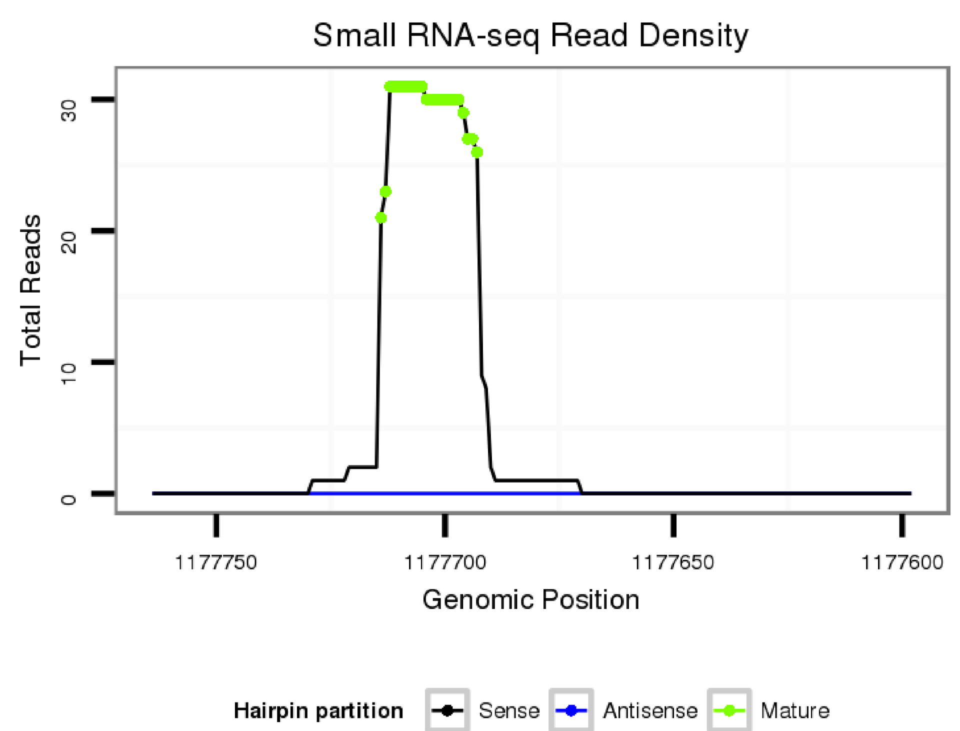
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

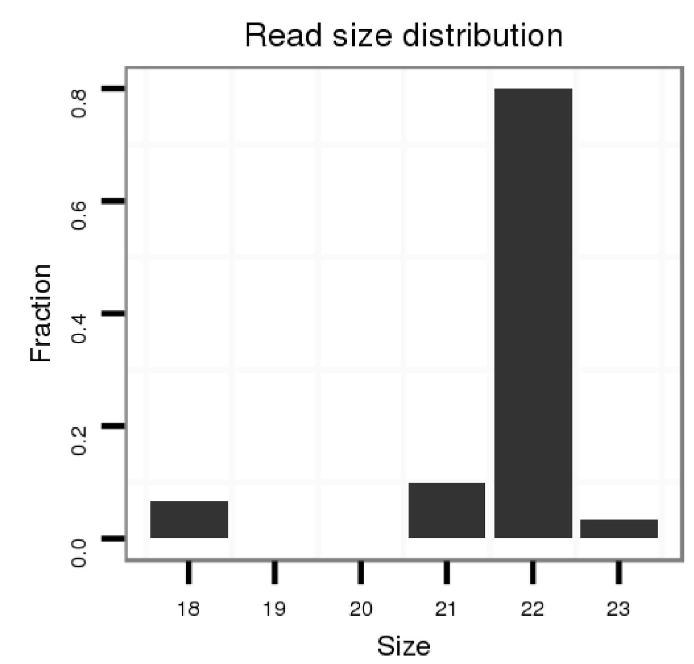
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_113	**scf2_1100000004585:1177648-1177714 -**	**confident-exception**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

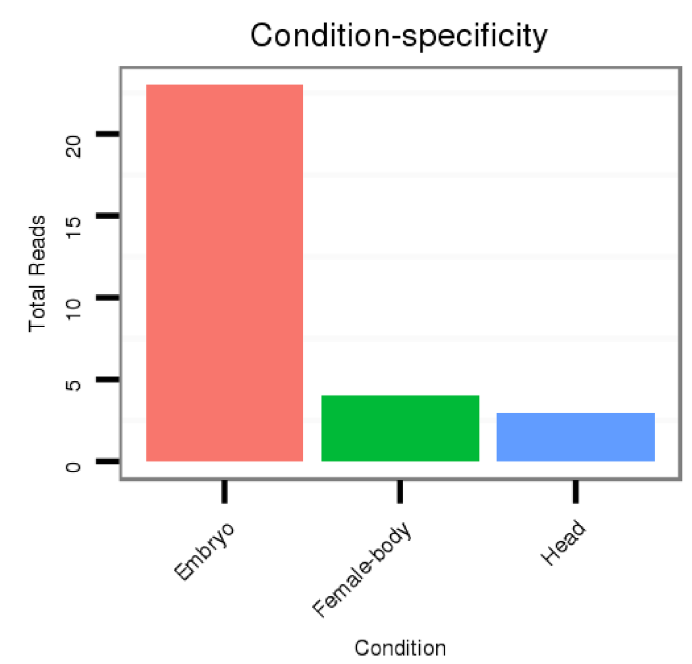
Legend: mature star mismatch in alignment mismatch in read

