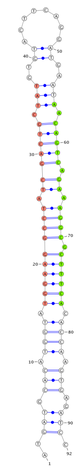
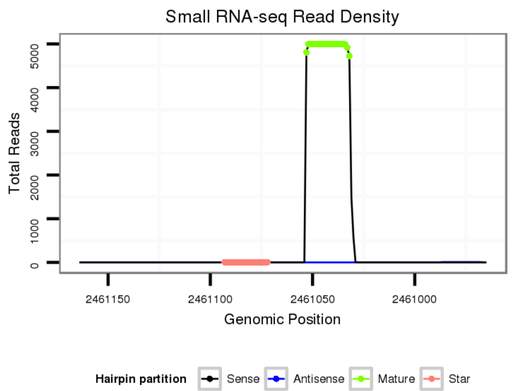
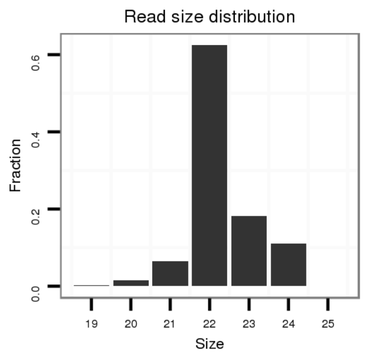
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_230	**scaffold_13417:2461015-2461114 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

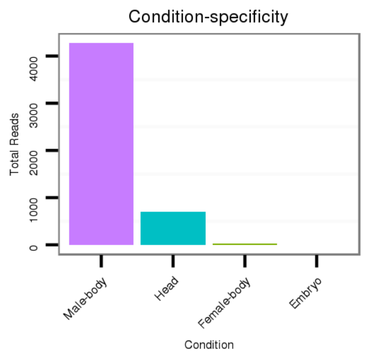
Legend: mature star mismatch in alignment mismatch in read

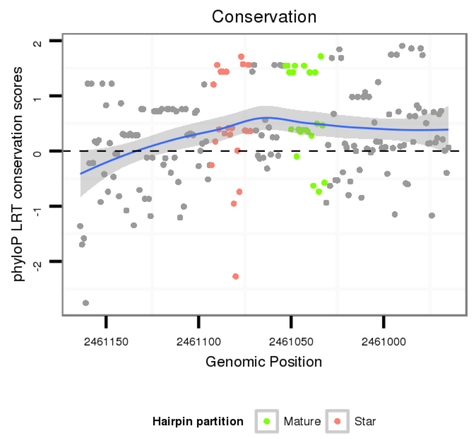
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GAATCCCGACTACAAACGTCCATTCCCTGCGCTATGAGGTGCCGTCCATGATCCGAATGATGCACATGGTATGGAAGGCCTATCGACTGCTATGTGTACTTCAGGATGAATAACAGTCAGAAAGGCGCTTTCACACCAAGTGAGATCCGGCCCCTGCAGACGTCGCGTCCCGTGACGGGCAGTTCCTGAACTGTCAAATA	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V106 head	V055 head	M044 female body	V039 embryo
**********..(((.(((.(((((.((((((((((.(((((((.(((..((........))..)))..)))))..)).)))).)))))).)))..))).**********										
.....AACAGTCAGAAAGGCGCTTTCA.....	22	0	1	3098.00	3098	2716	306	71	5	0
.....AACAGTCAGAAAGGCGCTTTCAC.....	23	0	1	887.00	887	746	105	30	5	1
.....AACAGTCAGAAAGGCGCTTTCACA.....	24	0	1	548.00	548	423	97	21	7	0
.....AACAGTCAGAAAGGCGCTTTC.....	21	0	1	187.00	187	174	8	4	0	1
.....ACAGTCAGAAAGGCGCTTTCA.....	21	0	1	133.00	133	106	23	4	0	0
.....AACAGTCAGAAAGGCGCTTTCAT.....	23	1	1	127.00	127	110	14	3	0	0
.....AACAGTCAGAAAGGCGCTTTCT.....	22	1	1	123.00	123	104	14	5	0	0
.....AACAGTCAGAAAGGCGCTTTCACT.....	24	1	1	80.00	80	63	12	3	2	0
.....AACAGTCAGAAAGGCGCTTT.....	20	0	1	72.00	72	64	4	3	1	0
.....ACAGTCAGAAAGGCGCTTTCAC.....	22	0	1	24.00	24	13	6	3	2	0
.....ACAGTCAGAAAGGCGCTTTCACA.....	23	0	1	23.00	23	12	8	1	2	0
.....AACAGTCAGAAAGGCGCTTTCACAT.....	25	1	1	20.00	20	18	2	0	0	0
.....AACAGTCAGAAAGGCGCTTTCATT.....	24	2	1	18.00	18	15	2	1	0	0
.....AACAGTCAGAAAGGCGCTTTT.....	21	1	1	14.00	14	14	0	0	0	0
.....AACAGTCAGAAAGGCGCTTTCATTT.....	25	3	1	10.00	10	9	1	0	0	0
.....AACAGTCAGAAAGGCGCTTTCAA.....	23	1	1	9.00	9	5	3	1	0	0
.....AACAGTCAGAAAGGCGCTTTCACAC.....	25	0	1	8.00	8	5	2	1	0	0
.....AACAGTCAGAAAGGCGCTTTCTT.....	23	2	1	7.00	7	7	0	0	0	0
.....AACAGTCAGAAAGGCGCTTTCACTT.....	25	2	1	6.00	6	6	0	0	0	0
.....ACAGTCAGAAAGGCGCTTT.....	19	0	1	6.00	6	4	1	1	0	0
.....AACAGTCAGAAAGGCGCTT.....	19	0	1	5.00	5	5	0	0	0	0
.....TGGAAGGCCTATCGACTGCTAT.....	22	0	1	4.00	4	1	0	1	2	0
.....AACAGTCAGAAAGGCGCTTTCC.....	22	1	1	4.00	4	4	0	0	0	0
.....AACAGTCAGAAAGGCGCTTTG.....	21	1	1	4.00	4	4	0	0	0	0
.....AACAGTCAGAAAGGCGCTTTTT.....	22	2	1	4.00	4	4	0	0	0	0
.....AACAGTCAGAAAGGCGCTTTA.....	21	1	1	4.00	4	3	1	0	0	0
.....ACAGTCAGAAAGGCGCTTTC.....	20	0	1	4.00	4	3	1	0	0	0
.....AACAGTCAGAAAGGCGCTTTCG.....	22	1	1	3.00	3	2	1	0	0	0
.....AACAGTCAGAAAGGCGCTTTCTTT.....	24	3	1	3.00	3	3	0	0	0	0
.....ACAGTCAGAAAGGCGCTTTCT.....	21	1	1	2.00	2	2	0	0	0	0
.....AACAGTCAGAAAGGCGCTTTCAG.....	23	1	1	2.00	2	0	2	0	0	0
.....AGTCAGAAAGGCGCTTTCACA.....	21	0	1	2.00	2	2	0	0	0	0
.....AACAGTCAGAAAGGCGCTTTCACG.....	24	1	1	2.00	2	2	0	0	0	0
.....AACAGTCAGAAAGGCGCTTTAT.....	22	2	1	2.00	2	2	0	0	0	0
.....AACAGTCAGAAAGGCGCTTTCACAA.....	25	1	1	2.00	2	2	0	0	0	0
.....AACAGTCAGAAAGGCGCTCA.....	20	2	1	1.00	1	1	0	0	0	0
.....AACAGTCAGAAAGGCGCTTTTTT.....	23	3	1	1.00	1	1	0	0	0	0
.....ACAGTCAGAAAGGCGCTTTCG.....	21	1	1	1.00	1	1	0	0	0	0
.....ACAGTCAGAAAGGCGCTTTCACAC.....	24	0	1	1.00	1	0	0	1	0	0
.....AACAGTCAGAAAGGCGCTTTGT.....	22	2	1	1.00	1	1	0	0	0	0
.....ACAGTCAGAAAGGCGCTTTC.....	21	1	1	1.00	1	1	0	0	0	0
.....AACAGTCAGAAAGGCGCTTCA.....	21	2	1	1.00	1	1	0	0	0	0
.....TCAGAAAGGCGCTTTCAT.....	18	1	1	1.00	1	1	0	0	0	0
.....ACAGTCAGAAAGGCGCTTTCAT.....	22	1	1	1.00	1	0	1	0	0	0
.....AGTCAGAAAGGCGCTTTCA.....	19	0	1	1.00	1	0	0	1	0	0
.....AACAGTCAGAAAGGCGCTTTCACATT.....	26	2	1	1.00	1	1	0	0	0	0
.....AACAGTCAGAAAGGCGCTTTCATG.....	24	2	1	1.00	1	1	0	0	0	0
.....ACAGTCAGAAAGGCGCTTTT.....	20	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

CTTAGGGCTGATGTTTGCAGGTAAGGGACGCGATACTCCACGGCAGGTACTAGGCTTACTACGTGTACCATACCTTCCGGATAGCTGACGATACACATGAAGTCCTACTTATTGTCAGTCTTTCCGCGAAAGTGTGGTTCACTCTAGGCCGGGGACGTCTGCAGCGCAGGGCACTGCCCGTCAAGGACTTGACAGTTTAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	V055 head	M058 embryo	V105 male body	V039 embryo
**********..(((.(((.(((((.((((((((((.(((((((.(((..((........))..)))..)))))..)).)))).)))))).)))..))).**********											
.....CCGTCAAGGACTTGACAGTTT..	21	0	1	4.00	4	3	0	0	0	1	0
.....CCGTCAAGGACTTGACAGTT...	20	0	1	3.00	3	2	1	0	0	0	0
.....CCGTCAAGGACTTGACAGTTTA.	22	0	1	1.00	1	1	0	0	0	0	0
.....GGTTCACTCTAGGCCGGGGACGT.....	23	0	1	1.00	1	0	1	0	0	0	0
.....CATACCTTCCGGATAGCTGAC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....CGTCAAGGACTTGACAGTT...	19	0	1	1.00	1	1	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13417:2460965-2461164 -	dan_230	GAAT----------CCCGACTACAAACGTCCATTCCCTGCGCTATGAGGTGCCGTCCATGATCCGAATGATGCACATGGTATGGAAGG-CC--TATCGACTGCTATGTGTACTTCAGGATGA------ATAACAGTCAGAAAGGCGCTTTCACACCAAGTGAGATCCGGCCCCTGCAGACGT----------CGCGTCCCGTGACGGGCAGTTCCTGAACTGTCAAATA
droBip1	scf7180000395874:32979-33175 -		GAAA----------CCCAACTCC---GGTCCTTTCACTGGCCATTATCTGCCGTCCATGATCTTACTGATGCACATGGTATGGAGGG-CC--TATCTACTGCTATGTGTACTCAGGATGA------ATAACAGTCAGAAAGGCGCTTTCAACACCAAGTGAGATCCGGCCCCTGCAACGT----------CGCGTCCCGTGACGGGCAGTTCCTGAACTGTCAAATA
droKik1	scf7180000302517:1186181-1186216 +		GCG----------[----------]--[--]----------[------]----------[----------]---TCCCGTGACAGGCAGTTCCTGAACGTGTCAAATA
droEle1	scf7180000491217:459290-459311 +		GAAT----------CTCGATTCCGACGG[----------]--[--]----------[------]----------[----------]CGA
droRho1	scf7180000777310:10085-10138 +		TAAA----------[----------]--[--]----------[------]ATAACTGTTAGAAAAGCTCGCTCAGCAATGAGACAGACTGTGCA-----[----------]GA
droTak1	scf7180000415812:136056-136115 +		GACC----------[----------]GAAGGGGGCGGAAGG-AGT-TATGCGGTGCGAGGTGTCGTTCAGGATGA------[----------]ATGCAGT
droEug1	scf7180000408987:110771-110831 +		GCGC----------[----------]--[--]----------[------]TGTCCAACTGCTGCCCACAGCCTCTGCTGACGT----------[----------]CGCTGCGCGCGAAAACGCTTC[----------]
dm3	chr2L:21773663-21773688 -		AAAC----------CCCGACCCAAACGT[----------]--[--]----------[------]----------[----------]GTA-[----------]TTCC
droSim2	2r:2586926-2586957 +		GCGC----------[----------]TATGCGGCGCGTATTATCACCAAAT[----------]--[--]----------[------]----------[----------]GA
droYak3	2L:18553219-18553275 -		TCAC----------[----------]--[--]----------[----------]ACCAGTGAGATTCAGCTCCTTCAGATGC----------C[----------]TCCAGTGCCACAAATGAGGACGA
droWil2	scf2_1100000004909:7960636-7960818 +		TGG----------[----------]AAGG-CC--ATCCGATTGTTATGTATCTATATCATAA-TACCCGATAACAGTCAGAAAGGCGCTTTCACTTCATGTGC----------CGA---ATAGAGTCAACGGCAGAACAAGCTAAAATTGTTATTGTG--------TTATACCAGAATCAAGAGCTA-CT----AA--TTGGCGTCTTTGTGACGGGCAGTTCCTGAAGTGTCAAATA
droVir3	scaffold_13042:903081-903277 -		GCAT----------[----------]ATGAAGCGAAAGG-CGCTTTCGACTGCTATGTGCATTTTTGACTATGTCATAGATAACAGTCTGAAAGGCCTTTGGCTCAGATGC----------AAAG--ACAGCGATAACG----------ATAACGATAACGATAACAATAACGATAACTTAA----GCGATAACGATAACGATAAGCGCATCTGGTGAGTAGGCGTTCCTGAAGTGTCAAATA
droMoj3	scaffold_6496:2844119-2844205 -		AGTCACTCTGGCAGCAATTAAACTTACCTGC---AGCTTTT[----------]--[--]---GCAGTGC----------CTT-----[----------]GT----------[----------]CAGTCCCGTTATGTGCAGGTCCTGCGATTTCAAATC
droGri2	scaffold_15081:2041204-2041374 -	dgr_24	CATT----------[----------]TGAGATGAAAGGCGCTTTTTTAGCTGCTATGTGCATTTTTGACTTATC---ATAACAGTTAACAGGGC-GTATCCTCTCAAATGAC----------GC---AC--GGGCAACA----------GCATTCGTGGCG----------GGGAATCTGA----GTGAGCCCG----AG--GATGCATCTGGTAAGTAGCGTTCCTGTGTAGCCAAATA

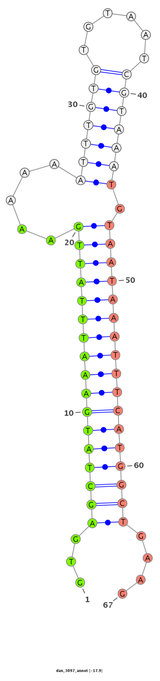
Generated: 09/08/2015 at 07:59 PM

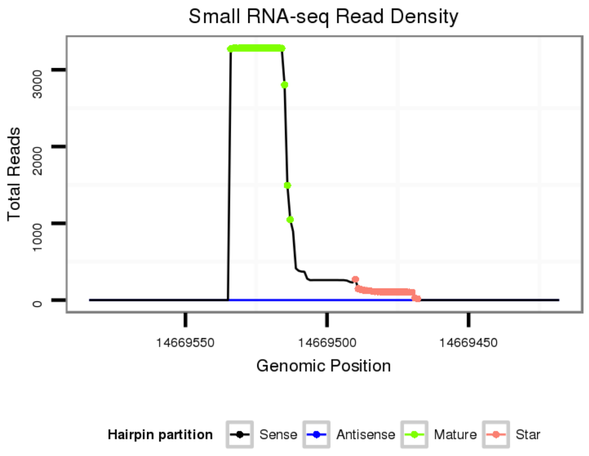
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	3
rescue.candidate	2

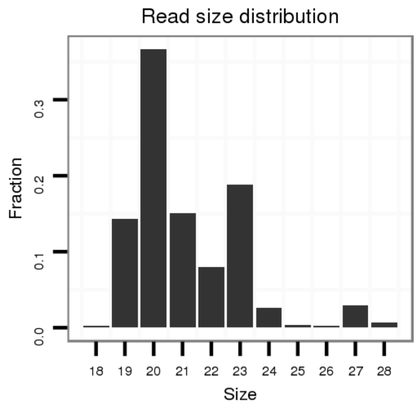
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_3097	**scaffold_13340:14669468-14669534 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

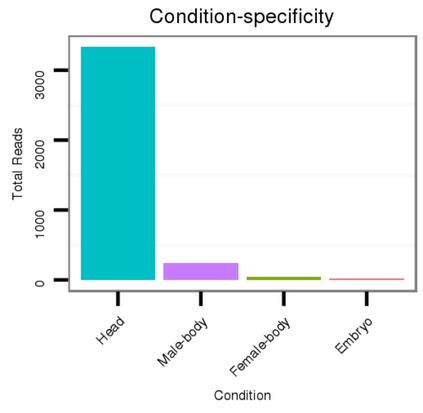
Legend: mature star mismatch in alignment mismatch in read

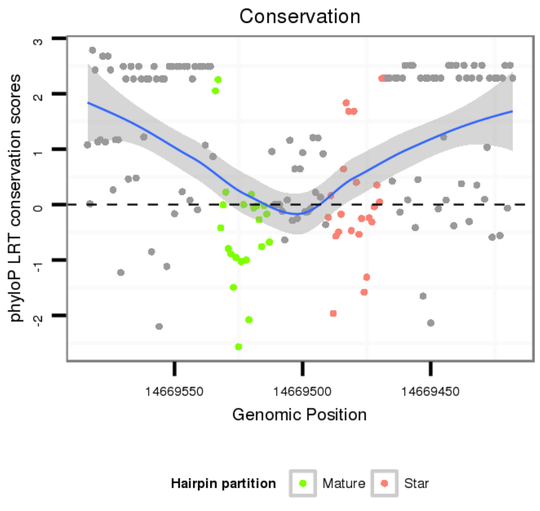
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF16580-in]; CDS [Dana\GF16580-cds]; CDS [Dana\GF16580-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GCTGGGAGTGTCCGAGCTGTTGTCGCTCCGGAAAGAACTACGACTACAAGGTGAGCTATGAAATTTATTGAAAAAATTTGTGTGTAATCGTAAATGTAATAAATTTCATGGCTGAAGCCCCGTCACTTCCGTGCCCGTCAAAAATCCTCGGAGGTTCGTCGAGTATC **...((((((((((((((((((.....(((((((.....)))))))..)))))))))))))))))....***	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V055 head	V105 male body	M044 female body	M058 embryo	V039 embryo
.....GTGAGCTATGAAATTTATTG.....	20	0	1	1304.00	1304	1128	77	84	13	1	1
.....GTGAGCTATGAAATTTATTGAAA.....	23	0	1	654.00	654	574	38	33	7	2	0
.....GTGAGCTATGAAATTTATT.....	19	0	1	477.00	477	453	9	15	0	0	0
.....GTGAGCTATGAAATTTATTGA.....	21	0	1	443.00	443	311	68	48	10	4	2
.....GTGAGCTATGAAATTTATTGAA.....	22	0	1	154.00	154	118	15	16	3	2	0
.....GTGAGCTATGAAATTTATTGAAAAAAT.....	27	0	1	105.00	105	98	0	7	0	0	0
.....AAATTTGTGTGTAATCGTAAAT.....	22	0	1	97.00	97	72	22	1	2	0	0
.....GTGAGCTATGAAATTTATTGAAAA.....	24	0	1	92.00	92	80	4	8	0	0	0
.....TGTAATAAATTTCATGGCTGA.....	21	0	1	46.00	46	38	4	3	1	0	0
.....TAATAAATTTCATGGCTGAAGT.....	22	1	1	28.00	28	2	2	16	3	5	0
.....AATTTGTGTGTAATCGTAAAT.....	21	0	1	28.00	28	22	5	1	0	0	0
.....GTGAGCTATGAAATTTATTT.....	20	1	1	26.00	26	23	1	2	0	0	0
.....GTGAGCTATGAAATTTATTGAAAAAATT.....	28	0	1	23.00	23	13	0	7	3	0	0
.....AAATTTGTGTGTAATCGTAAA.....	21	0	1	19.00	19	9	10	0	0	0	0
.....AATTTGTGTGTAATCGTAAATG.....	22	0	1	18.00	18	13	3	1	1	0	0
.....AAATTTGTGTGTAATCGTA.....	19	0	1	17.00	17	6	5	6	0	0	0
.....TAATAAATTTCATGGCTGA.....	19	0	1	16.00	16	10	3	1	2	0	0
.....AAATTTGTGTGTAATCGTAA.....	20	0	1	16.00	16	9	6	0	1	0	0
.....AAATTTGTGTGTAATCGTAAATG.....	23	0	1	15.00	15	8	7	0	0	0	0
.....GTGAGCTATGAAATTTATTGAAAAA.....	25	0	1	13.00	13	10	0	3	0	0	0
.....ATGTAATAAATTTCATGGCTGA.....	22	0	1	10.00	10	6	1	0	1	2	0
.....TGTAATAAATTTCATGGCTGAAG.....	23	0	1	9.00	9	4	1	0	0	3	1
.....GTGAGCTATGAAATTTATTGT.....	21	1	1	8.00	8	6	1	1	0	0	0
.....TGTAATAAATTTCATGGCTGAA.....	22	0	1	7.00	7	6	1	0	0	0	0
.....TAATAAATTTCATGGCTGAAG.....	21	0	1	7.00	7	1	1	2	2	1	0
.....GTGAGCTATGAAATTTATTGAAAT.....	24	1	1	6.00	6	5	0	0	0	1	0
.....TGAGCTATGAAATTTATTG.....	19	0	1	5.00	5	3	2	0	0	0	0
.....AAATTTGTGTGTAATCGT.....	18	0	1	5.00	5	2	3	0	0	0	0
.....AATTTGTGTGTAATCGTAAATGT.....	23	0	1	5.00	5	3	2	0	0	0	0
.....GTGAGCTATGAAATTTAT.....	18	0	1	4.00	4	3	1	0	0	0	0
.....AATTTGTGTGTAATCGTAA.....	19	0	1	4.00	4	2	1	0	1	0	0
.....GTGAGCTATGAAATTTATTGAAAAAA.....	26	0	1	4.00	4	3	0	1	0	0	0
.....ATGTAATAAATTTCATGGCTGT.....	22	1	1	3.00	3	1	0	1	1	0	0
.....AATTTGTGTGTAATCGTAAA.....	20	0	1	3.00	3	1	2	0	0	0	0
.....GTGAGCTATGAAATTTATTGAAT.....	23	1	1	3.00	3	3	0	0	0	0	0
.....AAATTTGTGTGTAATCGTAAATGTAAT.....	27	0	1	3.00	3	2	1	0	0	0	0
.....TGAGCTATGAAATTTATTGA.....	20	0	1	3.00	3	1	0	1	1	0	0
.....GTGAGCTATGAAATTTATTGAAG.....	23	1	1	3.00	3	3	0	0	0	0	0
.....TTGTGTGTAATCGTAAATGTA.....	21	0	1	3.00	3	1	1	1	0	0	0
.....TAATAAATTTCATGGCTGAA.....	20	0	1	3.00	3	2	0	1	0	0	0
.....GTAATAAATTTCATGGCTGA.....	20	0	1	3.00	3	3	0	0	0	0	0
.....AAATTTGTGTGTAATCGTT.....	19	1	1	2.00	2	0	2	0	0	0	0
.....ATTTGTGTGTAATCGTAAATG.....	21	0	1	2.00	2	0	0	1	1	0	0
.....AAATTTGTGTGTAATCGTAAATGT.....	24	0	1	2.00	2	1	0	0	0	1	0
.....TTGTGTGTAATCGTAAATGTAA.....	22	0	1	2.00	2	0	1	1	0	0	0
.....AATTTGTGTGTAATCGTAAATGTAAT.....	26	0	1	2.00	2	1	1	0	0	0	0
.....TGAGCTATGAAATTTATTGAAA.....	22	0	1	2.00	2	0	1	0	1	0	0
.....TTGTGTGTAATCGTAAATGTAATA.....	24	0	1	2.00	2	2	0	0	0	0	0
.....TGTGTGTAATCGTAAATGTAAT.....	22	0	1	2.00	2	1	1	0	0	0	0
.....AAATTTGTGTGTAATCGTAT.....	20	1	1	2.00	2	0	2	0	0	0	0
.....TAATAAATTTCATGGCTGAAGA.....	22	1	1	2.00	2	1	0	0	1	0	0
.....TTGTGTGTAATCGTAAATGTAAT.....	23	0	1	2.00	2	1	0	1	0	0	0
.....TTGTGTGTAATCGTAAATGT.....	20	0	1	2.00	2	0	1	1	0	0	0
.....TTGTGTGTAATCGTAAATGTAATAA.....	25	0	1	1.00	1	1	0	0	0	0	0
.....GTGAGCTATGAAATTTATA.....	19	1	1	1.00	1	0	0	1	0	0	0
.....TTTGTGTGTAATCGTAAATG.....	20	0	1	1.00	1	0	1	0	0	0	0
.....ATGTAATAAATTTCATGGCTGAAA.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TGTAATAAATTTCATGGCT.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TGTAATAAATTTCATGGCTGG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....GTGAGCTATGAAATTTATTGAT.....	22	1	1	1.00	1	0	0	0	1	0	0
.....GTGAGCTATGAAATTTATG.....	19	1	1	1.00	1	1	0	0	0	0	0
.....GTGTGTAATCGTAAATGTAAT.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TTTGTGTGTAATCGTAAATGT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....ATGTAATAAATTTCATGGCT.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TTGTGTGTAATCGTAAATGTAAA.....	23	1	1	1.00	1	1	0	0	0	0	0
.....ATTTGTGTGTAATCGTAAAT.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TGTAATAAATTTCATGGCTGAAGA.....	24	1	1	1.00	1	0	0	0	0	1	0
.....ATAAATTTCATGGCTGAAGT.....	20	1	1	1.00	1	0	0	1	0	0	0
.....TGTGTGTAATCGTAAATGTAATAAATTT.....	28	0	1	1.00	1	1	0	0	0	0	0
.....ATGTAATAAATTTCATGGCTG.....	21	0	1	1.00	1	0	0	0	0	0	1
.....TTGTGTGTAATCGTAAATGTAATAAA.....	26	0	1	1.00	1	1	0	0	0	0	0
.....AAATTTGTGTGTAATCGTAAAA.....	22	1	1	1.00	1	0	1	0	0	0	0
.....TAATAAATTTCATGGCTGAAG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....GTAATAAATTTCATGGCTGAAGT.....	23	1	1	1.00	1	0	0	0	1	0	0
.....AAATTTGTGTGTAATCGTAG.....	20	1	1	1.00	1	1	0	0	0	0	0
.....AATTTGTGTGTAATCGTAAATGTA.....	24	0	1	1.00	1	0	1	0	0	0	0
.....ATTGAAAAAATTTGTGTGTAATC.....	23	0	1	1.00	1	0	0	0	0	1	0
.....AAAATTTGTGTGTAATCGTAA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TGTAATAAATTTCATGGCTGAAA.....	23	1	1	1.00	1	0	1	0	0	0	0
.....TGTGTGTAATCGTAAATGTAATAAAT.....	26	0	1	1.00	1	1	0	0	0	0	0
.....TTGTGTGTAATCGTAAATGTAATAAAT.....	27	0	1	1.00	1	1	0	0	0	0	0
.....GTGAGCTATGAAATTTATTGAAAG.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TAATAAATTTCATGGCTGTT.....	20	2	1	1.00	1	0	0	0	1	0	0
.....TAATAAATTTCATGGCTGAAGTT.....	23	2	1	1.00	1	1	0	0	0	0	0
.....GTGAGCTATGAAATTTATTGC.....	21	1	1	1.00	1	1	0	0	0	0	0
.....GTGAGCTATGAAATTTATTC.....	20	1	1	1.00	1	0	1	0	0	0	0
.....GCTATGAAATTTATTGAAA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TGTAATAAATTTCATGGCTG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....ATAAATTTCATGGCTGAAG.....	19	0	1	1.00	1	0	0	0	1	0	0