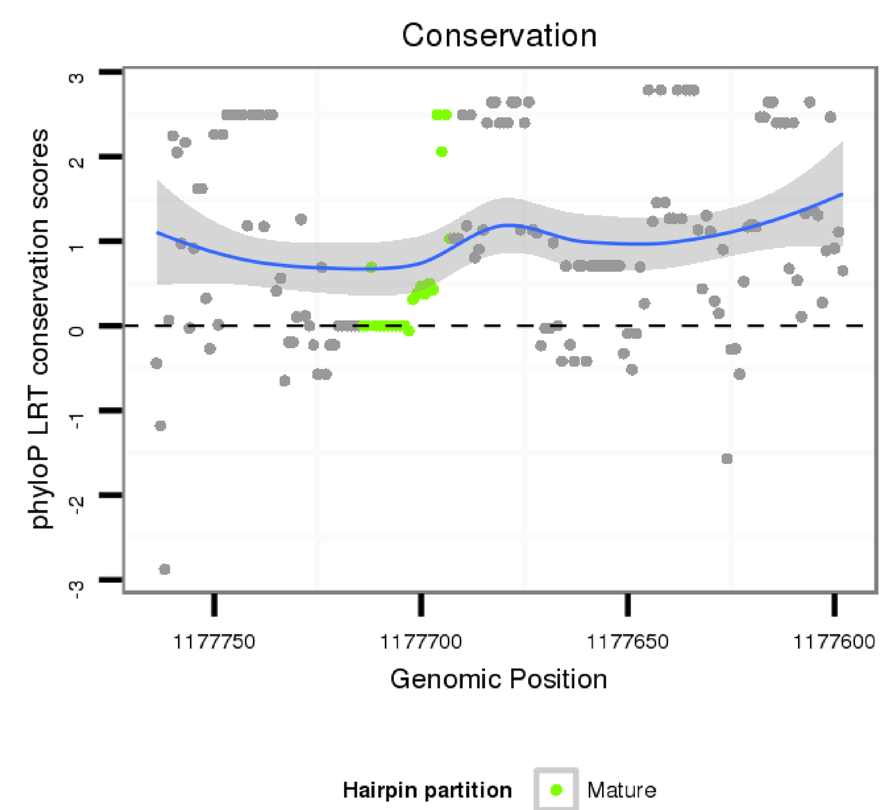
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dwil\GK24496-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTCAACTTTTATGCTATATTATTTATATACCCATTAAGAGTGATAGAGCGAGATAGAAACAGTGGGCCAGTGCGTTTTGGGTTGGCAAGCAGCGCTGGGTCGTTGTTTTTTTTTTTGTTTTGTTACCTCTTTTTTGAACAACAAATTTATTGGCAGCCAAAATGAAAT **********************************((((((((((((((((.((((((((((.(((((((..((((......))))..))))))).))))))))))).)))))))))))).))))).. **********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	M045 female body	V119 head	V117 male body	M020 head
....AGATAGAAACAGTGGGCCAGTG..	22	0	1	17.00	17	15	2	0	0	0
....ATAGAAACAGTGGGCCAGTGCG..	22	0	1	6.00	6	5	0	1	0	0
....GATAGAAACAGTGGGCCA...	18	0	1	1.00	1	0	1	0	0	0
....AGATAGAAACAGTGGGCC..	18	0	1	1.00	1	0	0	0	0	1
....GATAGAAACAGTGGGCCAGTG..	21	0	1	1.00	1	0	1	0	0	0
....ATAGAAACAGTGGGCCAGTGC...	21	0	1	1.00	1	1	0	0	0	0
....AGATAGAAACAGTGGGCCAGT...	21	0	1	1.00	1	1	0	0	0	0
....TAGAGCGAGATAGAAACAGTGGGCCA...	26	0	1	1.00	1	1	0	0	0	0
....ATAGAAACAGTGGGCCAGTGCGT...	23	0	1	1.00	1	0	0	1	0	0
...................................AAGAGTGATAGAGCGAGATAGAAAC..	25	0	1	1.00	1	0	0	0	1	0
....AGATAGAAACAGTGGGCCAGTGT...	23	1	1	1.00	1	1	0	0	0	0
....CGTTTTGGGTTGGCAAGCAGCG..	22	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