Anti-sense strand reads

CGACCCTCACAGGCTCGACAACAGCGAGGCCTTTCTTGATGCTGATGTTCCACTCGATACTTTAAATAACTTTTTTAAACACACATTAGCATTTACATTATTTAAAGTACCGACTTCGGGGCAGTGAAGGCACGGGCAGTTTTTAGGAGCCTCCAAGCAGCTCATAG **...((((((((((((((((((.....(((((((.....)))))))..)))))))))))))))))....***	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head
.....AATTTGTGTGTAATCGTAAATGTAAT.....	26	0	1	2.00	2	1
.....TGAGCTATGAAATTTATTGAAA.....	22	0	1	2.00	2	0
.....TTGTGTGTAATCGTAAATGTAATA.....	24	0	1	2.00	2	2
.....TGTGTGTAATCGTAAATGTAAT.....	22	0	1	2.00	2	1
.....AAATTTGTGTGTAATCGTAT.....	20	1	1	2.00	2	0
.....TAATAAATTTCATGGCTGAAGA.....	22	1	1	2.00	2	1
.....TTGTGTGTAATCGTAAATGTAAT.....	23	0	1	2.00	2	1
.....TTGTGTGTAATCGTAAATGT.....	20	0	1	2.00	2	0
.....TTGTGTGTAATCGTAAATGTAATAA.....	25	0	1	1.00	1	1
.....GTGAGCTATGAAATTTATA.....	19	1	1	1.00	1	0
.....TTTGTGTGTAATCGTAAATG.....	20	0	1	1.00	1	0
.....ATGTAATAAATTTCATGGCTGAAA.....	24	1	1	1.00	1	1
.....TGTAATAAATTTCATGGCT.....	19	0	1	1.00	1	1
.....TGTAATAAATTTCATGGCTGG.....	21	1	1	1.00	1	1
.....GTGAGCTATGAAATTTATTGAT.....	22	1	1	1.00	1	0
.....GTGAGCTATGAAATTTATG.....	19	1	1	1.00	1	1
.....GTGTGTAATCGTAAATGTAAT.....	21	0	1	1.00	1	0
.....TTTGTGTGTAATCGTAAATGT.....	21	0	1	1.00	1	1
.....ATGTAATAAATTTCATGGCT.....	20	0	1	1.00	1	1
.....TTGTGTGTAATCGTAAATGTAAA.....	23	1	1	1.00	1	1
.....ATTTGTGTGTAATCGTAAAT.....	20	0	1	1.00	1	1
.....TGTAATAAATTTCATGGCTGAAGA.....	24	1	1	1.00	1	0
.....ATAAATTTCATGGCTGAAGT.....	20	1	1	1.00	1	0
.....TGTGTGTAATCGTAAATGTAATAAATTT.....	28	0	1	1.00	1	1
.....ATGTAATAAATTTCATGGCTG.....	21	0	1	1.00	1	0
.....TTGTGTGTAATCGTAAATGTAATAAA.....	26	0	1	1.00	1	1
.....AAATTTGTGTGTAATCGTAAAA.....	22	1	1	1.00	1	0
.....TAATAAATTTCATGGCTGAAG.....	21	1	1	1.00	1	1
.....GTAATAAATTTCATGGCTGAAGT.....	23	1	1	1.00	1	0
.....AAATTTGTGTGTAATCGTAG.....	20	1	1	1.00	1	1
.....AATTTGTGTGTAATCGTAAATGTA.....	24	0	1	1.00	1	0
.....ATTGAAAAAATTTGTGTGTAATC.....	23	0	1	1.00	1	0
.....AAAATTTGTGTGTAATCGTAA.....	21	0	1	1.00	1	1
.....TGTAATAAATTTCATGGCTGAAA.....	23	1	1	1.00	1	0
.....TGTGTGTAATCGTAAATGTAATAAAT.....	26	0	1	1.00	1	1
.....TTGTGTGTAATCGTAAATGTAATAAAT.....	27	0	1	1.00	1	1
.....GTGAGCTATGAAATTTATTGAAAG.....	24	1	1	1.00	1	1
.....TAATAAATTTCATGGCTGTT.....	20	2	1	1.00	1	0
.....TAATAAATTTCATGGCTGAAGTT.....	23	2	1	1.00	1	1
.....GTGAGCTATGAAATTTATTGC.....	21	1	1	1.00	1	1
.....GTGAGCTATGAAATTTATTC.....	20	1	1	1.00	1	0
.....GCTATGAAATTTATTGAAA.....	19	0	1	1.00	1	1
.....TGTAATAAATTTCATGGCTG.....	20	0	1	1.00	1	1
.....ATAAATTTCATGGCTGAAG.....	19	0	1	1.00	1	0

Show Alignment With Reads

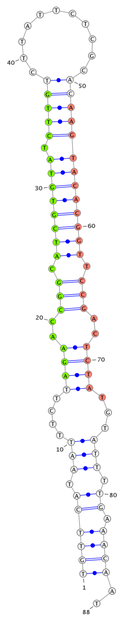
Re-alignment of all predicted orthologs

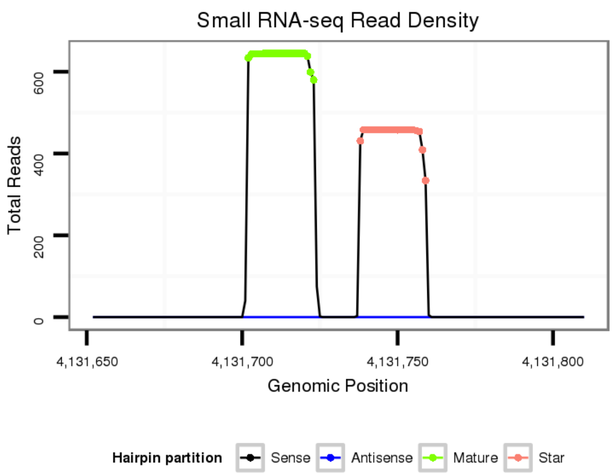
Species	Coordinate	ID	Alignment
droAna3	scaffold_13340:14669418-14669584 -	dan_3097	GCTGGGAGTGTCCGAGCTGTTGTCGCTCCGGAAAGAACTACGACTACAAGGTGAGCTATGAAATT----------TA--TT--------------G-----AAAAAA---TTTGTGTGTAATCGTAAAT----------------------------------GTAAT----AA----------AT-----TTCATGGCTGAAGCCCCGTCACTTCCGTGCCCGTCAAAAATCCTCGGAGGTTCGTCGAGTATC
droBip1	scf7180000395971:516483-516641 +		GCTGGGAGTGTCCTAGCTGTTGTCGCTCCGGAAAGAACTACGACTACAAGGTGAGCTATTAAACT---------T--TT------TTCAAAATTTG-----ACA---TTT----------------------------------AAACCTTATTATATATTT-----TT------TATGCTACATAGCCCCGTCACTTCCGTGCCCGTCAGAAATCCTCGGAGGTTAGACGAGTCTC
droKik1	scf7180000302355:1102314-1102476 -		GCTGGGAGTGTCCCAGTTGCTGTCGATCCGGCAAAAACTACGACTACAAGGTAGGCACCAGAAA-----------CCATTGGGTTT---------------------CTTGAAC----------------------------------ACCACACACTAATCTTCTT-----TT------TGTCTTCCACAGCCCCGTCACTTCAGCGCACGTCAGAAGTCCTCCGAGGTGCGTCGTGTTTC
droFic1	scf7180000454106:2299354-2299518 -		GCTGGGAGTGTCCCAGCTGTTGTCGCTCCGGCAAGAACTACGATTACAAGGTTGCAATTCGAGTT---------TA--TT--------T---TATAGTGTACA-----CG-GT----------------------------------TTATCTTATTAATCTC-----TAA-----TTTATCACCACAGCCCCGTCATTTCCGCGCCCGCCAGAAGTCCTCGGAAAGTGCGACGCGTTTC
droEle1	scf7180000491194:784446-784501 -		GTTGGGAGTGCCCCAGCTGCTGTCGCTCCGGCAAGAACTACGATTACAAGGTGAGC---------------------------------

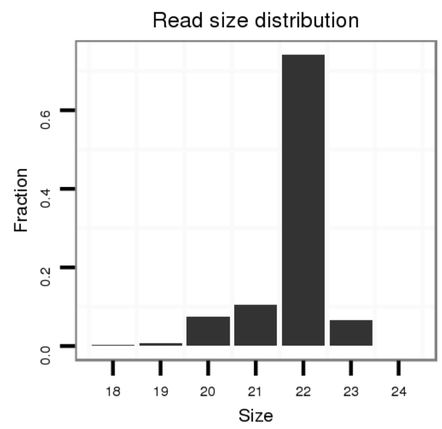
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_40	**scaffold_13266:4131702-4131760 +**	**confident**	**Canonical miRNA**	**3pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

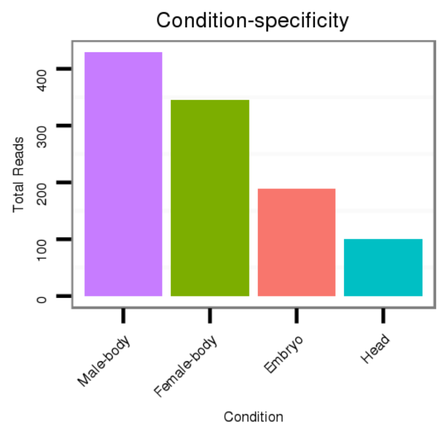
Legend: mature star mismatch in alignment mismatch in read

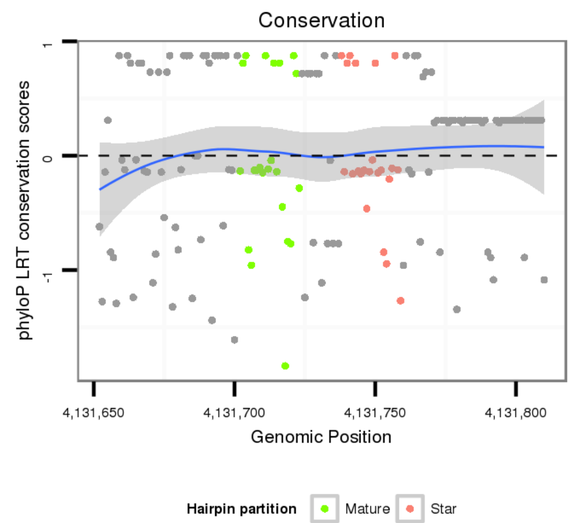
Predicted structure











Show Alternate Folds

Flybase annnotation

utr3 [utr3_minus_3275]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TAAAGTGATTTCTTGGAATTAAAGAAAAAAAAAGTTGTTCATAATTTCTTAGAACCGGCATCGTGTATCTTGTCTTATTCTCGCACAAGTACACGGTTCCGACTCTATGTATTTTGAAACAATTCTTCTGAATTAAGTGTGTGAATATTTTATATTAAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	M044 female body	M058 embryo	V055 head	V106 head	V039 embryo
**********(((((((.(((....((((..(((.(((((((((.(((((.....)))))))))))))).)))..))))...)))).)).)))))..**********											
.....AGAACCGGCATCGTGTATCTTG.....	22	0	1	469.00	469	316	114	2	18	14	5
.....AAGTACACGGTTCCGACTCTAT.....	22	0	1	310.00	310	25	127	110	22	10	16
.....AAGTACACGGTTCCGACTCTA.....	21	0	1	71.00	71	15	15	17	5	12	7
.....AGAACCGGCATCGTGTATCTTGT.....	23	0	1	68.00	68	28	27	7	5	1	0
.....AAGTACACGGTTCCGACTCT.....	20	0	1	43.00	43	5	16	15	6	1	0
.....AGAACCGGCATCGTGTATCT.....	20	0	1	34.00	34	25	4	3	0	1	1
.....TAGAACCGGCATCGTGTATCTTG.....	23	0	1	29.00	29	15	9	0	0	3	2
.....AAGTACACGGTTCCGACTCTAC.....	22	1	1	27.00	27	0	1	26	0	0	0
.....AGAACCGGCATCGTGTATCTT.....	21	0	1	17.00	17	7	10	0	0	0	0
.....AGTACACGGTTCCGACTCTAT.....	21	0	1	17.00	17	2	11	1	2	0	1
.....AAGTACACGGTTCCGACTCTATA.....	23	1	1	16.00	16	1	0	12	1	1	1
.....AGTACACGGTTCCGACTCTATT.....	22	1	1	9.00	9	1	6	1	0	1	0
.....AAGTACACGGTTCCGACTCTATT.....	23	1	1	8.00	8	2	3	1	1	1	0
.....AGAACCGGCATCGTGTATCTTGTT.....	24	1	1	7.00	7	7	0	0	0	0	0
.....GAACCGGCATCGTGTATCTTG.....	21	0	1	7.00	7	0	7	0	0	0	0
.....AGTACACGGTTCCGACTCTATG.....	22	0	1	5.00	5	2	2	0	1	0	0
.....AGAACCGGCATCGTGTATCTTGTA.....	24	1	1	5.00	5	3	2	0	0	0	0
.....TAGAACCGGCATCGTGTATCT.....	21	0	1	5.00	5	1	3	1	0	0	0
.....AGAACCGGCATCGTGTATC.....	19	0	1	5.00	5	3	0	0	2	0	0
.....AAGTACACGGTTCCGACTCTATAA.....	24	2	1	5.00	5	0	2	3	0	0	0
.....AAGTACACGGTTCCGACTCC.....	20	1	1	4.00	4	0	0	4	0	0	0
.....AAGTACACGGTTCCGACTCTAA.....	22	1	1	3.00	3	0	0	1	0	0	2
.....AGTACACGGTTCCGACTCTA.....	20	0	1	3.00	3	0	3	0	0	0	0
.....AAGTACACGGTTCCGACTC.....	19	0	1	2.00	2	0	0	2	0	0	0
.....AGAACCGGCATCGTGTATCTTGA.....	23	1	1	2.00	2	1	0	1	0	0	0
.....GAACCGGCATCGTGTATCTTGT.....	22	0	1	2.00	2	0	2	0	0	0	0
.....AAGTACACGGTTCCGACT.....	18	0	1	2.00	2	0	1	1	0	0	0
.....TAGAACCGGCATCGTGTATCTT.....	22	0	1	2.00	2	1	0	1	0	0	0
.....TAGAACCGGCATCGTGTATCTTGT.....	24	0	1	2.00	2	2	0	0	0	0	0
.....TAGAACCGGCATCGTGTATC.....	20	0	1	2.00	2	1	0	1	0	0	0
.....CAAGTACACGGTTCCGACTCTAT.....	23	0	1	2.00	2	1	0	1	0	0	0
.....AGTACACGGTTCCGACTCT.....	19	0	1	2.00	2	0	2	0	0	0	0
.....AGAACCGGCATCGTGTATCTTC.....	22	1	1	1.00	1	0	1	0	0	0	0
.....CAAGTACACGGTTCCGACTCC.....	21	1	1	1.00	1	0	0	1	0	0	0
.....AGTACACGGTTCCGACTCTAC.....	21	1	1	1.00	1	0	0	1	0	0	0
.....AGAACCGGCATCGTGTATCTTGC.....	23	1	1	1.00	1	0	0	1	0	0	0
.....AGAACCGGCATCGTGTATCTTGTC.....	24	0	1	1.00	1	0	1	0	0	0	0
.....AACCGGCATCGTGTATCTTGTC.....	22	0	1	1.00	1	0	1	0	0	0	0
.....AAGTACACGGTTCCGACTCTAG.....	22	1	1	1.00	1	0	1	0	0	0	0
.....AGAACCGGCATCGTGTATCTTAAA.....	24	3	1	1.00	1	0	1	0	0	0	0
.....AGAACCGGCATCGTGTATCTTA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TAGAACCGGCATCGTGTATCTTGTAG.....	26	2	1	1.00	1	1	0	0	0	0	0
.....AGAACCGGCATCGTGTATCTTT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....GTACACGGTTCCGACTCTATT.....	21	1	1	1.00	1	0	1	0	0	0	0
.....CAAGTACACGGTTCCGACTCTA.....	22	0	1	1.00	1	0	1	0	0	0	0
.....AGAACCGGCATCGTGTAAA.....	19	2	1	1.00	1	1	0	0	0	0	0
.....CGGCATCGTGTATCTTGT.....	18	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

ATTTCACTAAAGAACCTTAATTTCTTTTTTTTTCAACAAGTATTAAAGAATCTTGGCCGTAGCACATAGAACAGAATAAGAGCGTGTTCATGTGCCAAGGCTGAGATACATAAAACTTTGTTAAGAAGACTTAATTCACACACTTATAAAATATAATTT	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head
**********(((((((.(((....((((..(((.(((((((((.(((((.....)))))))))))))).)))..))))...)))).)).)))))..**********						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13266:4131652-4131810 +	dan_40	TAAAGTGATTTCTTGGAATTAAAGAAA----AAAAAAGTTGTTCATAATTTCTTAGAACCGGCA-TCGTGTATCTTGTCTTAT-TC-----------TCGC-ACAAGTACAC-GGTTCCGACTCTATGTATTTTGAAACAATTCTTCTGAATTAAGTGTGTGAATATTT-TATATTAAA
droBip1	scf7180000396427:2574418-2574575 +		TGAAAAATTTCCTGGTATACAAAAAC----AAAAAAA---ATTGTTAATTTCCTTGAATCGGTA--CCCGGCACTTGTATTTTGTT-----------TCGC-ACAGGTACTC-GTCTCTGCTTTTAATATTTAGAAACACTTCTTGTGAATTAAGTAATTGAATATTTTTTTATTAAC
droEle1	scf7180000491201:737269-737387 -		GT----GAATTCTAGGA--------ACTTTTTCAAAAA---TTTCATAAATTTGTAGACTTACTAAATGTGTTTTTTTTTTTT-TATTACTCATTGGTTAAAAAAAAGTCACCATTACTAGCTCTACATACTT---
droTak1	scf7180000415401:101242-101352 -		AAG---TAACTCAAGGAGTCCAGGAATTTTTGGTAAAT--TTTCCTAAGTAGCTAGAGCCGATA-ATGTGTG-GT--------------TGCTTGAG-AGAAGTACAA-GTTACTGTGCGTGTTTTGAGA-----------------------------------

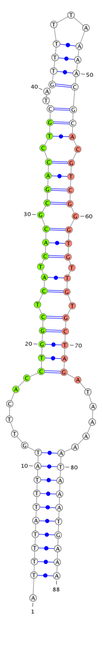
Generated: 09/08/2015 at 07:37 PM

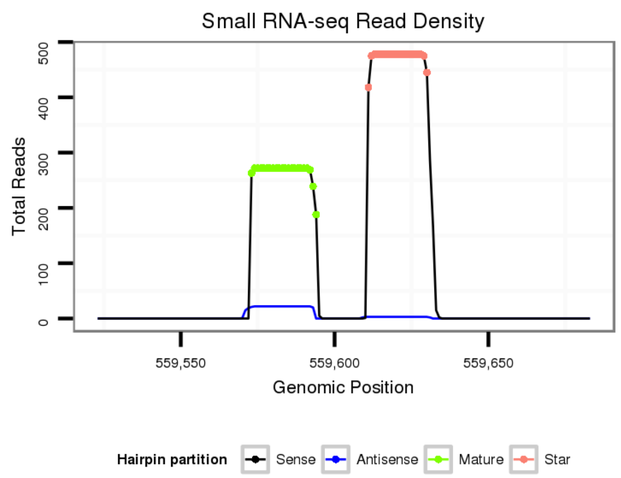
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

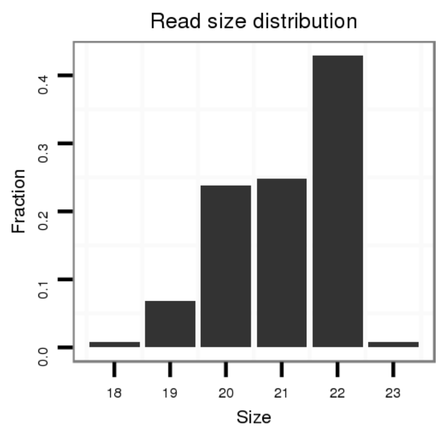
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_43	**scaffold_12903:559573-559633 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

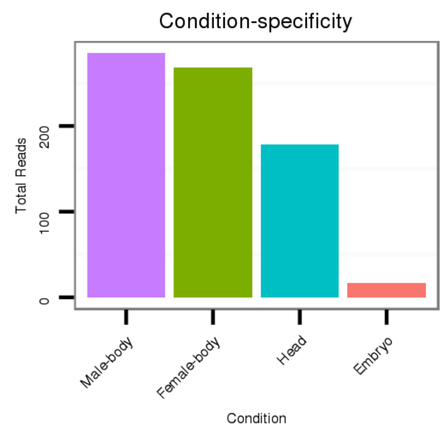
Legend: mature star mismatch in alignment mismatch in read

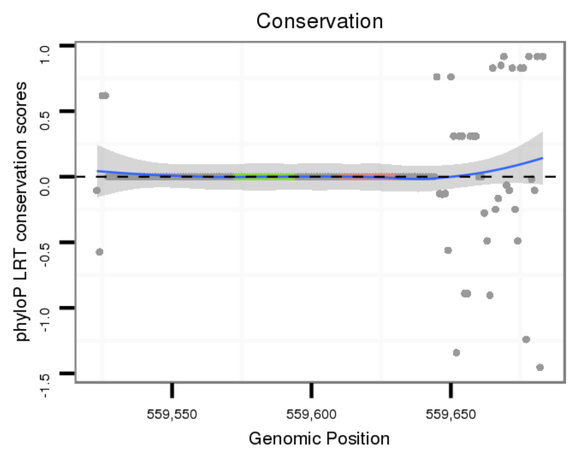
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TATTCTAATCAAATATTTAATTTTAAATGATTCTTATTTTATTTATGTTCACCTGGCTCATCACGCGACCTGCTAGTTTTTAAAACGCACGTCGGGTGTTGTGCTAGATAAAAATAAATGAAAGTGCAAGAATTAAAATCTTAAACAATTTAAAAAATATA	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	M044 female body	V106 head	V055 head	M058 embryo	V039 embryo
**********.((((((((((.....(((((.((.(((.((((.(((..((((...)))))))).))))).)))..)).)))))......))))))))))**********											
.....ACCTGGCTCATCACGCGACCTG.....	22	0	1	179.00	179	4	145	10	14	6	0
.....ACGTCGGGTGTTGTGCTAGA.....	20	0	1	139.00	139	66	15	52	5	1	0
.....ACGTCGGGTGTTGTGCTAGATA.....	22	0	1	129.00	129	83	15	21	9	0	1
.....ACGTCGGGTGTTGTGCTAGAT.....	21	0	1	111.00	111	69	19	10	13	0	0
.....ACCTGGCTCATCACGCGACCT.....	21	0	1	50.00	50	3	35	6	3	3	0
.....ACCTGGCTCATCACGCGACC.....	20	0	1	30.00	30	8	5	7	5	4	1
.....ACGTCGGGTGTTGTGCTAG.....	19	0	1	28.00	28	23	2	2	1	0	0
.....CGTCGGGTGTTGTGCTAGATA.....	21	0	1	21.00	21	9	9	3	0	0	0
.....CGTCGGGTGTTGTGCTAGA.....	19	0	1	19.00	19	9	5	4	1	0	0
.....ACGTCGGGTGTTGTGCTAGATT.....	22	1	1	12.00	12	6	1	1	4	0	0
.....ACCTGGCTCATCACGCGACCTGT.....	23	1	1	12.00	12	3	7	1	0	1	0
.....CGTCGGGTGTTGTGCTAGATAA.....	22	0	1	8.00	8	4	0	2	2	0	0
.....CGTCGGGTGTTGTGCTAGAT.....	20	0	1	7.00	7	1	5	1	0	0	0
.....ACGTCGGGTGTTGTGCTAGATAA.....	23	0	1	5.00	5	4	0	1	0	0	0
.....ACCTGGCTCATCACGCGACCTT.....	22	1	1	5.00	5	1	4	0	0	0	0
.....CCTGGCTCATCACGCGACCTG.....	21	0	1	4.00	4	0	4	0	0	0	0
.....CCTGGCTCATCACGCGACCTGC.....	22	0	1	4.00	4	0	4	0	0	0	0
.....ACCTGGCTCATCACGCGAC.....	19	0	1	3.00	3	1	0	0	1	1	0
.....ACGTCGGGTGTTGTGCTA.....	18	0	1	3.00	3	0	0	2	1	0	0
.....ACGTCGGGTGTTGTGCTAGT.....	20	1	1	2.00	2	1	0	1	0	0	0
.....ACGTCGGGTGTTGTGCTAGATAG.....	23	1	1	2.00	2	2	0	0	0	0	0
.....ACGTCGGGTGTTGTGCTAGATAAA.....	24	0	1	2.00	2	0	0	2	0	0	0
.....CGTCGGGTGTTGTGCTAG.....	18	0	1	2.00	2	1	0	0	1	0	0
.....ACCTGGCTCATCACGCGACCTA.....	22	1	1	1.00	1	0	1	0	0	0	0
.....ACGTCGGGTGTTGTGCTAGATG.....	22	1	1	1.00	1	0	0	0	1	0	0
.....ACCTGGCTCATCACGCGAA.....	19	1	1	1.00	1	1	0	0	0	0	0
.....ACGTCGGGTGTTGTGCTAA.....	19	1	1	1.00	1	0	1	0	0	0	0
.....CCTGGCTCATCACGCGACCT.....	20	0	1	1.00	1	0	1	0	0	0	0
.....GTCGGGTGTTGTGCTAGAT.....	19	0	1	1.00	1	0	1	0	0	0	0
.....ACGTCGGGTGTTGTGCTATT.....	20	2	1	1.00	1	0	0	0	1	0	0
.....ACCTGGCTCATCACGCGACCTGC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....GTCGGGTGTTGTGCTAGATA.....	20	0	1	1.00	1	0	1	0	0	0	0
.....ACCTGGCTCATCACGCGACCTGA.....	23	1	1	1.00	1	0	0	0	1	0	0
.....ACGTCGGGTGTTGTGCTAGATAGT.....	24	2	1	1.00	1	0	0	1	0	0	0
.....ACGTCGGGTGTTGTGCTAGAG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....ACGTCGGGTGTTGTGCTAGTAG.....	22	3	1	1.00	1	1	0	0	0	0	0
.....GTCGGGTGTTGTGCTAGA.....	18	0	1	1.00	1	0	1	0	0	0	0
.....CACGTCGGGTGTTGTGCTAGAT.....	22	0	1	1.00	1	0	0	1	0	0	0
.....ACCTGGCTCATCACGCGACCC.....	21	1	1	1.00	1	0	0	0	0	1	0
.....ACGTCGGGTGTTGTGCTAGTC.....	21	2	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

ATAAGATTAGTTTATAAATTAAAATTTACTAAGAATAAAATAAATACAAGTGGACCGAGTAGTGCGCTGGACGATCAAAAATTTTGCGTGCAGCCCACAACACGATCTATTTTATTTACTTTCACGTTCTTAATTTTAGAATTTGTTAAATTTTTTATAT	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V106 head	V055 head	M058 embryo
**********.((((((((((.....(((((.((.(((.((((.(((..((((...)))))))).))))).)))..)).)))))......))))))))))**********									
.....AGTGGACCGAGTAGTGCGCTGGA.....	23	0	1	13.00	13	9	2	1	1
.....GTGGACCGAGTAGTGCGCTGGA.....	22	0	1	4.00	4	3	1	0	0
.....TGGACCGAGTAGTGCGCTGGA.....	21	0	1	2.00	2	2	0	0	0
.....TGTGGACCGAGTAGTGCGCTGGA.....	23	1	1	2.00	2	2	0	0	0
.....AAGTGGACCGAGTAGTGCGCTGGA.....	24	0	1	1.00	1	0	1	0	0
.....GTGCAGCCCACAACACGATCTA.....	22	0	1	1.00	1	1	0	0	0
.....GGACCGAGTAGTGCGCTGG.....	19	0	1	1.00	1	1	0	0	0
.....CGTGCAGCCCACAACACGATCT.....	22	0	1	1.00	1	1	0	0	0
.....CGTGCAGCCCACAACACGATCTA.....	23	0	1	1.00	1	1	0	0	0
.....AGTGGACCGAGTAGTGCGCTGG.....	22	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:559523-559683 +	dan_43	TATTCTAATCAAATATTTAATTTTAAATGATTCTTATTTTATTTATGTTCACCTGGCTCATCACGCGACCTGCTAGTTTTTAAAACGCACGTCGGGTGTTGTGCTAGATAAAAATAAATGAAAGTGCAAGAATTAAAATCTTAAACAATTTAAAAAATA---TA
droBip1	scf7180000395925:48715-48746 -		AA----------AGTGTAACAAAAAA-------ACAAA-----TAAATGTGA
droRho1	scf7180000778082:74501-74525 -		TCTT----------AAAAGCAATTTTAAGAGTA---AA
droYak3	2R:7536006-7536035 +		TT----------AAACA----------TCAGACATTTCAAAAAGTA---TA

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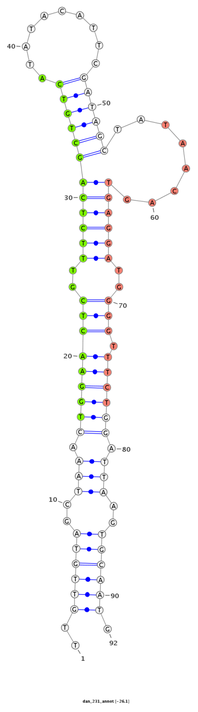
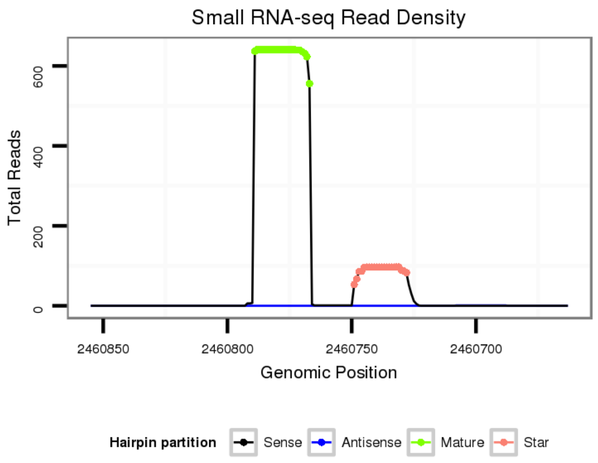
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

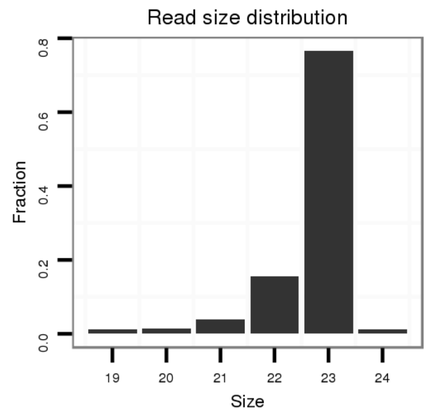
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_231	**scaffold_13417:2460713-2460805 -**	**confident**	**Testes-restricted**	**antisense_to_CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

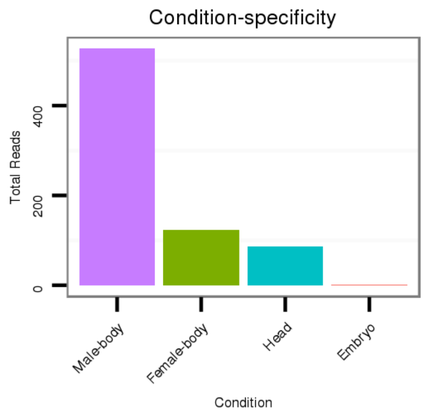
Legend: mature star mismatch in alignment mismatch in read

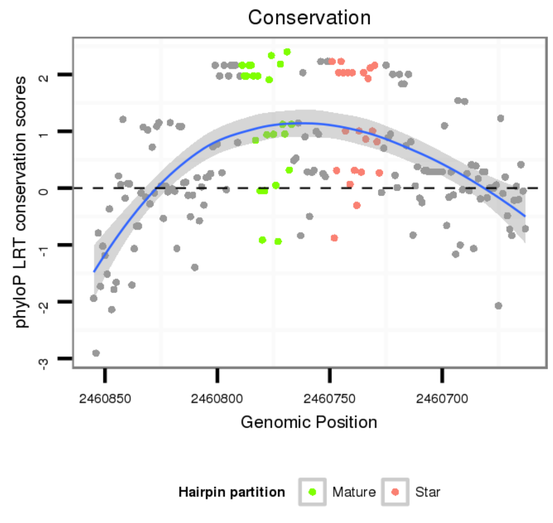
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to CDS [Dana\GF20485-cds]; Antisense to intron [Dana\GF20485-in]; Antisense to CDS [Dana\GF20485-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AGGACGATCCAGGCGGTGCAATAGCGGGGATCACTTTGGGTCGGCCAGCGATTGTTGTAGCTAAACTGGAACTCGTTTCTCAGCTGTCATATACATTCGATAGCTATAACAGTGAGGATGGGGTTTCTGGATTAAGTGCAATGGTATTACGGGCCGACCACTGTGACTGGGTCCCACCGTGAAGTGGGTGCGG	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	M044 female body	V055 head	V106 head	M058 embryo	V039 embryo
**********..(((((((..(((.(((((((((..(((((((((((.....)))))).....)))))))..))).)))))))..)))..))))))).**********											
.....TGGAACTCGTTTCTCAGCTGTCA.....	23	0	1	549.00	549	418	87	32	10	1	1
.....TGGAACTCGTTTCTCAGCTGTC.....	22	0	1	66.00	66	47	12	5	2	0	0
.....TAACAGTGAGGATGGGGTTTCT.....	22	0	1	24.00	24	13	3	2	6	0	0
.....TGGAACTCGTTTCTCAGCTGTCT.....	23	1	1	19.00	19	16	0	3	0	0	0
.....TGGAACTCGTTTCTCAGCTGT.....	21	0	1	9.00	9	6	3	0	0	0	0
.....TAACAGTGAGGATGGGGTTTCTG.....	23	0	1	9.00	9	3	2	2	2	0	0
.....TAACAGTGAGGATGGGGTT.....	19	0	1	8.00	8	5	0	1	2	0	0
.....ACAGTGAGGATGGGGTTTCTGG.....	22	0	1	7.00	7	5	1	0	1	0	0
.....AACAGTGAGGATGGGGTTTCTG.....	22	0	1	6.00	6	2	2	0	2	0	0
.....ACAGTGAGGATGGGGTTTCTG.....	21	0	1	6.00	6	4	2	0	0	0	0
.....AACAGTGAGGATGGGGTTTCT.....	21	0	1	5.00	5	2	1	0	2	0	0
.....TAACAGTGAGGATGGGGTTTCTGG.....	24	0	1	5.00	5	2	0	1	2	0	0
.....AGTGAGGATGGGGTTTCTGGAT.....	22	0	1	4.00	4	4	0	0	0	0	0
.....TAACAGTGAGGATGGGGTTTC.....	21	0	1	4.00	4	3	0	0	1	0	0
.....ACAGTGAGGATGGGGTTTCTGGA.....	23	0	1	4.00	4	1	0	0	3	0	0
.....AACTGGAACTCGTTTCTCAGCT.....	22	0	1	4.00	4	1	2	1	0	0	0
.....AACAGTGAGGATGGGGTTTCTGG.....	23	0	1	3.00	3	3	0	0	0	0	0
.....TAACAGTGAGGATGGGGTTTCTTT.....	24	2	1	3.00	3	1	0	0	2	0	0
.....GGAACTCGTTTCTCAGCTGTCA.....	22	0	1	3.00	3	0	3	0	0	0	0
.....AGTGAGGATGGGGTTTCTGG.....	20	0	1	3.00	3	1	0	2	0	0	0
.....TAACAGTGAGGATGGGGTTTCTT.....	23	1	1	3.00	3	1	0	0	2	0	0
.....AGTGAGGATGGGGTTTCTGGA.....	21	0	1	3.00	3	2	1	0	0	0	0
.....TGGAACTCGTTTCTCAGCTGTCAT.....	24	0	1	3.00	3	2	1	0	0	0	0
.....TGGAACTCGTTTCTCAGCTG.....	20	0	1	3.00	3	0	3	0	0	0	0
.....ACAGTGAGGATGGGGTTTCTGGT.....	23	1	1	3.00	3	2	0	0	1	0	0
.....AACAGTGAGGATGGGGTTTCTTT.....	23	2	1	2.00	2	0	0	1	1	0	0
.....TAACAGTGAGGATGGGGTTT.....	20	0	1	2.00	2	2	0	0	0	0	0
.....AGTGAGGATGGGGTTTCTGGAC.....	22	1	1	2.00	2	2	0	0	0	0	0
.....ACAGTGAGGATGGGGTTTCT.....	20	0	1	2.00	2	0	0	0	2	0	0
.....ACAGTGAGGATGGGGTTTCTTT.....	22	2	1	2.00	2	1	0	0	1	0	0
.....GTGAGGATGGGGTTTCTGGATT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....AACAGTGAGGATGGGGTTTCTT.....	22	1	1	1.00	1	0	1	0	0	0	0
.....TGGAACTCGTTTCTCAGCTGTCATT.....	25	1	1	1.00	1	0	0	1	0	0	0
.....TGGAACTCGTTTCTCAGCTGC.....	21	1	1	1.00	1	0	1	0	0	0	0
.....TAACAGTGAGGATGGGGTTTCTC.....	23	1	1	1.00	1	0	0	0	1	0	0
.....AACTGGAACTCGTTTCTCAGCTG.....	23	0	1	1.00	1	0	0	1	0	0	0
.....TAACAGTGAGGATGGGGTTTCA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TGGAACTCGTTTCTCAGCTGTCAC.....	24	1	1	1.00	1	0	1	0	0	0	0
.....CTGGAACTCGTTTCTCAGCTGTCA.....	24	0	1	1.00	1	0	0	1	0	0	0
.....CAGTGAGGATGGGGTTTCTGGT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....ACAGTGAGGATGGGGTTTCTT.....	21	1	1	1.00	1	0	0	0	1	0	0
.....TAACAGTGAGGATGGGGTTTCTGGT.....	25	1	1	1.00	1	0	0	1	0	0	0
.....AGTGAGGATGGGGTTTCTGGT.....	21	1	1	1.00	1	0	1	0	0	0	0
.....TATACATTCGATAGCTATAAC.....	21	0	1	1.00	1	0	0	0	1	0	0
.....AACTGGAACTCGTTTCTCAG.....	20	0	1	1.00	1	0	0	0	1	0	0
.....GGAACTCGTTTCTCAGCTGTC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....AGTGAGGATGGGGTTTCTG.....	19	0	1	1.00	1	0	0	0	1	0	0
.....TGGAACTCGTTTCTCAGCTGTT.....	22	1	1	1.00	1	0	1	0	0	0	0
.....TGGAACTCGTTTCTCAGCTGTCAC.....	24	1	1	1.00	1	1	0	0	0	0	0
.....ACAGTGAGGATGGGGTTTCTTTT.....	23	3	2	0.50	1	1	0	0	0	0	0
.....CAGTGAGGATGGGGTTTCTGTTC.....	23	3	2	0.50	1	0	1	0	0	0	0

Anti-sense strand reads

TCCTGCTAGGTCCGCCACGTTATCGCCCCCTAGTGAAACCCAGCCGGTCGCTAACAACATCGATTTGACCTTGAGCAAAGAGTCGACAGTATATGTAAGCTATCGATATTGTCACTCCTACCCCAAAGACCTAATTCACGTTACCATAATGCCCGGCTGGTGACACTGACCCAGGGTGGCACTTCACCCACGCC	Read size	# Mismatch	Hit Count	Total Norm	Total	V039 embryo	M044 female body	M058 embryo	V106 head
**********..(((((((..(((.(((((((((..(((((((((((.....)))))).....)))))))..))).)))))))..)))..))))))).**********									
.....ATGCCCGGCTGGTGACACTGA.....	21	0	1	1.00	1	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13417:2460663-2460855 -	dan_231	AGGACGATCCAGGCGGTGCAATAGCGGGGATCACTTTGGGTCGGCCAGCGATTGTTGTAGCTAAACTGGAACTCGTTTCTCAGCTGTCATATACATTCGATAGCTATAACAGTGAGGATGGGGTTTCTGGATTAAGTGCAAT---GGTATTACGGGCCGACCACTGT--GACTGGGTC--CC----------ACCGTGAAGTGGGTGCGG
droBip1	scf7180000395874:32722-32890 -		GTACA----------GGGATCACTTTTGGTCGACCAACGATTGTTGTAGCTAAACTGGAACTCGTTTCTCACTGTCATATACATCCGATAGCTATAACAGTGAGGATTGGGTTTCTGGATTAAGTGCAAT---GGTGTTACGGGCCGACTACTGT--GACTGGGC--CC----------A---CCAAGTGGGTGCGG
droKik1	scf7180000302517:1186301-1186441 +		CAACACGGATCGGCG----------GTCCACAATTGTTGCAACTAAACTGGAACTCGCTCCTCATGTGTCATGTGCATTCGTAGCTATTACAGTGAGGTGGAGTTTCTGGATTAAGTGCAAT---GGTG---------ATTACCG--------T---ACCAAT----------ATGG---CCA---------AG
droFic1	scf7180000454073:1735817-1735956 +		TCG----------ATTGCGCATTGTTGCAGCTAAACTGGAACTCAAATCTCAGCTGTCATATGCATTCAATAG-TATGCGCAGTGGGGGTGGG--TTCTAGAACAAGTGCAAT---CCTC----------GCGGGC--AATCGCTTCCG--T---GTCAAA----------AAAG-AAAGAAGGAGA
droEle1	scf7180000490751:1121746-1121825 +		----------CAGCTGTCAAACACATGCGATAGGTATGCACAGTGTGAATGGGGTC----------------------------------GAGTCGGA--TCGCGACAAAAAGAATGGAACGGAAGT----------G
droRho1	scf7180000761121:187405-187535 -		G----------ACAAACGATTGTTGCAGCTAAACTGGAACTCATGTCTCAGCTGTCATATACATTATGATAGGTATAACAGTGAGGATGGGGTTTCTGGAATAAGTGCAAT---GGCG---------ACCAGAGCAAGATCGGGTTTG--T----------TGCGG
droBia1	scf7180000302069:1148270-1148395 -		----------TTGCAGCTAAACTGGAACCCTGGTCTCAACTGTCATGTGCAGTTGATATGTATAACAGTGAGGACGGGGTTTCTGGAATAA-TGCAAT---GGTGG---------CAGAGT--GATCGAGTCCA--TCG----------CGAGGGGAAAGGA
droTak1	scf7180000415169:842210-842319 -		G----------ACGAACGATTGTTGCAGCTAAACTGGAACCCAACT-TGCGCTGTGATATTCATTTGATAGGTATAACAGCGGGATGGGGTTTTCTGGAATAAGTGCAAT---AGTG----------------------------------AGTGCAG
droEug1	scf7180000409230:877491-877616 -		A----------TAGTTGCAGCTAAACTGGAACTCAAGTCTCAGCTGTCATATTCATTTGATAGTTATGCACAGTGAGGATGGGGTTTCTGGAATAACTGCAACAATTGTG---------AGCAGTGA--GATCGAGTTTA--TCG----------CAA---------GG
droYak3	v2_chrUn_2706:8-58 -		ACGGCGATGGGGGCAGTGTGGCAAGAGAGACGCTCCGGGTGCTCCA--GCGA
droEre2	scaffold_4845:21531680-21531699 +		AGAGCACTCCAGGCAGTCCA---
dp5	Unknown_group_129:12001-12027 -		CTGGTG----------TCACCGTGGGAT----------CCA----------
droWil2	scf2_1100000004909:7960923-7961071 +	dwi_144	ATGATTAACCAACAACCAACTAAC----------TAACTAGCTGTTGTAACTAAACTGGAACTCATTTCTCAGTGTCATATACATACAATAGCTATAACAGTGAGACTAGGGTTTCTGGATTAAATGCAAT---AA----------GTGA---AACAACG---T---AC----------ATACATACAT
droVir3	scaffold_13042:902858-902983 -	dvi_76	GATCCGGAGAC----------AGATGAGTCTTGGATGATAACGCGATGTGGCATCTAACCTGGAACTCGATTCTCCTGTCATATGCGGACGATAACTATGGCAGTGAGGGTGGGGTTTCCTTATTAGATGGCAT----------
droMoj3	scaffold_6328:2897207-2897290 -		G----------ATGATGGCATCTAAGCTGGAACTCGATTCTCCTGTCATATGCACGCGACAACTATGGCAGTGAGGGTGGGGTTTCCCTATT----------

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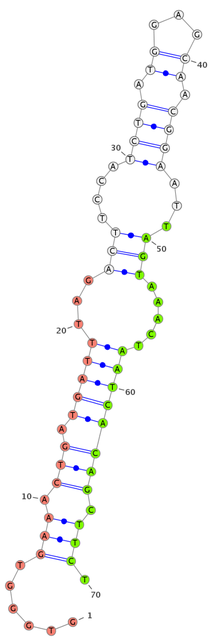
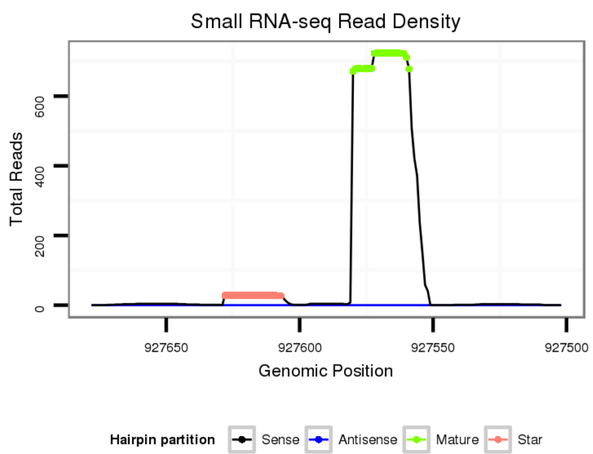
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	4
rescue.candidate	0

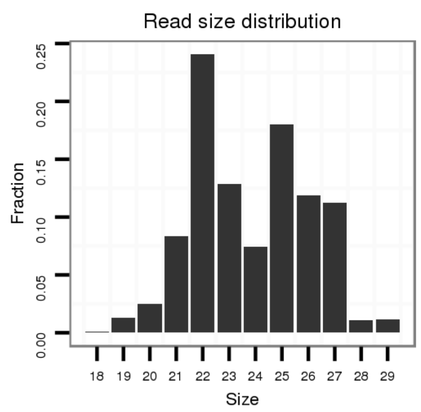
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_889	**scaffold_12943:927552-927628 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

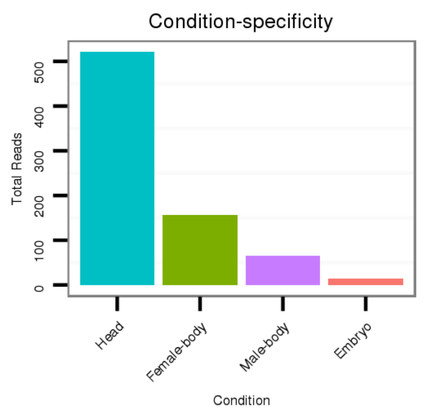
Legend: mature star mismatch in alignment mismatch in read

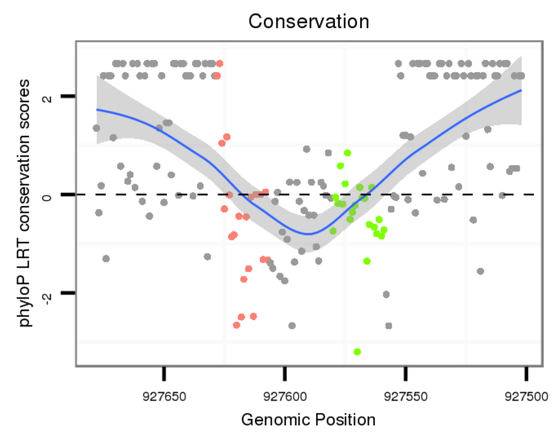
Predicted structure











dan_889_annot [-10,6]

Show Alternate Folds

Flybase annnotation

intron [Dana\GF21962-in]; CDS [Dana\GF21962-cds]; CDS [Dana\GF21962-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGCGCCGCAACAGCCTGACGGACAAGACCGGCAAGAAGGGCTTCCTGATGGTGGGTGAAACTGATGATTTAGACTTCCATCTGATGGAGCAACGGAATTAGTAAACTAATCACAGCTTCTTCCATAGGGCCTCAAAATGCGAAAGCAGCGCAGCACCGGGGATCTGGAGAAGCGGGG	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V055 head	M044 female body	V105 male body	M058 embryo	V039 embryo
**********.....(((.(((.(((((...(((....((((.((...)).)))).)))).....)))).....)))))))).)))..**********											
.....TAATCACAGCTTCTTCCATAGT.....	22	1	1	212.00	212	132	6	54	13	3	4
.....TAGTAAACTAATCACAGCTTCT.....	22	0	1	169.00	169	81	51	14	22	1	0
.....TAGTAAACTAATCACAGCTTCTTCC.....	25	0	1	131.00	131	62	28	26	8	7	0
.....TAGTAAACTAATCACAGCTTCTTCCAT.....	27	0	1	85.00	85	52	13	18	1	1	0
.....TAGTAAACTAATCACAGCTTCTT.....	23	0	1	85.00	85	37	30	15	3	0	0
.....TAGTAAACTAATCACAGCTTCTTCCA.....	26	0	1	85.00	85	37	19	24	4	1	0
.....TAGTAAACTAATCACAGCTTCTTC.....	24	0	1	48.00	48	22	17	6	3	0	0
.....TAGTAAACTAATCACAGCTTC.....	21	0	1	33.00	33	3	10	7	13	0	0
.....TAATCACAGCTTCTTCCATAG.....	21	0	1	29.00	29	5	0	22	0	2	0
.....TAATCACAGCTTCTTCCATAGTT.....	23	2	1	10.00	10	9	0	0	1	0	0
.....TAGTAAACTAATCACAGCTTCTTCCATAG.....	29	0	1	9.00	9	1	0	8	0	0	0
.....TAATCACAGCTTCTTCCATA.....	20	0	1	9.00	9	6	1	0	2	0	0
.....TAATCACAGCTTCTTCCATAGA.....	22	1	1	9.00	9	7	0	2	0	0	0
.....GTGGGTGAAACTGATGATTTAG.....	22	0	1	9.00	9	7	0	0	2	0	0
.....GTGGGTGAAACTGATGATTTAGA.....	23	0	1	8.00	8	1	0	0	6	1	0
.....TAGTAAACTAATCACAGCTT.....	20	0	1	8.00	8	2	3	2	1	0	0
.....TAGTAAACTAATCACAGCTTCTTCCATA.....	28	0	1	8.00	8	5	1	1	0	0	1
.....TAATCACAGCTTCTTCCAT.....	19	0	1	6.00	6	5	1	0	0	0	0
.....GTGGGTGAAACTGATGATTTAGAC.....	24	0	1	6.00	6	6	0	0	0	0	0
.....AATCACAGCTTCTTCCATAGT.....	21	1	1	6.00	6	2	0	4	0	0	0
.....TAGTAAACTAATCACAGCTTCTTCCATT.....	28	1	1	3.00	3	1	1	1	0	0	0
.....TAGTAAACTAATCACAGCTTCTTCG.....	25	1	1	3.00	3	3	0	0	0	0	0
.....TAGTAAACTAATCACAGCTTCTTCT.....	25	1	1	3.00	3	3	0	0	0	0	0
.....GTGGGTGAAACTGATGATTTAGACT.....	25	0	1	3.00	3	3	0	0	0	0	0
.....TAATCACAGCTTCTTCCATAGC.....	22	1	1	2.00	2	1	0	0	0	1	0
.....AGTAAACTAATCACAGCTTCTTCC.....	24	0	1	2.00	2	0	0	2	0	0	0
.....TTAGTAAACTAATCACAGCTTCTTCC.....	26	0	1	2.00	2	1	0	1	0	0	0
.....TAATCACAGCTTCTTCCATAGCC.....	22	2	1	2.00	2	0	0	2	0	0	0
.....TAGTAAACTAATCACAGCTTCTTCCT.....	26	1	1	2.00	2	1	1	0	0	0	0
.....AGTAAACTAATCACAGCTT.....	19	0	1	2.00	2	0	0	2	0	0	0
.....GATGGAGCAACGGAATTAGTAA.....	22	0	1	2.00	2	2	0	0	0	0	0
.....TAATCACAGCTTCTTCCATT.....	20	1	1	2.00	2	2	0	0	0	0	0
.....TTAGTAAACTAATCACAGCTTCT.....	23	0	1	2.00	2	2	0	0	0	0	0
.....AATCACAGCTTCTTCCATAGTT.....	22	2	1	2.00	2	2	0	0	0	0	0
.....AGTAAACTAATCACAGCTTCTTCCAT.....	26	0	1	2.00	2	0	0	2	0	0	0
.....TAGTAAACTAATCACAGCT.....	19	0	1	1.00	1	0	0	1	0	0	0
.....AGTAAACTAATCACAGCTTCTT.....	22	0	1	1.00	1	0	0	1	0	0	0
.....TAGTAAACTAATCACAGCTTCTTCCG.....	26	1	1	1.00	1	1	0	0	0	0	0
.....TAGTAAACTAATCACAGCTTCTG.....	23	1	1	1.00	1	1	0	0	0	0	0
.....GGCAAGAAGGGCTTCCTGAT.....	20	0	1	1.00	1	0	0	0	0	1	0
.....GTGGGTGAAACTGATGATTT.....	20	0	1	1.00	1	1	0	0	0	0	0
.....ACGGACAAGACCGGCAAGAAGGGC.....	24	0	1	1.00	1	1	0	0	0	0	0
.....ACAGCCTGACGGACAAGACCGGCAAGA.....	27	0	1	1.00	1	1	0	0	0	0	0
.....TAGTAAACTAATCACAGCTTCTTT.....	24	1	1	1.00	1	0	1	0	0	0	0
.....TAGTAAACTAATCACAGC.....	18	0	1	1.00	1	0	0	1	0	0	0
.....TAATCACAGCTTCTTCCATACT.....	22	2	1	1.00	1	1	0	0	0	0	0
.....GCAACAGCCTGACGGACAAGACC.....	23	0	1	1.00	1	0	0	0	1	0	0
.....TAGTAAACTAATCACAGCTTCTTCCAC.....	27	1	1	1.00	1	0	0	0	0	1	0
.....ATGCGAAAGCAGCGCAGCACCGGGG.....	25	0	1	1.00	1	1	0	0	0	0	0
.....CTAATCACAGCTTCTTCCATAG.....	22	0	1	1.00	1	0	0	1	0	0	0
.....GCAGCACCGGGGATCTGGAGAAGCA...	25	1	1	1.00	1	0	0	0	1	0	0
.....AATCACAGCTTCTTCCATAG.....	20	0	1	1.00	1	0	0	1	0	0	0
.....AACTAATCACAGCTTCTTC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....GCCTGACGGACAAGACCGGCA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TGATGGAGCAACGGAATTAGTAAAC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....GCAGCGCAGCACCGGGGATCTGGAGA.....	26	0	1	1.00	1	1	0	0	0	0	0
.....ACTAATCACAGCTTCTTCCATAG.....	23	0	1	1.00	1	0	0	1	0	0	0
.....AGCGCAGCACCGGGGATCTGGAG.....	23	0	1	1.00	1	0	0	1	0	0	0
.....GTGGGTGAAACTGATGATTTAGACTT.....	26	0	1	1.00	1	1	0	0	0	0	0
.....AATCACAGCTTCTTCCATAGA.....	21	1	1	1.00	1	0	0	1	0	0	0
.....TAATCACAGCTTCTTCCATAGTA.....	23	2	1	1.00	1	1	0	0	0	0	0
.....TTAGTAAACTAATCACAGCTT.....	21	0	1	1.00	1	0	1	0	0	0	0
.....AGTAAACTAATCACAGCTTCTTCCA.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TAGTAAACTAATCACAGCTTCC.....	22	1	1	1.00	1	1	0	0	0	0	0
.....ACTTCCATCTGATGGAGCAACGG.....	23	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