GAGTTGAAAATACGATATAATAAATATATGGGTAATTCTCACTATCTCGCTCTATCTTTGTCACCCGGTCACGCAAAACCCAACCGTTCGTCGCGACCCAGCAACAAAAAAAAAAACAAAACAATGGAGAAAAAACTTGTTGTTTAAATAACCGTCGGTTTTACTTTA **********************************((((((((((((((((.((((((((((.(((((((..((((......))))..))))))).))))))))))).)))))))))))).))))).. **********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V119 head	M045 female body	V118 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004585:1177598-1177764 -	dwi_113	CTCAACTTTTATGC------------TATA---------------TTATTTATATACCCATTAAGAGTGATAGAGCGAGATAGAAACAGTGGGCCAGTGCGTTTT-----------------------------------G--GGTTGGCAA--GCAGC-G---CTGG-----------------GTCGTTGTTTTTTTTTTTGTTTTGTTACCTCTTTTTTG-------------------------------AAC-----AACAAATTTATTGGCAG---CCAAAA-TGAAAT-----------
droVir3	scaffold_12963:6492969-6493047 -		---GTTGGCAA--GCAGC-AAC-------------------TG-------------------GCTGTTACCTCTTTTTTATTTTTTC----------CTA------------GCC-----CGACAATTTATTGGCTG---CCAAAT-CCACTC-----------
droMoj3	scaffold_6473:1760016-1760059 -		AGC---G---CCGA-----------------TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT--
droGri2	scaffold_15252:9717641-9717787 -		ATATACATATATAA------------ ---A---------------TTATATATATATA----------------------TATATATA-TATATAT-ATATATATTT----ACCC-------TA-AAA------C--TGTTGGCAATGACAGCTAAC---------------------TA-------------------GCTGTTACCTCTTTTGCTAGTACTGC-----------AG-CG--------CCC-----TGATAATTTATTGGCAG---CCAAAA-GCACTC-----------
dp5	4_group3:2799856-2800020 -		CTGAACTTCC-----ATTTAGCGAGTTGTACGGAGTATACGAGTCTTATTTATATACTC--CAC-GCTCGC--------A--------CACACACAGTGCGTTTGTTATGTATTC------------------GA------C--TGTTGGCAA--GCAGC-AGCGTTGGCGCTGGCGCTGGCGCTG---------------GCACTGTGCTACCTCTTTC--TTGGCAG---CCAAAA-------------------
droPer2	scaffold_1:4285130-4285288 -		CTGAACTTCC-----ATTTAGCGAGTTGTACGGAGTATACGAGTCTTATTTATATACTC--CAC-GCTCGC--------A--------CACACACAGTGCGTTTGTTATGTATTC------------------GA------C--TGTTGGCAA--GCAGC-AGCGTTGGCGCTG------GCGCTG---------------GCACTGTGCTACCTCTTTC--TTGGCAG---CCAAAA-------------------
droAna3	scaffold_12916:10051767-10051914 -		TCT-----------AACTGGCGATTTATA---------------TTATTTATCTACT----------------------GGCGCTTAGTGCGTTTGTTATGTACTC----GCCG---------CCGA------C--TGTTGGCAA--GCAG--TTTGTTACCTCTTTCCTT-------C------GGA-CCAGCCGCCAAC--A-ACATATTATAGGTCTATTGGCAG---GCGAAAGGCA---------------
droBip1	scf7180000396580:982680-982841 +		CAGAACTTCT-----ATCTGGCGATTTGTA---------------TTATTTATATACTGGCTAC---------------------TGGCGCTCAGTGCGTTTGTTATGTATTCGG-TGC--------C--ACCGA------C--TGTTGGCAA--GCAG--TTTGTTACCTCTTTCCTT-------C------GGA-CCAG-CCAACTA--AAA-----TATAAGTCTATTGGCAG---TCGAAAGGCACT-------------
droKik1	scf7180000302643:752650-752799 -		CTAAACTTCT-----ATCTGGCGATTTATA---------------TTATTTATATACT----------------------CGCGCACAGTGCGTTTGTTATGTATTCGCTTGCCA-------TATTGA------C--TGTTGGCAA--GCAG--TTTGTTACCTCTTTCCTT-------C--T-GGGC-CCC-------------A-----CAAATATTTATTGGCAG---CCAAAAAGCACT-------------
droFic1	scf7180000453842:1131358-1131501 -		TTT-----------AACTGGCGATTTATA---------------TTATTTATATAGTA--TAC---------------------TGGCGCACAGTGCGTTTGTTATGTATTC----GCCA-------CATCGA------C--TGTTGGCAA--GCAG--TTTGTTACCTCTTTCCTT-------C------GGC-CGA------------AAA-----GGAAAATTTATTGGCAG---CCAAAA-GCACTC-----------
droEle1	scf7180000491273:104146-104293 -		CCGAACTTCTAT---ATCT--CGATTTATA---------------TTATTTATATACT----------------------GGCGCACAGTGCGTTTGTTATGTATTC----GCCG-------CATCGA------C--TGTTGGCAA--GCAA--TTTGTTACCTCTTTCCTT-------G------GGT-CGA------------AAA-----TATAAATTTATTGGCAGCAGCGAAGA-GCACT------------
droRho1	scf7180000779577:107183-107323 -		TCT-----------AACTGGCGATTTATA---------------TTATTTATATACT----------------------GGCGCACAGTGCGTTTGTTATGTATTC----GCCG-------CATCGG------C--TGTTGGCAA--GCAA--TTTGTTACCTCTTTCCTT-------G------GGT-CGA------------A-------AAGAATTTATTGGCAG---CGAAAA-GCACTCGAACT------
droBia1	scf7180000302261:553016-553162 +		CCCGACT--------ATCTGGCGATTTGTA---------------TTATTTATATACT----------------------GGCGCACAGTGCGTTTGTTATGTATTC----GCCC-------CGTCGG------C--TGTTGGCAA--GCAG--TTTGTTACCTCTTTCCTT-------G------GGC-CGGGTCG-------AAA-----CGGGAATTTATTGGCAG---CCAAAA-GCACTC-----------
droTak1	scf7180000415204:14731-14899 -		TTATACTTTTATACTATCTGGCGATTTATA---------------TTATTTATATACT----------------------GGCGCACAGTGCGTTTGTTATGTATTC----GCCC-------CATCGACTACTAC--TGTTGGCAA--GCAG--TTTGTTACCTCTTTCCTT-------G------GGTTCGG----AAAAAGAAGA------GGGAATTTATTGGCAG---CGAAAA-GCACTCGAACT------
droEug1	scf7180000409005:1000126-1000280 +		CCGAACTTCTATAGTATCTGGCGATTTATA---------------TTATTTATATACT----------------------GGCGCACAGTGCGTTTGTTATGTATTC----GCCA-------CATCGA------C--TGTTGGCAA--GCAG--TTTGTTACCTCTTTCCTT-------T------GGC---------------------AGGAATTTATTGGCAG---CCAAAA-GCACTCGAACTACCCCT
dm3	chr2L:5111615-5111778 +		CAGAACTTCTATACTATCTGGCGATTTATA---------------TTATTTATATACT----------------------GGCGCACAGTGCGTTTGTTATGTATTC----GCCCCATGCC--ATCGA------C--TGTTGGCAA--GCAG--TTTGTTACCTCTTTCCTT-------G------GAT-CGGG-GGAAAAA--AAA-----GGGAAAATTATTGGCAG---CGAAAA-GCACTC-----------
droSim2	2l:4924914-4925077 +		CAGAACTTCTATACTATCTGGCGATTTATA---------------TTATTTATATACT----------------------GGCGCACAGTGCGTTTGTTATGTATTC----GCCCCACGCC--ATCGA------C--TGTTGGCAA--GCAG--TTTGTTACCTCTTTCCTT-------G------CAT-CGGGCGGAAAAA--AAA-----GGGAAAATTATTGGCAG---CGAAAA-GCACT------------
droSec2	scaffold_5:3198165-3198329 +		CAGAACTTCTATACTATCTGGCGATTTATA---------------TTATTTATATACT----------------------GGCGCACAGTGCGTTTGTTATGTATTC----GCCCCACGCC--ATCGA------C--TGTTGGCAA--GCAG--TTTGTTACCTCTTTCCTT-------G------CAT-CGGGTGGAAAAA--AAA-----GGGAAAATTATTGGCGG---CGAAAA-GCACTC-----------
droYak3	2L:10412510-10412672 -		CAGAACTTCTATACTATCTGGCGATTTATA---------------TTATTTATATACT----------------------GGCGCACAGTGCGTTTGTTATGTATTC----GCCCCACTCCACAACGA------CTCTGTTGGCAA--GCAG--TTTGTTACCTCTTTCCTT-------G------CCT-CGG------AAA--AAA-----GGGAAAATTATTGGCAG---CGAAAA-GCACTC-----------
droEre2	scaffold_4929:5192779-5192948 +		CAGAACTTCTATACTATCTGGCGATTTATA---------------TTATTTATATACT----------------------GGCGCACAGTGCGTTTGTTATGTATTC----GGCCCACTCC--ATCGA------C--TGTTGGCAA--GCAG--TTTGTTACCTCTTTCCTTTCCTTTTGCCTCGGGG-CA-------AAA--AAA-----GGGAAAATTATTGGCAG---CGAAAA-GCACTC-----------