ACGCGGCGTTGTCGGACTGCCTGTTCTGGCCGTTCTTCCCGAAGGACTACCACCCACTTTGACTACTAAATCTGAAGGTAGACTACCTCGTTGCCTTAATCATTTGATTAGTGTCGAAGAAGGTATCCCGGAGTTTTACGCTTTCGTCGCGTCGTGGCCCCTAGACCTCTTCGCCCCC	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head	V106 head	M058 embryo	V105 male body
**********.....(((.(((.(((((...(((....((((.((...)).)))).)))).....)))).....)))))))).)))..**********									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12943:927502-927678 -	dan_889	TGCGCCGCAACAGCCTGACGGACAAGACCGGCAAGAAGGGCTTCCTGATGGTGGGTGAAACTGAT---GATTTAGAC----------TTCCATCTGATGGA--GC----AAC----------GGAATTAGTAAACTAATCAC-------AGC---T-TCTTCCATAGGGCCTCAAAATGCGAAAGCAGCGCAGCACCGGGGATCTGGAGAAGCGGGG
droBip1	scf7180000396728:2209031-2209194 +		TGCGCCGCAACAGCCTGACGGACAAGACCGGCAAGAAGGGCTTCCTGATGGTGGGTGAACCTG---------------------ATGATG-GATGGA--GC----AAC----------TGAATCAGTAAACTAACCAT-------AGC---T-TCTCTTATAGGGCCTCAACATGCGAAAGCAGCCAAGCACCGGGGACCTGGAGAAGCCTGG
droKik1	scf7180000302472:1886542-1886702 -		TGAGGCGCAACAGTTGACGGACAAGACGGGCAAAAAGGGATTCTCTAATGGTGAGCAGGAG----GGAA---CTCCT----------TGAAGGATT--TTA--AA-TG----------TA-GCATATTTG-------GGC---C-TGCCTTTTAGGGCCTCAAGATGCGCAAGCAGCGCAGCACGGGATGATCTGGAAAAGAGGGG
droFic1	scf7180000449392:3515-3675 -		TGCGACGAAAAAGTTGACGGATAAAACCGGCAAGAAGGGATTCCTGATGGTGAGTTTGGAAGGGA--G---ATCTA----------TT------CTATTATT--TTG---T----------TA-TTATTAT-------TTC---T-TTTTATCAGGGTCTTAAGATGCGAAAGCAGCCTAGTACCGGGATCTGGAGAAGCGGGG
droEle1	scf7180000491186:2543392-2543568 -		TGCGGCGCAACAGTCTGACGGACAAGACCGGAAAGAAGGGATTCCTAATGGTGAGTTTGGCAGGG---C---TTGA----------TCTCTTAGTGGCGAATTCCTATTCCTG---------TAAA-----TGT-------A-TCGGT---ATC------A----TCGCCTAACAGGGCCTCAAGATGCGAAACAGCGCAGCACGGGATCTGGAGAAGAGGGG
droRho1	scf7180000778085:407695-407864 +		TCAGGCGCAACAGTCTGACGGATAAGACCGGAAAGAAGGGATTCCTTATGGTGAGTCCGAAGGGG---T---ATTAA----------TTATTTGTGGTGACGAATTCCTATTC--AAT-TCTGT---ATC------A----TCCCACAACAGGGCCTCAAGATGCGCAAACAGCGCAGCACCGGGATCTGGAGAAGAGGGG
droBia1	scf7180000302408:3621758-3621920 +		TGCGACGCAACAGCTTGACGGACAAGACCGGCAAGAAGGGATTCCTGATGGTGAGTTTGGGCGAGG----GATTTGCATCT---------------CATT--TCA---T---TTATTCAC----------TGTGC---CAA----T--A----TTCCGAACAGGGTCTCAAGATGCGCAAACAGCGCAGCACGGGCGATCTGGAGAAGCGGGG
droTak1	scf7180000415880:348415-348590 +		TGCGGCGCAACAGTTTAACAGATAAGACTGGCAAGAAGGGATTCCTGATGGTGAGTTGGGGAGGGG----TAATGTCATGT-----CATT------TCATTTA---T---CTTTATT----------TAA-CCCTT---CCTTATTT--TCTTGTCGAAAAACAGGGCCTTAAGATGCGCAAACAGCGCAGCACGGGCGATCTGGAGAAACGGGG
dm3	chr2L:9553890-9554049 -		TCCGGCGCAACAGTTTGACGGACAAGACGGCAAAAAGGGATTTGTGATGGTGTGTTCGAAG---T---------------CTCCTATGGTGACACT--ATTATC----------TAA-TGCT---TCA----T--A----CTGATTAATAGAACCTCAAGATGCGCAAGCAGCGCAGCACGGGTGATCTGGAAAAGCGGGG
droSim2	2L:9237439-9237606 -		TTCGGCGCAACAGTTTGACGGACAAGACGGGCAAAAAGGGATTCCTGATGGTGCGTTTCGTAGAG---T---ATTAC----------TTATATGGTGGCCATA--ACTATTA----------TAA-TTTAT---CCA----T--A----CTGCTTAACAGAACCTCAAGATGCGCAAGCAGCGCAGCACGGGTGATCTGGAAAAGCGGGG
droSec2	scaffold_3:5001211-5001378 -		TTCGGCGCAACAGTTTGACGGACAAGACGGGCAAAAAGGGATTCCTGATGGTGCGTTTGTAGTG---T---ATTAC----------TTACTATGGTGGCCACA--ACTATTA----------TAA-TTTAT---CCA----T--A----CTGCTTAACAGAACCTCAAGATGCGCAAGCAGCGCAGCACGGGTGATCTGGAAAAGCGGGG
droYak3	2L:12235231-12235406 -		TGAGGCGCAACAGTTTGACGGACAAGACCGGCAAAAAGGGATTCCTGATGGTGCGTTTCAATGGG---C---ATTAGATATCC-----CAAT------TCCTGGCC---T--ACTAAGC----------TAA-TTTTT---CCATACTC--TGAAC-CTCTGAAGAGAACCTGAAGATGCGCAAGCAGCGCAGCACGGGTGATCTGGAGAAGCGGGG
droEre2	scaffold_4929:10159428-10159594 -		TCCGGCGCAACAGTTTGACGGACAAGACCGGCAAGAAGGGTTTCCTCATGGTGCGTTTCGAGGA---C---ATCAG----------CTCCCATGGTGGCAAC--AGCATC----------TAA-TCTCT---TCA----T--A----CTCCCAACAGAACCTCAAGATGCGCAAGCAGCGCAGCACGGGTGATCTGGAAAAGCGGGG
dp5	4_group3:623225-623391 +		TGCGCCGCAACAGTCTGACGGACAAGACC---AAGAAGGGATTCCTCATGGTGGGTCTTCATCTGGGAT---CTCTC----------TTCTCTTCGAAGGA--GCCTTCAAC----------TGA-TTTCT---CTC----C--A----CTCTCTGCAGGGCCTCAAGATGCGCAAGCAGCGCTAGCACGGGATGATCTGGAGAAGCCTGGG
droPer2	scaffold_1:2098970-2099136 +		TGCGCCGCAACAGTCTGACGGACAAGACC---AAGAAGGGATTCCTCATGGTGGGTCTTCATCTGGGAT---CTCTC----------TTCTCTTCGAAGGA--GCCTTCAAC----------TGA-TTTCT---CTC----C--A----CTCTCTGCAGGGCCTCAAGATGCGCAAGCAGCGCAGCACGGGATGATCTGGAGAAGCCTGG
droWil2	scf2_1100000004521:12222131-12222298 +		TGCGAGCGAAATAGTCTAACAGACAAATCC---AAAAAAGGGTTTCCTAATGGTAAAATAATTATCA---------C----CAAAATCATTAA-----------------GCATTCAGAATTGAAATGTTAAACTCTT---CTT----T--T----CTATTTTAAAGGGCTTAAAATGCGCAAACAACGCAGCACAGGGGATCTGGAGAAACGTGG
droVir3	scaffold_12723:4022517-4022673 -		TTCGACGCAACAGTCTCACGGAAAGACG---AAGAAGGGATTTCTAATGGTAAGCAGCCGAA---T---CCCT----------AGCACGTTCCAAGA--GCTTTGTAA----------TGG-GTATT---C-------T---C-CTTCGGCAGGGTCTGAAAATGCGTAAACAACGCAGCACTGGGATCTGGAGAAACGTGG
droMoj3	scaffold_6500:14700945-14701109 +		TGCGCCGCAACAGCCTCACGGACAAGACG---AAGAAGGGCTTTCTGATGGTAATGTCAACAGCTG---C---CTAAT----------AAGCTCGCACATTATA--TTGATTG----------TTT-TTTG---TTT----T--T---CATTTTCGCAGGGGCTGAAAATGCGTAAGCAGCGCAGCACTGGAGATTTGGAAAACGTGG
droGri2	scaffold_15252:3636787-3636945 +		CGCGGCGCAACAGTCTCACGGACAAGACG---AAGAAGGGATTTCTGATGGTAAGCAACGCGAA---T---AT--T----TCAAAACAT----------TTTGCAAACATTATTT------GAA-CGT-----T---C-ATCCTGGCAGGGTCTGAAAATGCGTAAGCAGCGCAGCACTGGTGATTTGGAGAAACGTGG

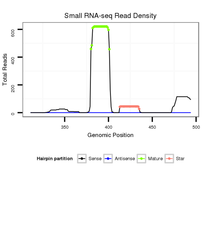
Generated: 09/08/2015 at 07:04 PM

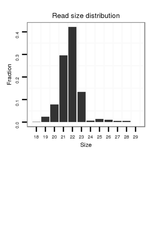
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

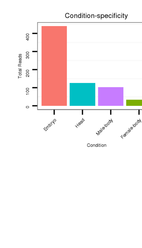
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_4035	scaffold_2263:361-444 +	confident	Canonical miRNA	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

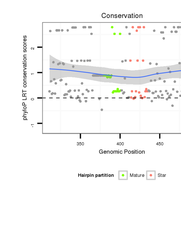
Legend: mature star mismatch in arm/star mismatch in loop

Predicted structure









Show Alternate Folds

FlyBase annotation

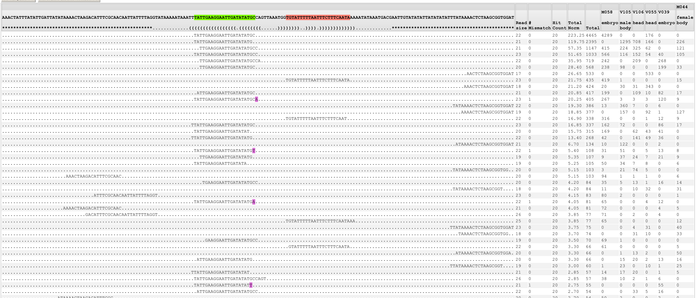
dsRNA:[Dsur2.0]dsRNA(CJT3600-RA)

No flyanatble elements found

mature	star
1. scaffold_2826:992-1013 - 2. scaffold_3108:1361-1382 - 3. scaffold_3159:666-687 - 4. scaffold_3159:1000-1021 - 5. scaffold_3164:897-918 - 6. scaffold_3368:964-985 - 7. scaffold_3434:1000-1021 - 8. scaffold_3434:824-846 - 9. scaffold_3450:1062-1083 - 10. scaffold_3453:980-1001 - 11. scaffold_3474:633-674 - 12. scaffold_3474:1000-1021 - 13. scaffold_4336:700-721 - 14. scaffold_4845:777-798 - 15. scaffold_4894:1000-1021 - 16. scaffold_4904:1061-1082 - 17. scaffold_5016:639-680 - 18. scaffold_5185:989-1010 - 19. scaffold_5352:8525-8545 - 20. scaffold_5352:8525-8545_MM4 21. dan_4035 scaffold_2263:286-405 + 22. scaffold_2264:233-254 - 23. scaffold_2847:58-81 + 24. scaffold_2847:58-81 + 25. scaffold_2624:589-610 - 26. scaffold_2837:586-607 + 27. scaffold_3261:240-261 + 28. scaffold_3261:240-261 + 29. scaffold_3402:341-362 + 30. scaffold_3404:584-605 + 31. scaffold_3432:586-607 + 32. scaffold_3496:2-23 + 33. scaffold_3496:2-23 + 34. scaffold_4374:586-607 + 35. scaffold_4374:616-638 + 36. scaffold_4374:616-638 + 37. scaffold_4569:91-112 + 38. scaffold_5100:369-390 + 39. scaffold_5124:577-598 + 40. scaffold_5183:6424-6445 + 41. scaffold_5183:6424-6445 + 42. scaffold_5094:1502-1523 + 43. scaffold_3402:385-406 +	1. dan_4035 scaffold_2263:410-431 + 2. scaffold_2264:306-368 + 3. scaffold_2387:385-425 + 4. scaffold_2624:632-653 + 5. scaffold_2624:632-644 + 6. scaffold_2837:639-661 + 7. scaffold_3402:384-405 + 8. scaffold_3405:609-631 + 9. scaffold_3403:276-306 + 10. scaffold_3403:248-269 + 11. scaffold_3450:613-639 + 12. scaffold_3474:613-639 + 13. scaffold_3496:25-51 + 14. scaffold_4045:677-679 + 15. scaffold_4045:677-679 + 16. scaffold_5035:631-651 + 17. scaffold_4879:274-306 + 18. scaffold_4569:961-1004 + 19. scaffold_5100:402-424 + 20. scaffold_5352:8525-8579 + 21. scaffold_5124:618-632 +

Sense Strand Reads

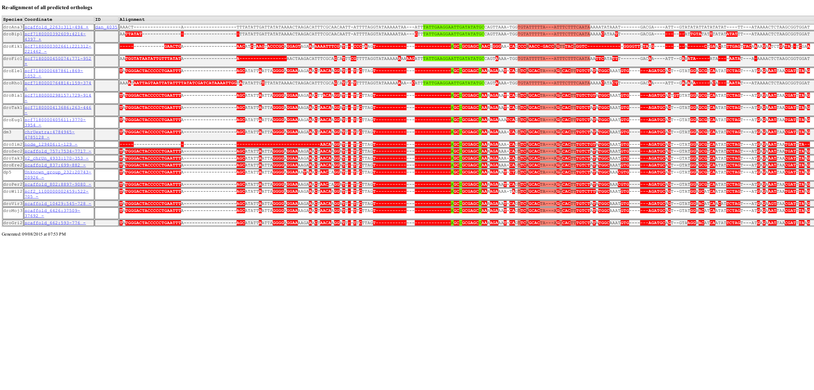
hide 3p reads | show mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

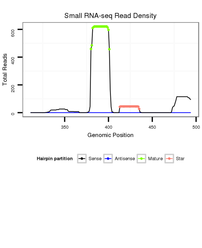


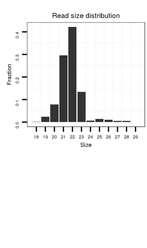
Generated 09/08/2015 at 07:53 PM

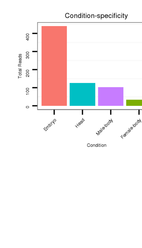
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_4035	scaffold_2263:361-444 +	confident	Canonical miRNA	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

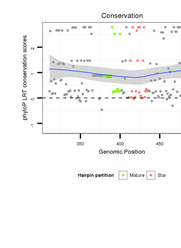
Legend: mature star mismatch in arm/star mismatch in loop

Predicted structure









Show Alternate Folds

FlyBase annotation

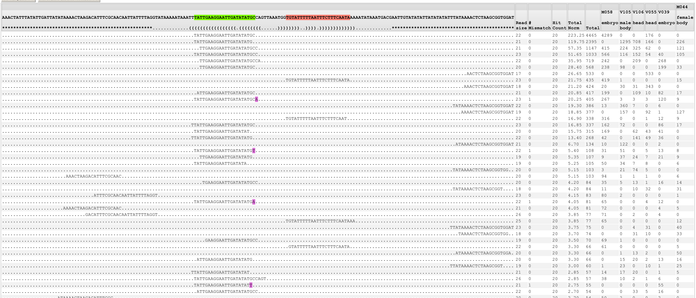
dsRNA:[Dsur2.0]dsRNA(CJT3600-RA)

No flyanatble elements found

mature	star
1. scaffold_2826:992-1013 - 2. scaffold_3108:1361-1382 - 3. scaffold_3159:666-687 - 4. scaffold_3159:1000-1021 - 5. scaffold_3164:897-918 - 6. scaffold_3368:964-985 - 7. scaffold_3434:1000-1021 - 8. scaffold_3434:824-846 - 9. scaffold_3450:1062-1083 - 10. scaffold_3453:980-1001 - 11. scaffold_3474:633-674 - 12. scaffold_3474:1000-1021 - 13. scaffold_4336:700-721 - 14. scaffold_4845:777-798 - 15. scaffold_4894:1000-1021 - 16. scaffold_4904:1061-1082 - 17. scaffold_5016:639-680 - 18. scaffold_5185:989-1010 - 19. scaffold_5352:8525-8545 - 20. scaffold_5352:8525-8545_MM4 21. dan_4035 scaffold_2263:286-405 + 22. scaffold_2264:233-254 - 23. scaffold_2847:58-81 + 24. scaffold_2847:58-81 + 25. scaffold_2624:589-610 - 26. scaffold_2837:586-607 + 27. scaffold_3261:240-261 + 28. scaffold_3261:240-261 + 29. scaffold_3402:341-362 + 30. scaffold_3404:584-605 + 31. scaffold_3432:586-607 + 32. scaffold_3496:2-23 + 33. scaffold_3496:2-23 + 34. scaffold_4374:586-607 + 35. scaffold_4374:616-638 + 36. scaffold_4374:616-638 + 37. scaffold_4569:91-112 + 38. scaffold_5100:369-390 + 39. scaffold_5124:577-598 + 40. scaffold_5183:6424-6445 + 41. scaffold_5183:6424-6445 + 42. scaffold_5094:1502-1523 + 43. scaffold_3402:385-406 +	1. dan_4035 scaffold_2263:410-431 + 2. scaffold_2264:306-368 + 3. scaffold_2387:385-425 + 4. scaffold_2624:632-653 + 5. scaffold_2624:632-644 + 6. scaffold_2837:639-661 + 7. scaffold_3402:384-405 + 8. scaffold_3405:609-631 + 9. scaffold_3403:276-306 + 10. scaffold_3403:248-269 + 11. scaffold_3450:613-639 + 12. scaffold_3474:613-639 + 13. scaffold_3496:25-51 + 14. scaffold_4045:677-679 + 15. scaffold_4045:677-679 + 16. scaffold_5035:631-651 + 17. scaffold_4879:274-306 + 18. scaffold_4569:961-1004 + 19. scaffold_5100:402-424 + 20. scaffold_5352:8525-8579 + 21. scaffold_5124:618-632 +

Sense Strand Reads

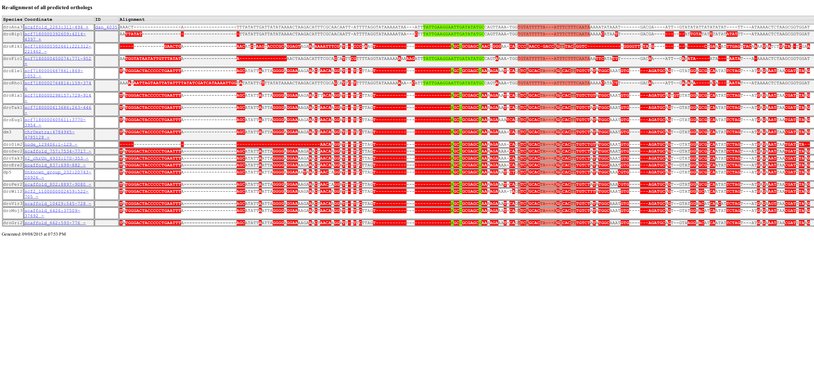
hide 3p reads | show mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs



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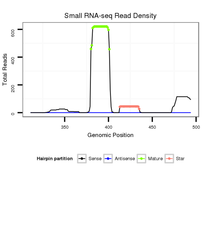
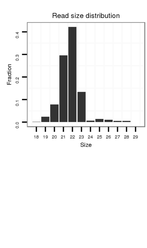
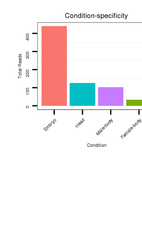
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_4035	scaffold_2263:361-444 +	confident	Canonical miRNA	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

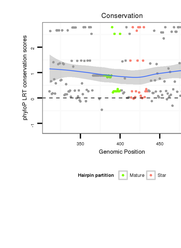
Legend: mature star mismatch in arm/star mismatch in loop

Predicted structure









Show Alternate Folds

FlyBase annotation

dsRNA:[Dsur2.0]dsRNA(CJT3600-RA)

No flyanatble elements found

mature	star
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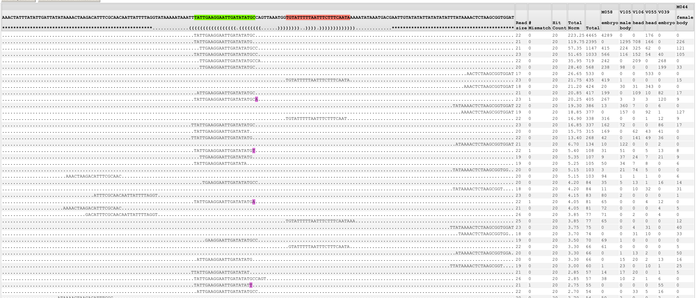
Sense Strand Reads

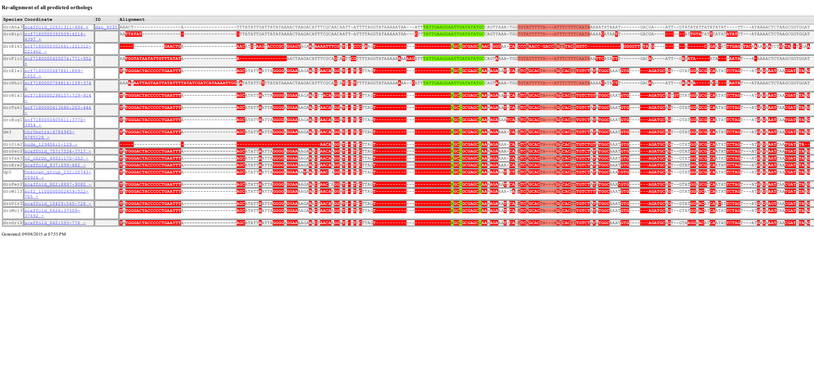
hide 3p reads | show mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

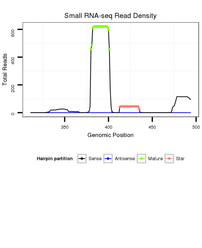


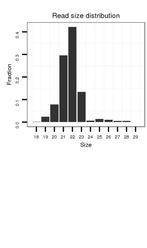
Generated 09/08/2015 at 07:53 PM

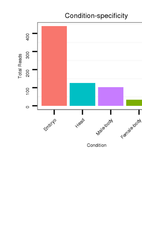
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_4035	scaffold_2263:361-444 +	confident	Canonical miRNA	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

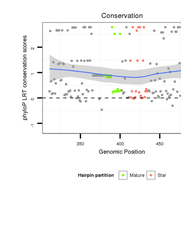
Legend: mature star mismatch in arm/star mismatch in loop

Predicted structure









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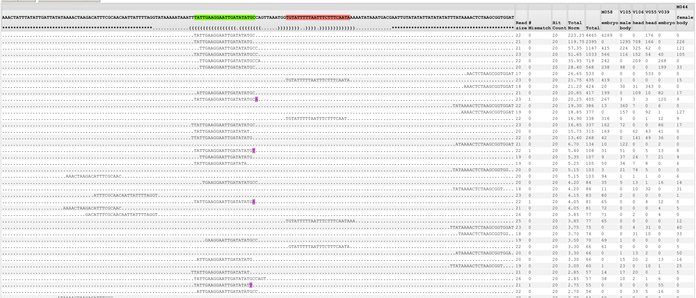
Sense Strand Reads

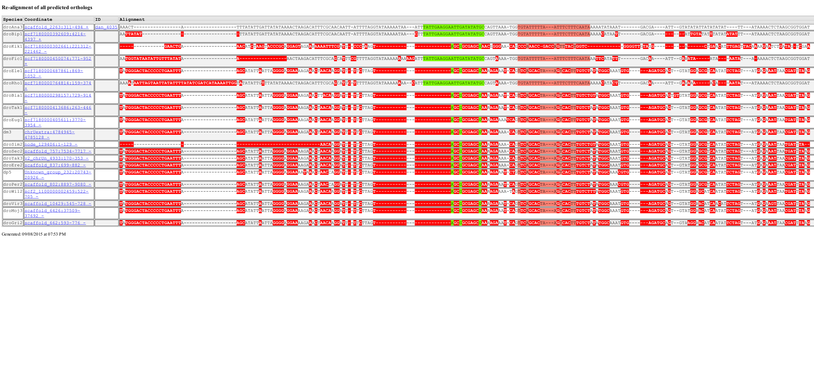
hide 3p reads | show mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs



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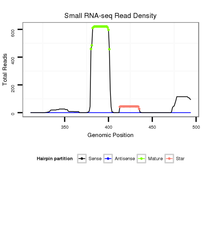

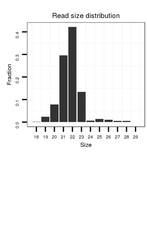

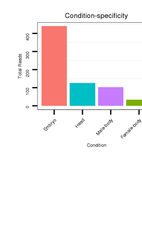

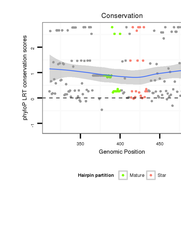

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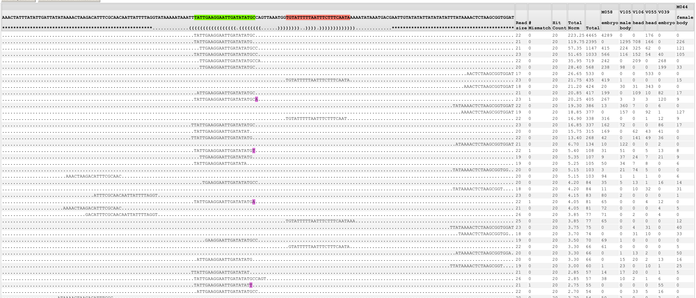
Sense Strand Reads

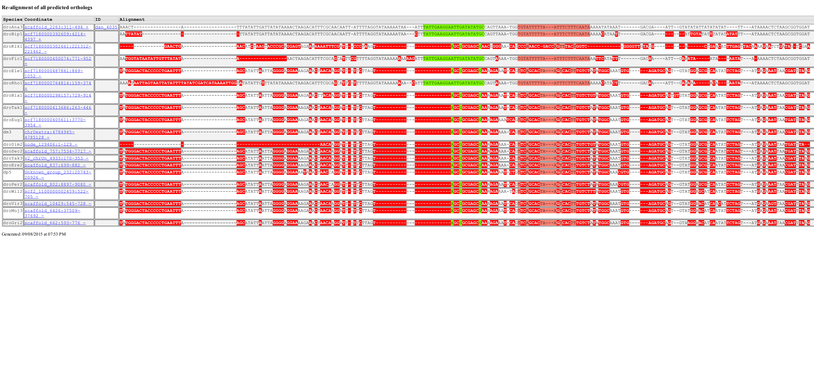
hide 3p reads | show mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs



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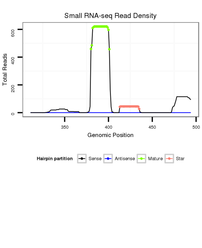