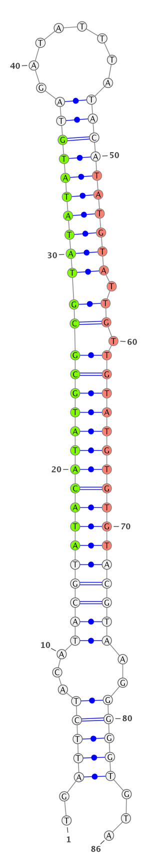
Generated: 09/08/2015 at 07:47 PM

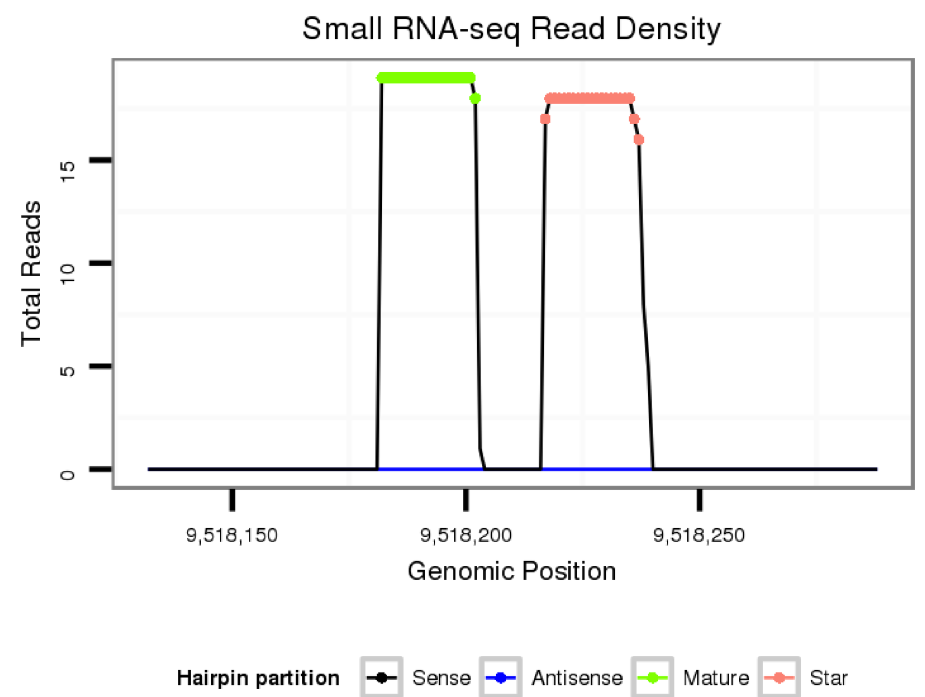
	PASS/FAIL
crit.star	0
crit.loop	1
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

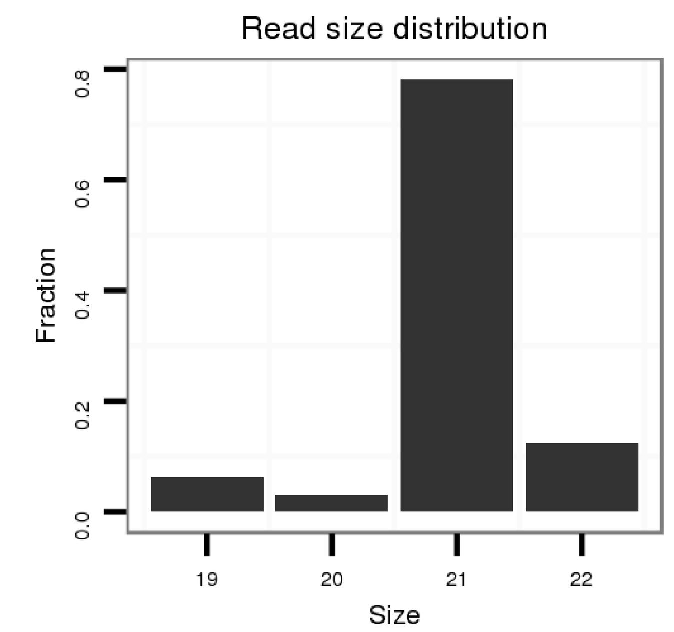
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_111	scf2_1100000004902:9518182-9518238 +	confident	Canonical miRNA	intergenic	[View on UCSC Genome Browser {Cornell Mirror}]

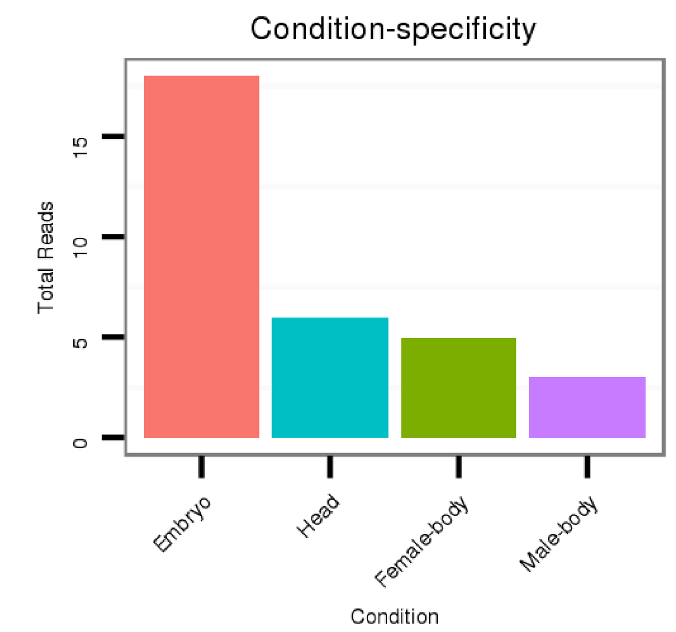
Legend: mature star mismatch in alignment mismatch in read

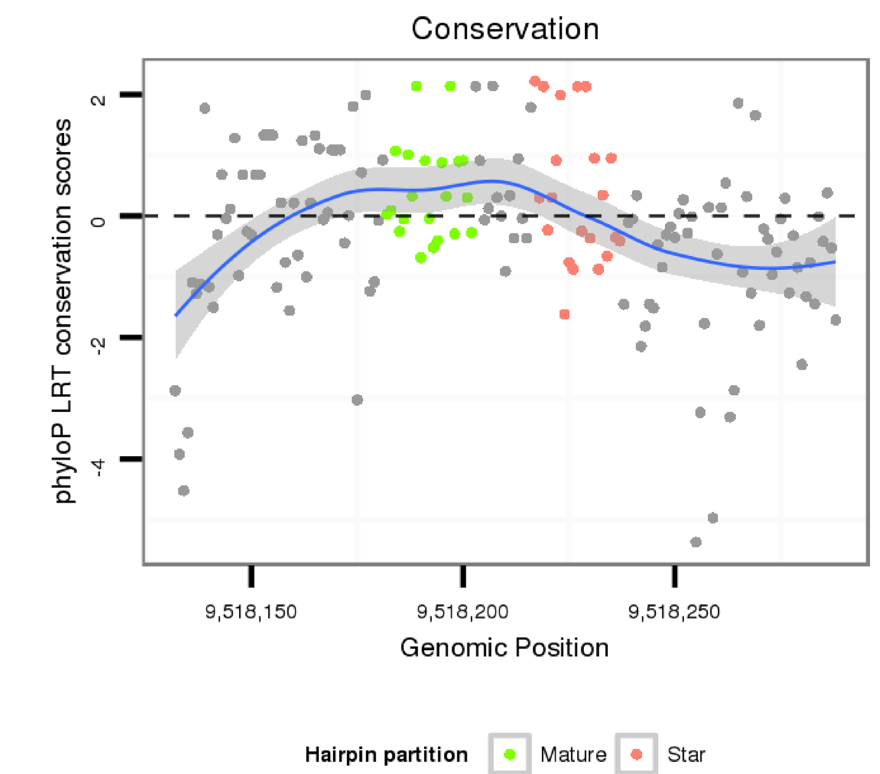
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
(TATATG)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTTTCCAATATTGTAGAGATAAATTAGCCGCCCATTGATTCTACATACGTATACATATGCGCGTATATATGTAGATATTTATACATATGTATTGTTGTATGTGTGTACGTAAGGGGGTGTAAAAATAAGCGCATGTATTCTTTGGCCTTTTCTGTAA **********************************..(((((...((((((((((((((((((((((((((((........)))))))))).)).))))))))))))))))..)))))...**********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V118 embryo	M045 female body	M020 head	V119 head	V117 male body
....ATACATATGCGCGTATATATG..	21	0	1	17.00	17	14	1	1	1	0
....TATGTATTGTTGTATGTGTGT...	21	0	1	8.00	8	2	1	0	3	2
....TATGTATTGTTGTATGTGTGTAC...	23	0	1	5.00	5	3	1	1	0	0
....TATGTATTGTTGTATGTGTGTA..	22	0	1	3.00	3	1	1	1	0	0
....TATGTATTGTTGTATGTGTGTACT..	24	1	1	1.00	1	1	0	0	0	0
....ATACATATGCGCGTATATAT...	20	0	1	1.00	1	0	1	0	0	0
....ATACATATGCGCGTATATATGT...	22	0	1	1.00	1	1	0	0	0	0
....TATGTATTGTTGTATGTGT...	19	0	1	1.00	1	0	0	0	0	1
....ATGTATTGTTGTATGTGTG..	19	0	1	1.00	1	0	1	0	0	0
....TATGTATTGTTGTATGTGTGTACC..	24	1	1	1.00	1	0	0	1	0	0

Anti-sense strand reads

AAAAGGTTATAACATCTCTATTTAATCGGCGGGTAACTAAGATGTATGCATATGTATACGCGCATATATACATCTATAAATATGTATACATAACAACATACACACATGCATTCCCCCACATTTTTATTCGCGTACATAAGAAACCGGAAAAGACATT **********************************..(((((...((((((((((((((((((((((((((((........)))))))))).)).))))))))))))))))..)))))...**********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	M045 female body	V117 male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droWil2	scf2_1100000004902:9518132-9518288 +	dwi_111	TTTT----------CCAATATTG-------------TAGAGATAAATTAGCCGCCCATTG-----ATTCTACA--TACGTATACATATGCGCGTATATATGTAGATA--TTTATACATATGTAT--TGTTGTATGTGTGTACGT--AAGGGG--------------------GTGTAAAAATAAGCGCATGT--ATTCTTTGGCCTTTT--CTGTAA----
droVir3	scaffold_12928:721424-721525 +		TTGT--ATA--TATATATATATATATATGTATATATGTATATA--TATATATATATTTAT--T--TATATATATATATAT--GTATGT--------------------ATTTATATATATAT------A------------------------------TGT--------------------------------GTATATAATC
droMoj3	scaffold_6473:2505872-2505998 -		CCTA----------TTGAT----------ACAG--A--TGAATATACATATGTATGTATGTATGTAAATA--TATGTACATATACATATG--TATTTATGTACATAG--ATGCAT--------------------ACATAAATACAT------ACA----------TATGTATGATGTGT----------------------------GGACATT--TCTTAA----
droGri2	scaffold_14853:3912228-3912376 -		TATA----------CCGAAAATA-------------TAT-----------------------------------ACA--TACATATATATATATATACATATGTA--TATATATATATA-----TATATATATATAT--ATATATATGTAAAGATATTTATATATATATAAAAACAT------A------------------------------TATATGTAAGTATACATATGC----ATAGCTTTCTATTGT----
dp5	2:16555359-16555489 -		GCTT----------ACTATT--GTGGAATATTAATTG--------AATCCGTCTCCC---TCTACCCCTATGCGACTG--------TG--CGTTTG--T--------------GTGTGTGTGTGTCAAAAGGG--------------------GTGTAAAAATAAGCGCATGTT----------TCCCTCTGCTTTTTTCC-CG----------------------------T--CTGTAA----
droPer2	scaffold_26:246560-246707 +		GCAT----------CTAATA----------ATGACTGCAAAATTAAATTATACACACA---AGTTAATTATAAATACATATG--TATGTGTATATATATATATATACATATATATA--TGTATA--TATATAT--G--TATGTACATATGTAT--GTATGT--------------------ATGTAAATATGT------A------------------------------TGT--------------------------------ATGTAT----
droAna3	scaffold_13266:14450004-14450129 +		TGTG----------GATA-----------------TAC-----AATTAATCGCCCATTATATGT-----ATC--TGCATATATATATATACGTATATAAATACATACAAACATA--TGTACAT--A--TATATATGTATGTGT--ATGTGC--------------------ATGTAAGCACAG------A------------------------------CGT--------------------------------TAGTAT----
droBip1	scf7180000396696:678530-678638 +		TTCT--ACA--TTCATATATATATGTATATATATATATATA--TTTATATATATAT--TGTTCAGTGTATGTGC--CAGTGG--------------------GCA----GTCAAGCTTATGA--TTCA----AAGGACC---TTTC----
droKik1	scf7180000302810:810234-810257 +		CTGC--GG--------------------GCAG---------------T--GAATTAG--CCACCC----
droFic1	scf7180000454114:237517-237557 +		AAG---GGG--------------------GTGTAAAACTGTTCGAGTAT--GT------GTGTGTG--CTGTAA----
droEle1	scf7180000490214:1253640-1253735 +		TATA--TATATACATATATACATATATATATATA--TATATATATATAT--TATTATATATATATAT--ATATAT--------------------ATATATATATAC------A------------------------------AGC--------------------------------ATATA-----
droRho1	scf7180000779322:146427-146474 -		ATGT---ATT--TAAAGGGG--------------------GTGTAAAACTGAGCGAGTGT--GTGTGTG--CTGTAA----
droBia1	scf7180000301141:6196-6288 +		TGTG--TGTGCGTGTGTGTGTGTGTGTGTGTGTGTG--CGTGTG--TGTGTGT--G--TGTGTGTGTGTGTGT--GCGTGC--------------------GTGCGTGCGTGT------G------------------------------CGT----------------------------------GTGTGT----
droTak1	scf7180000415712:636443-636510 +		TTAA--------------A---G---GCGTACACGT---ACT--GAAAGGGG--------------------GTGTAAAACAGATCGCCTGT--GTGTGCGTGTGTG--CTGTAA----
droEug1	scf7180000409488:354085-354121 -		AAG---GGG--------------------GTGTAGGATAGAGCGTGT--GTGTGTG--CTGTAA----
dm3	chr3R:27551021-27551222 +		ATAAGTTTAAACTTCTAAT-------ACAAACTG--------AATAAGGTGCTTATAATGTTTATTTAACATACA----------TATAGTGATAGTTTCAGAAGAACATAAATTCAAACTTAAAATACAATACGTACAAATAT--------------------------------GTAATCG--T--------------ATACAAAACAGT--GACGAG--------------------GAGCGAAAATGGAAGGCTGTATAGTAATTTAGGACC-----------T-------------TGTA----TATGCGATAT--CTGCCA----
droSim2	3r:26826906-26826969 +		TTAA--------------A---G---GCGTACACGT---ACC--CAAAGGGG--------------------GTGTAAAGCAGAGCGTATGT--GTCC----GTGTCCC--CTGTAA----
droSec2	scaffold_31:205581-205792 +		ATAAGTTTAAACTTCTAAT-------ACAAACTG--------AATAAGGTGCTTATAATGTTTATTTAACATACATACATATGGATACATATAGTGATAGTTTCTGAAGATCATAAATTCGAACTTAAAATACATTACGTACAAATAT--------------------------------GTAATCG--T--------------ATACAAAACAGT--GACGAG--------------------GAGCGAAAATGGAAGGCTGTATAGTAATTTAGGACC-----------T-------------TGTA----CATGCGATAT--CTGCCA----
droYak3	3R:28485610-28485667 +		GCGT---ACACGT---ACC--CAAAGGGG--------------------GTGTAAAGCAGAGCGTATGT--GTGC----GTGTCCC--CTGTAA----
droEre2	scaffold_4690:12033840-12033936 -		TATG--TATGTATACATATGTATGTATGTATGTATGTA--TGTATACATATGTAT--GTATGTATGTATGTAT--ATATAT--------------------ATGTATGTATGT------A------------------------------TGT--------------------------------ATGTAT----