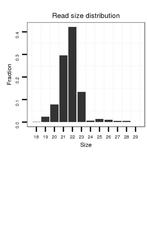

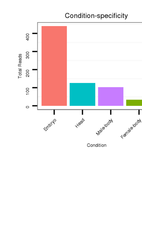

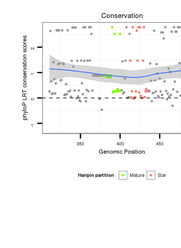

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Sense Strand Reads

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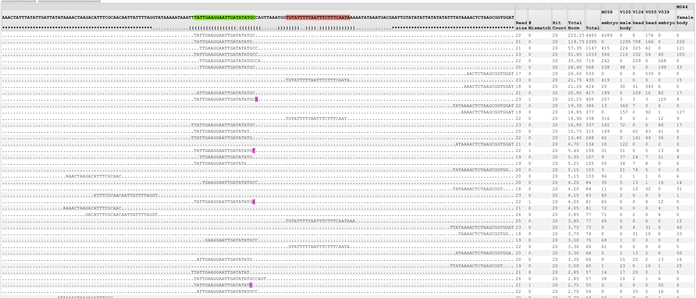

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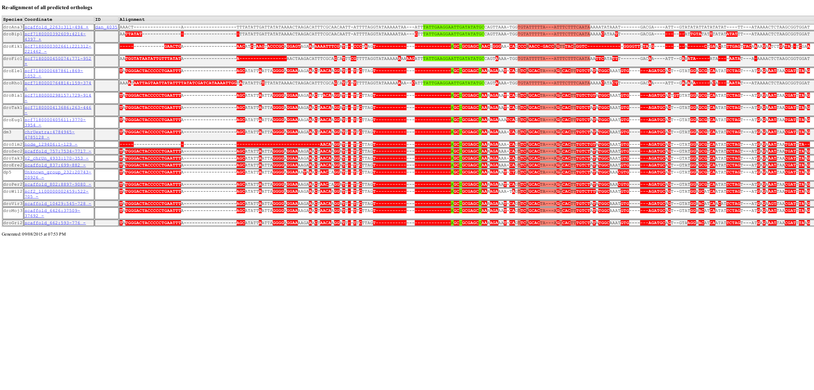
Re-alignment of all predicted orthologs

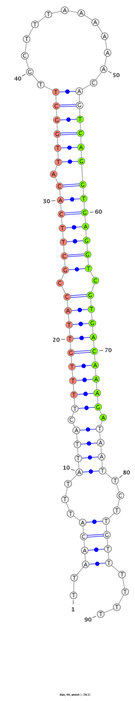


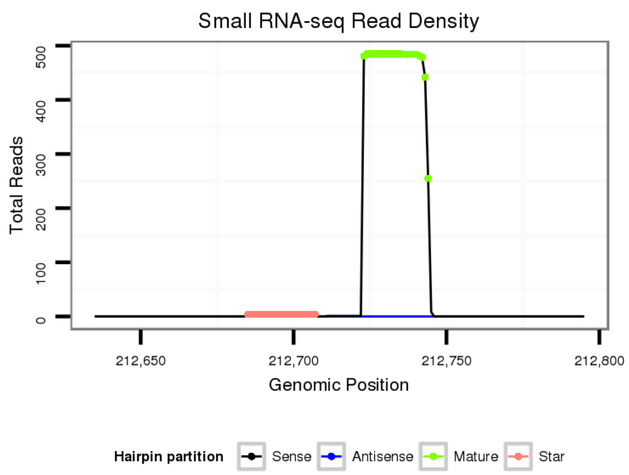
Generated 09/08/2015 at 07:53 PM

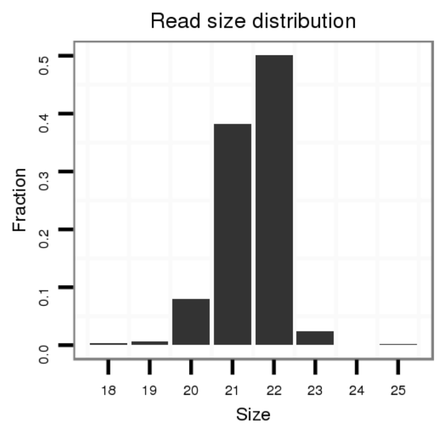
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_46	**scaffold_13335:212685-212745 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

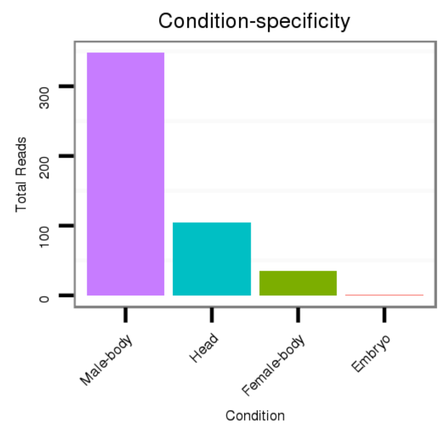
Legend: mature star mismatch in alignment mismatch in read

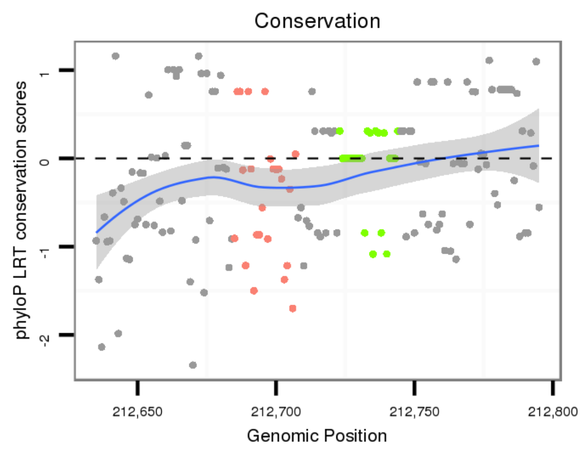
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AATAAAAAGTTAAATTCAAAATATGAAGACAGTTATTAACATTTATTACTTTTGTTACCGCTTCACATTGGCTTGCTTTAAAAAACAGTCAGGTGAGGTCGTGACAAAGATAATTCTTGTTTTTTCAACTCTTTAAACCAATAATTTTAAAGGTTGCCCTC	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V106 head	M044 female body	V055 head	V039 embryo
**********..((((...((((.(((((((((.(((((((.((((((.............)))))))))))))).)))))))).))))...)))))....**********											
.....TCAGGTGAGGTCGTGACAAAGA.....	22	0	1	245.00	245	179	46	14	6	0
.....TCAGGTGAGGTCGTGACAAAG.....	21	0	1	185.00	185	132	34	11	7	1
.....TCAGGTGAGGTCGTGACAAA.....	20	0	1	37.00	37	27	7	2	1	0
.....TCAGGTGAGGTCGTGACAAAGAA.....	23	1	1	15.00	15	11	1	1	2	0
.....TCAGGTGAGGTCGTGACAAAGAT.....	23	0	1	8.00	8	4	2	1	1	0
.....TCAGGTGAGGTCGTGACAAAGT.....	22	1	1	4.00	4	3	1	0	0	0
.....TTTGTTACCGCTTCACATTGGCT.....	23	0	1	4.00	4	1	0	3	0	0
.....TCAGGTGAGGTCGTGACAAAT.....	21	1	1	3.00	3	1	1	0	1	0
.....TCAGGTGAGGTCGTGACAA.....	19	0	1	3.00	3	3	0	0	0	0
.....TCAGGTGAGGTCGTGACAAAA.....	21	1	1	2.00	2	2	0	0	0	0
.....TCAGGTGAGGTCGTGACA.....	18	0	1	2.00	2	0	1	1	0	0
.....CAGGTGAGGTCGTGACAAAG.....	20	0	1	2.00	2	0	0	2	0	0
.....CAGGTGAGGTCGTGACAAAGA.....	21	0	1	2.00	2	1	0	1	0	0
.....TCAGGTGAGGTCGTGACAAT.....	20	1	1	1.00	1	1	0	0	0	0
.....TTTAAAAAACAGTCAGGTGAGGTCG.....	25	0	1	1.00	1	1	0	0	0	0
.....TCAGGTGAGGTCGTGACAAAGAAT.....	24	2	1	1.00	1	1	0	0	0	0
.....TCAGGTGAGGTCGTGACAAAC.....	21	1	1	1.00	1	0	1	0	0	0
.....TCAGGTGAGGTCGTGACAAAGAAC.....	24	2	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

TTATTTTTCAATTTAAGTTTTATACTTCTGTCAATAATTGTAAATAATGAAAACAATGGCGAAGTGTAACCGAACGAAATTTTTTGTCAGTCCACTCCAGCACTGTTTCTATTAAGAACAAAAAAGTTGAGAAATTTGGTTATTAAAATTTCCAACGGGAG	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V055 head	V039 embryo
**********..((((...((((.(((((((((.(((((((.((((((.............)))))))))))))).)))))))).))))...)))))....**********									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13335:212635-212795 +	dan_46	AATAAAAAGTTAAATTCAAAA-T----------ATGAAGACAGTTATTAA--CATTTATTACTTTTGTTACCGCTTC----------ACATTGGCTTGCTTTAAAAAACAGTCAGGTGAGGTCGTGACAAAGATAATTCTTGTTTTTTCAACTCTTTAAACCAATAATTTTAAAGG---------TTGCCCTC
droBip1	scf7180000395839:422358-422511 -		AACAAAAATTTTCAACCATAT-TTTTAAAAT----------TTTCTAATGCACTTGTAATCCTTGCTAGATTTCC----------ACATAACGTCATCATAGTAGACAAT-------ATCTTGGCC---ATATTTTTTATCTTACTCAATATTTAG------ACCTTAAAAGGTTTTGAAATATATCCTC
droKik1	scf7180000302610:1791641-1791705 +		AAAGAAAATTATT-------ACAATAAAAAATTATTAAAAAAATAAACCCCTCAAAAACACCCACAA--AA----------TC
droEle1	scf7180000491011:2115643-2115679 +		TTTAAATATTAT--------ATATTAATATAT----------TTCCAA--ATCC----------ATC
droRho1	scf7180000763611:399832-399870 +		TAAAGCGAGCTAAGTTTTAAA-C----------ATAAAGACAGTTTTTA--A
droTak1	scf7180000415394:1165740-1165744 +		CCAC----------C
droEug1	scf7180000409076:258666-258707 -		TGGTTT----------ATTAACT----------CTGCAGCCGAATATCAAATGAAATT----------ATA
droSim2	x:3953143-3953163 -		TTAAGT----------AAACAACTTTAAAAG----------
droSec2	scaffold_4:2466335-2466355 +		TTAAGT----------AAACAACTTTAAAAG----------
droEre2	scaffold_4820:6149490-6149575 +		ATTAAAAAAA----------CACCTGGGATATACAAATTACCGATACAATTTGCAA--GATTTATTTCTCTTAGTGTCGCTTT----------GCTGTTGTTTGTTTG----------
dp5	XL_group1a:3804489-3804492 +		CCCT----------
droPer2	scaffold_11:366359-366362 +		CCCT----------
droMoj3	scaffold_6328:2692240-2692274 -		TAATTT----------TGATTTTTCAAAATCAAAAACCGTTA--------A----------G

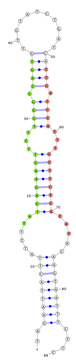
Generated: 09/08/2015 at 08:00 PM

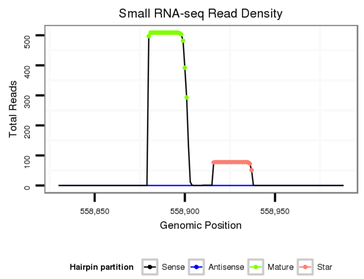
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

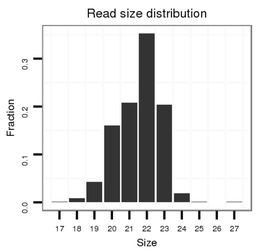
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_47	**scaffold_12903:558880-558938 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

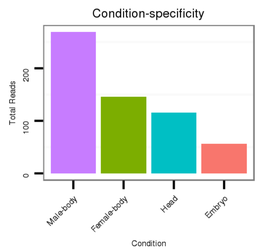
Legend: mature star mismatch in alignment mismatch in read

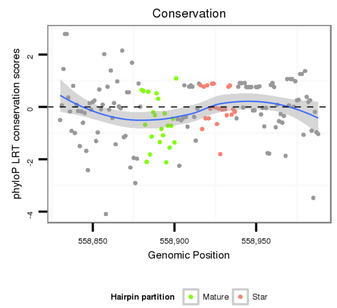
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTTTTTTTTTTTTTTTTCAATTTTATTTTCAGTGCCTAGAATTACTTATTTATGAGAAGTTCTTGGGCCAGTGTTGTATCTGATCATTGATCCATTTGCTTCTCACATACAAGTAATTTCTTCAGCCTCATTAAGTGAGATTTAATATTTAAAATTAAT							V105	M044 female	V106	M058	V055	V039
********************************..(((((((((.....(((((((...(((.(((((..........)))))).)))).)).....)))))))))....)))))))))....********************************	Read size	# Mismatch	Hit Count	Total Norm		Total	male body	body	head	embryo	head	embryo
..........TATGAGAAGTTCTTGGGCCAGT..	22	0	1	156.00	156	96	26	9	15	8	2	
..........TATGAGAAGTTCTTGGGCCAGTG..	23	0	1	119.00	119	66	32	11	3	7	0	
..........TATGAGAAGTTCTTGGGCCAG..	21	0	1	96.00	96	46	25	4	14	7	0	
..........TATGAGAAGTTCTTGGGCCA..	20	0	1	87.00	87	33	11	29	5	9	0	
..........TTGATCCATTTGCTTCTCACAT..	22	0	1	49.00	49	4	25	6	11	3	0	
..........TTGATCCATTTGCTTCTCACA..	21	0	1	21.00	21	2	6	6	2	4	1	
..........TATGAGAAGTTCTTGGGCCAGTT.	23	1	1	21.00	21	14	0	4	1	2	0	
..........TATGAGAAGTTCTTGGGCC..	19	0	1	21.00	21	10	3	6	1	1	0	
..........TATGAGAAGTTCTTGGGCCT..	20	1	1	13.00	13	3	1	9	0	0	0	
..........TATGAGAAGTTCTTGGGCCAGTGT.	24	0	1	11.00	11	6	4	1	0	0	0	
..........TATGAGAAGTTCTTGGGCT..	19	1	1	6.00	6	6	0	0	0	0	0	
..........TTGATCCATTTGCTTCTCACT..	21	1	1	5.00	5	0	4	1	0	0	0	
..........TATGAGAAGTTCTTGGGC..	18	0	1	5.00	5	1	0	2	1	1	0	
..........TTGATCCATTTGCTTCTCAC..	20	0	1	4.00	4	2	1	0	1	0	0	
..........TATGAGAAGTTCTTGGGCCAGTA.	22	1	1	4.00	4	2	0	1	1	0	0	
..........ATGAGAAGTTCTTGGGCCAGT..	21	0	1	4.00	4	0	4	0	0	0	0	
..........TATGAGAAGTTCTTGGGCCAGTGA.	24	1	1	3.00	3	2	1	0	0	0	0	
..........ATGAGAAGTTCTTGGGCCAG..	20	0	1	3.00	3	0	3	0	0	0	0	
..........ATGAGAAGTTCTTGGGCCA..	19	0	1	3.00	3	0	3	0	0	0	0	
..........TATGAGAAGTTCTTGGGCCAGA.	22	1	1	3.00	3	0	0	0	3	0	0	
..........TTGATCCATTTGCTTCTCACATA.	23	1	1	3.00	3	0	3	0	0	0	0	
..........ATGAGAAGTTCTTGGGCCAGTG..	22	0	1	2.00	2	0	2	0	0	0	0	
..........TATGAGAAGTTCTTGGGCCAGTAAA..	25	3	1	2.00	2	0	0	0	2	0	0	
..........TATGAGAAGTTCTTGGGCCAA.	21	1	1	2.00	2	0	0	1	1	0	0	
..........TATGAGAAGTTCTTGGGCCAGTGAA..	25	2	1	2.00	2	1	0	0	0	0	1	
..........TATGAGAAGTTCTTGGGCCAGTGTT.	24	1	1	2.00	2	2	0	0	0	0	0	
..........TATGAGAAGTTCTTGGGCCAGTTA..	24	2	1	1.00	1	1	0	0	0	0	0	
..........TATGAGAAGTTCTTGGGCCAGTGTTT..	25	0	1	1.00	1	1	0	0	0	0	0	
..........TTGATCCATTTGCTTCTCACG.	21	1	1	1.00	1	1	0	0	0	0	0	
..........TATGAGAAGTTCTTGGGCCAGA..	22	1	1	1.00	1	0	1	0	0	0	0	
..........TATGAGAAGTTCTTGGGCCAGTGTTAAA..	27	3	1	1.00	1	1	0	0	0	0	0	
..........TTGATCCATTTGCTTCTCACAT.	22	1	1	1.00	1	0	0	0	1	0	0	
..........TGATCATTGATCCATTTGCTTCTCACA.	27	0	1	1.00	1	1	0	0	0	0	0	
..........TATGAGAAGTTCTTGGGCCAGTGTTT.	26	1	1	1.00	1	1	0	0	0	0	0	
..........TATGAGAAGTTCTTGGGCCAGTTA..	24	2	1	1.00	1	1	0	0	0	0	0	
..........TTGATCCATTTGCTTCTCAT.	20	1	1	1.00	1	0	0	1	0	0	0	
..........TATGAGAAGTTCTTGGGCA..	19	1	1	1.00	1	0	0	1	0	0	0	
..........TATGAGAAGTTCTTGGGTT..	19	2	3	0.67	2	1	1	0	0	0	0	
..........TATGAGAAGTTCTTGGGA..	18	1	2	0.50	1	0	0	0	0	0	1	
..........TATGAGAAGTTCTTGGGTA..	19	2	3	0.33	1	1	0	0	0	0	0	

Anti-sense strand reads

AAAAAAAAAAAAAAAAAGTTAAAATAAAAGTCACGGATCTTAATGAATAAAATACTCTTCAAGAACCCGGTCACAACATAGACTAGTAACTAGGTAAACGAAGAGTGTATGTTCATTAAAGAAGTCGGAGTAATTCACTCTAAATTATAAATTTTAATTA							V039	V055	M058	M044 female	V106
********************************..(((((((((.....(((((((...(((.(((((..........)))))).)))).)).....)))))))))....)))))))))....********************************	Read size	# Mismatch	Hit Count	Total Norm	Total		embryo	head	embryo	body	head
..........TATGAGAAGTTCTTGGGCCAGTGAT..	24	1	1	2.00	2	2	0	0	0	0	0	
..........TATGAGAAGTTCTTGGGCCAGTGTTTT..	26	2	3	1.33	4	3	0	1	0	0	0	

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:558830-558988 +	dan_47	TTTTTTTTTTTTTTTTTCAATTTTATTTTCAGTGCCTAGAATTACTTATTTATGAGAAGTTCTTGGGCCAGTGTTGTATCTGATCATTGATCCATTTGCTTCTCACATACAAGTAATTTCTTCAGCCTCATTAAGTGAGATTTAATATTTAAAATTAAT
droBip1	scf7180000395912:27747-27883 +		TTTTTTTATTTATAT----------TGTTTTCAGTGT-------GA-TTTAAATC-A--------TCAA----------A-T-----------GTAAA---T----------------------T-TGC---ATGAGAAGTTCTTGGGCCAGT-GCG---------------------------A-----------------AAGTAATTTCTTGA-GAATCAAATTCCGTGAAAAATGTGT-C-TA----------------------A--C-GAT-TT----------TG-------------------GAAAAC
droKik1	scf7180000302577:1299837-1299993 -		TTTTTTTGTTTTTT----------TT-------ACT---------TT-----TTTTT---------TAT---------TACCTAAACGTTATTTTT-GT----------------------A---ATTTACTTTAAGT---------TA---------------------------A---T
droFic1	scf7180000453839:1599715-1599782 +		TTTTTTAGTGCTTT----------GT-------TTTTATGTTTTAATTAATTTATT-A---------GTTA----------A-T-----------GTAAA---AA----------------------T---TATTACAATAAGT---------GT---------------------------A---T
droEle1	scf7180000490999:100297-100348 +		TGTTTTTCACTTTT----------TT-------TTT-CA-T----------AATTT----------G-----------T----------------------T---A-TT----------------------T-----TAT---------------------------A---T
droRho1	scf7180000780108:361776-361932 -		TTTTTTATTTTAGC----------TT-------GTT-AG-T----------CATTAG-T----------A-----------T----------------------T---TTAAGTTAAA---AAAGATTTTTGAATTCGTATGTACAAAAATCCTTCT---------------------------ATCTATTTGGAACT--TCCGAAATCGGACGATTATATCATACAGCCAAAATTTAATCG---------------------------A-----------A-AGAA-TTAATA-C-GAAAA---------TATA
droBia1	scf7180000302422:2714886-2714989 +		GATTTTTTTTTCGCTTCGAATT-------TGGTTTTATTT-T----------TTATTTATTT----------TTA----------A-T-----------GTTAA---T----------------------T-GCGT---------------------------A---T
droTak1	scf7180000415261:299663-299784 +		TTTTTTTACTTTAATAAAACGTGTTTTTTG----------TTT-------TT---TTTATTT----------AC-A----------A-T-----------GTCTA---T----------------------T---AGTT---------TTTTGTGGGGCACTTAGTATCTGATTGACTTT---------CA---------GGGTTGTCCATATCATTTCATTGCAAAT---------------------------A---T
droEug1	scf7180000409466:818269-818426 -		CTTTTTAATTTTT----------TT-------GGTA---------T----------GAATTCTAACTTGAATTTATAAATA----------A-T-----------GTCTT---T----------------------T---TTAAATATGGAAAA---TATGT---CAGAAGAATTTTTTGGATGGCAATTAACTATTTG---------------------------A-----------ATATTAATAAATATTTTAATAA-CAGAATTTTAATATT-A----------AATT
dm3	chr2R:2053567-2053638 +		TTTTTCTTTTTAT----------AC-------AA---------A----------TT-----TTT----------T----------A-T-----------GGGAAAAATGTTTTTATCTTCTAAGCTTCATTATTTACTATTT---------TT---------------------------A---T
droSim2	2r:16471713-16471797 +		TTTTTTTTTCTTT----------TT-------TTT----------T----------TATAGT---AATCTGTTACAATCGCTTAGTTTTTGTAT----------TA-ATAAA-TTA----------A-T-----------TCTAA---T----------------------T---------------------------A---T
droSec2	scaffold_6:2408150-2408291 -		TTTTTATTTTTTT----------TT-------TAATTATTTATT----------TTA----------A-T-----------GCTAA---TGT----------------------TTTAT---------------------------GCGGGCTTGGTTCGATCCATAACCGTATATAGAACA---------------------------A---T
droYak3	2R:7529491-7529654 +		GTTTTTTATTTATT----------TC-------ATT----------T----------CATTTTCTTT----------A-T-----------GTAA---T----------------------T---TTACAAATCAGAA---------AATTA-T-CGTTAGGCAATTTTTTCTCGTCACGTTCA---------TA---------AAATAGATATAGATAA---------------------------A---T
droEre2	scaffold_4845:18253586-18253675 -		TTTTTTTGTTTTTT----------TC-------CTT----------T----------AATTTTTTTTCTC----------A-T-----------AGGA---TGC----------------------T---ATTTTTTCGGATTGGA---------CA---------------------------A---T
dp5	4:1124312-1124457 +		CGTTTTTTTGTTTT----------TC-------CAT----------T----------TTTTTTGTTG----------A-T-----------GTAAATAATA---T----------------------T---------------------------A---T
droPer2	scaffold_2:1281160-1289205 +		CGTTTTTTTGTTTT----------TC-------CAT----------T----------TTTTTTGTTG----------A-T-----------GTAAATAATA---T----------------------T---------------------------A---T
droWil2	scf2_1100000004513:4631877-4631924 -		ATTTTTTGTTTTTT----------TC-------AGT----------T----------TTTTT----------A-T-----------G---GTAAATAATA---T----------------------T---------------------------A---T
droVir3	scaffold_12875:4798418-4798492 +		TTTTTTTTTATTT----------TC-------TCA----------A----------TT-----TTT----------A-T-----------AAAT---------------------AATTAGA---------------------------ATTCAT---GTTTATAAAGTT---------TT---------------------------A---T
droMoj3	scaffold_6540:28993729-28993787 +		TTTTTTGTTTTTTT----------GT-------CAA----------TT---------TTATTTT----------GA-T-----------A---AATAA---T----------------------A---------------------------A---T
droGri2	scaffold_15245:189382-189446 -		GTTTTTTTTTAATTT----------TGGTGTTTTATT----------TT-TATTATTTT----------TTA----------A-T-----------GTTTAAATGCTTTTATAGTTA---------TA---------------------------A---T

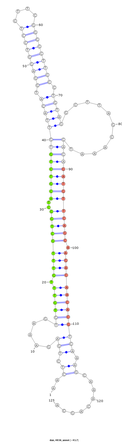
Generated: 09/08/2015 at 08:00 PM

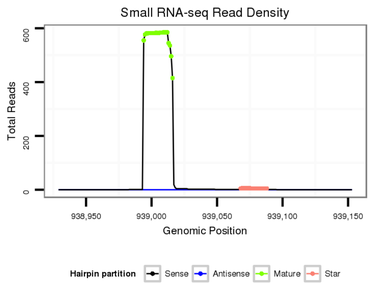
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.mfe	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	0
rescue.candidate	0

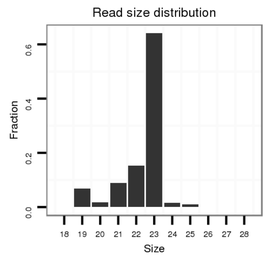
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_4036	**scaffold_13340:938979-939103 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

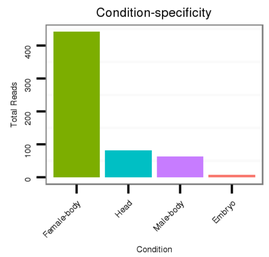
Legend: mature star mismatch in alignment mismatch in read

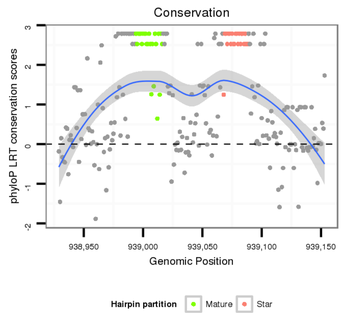
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dana/GF17529-in]

No Repeatable elements found

Sense Strand Reads

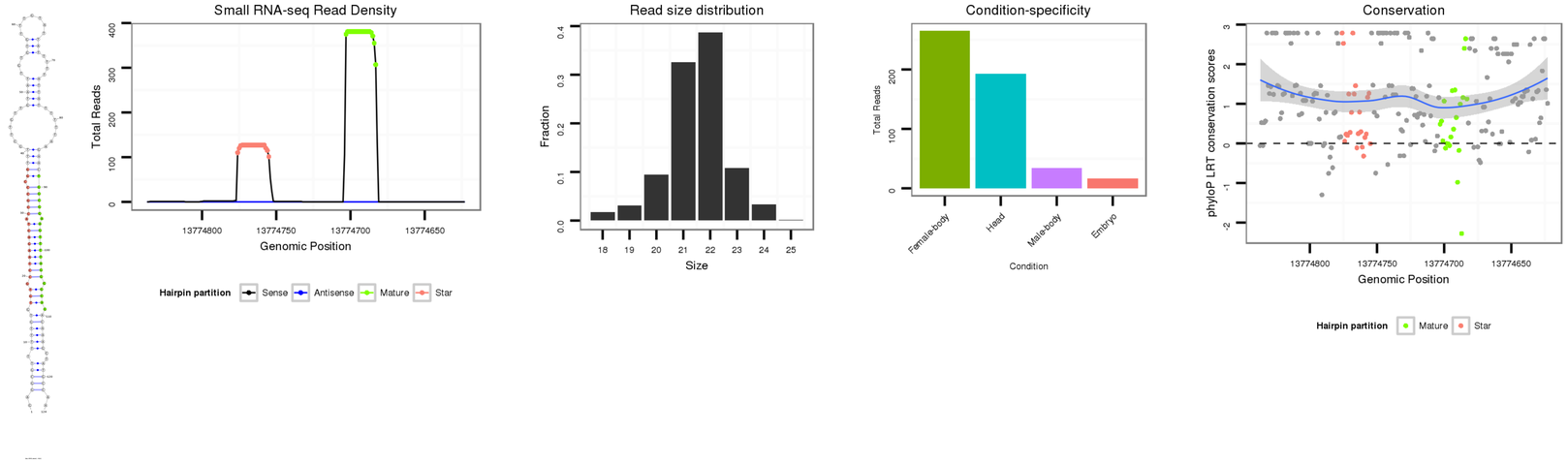
hide 3p reads | show mid mismatch reads

ACACCCAGGATCTGGATCTGGATCTGGAACTGAATCTGGAGCAGCATGAGAACTCTGAGAAAGTGTGTTTGTTTGCTGGCTACGTCTGTGTTACATGGAGGTCCTCTTCGGGGCTTCCCTGTAGGCTTAGCAAATCACAGATGTTCAGCAAGACAACACGTCAAAGCAAACAGCAGGACAACTACTACATCAAAGTGATTCCAATTCAAACAATGGACAAATAAA	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V106 head	V105 male body	V055 head	M058 embryo	V039 embryo
..(.(.(((.....(((((((.(((((((((..(((((((((((((.(((((((((....)))))))))..)))))).....)))))))))))))).))))))).))).)).....)))))))))))))