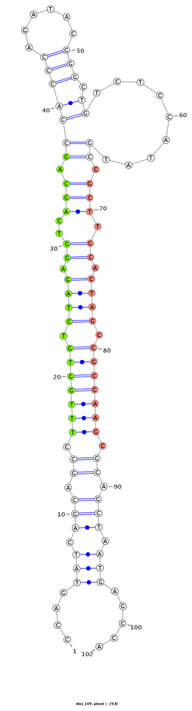
Generated: 09/08/2015 at 07:43 PM

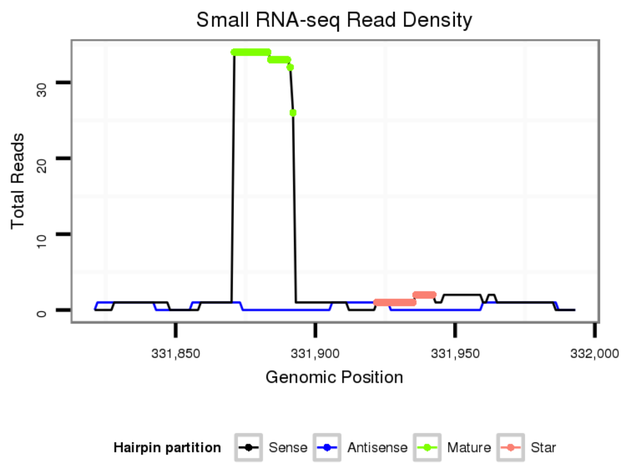
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

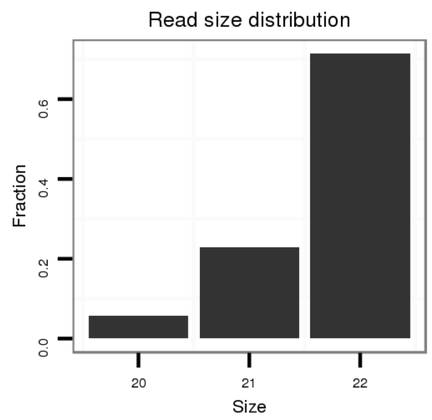
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dwi_109	**scf2_1100000004921:331871-331943 +**	**confident-exception**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

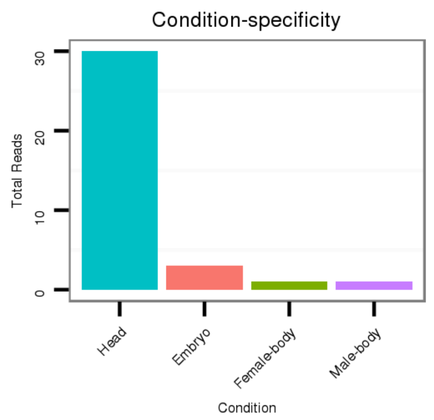
Legend: mature star **mismatch in alignment** mismatch in read

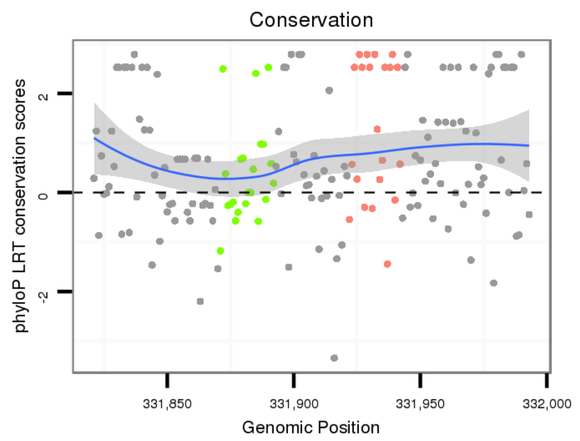
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dwil\GK22589-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TCCATTTCACCTCCACATTCGCCAACTCATGCGGCCCAGTATCAGCAGCCTTTGGTGTCTAGAGGTCAGCAGCCACCCAGATACGGGCTGTCTCCATATGCCGCTTCCACTAGCCGCCAAGCGCAGCTAATGAGCCAACAGCCTCAGCCTCAGCAGCGCAAGCGTCGATTAAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V119 head	M020 head	M045 female body	V118 embryo	V117 male body
************************************....(((.(((.((.(((((((.(((((.((..(((.(((((((.....))))).))).........)).))))..)))))..)))))))..)).)))).)))).....************************************										
....TTTGGTGTCTAGAGGTCAGCAG.....	22	0	1	25.00	25	19	3	0	3	0
....TTTGGTGTCTAGAGGTCAGCA.....	21	0	1	7.00	7	7	0	0	0	0
....................................GTATCAGCAGCCTTTGGTGTCTAGA.....	25	0	1	1.00	1	0	0	0	1	0
....GCCAAGCGCAGCTAATGAGCCAAC.....	24	0	1	1.00	1	0	0	1	0	0
.......CACCTCCACATTCGCCAACT.....	20	0	1	1.00	1	0	0	1	0	0
....GCTAATGAGCCAACAGCCT.....	19	0	1	1.00	1	0	0	1	0	0
....CGCTTCCACTAGCCGCCAAGC.....	21	0	1	1.00	1	0	1	0	0	0
....GCCACCCAGATACGGGCTGT.....	20	0	1	1.00	1	0	0	0	0	1
....CCTCAGCCTCAGCAGCGCAAGCGT.....	24	0	1	1.00	1	0	0	0	0	1
....TTTGGTGTCTAGAGGTCAGC.....	20	0	1	1.00	1	0	0	1	0	0
....TTTGGTGTCTAGAGGTCAGCAGT.....	23	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