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_4040	**scaffold_12916:13774673-13774787 -**	**confident**	**Canonical miRNA**	**3pUTR**	[View on UCSC Genome Browser [Cornell Mirror]]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

utr3 [utr3_minus_966]; intron [Dana\GF14149-in]; CDS [Dana\GF14149-cds]

Repeatable elements

Name	Class	Family	Strand
AT_rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TCCTTTTCTTGTTAACAGCTTTTGCTTTTTTTTTTATGTACCTCAGAGGCGTTTTTGTGTGCCTAAGACTACCGCCCGGTTTGCTTGTTGTAATTGTGTGTTTGTATTATTTTTATTATTTTTTAAGAACTGGCGGAAGTTTTAGGGGCAGACAAAGCTATGCCAACAGATTCAACTTTTCAAAATTGCCAACTTGTGAACATATTATAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V106 head	V105 male body	V055 head	M058 embryo	V039 embryo
..(((((.(((((((.(((.(((((((((((.((((((.(((((.....(((((...(((.....)))....)))))).....)))))))))).)))))))).)))))))..)))))..**********												
.....TGGCGGAAGTTTTAGGGGCAG.....	21	0	1	127.00	127	57	57	5	7	1	0
.....TGGCGGAAGTTTTAGGGGCAGA.....	22	0	1	100.00	100	28	44	12	10	5	1
.....CTGGCGGAAGTTTTAGGGGCAG.....	22	0	1	45.00	45	24	13	2	4	2	0
.....TGTGCCTAAGACTACCGCCGG.....	22	0	1	42.00	42	41	0	0	0	1	0
.....TGGCGGAAGTTTTAGGGGCA.....	20	0	1	30.00	30	6	15	5	4	0	0
.....CTGGCGGAAGTTTTAGGGGCAGA.....	23	0	1	30.00	30	11	10	5	2	2	0
.....TGTGCCTAAGACTACCGCCCGGTT.....	24	0	1	17.00	17	16	0	0	0	1	0
.....TGTGCCTAAGACTACCGCCCG.....	21	0	1	13.00	13	11	2	0	0	0	0
.....CTGGCGGAAGTTTTAGGGGC.....	20	0	1	8.00	8	2	6	0	0	0	0
.....TGGCGGAAGTTTTAGGGGC.....	19	0	1	7.00	7	2	3	1	1	0	0
.....TGTGCCTAAGACTACCGCC.....	19	0	1	7.00	7	7	0	0	0	0	0
.....TGGCGGAAGTTTTAGGGGCAGAT.....	23	1	1	7.00	7	2	3	1	1	0	0
.....TGGCGGAAGTTTTAGGGG.....	18	0	1	6.00	6	4	2	0	0	0	0
.....GTGCCTAAGACTACCGCCCGGT.....	22	0	1	5.00	5	5	0	0	0	0	0
.....GTGCCTAAGACTACCGCCCGG.....	21	0	1	4.00	4	4	0	0	0	0	0
.....TGTGCCTAAGACTACCGCCC.....	20	0	1	4.00	4	4	0	0	0	0	0
.....CTGGCGGAAGTTTTAGGGGCAT.....	23	1	1	4.00	4	1	0	1	2	0	0
.....TGCTTGTTGTAATTGTGTGT.....	20	0	1	1.00	1	0	0	0	1	0	0
.....CTGGCGGAAGTTTTAGG.....	18	1	1	1.00	1	1	0	0	0	0	0
.....TGTGCCTAAGACTACCGCCCGGTTT.....	25	0	1	1.00	1	1	0	0	0	0	0
..CTTTTCTTGTTAACAGCTTTTGCT.....	24	0	1	1.00	1	0	0	0	0	1	0
.....GTACCTCAGAGGCGTTTTTTGTG.....	23	0	1	1.00	1	0	1	0	0	0	0
.....GTGCCTAAGACTACCGCCCG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GTGCCTAAGACTACCGCCCGGTT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GGCGGAAGTTTTAGGGGC.....	18	0	1	1.00	1	1	0	0	0	0	0
.....GCGGAAGTTTTAGGGGCAGATTT.....	23	3	1	1.00	1	1	0	0	0	0	0
.....TGTGTGCCTAAGACTACCGCCC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TGTGCCTAAGACTACCGCA.....	19	1	1	1.00	1	1	0	0	0	0	0
.....CTGGCGGAAGTTTTAGGGGCT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TGGCGGAAGTTTTAGGGGCAGTAT.....	24	3	1	1.00	1	0	0	1	0	0	0
.....GCCTAAGACTACCGCCCGGTT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CTGGCGGAAGTTTTAGGGGCATT.....	23	2	1	1.00	1	0	1	0	0	0	0
.....TGGCGGAAGTTTTAGGGGCAGATTT.....	25	3	1	1.00	1	0	1	0	0	0	0
.....CTGGCGGAAGTTTTAGGGGCAGTA.....	24	2	1	1.00	1	0	0	1	0	0	0
.....TGTGCCTAAGACTACCGCCCGGTA.....	24	1	1	1.00	1	0	0	0	1	0	0
.....CTGGCGGAAGTTTTAGGGGCAGTTT.....	24	3	4	0.50	2	0	2	0	0	0	0
.....CTGGCGGAAGTTTTAGGGGCAGTTT.....	25	3	3	0.33	1	0	1	0	0	0	0

Anti-sense strand reads

AGGAAAAGAACAATTGTCGAAAACGAAAAAAAAAAATACATGGAGTCTCCGCAAAAAACACACACGGATTCTGATGGCGGGCCAAACGAACAACATTAACACACAAACATAATAAAAATAATAAAAAATTCTTGACCGCCTTCAAAATCCCCGTCTGTTTCGATACGGTTGTCTAAGTTGAAAAAGTTTTAACGGTTGAACACTTGTATAATATG	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head	M058 embryo	M044 female body	V105 male body
..(((((.(((((((.(((.(((((((((((.((((((.(((((.....(((((...(((.....)))....)))))).....)))))))))).)))))))).)))))))..)))))..**********									
.....AAAACGAAAAAAAAAAATA.....	19	0	3	0.33	1	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12916:13774623-13774837 -	dan_4040	TCCTTT-T--CTTGTTAACAGCTTT-TGCTTTTT--TTTTTTATGTACCTCAGAGG----------CGTTTTTGTGTGTGCCTAAGACTAC-CG-CCCG-----GTTTGCTTGTTGTAA-TTGTGTGTTTGTA--T--TA---TTTTTATTATTT----------TTTAAGAACTGGC-GGAAGTTT-TAGGGGCAGACAAAGCTATGCCA-ACAGATT---C----------AACT--TTTTCAAAATTGCCAACTTGT----------G-AACAT---ATTATAC
droBip1	scf7180000396535:738649-738846 -		TGTTTT-T--CTTGTTAACAGCTTT-TGCTTTTTTTTG---T----ACCTCAGAGG----------CC-CTTTGTTGTGCCCAAGACTACCTC-CCCG-----ATTTGCTTGTTGTGA-TTGTGTGTTTGTA--T--TA---TT-TTTATTTTTTTTTC----------TTTAAGGACGGC-GC-CAGTTT-TAAGCCAGACAAA--------T---GATT---C----------AACT--TTTTCAAAATTGCCAATTTAT----------G-AACAT---ATAC
droKik1	scf7180000302677:189880-190095 +		TCCTTT-T--CTTGTTAAGTGCTTT-TGCTTATT-TTA----T----ACCTCATTGCG----------CCG-CTTTGTTGTGCCTAAGATCTCTGCCGTTGCCTTGATTATGTCA-TTGTGTGTTTGTA--T--TA---TT-TTTAGTTTT----------TTTAAGGACGAAC-GATAAGT-TAGCTGCCAGGCAAAGCCAAAGCCA-AAAGATT---C----------AACG--TTTTCGATTATTGCCAATTAATT----------G-AACATATATTCTATAC
droFic1	scf7180000454144:360267-360471 -		ACCTTT-T--CTTGTTAACAGCTTT-TGCTTTTTTTTT---T----ACCTCAGTGG----------C--TTTTTGCCTGCGCCAAGAGTCGTCGATCGCGGGGT-TTTGATTGTTGTGA-TTGTGTGTTTGTA--T--TATA---TATTA---TT-TTTATTAT---------TTTAAGGACGATGCGAATGGTGTTGTCGGGGCAGCCAAAGCGATGGCA-AAAGATT---C----------AACG--TTTTCAAAATTGCCAATTAAT----------G-AACAT---ATAC
droEle1	scf7180000491186:2985981-2986183 -		ACCTTTGT--CTTGTTAACAGCTTT-TGCTTTTT-TTT---T----ACCTCAGTGG----------T--GGTTGTGCCTGCGCCAAGAGCGTCGATCGCGGGGT-TTTGATTGTTGTGA-TTGTGTGTTTGTA--T--TA---TT-TTTATTAT---------TTTAAGGACGATGCGAATGGTGTTGTCGGGGCAGCCAAAGCGATGGCA-AAAGATT---C----------AACG--TTTTCAAAATTGCCAATTAGT----------G-AACAT---ATAC
droRho1	scf7180000779234:260071-260270 +		ACCTTTGT--CTTGTTAACAGCTTT-TGCTTTTT-TTT---T----ACCTCAGTGG----------C--TTTTTGCCTGCGCCAAGAGTCGTCGATCGCGGGGT-TTTCATTGTTGTGA-TTGTGTGTTTGTA--T--TA---TT-TTTATTAT---------TTTAAGGACGATGCGAATGGTGTTGTCGGGGCAGCCAAAGCGATGGCA-AAAGATT---C----------AACG--TTTTCAAAATTGCCAATTAGT----------G-AACAT---ATAC
droBia1	scf7180000301468:35124-35335 -		ACCTTT-T--CTTGTTAACAGCTTT-TGCTTTTT-TTT---T----ACCTCAGCGTTGCAT----------CCC-TTTTGCTGCCTGCGCCAAGATCGTCGATCGTGGGGT-TTTCATTGTTGTGA-TTGTGTGTTTGTA--TTGTATTA---TA---TT-TTTATTAG---------TTTAAGGACGATGCGAATGGTGTTGTCGGGGCAGCCAAAGCGATGGCA-AAAGATT---C----------AAGTTTTTTCAAAATTGCCAATTAGT----------G-AACAT---ATTATGC
droTak1	scf7180000415667:579341-579542 +		ACCTTT-T--CTTGTTAACAGCTTT-TGCTTTTT-TTT---T----ACCTCAGCGGG---------C--TTTTTGCCTGCGCCAAGATCGTCGATCGTGGGGT-TTTGATTGTTGTAA-TTGTGTGTTTGTA--TTGTATTA---TA---TT-TTATTAT---------TTTAAGGACGATGCGATGATGGTGTTGTCGGGGCAGCCAAAGCGATGGCGT-AAAGATT---C----------AACG--TTTTCAAAATTGCCAATTAGT----------G-AACAT---ATAC
droEug1	scf7180000409554:4977644-4977846 +		ACCTTT-T--CTTGTTAACAGCTTT-TGCTTTTT-TTT---T----ACCTCAGCGGG---------C--TTTTTGCCTGCGCCAAGATCGTCGATCGTGGGGT-TTTCATTGTTGTAA-TTGTGTGTCCC-ATA---TTTT---TA--TTATTAT---------TTTAAGGGCGATGCGAATGGTGTTAGGCAGCCAAAGCGATGGCA-AAAGATT---C----------AACG--TTTTCAAAATTGCCAATTAGT----------G-AACAT---ATAC
dm3	chr2L:9935022-9935224 -		ACCTTT-T--CTTGTTAACAGCTTT-TGCTTTTTTTTT---T----ACCTCAGCGGG---------C--TTTTTGCCTGCGCCAACAGAGCGTCGATCGTGGGGT-TTTCATTGTTGTAA-TTGTGTGTCGTTA--TA---TA---TTTTTATTAT---------TTTAAGCACGATGCTTGTGGCTGCGAACAGCGAAAGCACAGCCA-AAAGATT---C----------AACG--TTTTCAAAATTGCCAATTAGT----------G-AACAC---ATAC
droSim2	2L:9633173-9633376 -		ACCTTT-T--CTTGTTAACAGCTTT-TGCTTTTT--TTTTTT----ACCTCAGCGGG---------C--TTTTTGCCTGCGCCACAGAGCGTCGATCGTGGGGT-TTTCATTGTTGTAA-TTGTGTGTCGTTA--TA---TA---TTTTTATTAT---------TTTAAGCACGATGCTTGTGGCTGCGAACAGCGAAAGCGCAGCCA-AAAGATT---C----------AACG--TTTTCAAAATTGCCAATTAGT----------G-AACAC---ATAC
droSec2	scaffold_3:5381849-5382053 -		ACCTTT-T--CTTGTTAACAGCTTT-TGCTTTTT--TTTTTT----TACCTCAGCGGG---------C--TTTTTGCCTGCGCCACAGAGCGTCGATCGTGGGGT-TTTCATTGTTGTAA-TTGTGTGTCGTTA--TA---TA---TTTTTATTAT---------TTTAAGCACGATGCTTGTGGCTGCGAACAGCGAAAGCGCAGCCA-AAAGATT---C----------AACG--TTTTCAAAATTGCCAATTAGT----------G-AACAC---ATAC
droYak3	2L:12625722-12625921 -		ACTTTT-T--CTTGTTAACAGCTTT-TGCTTTT-TTT---T----ACCTCAGTGG----------C--TTTTTGCCTGCGCCAAGAGCGTCGATCGTGGGGT-TTTCATTGTTGTAA-TTGTGTGTCGTTA--TA---TT-TTTATTAT---------TTTAAGCACGATGCTTGTGGCTGCGGGGCAGCGAAAGCGCAGCCA-AAAGATT---C----------AACG--TTTTCAAAATTGCCAATTAGT----------G-AACAC---ATAC
droEre2	scaffold_4929:10555272-10555471 -		ACCTTT-T--CTTGTTAACAGCTTT-TGCTTTT-TTT---T----ACCTCAGTGG----------C--TTTTTGCCTGCGCCAAGAGCGTCGATCGTGGGGT-TTTCATTGTTGTAA-TTGTGTGTCGTTA--TA---TA---TT-TTTATTAT---------TTTAAGCACGATGCTTGTGGCTGCGGTCAGCGAAAGCGCTACCA-AAAGATT---C----------AACG--TTTTCAAATTGCCAATTAGT----------G-AACAC---ATAC
dp5	4_group3:234365-234568 +	dps_243	ATTAAT-T--CTTGTTAACAGCTTT-TGCTTTTTTGTT---T----ACCTCACTGG----------C--AATTTGTCTGTATTAAAACGTTTGTTGCGGGGT-TTTATTGTTGTGA-TTGTGTGTTAA-TTA---TT-GCATTGTT---------TTTAATGCACGAAGTGATGTTTAAATATAATGAGCAAAGTGCA----AGTTT---C----------ACGT--TTTTCGAAATTGCCAATTAGT----------ATGAAAATATTTATTATAC
droPer2	scaffold_1:1709203-1709406 +	dps_322	ATTAAT-T--CTTGTTAACAGCTTT-TGCTTTTTTGTT---T----ACCTCACTGG----------C--AATTTGTCTGTATTAAAACGTTTGTTGCGGGGT-TTTATTGTTGTGA-TTGTGTGTTAA-TTA---TT-GCATTGTT---------TTTAATGCACGAAGTGATGTTTAAATATAATGAGCAAAGTGCA----AGTTT---C----------ACGT--TTTTCGAAATTGCCAATTAGT----------ATGAAAATATTTATTATAC
droWil2	scf2_1100000004521:12231576-12231852 -		CGT-AT-C--CTTGTTAAGTGCTTTGTCTTTT-T--T----ACCTCACTCAA----------C--AGTTTGTATGTAATTGTAAAGTGTTTAAAGTA-------GTTTGCCTTGTTGTGAATAGTGTCA--TT--T--TCTTT-TTTTTAC-TAATTTAATTTAATTATTTTTTGCATAAAGCGCTGAACGTGGTCGCAAAGTGATGAAAGTGTTTTTG---GCGTT---CTACGTTTT---CATTGTA----T--ACATATATAT---TT---------ATACTATTATAAAATAGTTTAAATT-GTTTTCAAAATTGCCAATTAGT----------CG-GACAT---ATTATAC
droVir3	scaffold_12723:4015043-4015334 +	dvi_23304	G-TTTT-T--TGTTTTAATTTTTTT-TCGTTTA--TTTTTT---T--TTTAAACGA----------CGTTTTGT---GCCTTGCTTGCGATTAAAGCGTGCAAGGTTTTCATTGTTGTAA-TTATATTTT-ATA--T--TA---TT-----CTTA--------TTAAAAGCGTTT-GATTTTT-GAATTGAAAAGTAGCAAGTGTTATTA---TCGTTGAGCTATGTTTT---TAACATACTACATACACATGCAGACATCCAGACAGGCAAACATAAATTTATAAAC------TTTT---T-------TAGTTTGTTTATTGAATGAAAAACAAATGGCCAACTTCTTG-GTTTAAATATTATAG
droMoj3	scaffold_6500:14710061-14710202 -		TCCTTTGTGCGCTTGTTGACAGCTTTGTCTTTT-TGATTT---T----ACCTCAGTT----------ATTTGTTTGATCACGAATTGG--GCTTTGCTTGCGGTTAAAGCTATTGAAGCGGGGTTTCATTGTTGTAG-TTATATATTT-ATA--T--TA---TT-TTA--------TTT----------TTAAGTGCGTTTTAATAGTTT-TGATGGAGCAAGTGTGTGTTT---AGATTTGACGCAAGTTTTTTTATCATACTATATAAACATACATAC----------TTTT---T-------TTAC-----------A-TGACAT---TTTATAT
droGri2	scaffold_15252:3644313-3644529 -		TCTT-T--CTTGTTAACAGCTTT-TGCTCTTTTTTT---T----ACCTCGATT----------CAG--GCTTTGCTTGCGGTTAAAGCGTTTAAAGCGGGGTTTCATTGTTGTAA-TTATATTAT-ATA--T--TA---TT-TTA--------TTT----------TTAAGTGCGTTTTAATAGTTT-TGATGGAGCAAGTGTGTGTTT---AGATTTGACGCAAGTTTTTTTATCATACTATATAAACATACATAC----------TTTT---T-------TTAC-----------A-TGACAT---TTTATAT

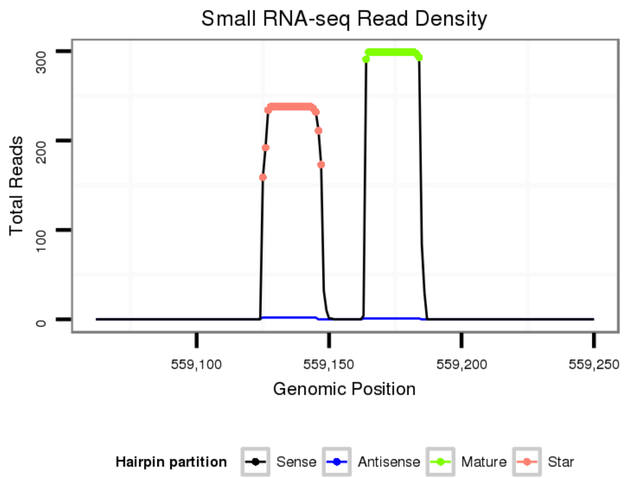
Generated: 09/08/2015 at 07:46 PM

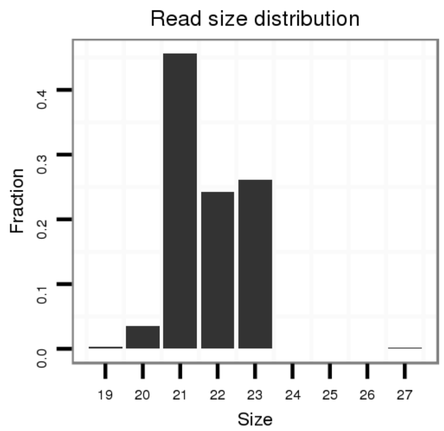
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	1

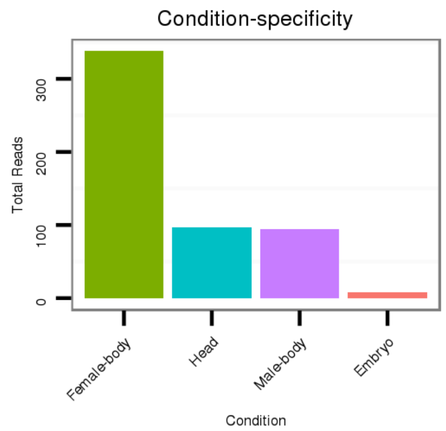
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_316	**scaffold_12903:559112-559200 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

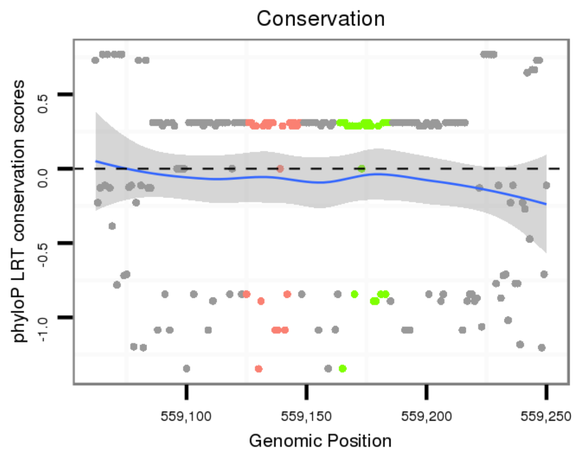
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GAATAATGTATTCTCACTCTCCAATTTTGCTCAGTGCAGTTTTAAGACTAGAAATTGCTTACTCTTGGCAGACATTTACTCTGAGTGTATTTTTCAAGCAACTGAGCGTCGATGTCAACCAGAAATAATCATTTTCCCAGCATCTATATTTTTTTTGCAGTGTTTTTATGCAGAAAAGTGGCAAGCGAA **********..(((((.((.(((...((((..(((((((.((.((.(((((.........)).)))).)).)).)))))).)))).)))...)))).)).)))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V105 male body	V106 head	V055 head	M058 embryo	V039 embryo
..........TGAGCGTCGATGTCAACCAGA..........	21	0	1	203.00	203	79	46	64	7	3	4
..........CTTGGCAGACATTTACTCTGAGT..........	23	0	1	101.00	101	90	6	2	3	0	0
..........TGAGCGTCGATGTCAACCAGAA..........	22	0	1	51.00	51	24	22	5	0	0	0
..........CTTGGCAGACATTTACTCTGAG..........	22	0	1	32.00	32	31	0	1	0	0	0
..........TGAGCGTCGATGTCAACCAGAAA..........	23	0	1	29.00	29	11	15	1	1	1	0
..........TTGGCAGACATTTACTCTGAGT..........	22	0	1	25.00	25	23	1	0	1	0	0
..........TGGCAGACATTTACTCTGAGTG..........	22	0	1	19.00	19	19	0	0	0	0	0
..........CTTGGCAGACATTTACTCTGA..........	21	0	1	19.00	19	14	1	4	0	0	0
..........TGGCAGACATTTACTCTGAGT..........	21	0	1	13.00	13	12	0	1	0	0	0
..........TGGCAGACATTTACTCTGAGTGT..........	23	0	1	9.00	9	7	2	0	0	0	0
..........TTGGCAGACATTTACTCTGAG..........	21	0	1	5.00	5	4	0	0	1	0	0
..........CTTGGCAGACATTTACTCTG..........	20	0	1	4.00	4	1	0	3	0	0	0
..........GAGCGTCGATGTCAACCAGA..........	20	0	1	4.00	4	4	0	0	0	0	0
..........TGAGCGTCGATGTCAACCAG..........	20	0	1	4.00	4	3	0	0	1	0	0
..........TGAGCGTCGATGTCAACCAGAAAA.....	24	1	1	3.00	3	2	1	0	0	0	0
..........GAGCGTCGATGTCAACCAGAA..........	21	0	1	3.00	3	3	0	0	0	0	0
..........TGAGCGTCGATGTCAACCAGAAT.....	23	1	1	3.00	3	2	0	1	0	0	0
..........CTTGGCAGACATTTACTCT..........	19	0	1	2.00	2	1	0	1	0	0	0
..........CTGAGCGTCGATGTCAACCAGA..........	22	0	1	2.00	2	1	1	0	0	0	0
..........TTGGCAGACATTTACTCTGA..........	20	0	1	2.00	2	2	0	0	0	0	0
..........CTGAGCGTCGATGTCAACCA..........	20	0	1	2.00	2	2	0	0	0	0	0
..........GGCAGACATTTACTCTGAGT..........	20	0	1	2.00	2	2	0	0	0	0	0
..........GGCAGACATTTACTCTGAGTG..........	21	0	1	2.00	2	2	0	0	0	0	0
..........GAGCGTCGATGTCAACCAGAAA..........	22	0	1	1.00	1	1	0	0	0	0	0
..........CTTGGCAGACATTTACTCTGAGTGTAT.....	27	0	1	1.00	1	0	0	1	0	0	0
..........TGAGCGTCGATGTCAACCAGG.....	21	1	1	1.00	1	1	0	0	0	0	0
..........TTGGCAGACATTTACTCTGAGTG.....	23	0	1	1.00	1	1	0	0	0	0	0
..........TGGCAGACATTTACTCTGAGTGC.....	23	1	1	1.00	1	0	0	1	0	0	0
..........CTTGGCAGACATTTACTCTGAGC.....	23	1	1	1.00	1	0	0	0	0	1	0
..........TGGCAGACATTTACTCTGAG..........	20	0	1	1.00	1	1	0	0	0	0	0
..........CTTGGCAGACATTTACTCTGAGTT.....	24	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