AGGTAAAGTGGAGGTGTAAGCGGTTGAGTACGCCGGGTCATAGTCGTCGGAAACCACAGATCTCCAGTCGTCGGTGGGTCTATGCCCGACAGAGGTATACGGCGAAGGTGATCGGCGGTTCGCGTCGATTACTCGGTTGTCGGAGTCGGAGTCGTCGCGTTCGCAGCTAATTT	Read size	# Mismatch	Hit Count	Total Norm	Total	V119 head	M045 female body	M020 head	V118 embryo	V117 male body
************************************....(((.(((.((.(((((((.(((((.((..(((.(((((((.....))))).))).........)).))).)).)))))..)))))))..)).)))).)))).....************************************										
....CCGACAGAGGTATACGGCGAA.....	21	0	1	1.00	1	1	0	0	0	0
....TCGGAGTCGGAGTCGTCGCGTTCGCAG.....	27	0	1	1.00	1	0	0	0	1	0
....................................GGTCATAGTCGTCGGAAA.....	18	0	1	1.00	1	0	0	1	0	0
.GGTAAAGTGGAGGTGTAAGCG.....	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
droWil2	scf2_1100000004921:331821-331993 +	dwi_109	TCCATTTCA---CCTCCACATTCGCCAACTCAT---------G-----CGGCCCAGTATCAGCAGCCTTTGGTGTCTAGAGGTCAGCAGCCACCCAGATACGGGCTGTCT------CCATATGC---CGCTTCCACTAGCCGCCAAGGCGCAGCTAATGAGC----------CAACAGCCTCAGCCT---CAGCAGCGCAAGCGTCGATT------AAA----------
droVir3	scaffold_13047:7943250-7943401 -		TCTATATCG---CGCCACAATCGCCTTGGCGG--------------------GTGTGCAC------AGCCAGCTGGTACCGAAATATAACAATC--------CGCA---TGGCTGAACCAGCCGACAGGCGCAGCTGCTTAGC----------GAACAGCAGCAGCAACAG---CACTGCGCAAGCCGCCGTCTGCAATTTCC----------
droMoj3	scaffold_6540:28246574-28246719 +		TCCATATCG---CCACCACAATCACCATGGCCGCCCATGCCC-----------------------------AGCCAGCCTATGCCGAAATATTCCATTC--------CATA---TGGCTCGACGAGCAGCAGGCGCAGCTGCTCACT----------GAACAGCAACAGCCTCCT---C------GGAAGCCGCCTCTTCAATTTGG----------
droGri2	scaffold_15074:1676947-1677100 +		TCCATATCG---CGCCACAGTCGCCTTGGCGG--------------------------------------CCAATGCCCATATATTCCATACC--------CTCGTA---TGGCTCAACCAGTCGCCAGGCGCAGCAGCAA---CAGCAGCAGCTCAGCGA--AGAGCATAAGCAGCAGCAGCAT---CCGTTTCGCAAGCCGACCTCTCC----AGT----------
dp5	2:9691411-9691613 +		TCGATCTCG---CCGCCCCAATCGCCGAGGCCG--------ACCCCGTCGCCCCCCATGTAGTCGCATGCCACGCTG--CGTGGGCCACCTCCCAGATATCCCATGCC-----ACCCCAAGC---TGGCTCCACCAGCCGCCAAGCCCAATTCTGTCTGAACAGCA-----GCAGCAGCAGCCGTCGCCACAGCAGCCG---CAGCAGCGCAAGCGTCGCAT------GGGTCAGAG-----
droPer2	scaffold_0:10789750-10789952 -		TCGATCTCG---CCGCCCCAATCGCCGAGGCCG--------ACCCCGTCGCCCCCATCTAGTCGCATGCCACGCTG--CGTGGGCCACCTCCCAGATATCCCATGCC-----ACCCCAAGC---TGGCTCCACCAGCCGCCAAGACCAATTCTGTCTGAACAGCA-----GCAGCAGCAGCCACGCCACAGCAGCCG---CACACAGCGCAAGCGTCGCAT------GGGTCAGAG-----
droAna3	scaffold_13340:19587525-19587723 +		CCCATGACCAGTCGACCGCACTCGCCAAGCATAC---TGCAAACCC--------------------ATCTGAAC------CGAGGTCCGCCGCCCAAGTATCCAACTCACAGCCAACATATGTGG---CCGCTCCACCAGTAGCCAAGCCATACAATGTCTACCCACCA-----GTTGACTCCGCATCAACACCAACAATTG---CAGACCGCCAAACCGCCGAAT------GGGCCAGAGCCCAA
droBip1	scf7180000396413:2798451-2798638 -		CCCATGACCAGTCGACCGCACTCGCCTAGATTGT---TGCAAACCC--------------------ATCTCAAC------CGAGGCCGCCGCCCAAGTATCCAACTCAGGGCCAACAGATGGG---CCGCTCCACCAAGTAGACAAGCCCATTTAATGTCCACCCACCA-----GTTGACTCCGCACCAGCATCAACAACTG---CAGACACGCAAACGCCGAAT------GGA----------
droKik1	scf7180000302705:158717-158918 -		GCGATGAACAGTCGCCCGCAGTCGCCTTGGCCAA---TGGCTTCTT--------------------TGTTGCCC------CGTGGACCGCCGCCCTAAGTATCCGATGGTCGGACAGCAAACGGGTGGTACTTCCACCAGCAGACATGGTCACATGATGTCCTCGCACCA-----ACTGACTCCTCATCAGCACCAGCAGCTT---CAGCCTCGCGAAGCGTCGCTT------GGGGCAGAGCCCAC
droFic1	scf7180000453826:611127-611325 +		TCGATGACCAGTCGACCGCAGTCGCCGTCTACGA---TGGCTGCCC--------------------TGTTGGCC------CGGGGACGCCGCCCGAAATACCGATGTCCGGGCAACAGACACAGG---CGGCTCCACCAGCAGACAGGCCACATCATGTCCTCCCACCA-----GTTGACCCCGATCGACATCAGCAGCTT---CAGTCGCGAAAGCGTCGGAT------GGGACAGAGTCCGG
droEle1	scf7180000491261:1574999-1575180 -		GTCACGTCCAGTCGCCCACAGTCGCCGGGGGA---TGGCCGGTCC--------------------TCTTGGCC------CGTGGACCGCCGCCCAAGTATCCGATGCCGGGCAACAAAGTGG---TGGCTCTACCAGCAGACAGGGTCACATCATGTCTTCCCACCA-----GTTGACTCCGCACAGCACCAGCAGCTCC---CAGCCGCGAAAGCGTCGCCT------GGG----------
droRho1	scf7180000780007:41838-42019 +		GTCACATCCAGTCGCCCACAGTCGCCGGGGGA---TGGCCGGTCC--------------------TTTTGAGC------CGTGGACCGCCGCCCAAGTATCCAATAGCCGGGCAACAGGGTGG---CGGCTCCACTAGCAGCAGGGTCACATTATGTCTTCCCACCA-----GTTGACCCCGTTCGCAGCACCAACAGCTC---CAGCCGCGCGAAGCGTCGTCT------GGT----------
droBia1	scf7180000302075:1845428-1845615 +		TCCGCGTCCAGTCGCCCGCAGACGCAGTCCACAG---TGGCTCGTCC--------------------TCCTGAGC------CGAGGTCCGCCGCCCAAGTAGCCGAATGCGGGGCAACAATCGGG---CGGCTCCACCAGCAGACAGGGTCACATCATGTCCTCGCACCA-----GTTGACCCCGCTGCAGCACCAGCAGCTT---CAGCCGCGCGAACGTCGCCT------GGG----------
droTak1	scf7180000415700:487267-487457 -		TCTCTTGGCCAGTCGACCGCAGTCGCCTTGCACGA---TGGCCGGTCC--------------------TGCTGACC------CGCGGACCGCCGCCCAAGTATCCGTTGCGTGGACAACGCGGCGGG---AGGCTCCACCAGCAGGCAGGCCACATTTAATGTCCAGCCACCA-----GTTGACCCCACTGCAGCATCAGCAGCTCCAACAGCCGCGCAAGCGTCGCCT------GGG----------
droEug1	scf7180000409770:573559-573752 -		TCAGCGTCCAGTCGACCACACAGTCGCCTTGAACGA---TGGCTGCTC--------------------TTTTGGCC------CGCGGACCGCCGCCCTAAGTATCCGATTTCTGGGCAGCAAGCAGG---TGGCTCTACAAAGAGACACGGCTCACATCATGTCTTCCCACCA-----GTTGACTCCACTGCAGCACCAGCAACAGTC---CAGCCGCGCGAAGCCGCGACT------GGGACAAAG-----
dm3	chr3R:23104009-23104196 -		TCCACGTCCAGTCGACCGCAGTCGCCGTCCACAA---TGTCCAGTC--------------------TCTTGGGT------CGCGGGCCGCCCACCGAAGTATCAGATAGCTGGTCAGCAAGCAGG---TGCTTCCACCAGCAGGCAGGCCACATCATGTCTTCCCACCA-----GCTGACACCGGTCGCAGCACCAACAGCTC---CAGCCGCGCAAAGCGTCGATT------GGG----------
droSim2	3r:22545675-22545862 -		TCCACGTCCAGTCGACCGCAGTCGCCGTCCCAAA---TGTCCAGTC--------------------TCCTGGGT------CGCGGACCGCCACCCAAGTATCAGATGCCTGGGCAGCAGGCAGG---TGCTTCCACCAGCAGACAGGCCACATCATGTCTTCCCACCA-----GCTGACACCGCTCGCAGCACCAACAGCTC---CAGCCGCGCAAACGTCGATT------AGG----------
droSec2	scaffold_13:1858132-1858319 -		TCCACGTCCAGTCGACCGCAGTCGCCGTCCCAAA---TGTCCAGTC--------------------TTCTGGGT------CGCGGACCGCCACCCAAGTATCAGATGCCTGGGCAGCAGGCAGG---TGCTTCCACCAGCAGACAGGCCACATCATGTCTTCCCACCA-----GCTGACACCGCTCGCAGCACCAACAGCTC---CAGCCGCGCAAAGCGTCGATT------AGG----------
droYak3	3R:23389488-23389675 +		TCCGTGTCCAGTCGACCACAGTCGCCGTCCACAA---TGGCCGGTCC--------------------TCTTGGCC------CGCGGACCGCCACCCAAGTATCCGATGCCTGGGCAACAAACGGG---TGCTTCTACCAGTAGACAGGCTCACATCATGTCTTCCCACCA-----GTTGACTCCGCTGCAGCACCAACAAGTC---CAGCCGCGCAAAGCGTCGATT------GGG----------
droEre2	scaffold_4820:4929916-4930103 +		TCCGGGTCCAGTCGACCGCAGTCGCCGTCCACAA---TGACCGGTCC--------------------TCATGGGA------CGCGGACCGCCACCCGAAGTATCCGATGCCTGGGCAACAGGCGGG---TGCTTCCACCAGCAGACAGGCTCACGATCATGTCTTCCCACCA-----GTTGACACCGCTCGCAGCACCAACAGCTC---CAGCCACGCAAAGCGTCGACT------GGG----------

Generated: 09/08/2015 at 07:47 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