CTTATTACATAAGAGTGAGAGGTTAAAACGAGTCACGTCAAAATTCTGATCTTTAACGAATGAGAACCGTCTGTAAATGAGACTCACATAAAAAGTTCGTTGACTCGCAGCTACAGTTGGTCTTTATTAGTAAAAGGGTCGTAGATATAAAAAAAACGTCACAAAAATACGTCTTTTCACCGTTCGCTT **********..((((.((.(((...((((..(((((((.((.((.(((((.........)).)))).)).)).)))))).)))).)))...)))).)).)))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V055 head	V106 head	M058 embryo	V105 male body
..........GACTCGCAGCTACAGTTGGTCT..........	22	0	1	1.00	1	1	0	0	0	0
..........AGAACCGTCTGTAAATGAGACT..........	22	0	1	1.00	1	1	0	0	0	0
..........GAACCGTCTGTAAATGAGACT..........	21	0	1	1.00	1	1	0	0	0	0
..........AAAAAAAACGTCACAAAA..........	18	0	3	0.33	1	0	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:559062-559250 +	dan_316	GAA--TAATGTATTCTCACTCTCCAA---TTTTGCTCAGTGCAGTTTTAAGACTAGAAATTGCTTACTCTTGGCAGACATTTACTCTGA---GTGTATTTTTCAAGCAACTGAGCGTCGATGTCAACCAGAAATAATCATTTTCCCAGCATCTATATTTTTTTTGCAGTGTTTTTATGCAGAAAAGTGGCAAGCGAA
droBip1	scf7180000395912:27955-28137 +		GAA--TAATGTTTTTCCAGTCTTCAATAATTGTGTTAAG----CTTCTAAGAATTGAAATTA-TTATTTTGGGTGACATGG-CGTTGAGGTGTATATTTTGCAACACACTTCAGCCCCG-TGTCTTCTTAAATATAATAAGTTTCCCAACATCAGTATTTTTGTAATTTTATTTTTTTTTGTAATTCT-----GCTGA
droEug1	scf7180000409711:983053-983110 -		GCTTTTGAACTTTTTTTGGGCCGCTTCA--GATTTTTACGTATCGAAGGAGAAAGCAAG

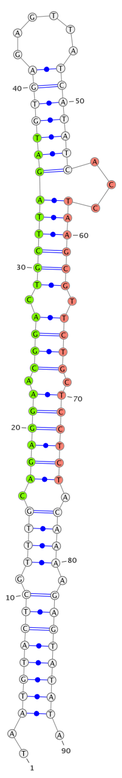
Generated: 09/08/2015 at 08:00 PM

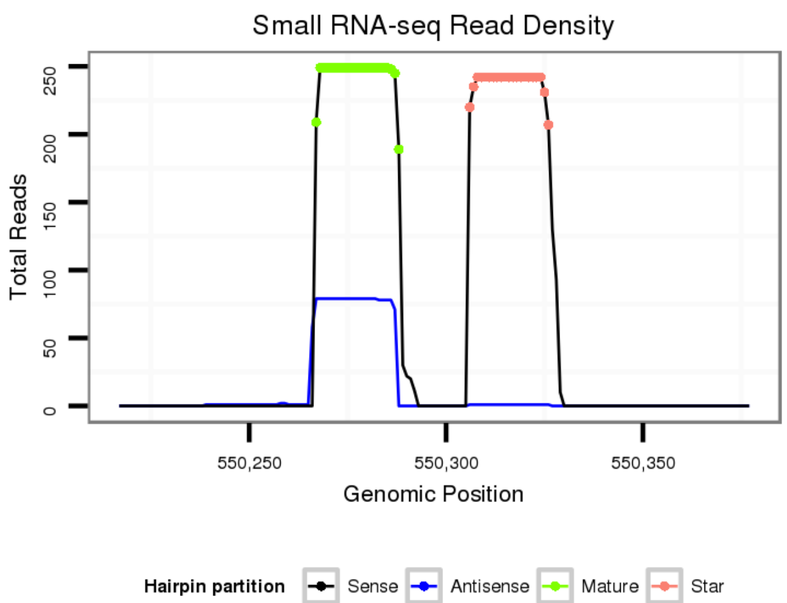
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

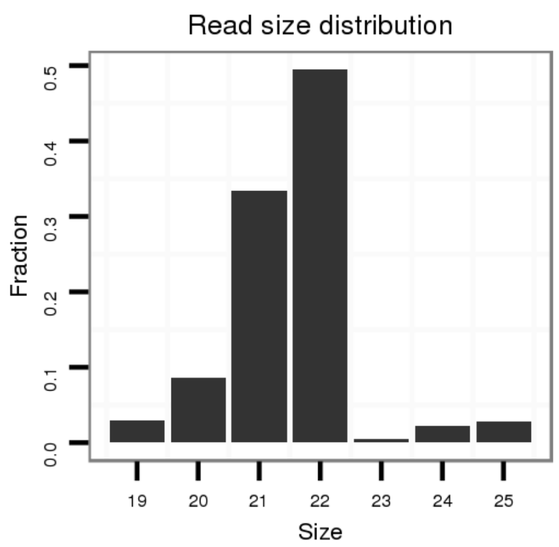
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_45	**scaffold_12903:550267-550327 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

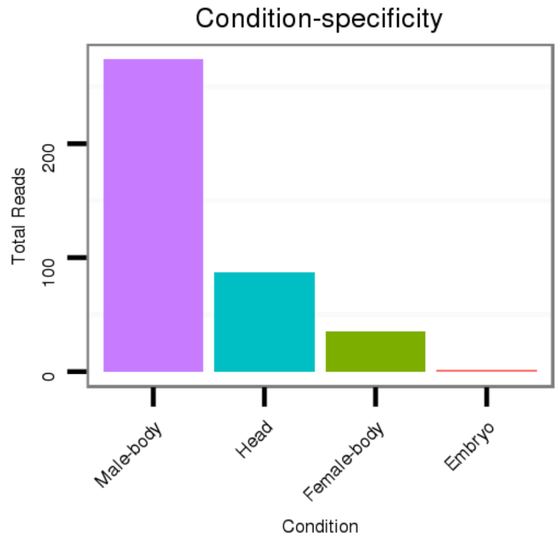
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dana\GF15947-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTCAGGATCTTCTATCTGTGAGGGGTTCCAGAGACTAATGTACTCGTTTGCAGAGGAACGGACTGCTTAGATGTGAGAGTTATCATATCACCTAAGCGTTCTGCTCCTCTACAAAAGAGTATATATCGCCAGTCGATCATCACAACTTCATAAATCACATC **********..(((((((.(((((.(((((((.((((.(((((((((((((.....)))))))...)))))))..))))..)))))))..))))..)))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V055 head	M044 female body	V106 head	M058 embryo	V039 embryo
.....CAGAGGAACGGACTGCTTAGAT.....	22	0	1	155.00	155	122	13	4	15	1	0
.....ACCTAAGCGTTCTGCTCCTCT.....	21	0	1	76.00	76	47	12	10	7	0	0
.....ACCTAAGCGTTCTGCTCCTCTAC.....	23	0	1	71.00	71	39	10	11	4	6	1
.....CAGAGGAACGGACTGCTTAGA.....	21	0	1	50.00	50	34	4	5	7	0	0
.....ACCTAAGCGTTCTGCTCCTCTA.....	22	0	1	34.00	34	22	6	6	0	0	0
.....ACCTAAGCGTTCTGCTCCTC.....	20	0	1	24.00	24	19	1	0	3	1	0
.....AGAGGAACGGACTGCTTAGATGTGA.....	25	0	1	11.00	11	5	1	3	2	0	0
.....ACCTAAGCGTTCTGCTCCT.....	19	0	1	11.00	11	3	5	1	2	0	0
.....AGAGGAACGGACTGCTTAGATGTG.....	24	0	1	9.00	9	6	0	1	2	0	0
.....ACCTAAGCGTTCTGCTCCTCTACT.....	24	1	1	8.00	8	5	0	2	1	0	0
.....AGAGGAACGGACTGCTTAGATG.....	22	0	1	8.00	8	4	0	2	2	0	0
.....CCTAAGCGTTCTGCTCCTCTAC.....	22	0	1	8.00	8	7	0	0	0	1	0
.....ACCTAAGCGTTCTGCTCCTCTT.....	22	1	1	7.00	7	4	0	2	1	0	0
.....AGAGGAACGGACTGCTTAGA.....	20	0	1	6.00	6	5	0	1	0	0	0
.....ACCTAAGCGTTCTGCTCCTCTAT.....	23	1	1	5.00	5	3	0	1	0	0	1
.....CTAAGCGTTCTGCTCCTCTAC.....	21	0	1	4.00	4	3	0	1	0	0	0
.....AGAGGAACGGACTGCTTAGAT.....	21	0	1	4.00	4	3	1	0	0	0	0
.....ACCTAAGCGTTCTGCTCCTCTACA.....	24	0	1	4.00	4	2	0	0	2	0	0
.....CCTAAGCGTTCTGCTCCTCTA.....	21	0	1	3.00	3	1	1	1	0	0	0
.....CAGAGGAACGGACTGCTTAG.....	20	0	1	3.00	3	2	1	0	0	0	0
.....CTAAGCGTTCTGCTCCTCTACA.....	22	0	1	3.00	3	3	0	0	0	0	0
.....CCTAAGCGTTCTGCTCCTCTACA.....	23	0	1	3.00	3	0	0	3	0	0	0
.....AGAGGAACGGACTGCTTAGATGT.....	23	0	1	2.00	2	0	1	0	1	0	0
.....CAGAGGAACGGACTGCTTAGATA.....	23	1	1	2.00	2	2	0	0	0	0	0
.....CAGAGGAACGGACTGCTTAGATT.....	23	1	1	2.00	2	2	0	0	0	0	0
.....ACCTAAGCGTTCTGCTCCTCA.....	21	1	1	2.00	2	2	0	0	0	0	0
.....ACCTAAGCGTTCTGCTCCTCTACC.....	24	1	1	2.00	2	1	0	1	0	0	0
.....AGAGGAACGGACTGCTTAGATGTGAA.....	26	1	1	1.00	1	1	0	0	0	0	0
.....AGAGGAACGGACTGCTTAGATT.....	22	1	1	1.00	1	0	0	1	0	0	0
.....AGAGGAACGGACTGCTTAGATTA.....	23	2	1	1.00	1	1	0	0	0	0	0
.....AGAGGAACGGACTGCTTAGATGC.....	23	1	1	1.00	1	0	0	1	0	0	0
.....CAGAGGAACGGACTGCTTA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....ACCTAAGCGTTCTGCTCCTCTTAG.....	24	3	1	1.00	1	1	0	0	0	0	0
.....CAGAGGAACGGACTGCTTAGTA.....	22	2	1	1.00	1	1	0	0	0	0	0
.....CAGAGGAACGGACTGCTTAGAAA.....	23	2	1	1.00	1	1	0	0	0	0	0
.....AGAGGAACGGACTGCTTAGATGTA.....	24	1	1	1.00	1	0	0	1	0	0	0
.....CAGAGGAACGGACTGCTTAGT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....ACCTAAGCGTTCTGCTCCTCTAA.....	23	1	1	1.00	1	0	0	1	0	0	0
.....ACCTAAGCGTTCTGCTCCTCTGT.....	23	2	1	1.00	1	1	0	0	0	0	0
.....CCTAAGCGTTCTGCTCCTCT.....	20	0	1	1.00	1	0	0	1	0	0	0
.....ACCTAAGCGTTCTGCTCCTCTTT.....	23	2	1	1.00	1	0	1	0	0	0	0
.....ACCTAAGCGTTCTGCTCCTT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....ACCTAAGCGTTCTGCTCCTC.....	21	1	1	1.00	1	0	0	0	0	1	0

Anti-sense strand reads

AAGTCCTAGAAGATAGACACTCCCCAAGGTCTCTGATTACATGAGCAAACGTCTCCTTGCCTGACGAATCTACACTCTCAATAGTATAGTGGATTCGCAAGACGAGGAGATGTTTTCTCATATATAGCGGTCAGCTAGTAGTGTTGAAGTATTTAGTGTAG **********..(((((((.(((((.(((((((.((((.(((((((((((((.....)))))))...)))))))..))))..)))))))..))))..)))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V106 head	V105 male body	M058 embryo	V055 head	V039 embryo
.....CGTCTCCTTGCCTGACGAATCT.....	22	0	1	55.00	55	48	3	4	0	0	0
.....GTCTCCTTGCCTGACGAATCT.....	21	0	1	16.00	16	13	3	0	0	0	0
.....GTCTCCTTGCCTGACGAATC.....	20	0	1	5.00	5	4	1	0	0	0	0
.....TGTCTCCTTGCCTGACGAATCT.....	22	1	1	4.00	4	2	2	0	0	0	0
.....CGTCTCCTTGCCTGACGAATC.....	21	0	1	2.00	2	2	0	0	0	0	0
.....TGAGCAAACGTCTCCTTGCCTGACG.....	25	0	1	1.00	1	0	0	0	1	0	0
.....CCCAAGGTCTCTGATTACATG.....	21	0	1	1.00	1	0	0	0	1	0	0
.....TGGATTCGCAAGACGAGGAGA.....	21	0	1	1.00	1	0	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:550217-550377 +	dan_45	TTCAGGATCTTCTATCTGTGAGGGGTTCCAGAGACTAATGTACTCGTTTGCAGAGGAACGGACTGCTTAGATGTGAGAGTTATCATATCACCTAAGCGTTCTGCTCCTCTACAAAAGAGTATATATCGCCAGTCGATCATCACAACTTCATAAATCACATC

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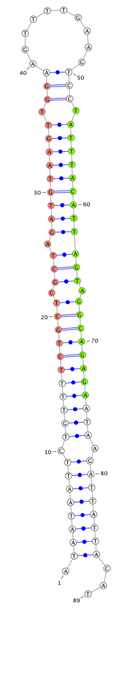
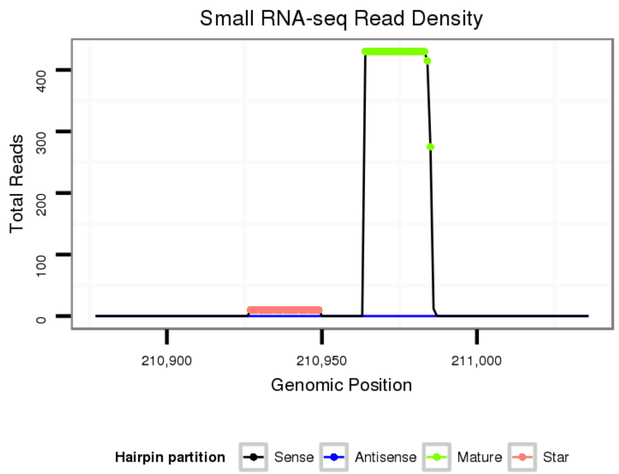
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

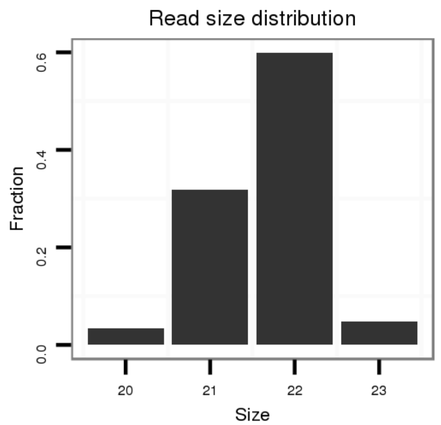
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_41	**scaffold_13335:210927-210986 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

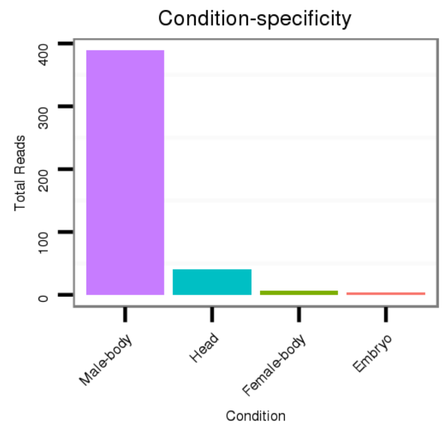
Legend: mature star mismatch in alignment mismatch in read

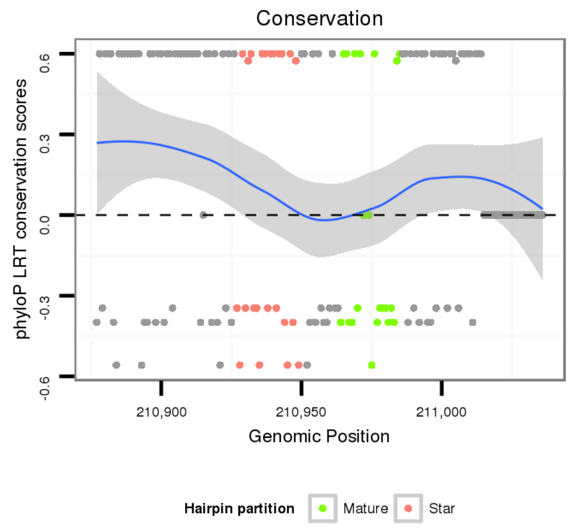
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATTAAATGAAAATAAAGTTAAAATATTGTAAATATATAATAATTCTGTTTTCTGCTCGCTAGATGTAAGTTGGAAGTTTTGAAGTCCTATTTACATTAGTAGGCAGAGAATAAGATTATTACATTCTACGAAATATATGTTATATATATTTAAGGAGTCT **********.(((((((((.((((((((((.(((.(((((((((.(((.....)))).)))))))))).)))))))))).)))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V055 head	V106 head	M044 female body	M058 embryo
.....TATTTACATTAGTAGGCAGAGA.....	22	0	1	263.00	263	234	18	7	2	2
.....TATTTACATTAGTAGGCAGAG.....	21	0	1	140.00	140	126	7	3	2	2
.....TATTTACATTAGTAGGCAGAGT.....	22	1	1	22.00	22	20	1	1	0	0
.....TATTTACATTAGTAGGCAGAGAT.....	23	1	1	15.00	15	12	2	0	1	0
.....TATTTACATTAGTAGGCAGA.....	20	0	1	15.00	15	14	1	0	0	0
.....TATTTACATTAGTAGGCAGAGAA.....	23	0	1	11.00	11	9	1	0	1	0
.....TCTGCTCGCTAGATGTAAGTTGG.....	23	0	1	10.00	10	6	1	2	1	0
.....TATTTACATTAGTAGGCAGAGAAA.....	24	1	1	6.00	6	5	0	0	0	1
.....TATTTACATTAGTAGGCAGAT.....	21	1	1	3.00	3	3	0	0	0	0
.....TTTACATTAGTAGGCAGAGT.....	20	1	1	2.00	2	2	0	0	0	0
.....TATTTACATTAGTAGGCAGAGTT.....	23	2	1	2.00	2	2	0	0	0	0
.....ATTTACATTAGTAGGCAGAGAAA.....	23	1	1	1.00	1	0	0	0	1	0
.....TATTTACATTAGTAGGCAGAGAAT.....	24	0	1	1.00	1	1	0	0	0	0
.....TATTTACATTAGTAGGCAGAGATAT.....	25	3	1	1.00	1	1	0	0	0	0
.....TATTTACATTAGTAGGCAGAGATC.....	24	2	1	1.00	1	1	0	0	0	0
.....TATTTACATTAGTAGGCAGACT.....	22	2	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

TAATTTACTTTTATTTCAATTTTATAACATTTATATATTATTAAGACAAAAGACGAGCGATCTACATTCAACCTTCAAAACTTCAGGATAAATGTAATCATCCGTCTCTTATTCTAATAATGTAAGATGCTTTATATACAATATATATAAATTCCTCAGA **********.(((((((((.((((((((((.(((.(((((((((.(((.....)))).)))))))))).)))))))))).)))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head	V039 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13335:210877-211036 +	dan_41	ATTAAATGAAAATAAAGTTAAAATATTGTAAATATATAATAATTCTGTTTTCTGCTCGCTAGATGTAAGTTGGAAGTTTTGAAGTCCTATTTACATTAGTAGGCAGAGAATAAGATTATTACATTCTACGAAATATATGTTATATATATTTAAGGAGTCT
droKik1	scf7180000302610:1797033-1797166 +		TTCAAAATAAAATAAATAATTATTTTATAAATATATT-TATTAATATATCATACTTAATAAATATATTTAGTAATATATATTATTTATTAATAAATA---TTTAATTATGAATTAAAATAAAATATTTTACAAAATTTTAT----------

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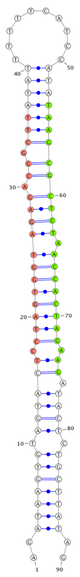
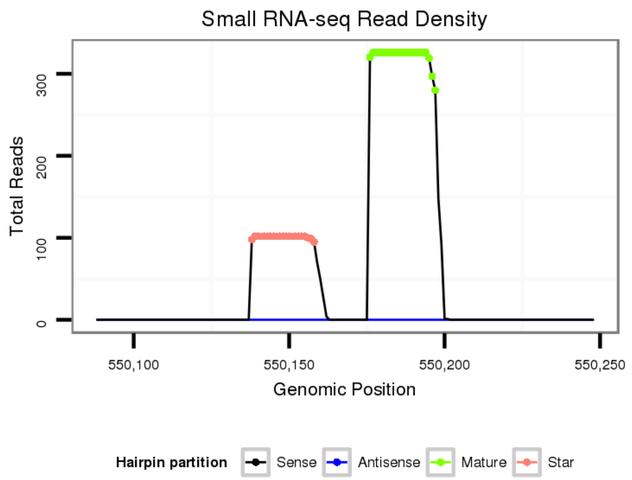
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

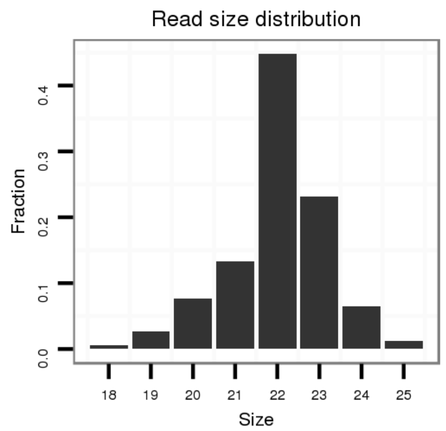
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_49	**scaffold_12903:550138-550198 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

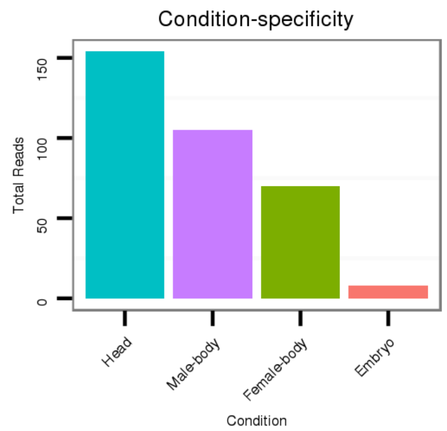
Legend: mature star mismatch in alignment mismatch in read

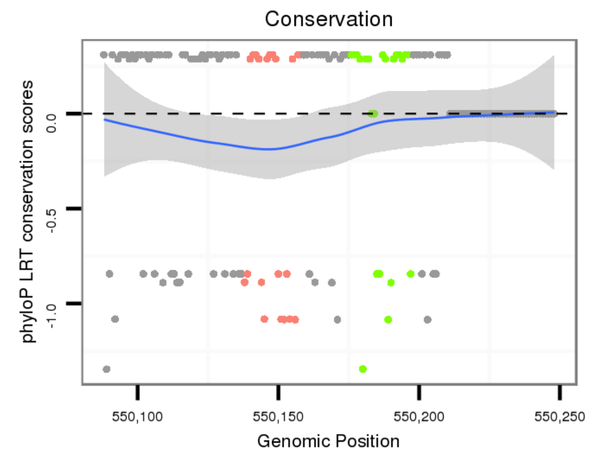
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dana\GF15947-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGGAGGAAAGTGAAGAGAGTTAAAGGATAACCCCCAGATAAGTGTAGTACTCCTAGTGGTAGAGACGGCTTATATTTTTTCATCCATATAAGCGCTCTAACCACTAGAAGATACTCTGCTTATAGAGTCTTCAGGATCTTCTATCTGTGAGGGGTTCCAGA **********..(((((((.(((((((.((((((((((((.((.(((((((.....)))))))))))))).))))))))).)).)))).)))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V106 head	M044 female body	V055 head	M058 embryo	V039 embryo
.....TAAGCGCTCTAACCACTAGAAG.....	22	0	1	129.00	129	23	89	8	6	3	0
.....TAAGCGCTCTAACCACTAGAAGAT.....	24	0	1	90.00	90	64	7	14	5	0	0
.....TAAGCGCTCTAACCACTAGAAGA.....	23	0	1	55.00	55	29	11	11	4	0	0
.....TCCTAGTGGTAGAGACGGCTT.....	21	0	1	25.00	25	14	2	5	3	1	0
.....TCCTAGTGGTAGAGACGGCTTAT.....	23	0	1	22.00	22	6	1	12	1	2	0
.....TCCTAGTGGTAGAGACGGCTTATA.....	24	0	1	22.00	22	10	5	6	1	0	0
.....TAAGCGCTCTAACCACTAGA.....	20	0	1	22.00	22	4	13	5	0	0	0
.....TCCTAGTGGTAGAGACGGCTTA.....	22	0	1	19.00	19	5	1	11	1	0	1
.....TAAGCGCTCTAACCACTAGAA.....	21	0	1	16.00	16	10	1	3	1	1	0
.....TAAGCGCTCTAACCACTAGAAGAA.....	24	1	1	9.00	9	5	0	2	1	1	0
.....TAAGCGCTCTAACCACTAGAAGATT.....	25	1	1	7.00	7	5	0	2	0	0	0
.....TCCTAGTGGTAGAGACGGCTTT.....	22	1	1	7.00	7	5	1	1	0	0	0
.....TAAGCGCTCTAACCACTAG.....	19	0	1	7.00	7	0	7	0	0	0	0
.....TCCTAGTGGTAGAGACGGCTTAA.....	23	1	1	6.00	6	2	1	2	0	0	1
.....TCCTAGTGGTAGAGACGGCTTATT.....	24	1	1	6.00	6	3	0	3	0	0	0
.....TCCTAGTGGTAGAGACGGCTTATAA.....	25	1	1	5.00	5	3	2	0	0	0	0
.....TCCTAGTGGTAGAGACGGCTTATAT.....	25	0	1	4.00	4	1	3	0	0	0	0
.....TCCTAGTGGTAGAGACGGCTTAAT.....	24	2	1	3.00	3	1	2	0	0	0	0
.....TCCTAGTGGTAGAGACGGCT.....	20	0	1	3.00	3	2	0	0	1	0	0
.....TAAGCGCTCTAACCACTAGAAA.....	22	1	1	3.00	3	2	1	0	0	0	0
.....TCCTAGTGGTAGAGACGGCTTATAAA.....	26	2	1	3.00	3	2	0	0	0	0	1
.....AAGCGCTCTAACCACTAGAAG.....	21	0	1	3.00	3	0	1	2	0	0	0
.....TCCTAGTGGTAGAGACGG.....	18	0	1	2.00	2	1	0	1	0	0	0
.....AAGCGCTCTAACCACTAGAAGA.....	22	0	1	2.00	2	0	0	2	0	0	0
.....CCTAGTGGTAGAGACGGCT.....	19	0	1	1.00	1	0	0	1	0	0	0
.....TAAGCGCTCTAACCACTAGAAGAAT.....	25	2	1	1.00	1	1	0	0	0	0	0
.....TCCTAGTGGTAGAGACGGCTTAGT.....	24	2	1	1.00	1	1	0	0	0	0	0
.....AAGCGCTCTAACCACTAGAA.....	20	0	1	1.00	1	0	0	1	0	0	0
.....TCCTAGTGGTAGAGACGGCTTAC.....	23	1	1	1.00	1	1	0	0	0	0	0
.....CCTAGTGGTAGAGACGGCTTA.....	21	0	1	1.00	1	0	0	1	0	0	0
.....CCTAGTGGTAGAGACGGCTTATA.....	23	0	1	1.00	1	0	1	0	0	0	0
.....TAAGCGCTCTAACCACTAGAAGATAC.....	26	0	1	1.00	1	0	0	1	0	0	0
.....TAAGCGCTCTAACCACTAGAAT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TCCTAGTGGTAGAGACGGT.....	19	1	1	1.00	1	1	0	0	0	0	0
.....TCCTAGTGGTAGAGACGGCTTATAAAA.....	27	3	1	1.00	1	0	1	0	0	0	0
.....CCTAGTGGTAGAGACGGCTTAT.....	22	0	1	1.00	1	0	0	1	0	0	0
.....AAGCGCTCTAACCACTAGAAGATT.....	24	1	1	1.00	1	0	0	1	0	0	0
.....TCCTAGTGGTAGAGACGGCTG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TAAGCGCTCTAACCACTAGAAC.....	22	1	1	1.00	1	0	1	0	0	0	0
.....TCCTAGTGGTAGAGACGGC.....	19	0	1	1.00	1	0	0	0	1	0	0

Anti-sense strand reads

ACCTCCTTTCACTTCTCTCAATTTCCTATTGGGGGTCTATTCACATCATGAGGATCACCATCTCTGCCGAATATAAAAAAGTAGGTATATTCGCGAGATTGGTGATCTTCTATGAGACGAATATCTCAGAAGTCCTAGAAGATAGACACTCCCCAAGGTCT **********..(((((((.(((((((.((((((((((((.((.(((((((.....)))))))))))))).))))))))).)).)))).)))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	V055 head	V039 embryo	M044 female body
Show Alignment With Reads										

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:550088-550248 +	dan_49	TGGAGGAAAGTGAAGAGAG----------TTAAAGGATAACCCCCAGATAAGTGTAGTACTCCTAGTGGTAGAGACGGCTTATATTT----TTTCATCCA-TATAAGCGCTCTAACCACTAGAAGATACTCTGCTTATAGAGTCTTCAGGATCTTCTATCTGTGAGGGGTTCCAGA
droBip1	scf7180000395912:15441-15590 +		TCAATGAAAGTGAAAAGAAAGTATAATAATTTAGTGAAAAATATTTAAAATAAATCCCCAGATGAGTATAATGTATCTAGATGTAGGTCTTGATTATGTATGCACTTTCTTAGATTATAAGGGC--CGATCTAGAAAATATTATATTTAT----------

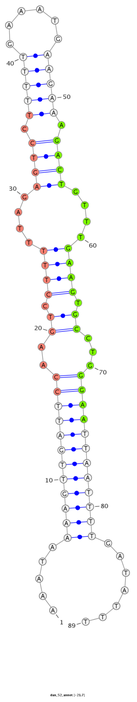
Generated: 09/08/2015 at 08:03 PM

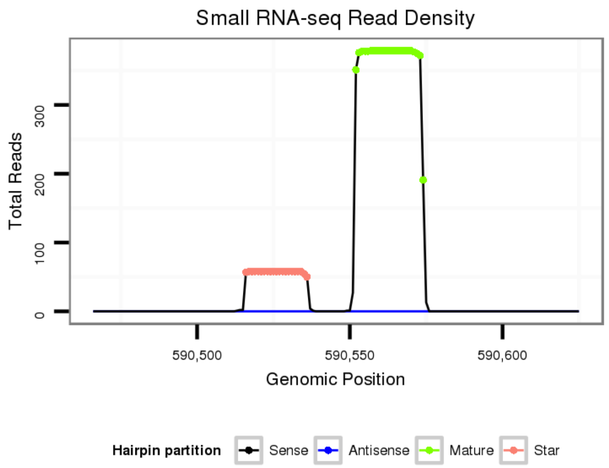
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

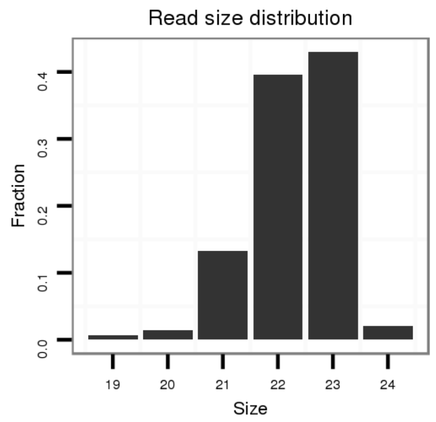
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_52	**scaffold_12903:590516-590575 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

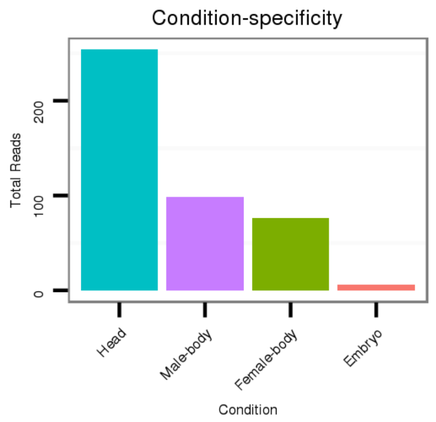
Legend: mature star mismatch in alignment mismatch in read

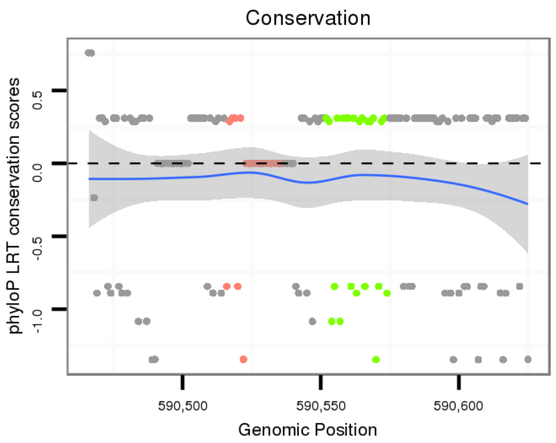
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TAAAATGAAAATATATCGAATGTGCAAGAAACTCAAAATAAAAGTTGATTCCAAGTCCTTTTTAGAGTCCTTTTTGAAATGAAGAAAGACTGTTTGAAGTGCCTGGGAATTAATTTTGATATTTAAGCAACAGTTTTGAAAGTGAAGAATGAATAAGTAC	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	M044 female body	V055 head	M058 embryo	V039 embryo
**********.....(((((((((((((..((.((((....((((.(((((.....)))))).))))....)))))..))...))))))))))).....**********											
.....AGACTGTTTGAAGTGCCTGGGAA.....	23	0	1	160.00	160	94	29	28	7	1	1
.....AGACTGTTTGAAGTGCCTGGGA.....	22	0	1	152.00	152	89	26	21	13	2	1
.....CCAAGTCCTTTTTAGAGTCCT.....	21	0	1	45.00	45	6	23	13	2	1	0
.....AAGACTGTTTGAAGTGCCTGGGA.....	23	0	1	23.00	23	10	10	2	1	0	0
.....GACTGTTTGAAGTGCCTGGGAA.....	22	0	1	16.00	16	12	3	1	0	0	0
.....AGACTGTTTGAAGTGCCTGGGAT.....	23	1	1	13.00	13	6	3	1	3	0	0
.....AGACTGTTTGAAGTGCCTGGGAAT.....	24	0	1	9.00	9	6	2	0	1	0	0
.....GACTGTTTGAAGTGCCTGGGA.....	21	0	1	6.00	6	4	0	2	0	0	0
.....AGACTGTTTGAAGTGCCTGGGAAA.....	24	1	1	5.00	5	5	0	0	0	0	0
.....CCAAGTCCTTTTTAGAGTCC.....	20	0	1	4.00	4	0	1	2	1	0	0
.....GACTGTTTGAAGTGCCTGGGAAT.....	23	0	1	3.00	3	2	1	0	0	0	0
.....AGACTGTTTGAAGTGCCTGGGT.....	22	1	1	3.00	3	2	0	0	1	0	0
.....AGACTGTTTGAAGTGCCTGGG.....	21	0	1	3.00	3	3	0	0	0	0	0
.....CCAAGTCCTTTTTAGAGTCCTT.....	22	0	1	3.00	3	0	1	2	0	0	0
.....CCAAGTCCTTTTTAGAGTC.....	19	0	1	2.00	2	1	0	1	0	0	0
.....AAGACTGTTTGAAGTGCCTGG.....	21	0	1	2.00	2	0	1	1	0	0	0
.....ACTGTTTGAAGTGCCTGGGAA.....	21	0	1	2.00	2	2	0	0	0	0	0
.....AGACTGTTTGAAGTGCCTGGGAAG.....	24	1	1	2.00	2	2	0	0	0	0	0
.....TTCCAAGTCCTTTTTAGAGTCC.....	22	0	1	1.00	1	0	0	1	0	0	0
.....AGACTGTTTGAAGTGCCTGGGATC.....	24	2	1	1.00	1	1	0	0	0	0	0
.....GAAAGACTGTTTGAAGTGCCTG.....	22	0	1	1.00	1	0	0	1	0	0	0
.....AAGACTGTTTGAAGTGCCTG.....	20	0	1	1.00	1	0	0	1	0	0	0
.....ACTGTTTGAAGTGCCTGGGG.....	20	1	1	1.00	1	1	0	0	0	0	0
.....GACTGTTTGAAGTGCCTGGGAAAA.....	24	2	1	1.00	1	1	0	0	0	0	0
.....AGACTGTTTGAAGTGCCTGGGAG.....	23	1	1	1.00	1	0	0	1	0	0	0
.....AGACTGTTTGAAGTGCCTGGT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....AGACTGTTTGAAGTGCCTGGAAG.....	24	1	1	1.00	1	0	0	1	0	0	0
.....GTTTGAAGTGCCTGGGAAT.....	19	0	1	1.00	1	0	1	0	0	0	0
.....GACTGTTTGAAGTGCCTGGGAAA.....	23	1	1	1.00	1	1	0	0	0	0	0
.....ATTCCAAGTCCTTTTTAGAGTC.....	22	0	1	1.00	1	0	0	1	0	0	0
.....ACTGTTTGAAGTGCCTGGGAAA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....CAAGTCCTTTTTAGAGTCCT.....	20	0	1	1.00	1	0	0	1	0	0	0
.....AGACTGTTTGAAGTGCCTGGGAC.....	23	1	1	1.00	1	0	0	1	0	0	0
.....AGACTGTTTGAAGTGCCTGGGC.....	22	1	1	1.00	1	0	0	0	1	0	0
.....CCAAGTCCTTTTTAGAGTCCTTT.....	23	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

ATTTTACTTTTATATAGCTTACACGTTCTTTGAGTTTTATTTTCAACTAAGGTTCAGGAAAAATCTCAGGAAAAACTTTACTTCTTTCTGACAAACTTCACGGACCCTTAATTAAAACTATAAATTCGTTGTCAAAACTTTCACTTCTTACTTATTCATG	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V055 head	V039 embryo
**********.....(((((((((((((..((.((((....((((.(((((.....)))))).))))....)))))..))...))))))))))).....**********								

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:590466-590625 +	dan_52	TAAAATGAAAATATA----------TCGAATGTGCAAGAAACTCAAAATAAAAGTTGATTCCAAGTCCTTTTTAGAGTCCTTTTTGAAATGAAGAAAGACTGTTTGA----AGTGCCTGGGAATTAATTTTGATATTTAAGCAACAG----TTTTGAAAGTGAAGAATGAATAAGTAC----------
droBip1	scf7180000395925:18902-19079 -		TAAATATGGTAACTTTTTATCCCCAAATATCGCATTTCG----------ATAAAAATAGAATTCAAAATG----------ATAAAGCAGAAAGCTTTTTTAATATATGTACCTCAGATTTAATCTCAATATTTAAGCATCTCTGCAAATCAAAACCAAAGAAACTATAAATAGGCAACAATTATAAACCTTTTTGTTTAA
droEre2	scaffold_4690:9468181-9468183 -		TAC----------]----------[----------]----[----------]----

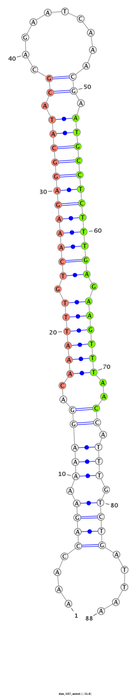
Generated: 09/08/2015 at 07:45 PM

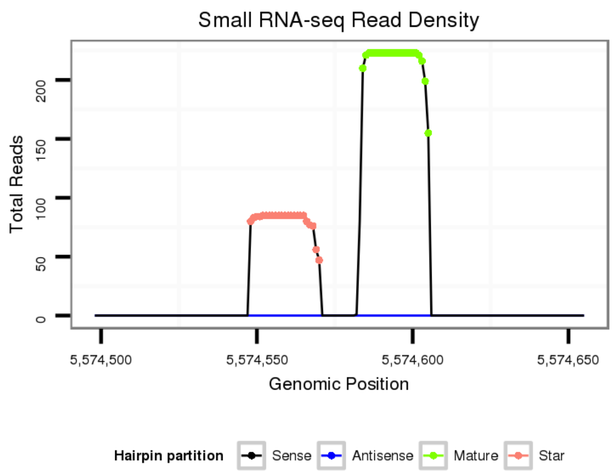
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

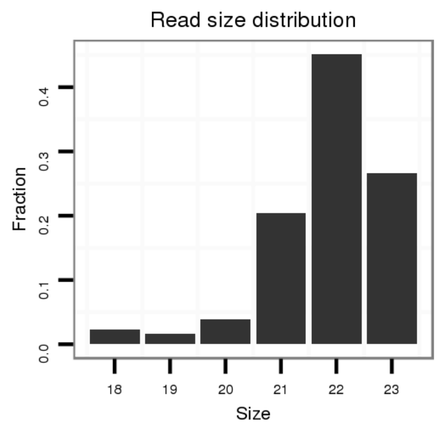
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_107	**scaffold_12916:5574548-5574605 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

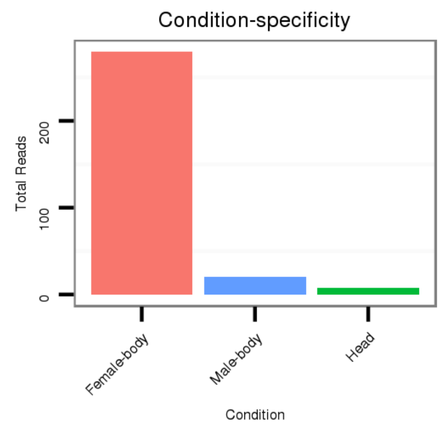
Legend: mature star mismatch in alignment mismatch in read

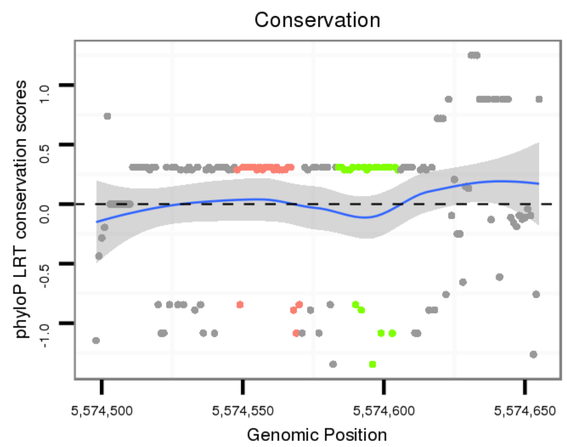
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GATGTTAATGTTAATTAATGTAAAGTTTAAGCCACAAACCAGAAAAAGGACAAATTTGTCAAAGAGGCATACGCAGAATCAAACGAATGCCTCTTTGAGAAGTTTAACCATTTGTCTGATTAAATACACCAACTAATAATTATAATTAAGCCACCTGT	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V105 male body	V106 head	V055 head	M058 embryo	V039 embryo
**********.....((((.(((((..(((((((.(((((((((((((.((..........)).)))))))))))))).))))))..)).)))).))))).....**********											
.....ATGCCTCTTTGAGAAGTTTAAC.....	22	0	1	105.00	105	103	2	0	0	0	0
.....CAAATTTGTCAAAGAGGCATACG.....	23	0	1	43.00	43	39	3	0	1	0	0
.....AATGCCTCTTTGAGAAGTTTAAC.....	23	0	1	39.00	39	38	0	1	0	0	0
.....AATGCCTCTTTGAGAAGTTTAA.....	22	0	1	23.00	23	21	1	1	0	0	0
.....ATGCCTCTTTGAGAAGTTTAA.....	21	0	1	20.00	20	15	0	5	0	0	0
.....CAAATTTGTCAAAGAGGCATA.....	21	0	1	20.00	20	9	11	0	0	0	0
.....AATGCCTCTTTGAGAAGTTTA.....	21	0	1	12.00	12	10	2	0	0	0	0
.....CAAATTTGTCAAAGAGGCATAC.....	22	0	1	9.00	9	9	0	0	0	0	0
.....TGCCTCTTTGAGAAGTTTAAC.....	21	0	1	9.00	9	9	0	0	0	0	0
.....ATGCCTCTTTGAGAAGTTTAACT.....	23	1	1	6.00	6	6	0	0	0	0	0
.....CAAATTTGTCAAAGAGGC.....	18	0	1	5.00	5	5	0	0	0	0	0
.....ATGCCTCTTTGAGAAGTTTAACA.....	23	1	1	5.00	5	4	0	1	0	0	0
.....ATGCCTCTTTGAGAAGTTTA.....	20	0	1	4.00	4	4	0	0	0	0	0
.....AATGCCTCTTTGAGAAGTTT.....	20	0	1	4.00	4	4	0	0	0	0	0
.....CAAATTTGTCAAAGAGGCA.....	19	0	1	2.00	2	2	0	0	0	0	0
.....GCCTCTTTGAGAAGTTTAAC.....	20	0	1	2.00	2	2	0	0	0	0	0
.....AAATTTGTCAAAGAGGCATACG.....	22	0	1	2.00	2	2	0	0	0	0	0
.....TGCCTCTTTGAGAAGTTTAACA.....	22	1	1	2.00	2	2	0	0	0	0	0
.....ATGCCTCTTTGAGAAGTT.....	18	0	1	1.00	1	1	0	0	0	0	0
.....GAATGCCTCTTTGAGAAGTTT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....AATGCCTCTTTGAGAAGTTTAACA.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TTTGTCAAAGAGGCATACG.....	19	0	1	1.00	1	1	0	0	0	0	0
.....CAAATTTGTCAAAGAGGCAT.....	20	0	1	1.00	1	0	1	0	0	0	0
.....AATGCCTCTTTGAGAAGTT.....	19	0	1	1.00	1	1	0	0	0	0	0
.....ATGCCTCTTTGAGAAGTTTAAA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TGCCTCTTTGAGAAGTTTAACG.....	22	1	1	1.00	1	1	0	0	0	0	0
.....AATTTGTCAAAGAGGCATACG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TGCCTCTTTGAGAAGTTTAA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TGCCTCTTTGAGAAGTTTA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....AAATTTGTCAAAGAGGCA.....	18	0	2	1.00	2	1	1	0	0	0	0

Anti-sense strand reads

CTACAATTACAATTAATTACATTTCAAATTCGGTGTTTGGTCTTTTTCCTGTTTAAACAGTTTCTCCGTATGCGTCTTAGTTTGCTTACGGAGAAACTCTTCAAATTGGTAAACAGACTAATTTATGTGGTTGATTATTAATATTAATTCGGTGGACA	Read size	# Mismatch	Hit Count	Total Norm	Total
**********.....((((.((((((..(((((((.(((((((((((((.((..........)).)))))))))))))).))))))..)).)))).))))).....**********					
No data available in table					

Show Alignment With Reads

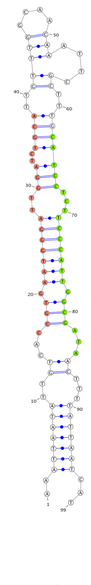
Re-alignment of all predicted orthologs

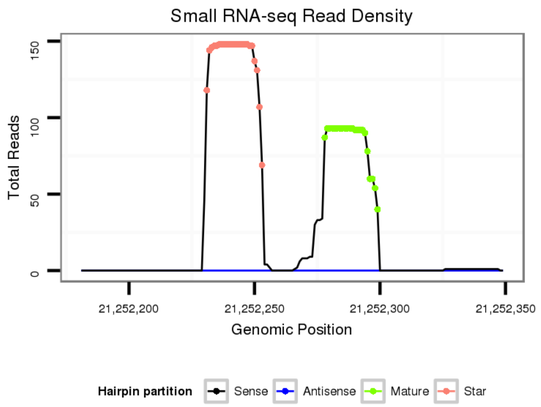
Species	Coordinate	ID	Alignment
droAna3	scaffold_12916:5574498-5574655 +	dan_107	GATGTTAATGTTAATTAATGTAAAGTTTAAGCCACAAACCAGAAAAAGGACAAATTTGTCAAAGAGGCATACGCAGAATCAAACGAATGCCTCTTTGAGAAGTTTAACCATTTGTCTGATTAAATACACCAACTAA---TAATTATAAT-TAAGCCACCTGT
droBip1	scf7180000396568:1258763-1258911 -		TAT---------ATTAATGTAGCTTCTAGTCACTAGACAGCAAAAGGACGAATTTGTCAAAGAGGCATTAAAAGTATAAAATCAATGCCTTTATGACAATTTTCACCATTTTGCTGTTAAAAACACCATCTAA---TAATAATAATTTAAGCCACCAGT
droRho1	scf7180000779523:214366-214408 +		ATA----------AAAAACATTTACTAAATTTAATTATTCAT-TATTGTTATCTT
droBia1	scf7180000302408:1816275-1816310 +		AGA----------ATACCGAATAA---TAATTATTAT-TTAGTCTTTTCT
droSec2	scaffold_24:655918-655919 +		GT----------------------

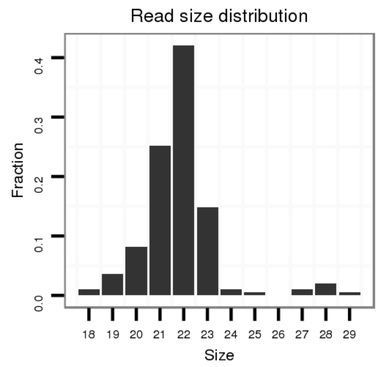
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_94	**scaffold_13340:21252231-21252299 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

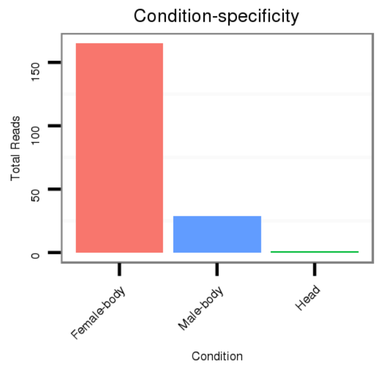
Legend: mature star mismatch in alignment mismatch in read

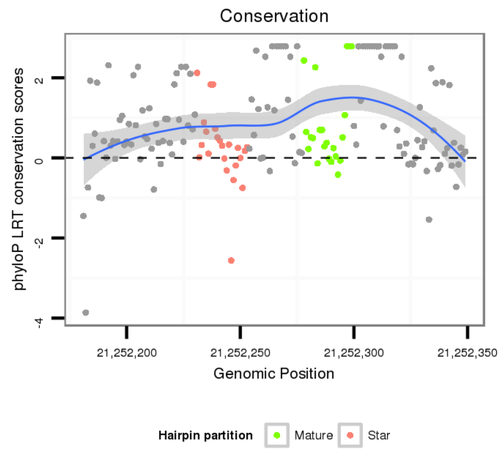
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TCCTGCAACACAATTTTAATGCGCAGTACAGCCAGAAATTAATATTGTCACCGTGAATGGGATTGGATCTGCATTGTTTGGCAACAAATTCGCTTTGCATCCTCTTCCCATTGGCGATAACTTTTATTAATCATTTAATTCGGCTGTAAAAAGTTGTGGGTGTATGGGT	Read size	# Mismatch	Hit Count	Total Norm	Total	female body	V105 male body	V055 head	V106 head
..CATCCTCTTCCCATTGGCGATT	22	1	1	48.00	48	47	1	0	0
..CATCCTCTTCCCATTGGCGATA	22	0	1	35.00	35	33	1	1	0
...CCGTGAATGGGATTGGATCTGCA	23	0	1	29.00	29	24	5	0	0
...ACCGTGAATGGGATTGGATCTGCA	24	0	1	23.00	23	21	2	0	0
...CCGTGAATGGGATTGGATCTGC	22	0	1	22.00	22	7	15	0	0
..CATCCTCTTCCCATTGGCGAT	21	0	1	13.00	13	11	2	0	0
...CCGTGAATGGGATTGGATCTG	21	0	1	12.00	12	11	1	0	0
...CGTGAATGGGATTGGATCTGCA	22	0	1	12.00	12	11	1	0	0
..TTTGCATCCTCTTCCCATTGGC	22	0	1	11.00	11	11	0	0	0
...ACCGTGAATGGGATTGGATCTGC	23	0	1	11.00	11	1	9	0	1
..TTTGCATCCTCTTCCCATTGG	21	0	1	10.00	10	9	1	0	0
..CATCCTCTTCCCATTGGCGATTT	23	2	1	6.00	6	6	0	0	0
...ACCGTGAATGGGATTGGATCTG	22	0	1	6.00	6	6	0	0	0
..CATCCTCTTCCCATTGGCGA	20	0	1	5.00	5	5	0	0	0
..ATCCTCTTCCCATTGGCGATA	21	0	1	5.00	5	5	0	0	0
...CCGTGAATGGGATTGGATC	19	0	1	5.00	5	5	0	0	0
...CGTGAATGGGATTGGATCTGC	21	0	1	5.00	5	3	2	0	0
...CCGTGAATGGGATTGGATCT	20	0	1	4.00	4	4	0	0	0
...ACCGTGAATGGGATTGGATC	20	0	1	4.00	4	2	2	0	0
..ATCCTCTTCCCATTGGCGATTT	22	2	1	4.00	4	4	0	0	0
...CGTGAATGGGATTGGATCTG	20	0	1	4.00	4	4	0	0	0
..ATTCGCTTTGCATCCTCTTCCCATTGGC	28	0	1	3.00	3	3	0	0	0
..TTTGCATCCTCTTCCCATTGGCT	23	1	1	3.00	3	2	1	0	0
..TTCGCTTTGCATCCTCTTCCCATTGGC	27	0	1	2.00	2	2	0	0	0
..CATCCTCTTCCCATTGGCGACT	22	2	1	2.00	2	2	0	0	0
..TTGCATCCTCTTCCCATTGG	20	0	1	2.00	2	2	0	0	0
..CATCCTCTTCCCATTGGCGATAT	23	1	1	2.00	2	2	0	0	0
...CCGTGAATGGGATTGGATCTGT	22	1	1	2.00	2	0	2	0	0
..ATCCTCTTCCCATTGGCGATTT	21	1	1	2.00	2	2	0	0	0
...CGTGAATGGGATTGGATCTGCATT	24	0	1	2.00	2	1	1	0	0
..CATCCTCTTCCCATTGGCGACTT	23	3	1	1.00	1	1	0	0	0
...CGTGAATGGGATTGGATCT	19	0	1	1.00	1	1	0	0	0
..CATCCTCTTCCCATTGGCGT	20	1	1	1.00	1	0	0	1	0
...CCGTGAATGGGATTGGATCTGCAC	24	1	1	1.00	1	1	0	0	0
..TTGCATCCTCTTCCCATTGGC	21	0	1	1.00	1	1	0	0	0
....AATGGGATTGGATCTGCATTG	21	0	1	1.00	1	1	0	0	0
...CGTGAATGGGATTGGATCTGCATTG	25	0	1	1.00	1	1	0	0	0
..TTTGCATCCTCTTCCCATTGGT	22	1	1	1.00	1	1	0	0	0
..TGAATGGGATTGGATCTG	18	0	1	1.00	1	1	0	0	0
...CGTGAATGGGATTGGATC	18	0	1	1.00	1	1	0	0	0
..ATTCGCTTTGCATCCTCTTCCCATTGGCT	29	1	1	1.00	1	1	0	0	0
..CATCCTCTTCCCATTGGCGATAC	23	1	1	1.00	1	1	0	0	0
...CGTGAATGGGATTGGATT	18	1	1	1.00	1	1	0	0	0
..GTAAAAAGTTGTGGGTGTATGG	22	0	1	1.00	1	0	1	0	0
...GTGAATGGGATTGGATCTG	19	0	1	1.00	1	1	0	0	0
..ATTCGCTTTGCATCCTCTTCCC	22	0	1	1.00	1	1	0	0	0
...ACCGTGAATGGGATTGGA	18	0	1	1.00	1	0	0	1	0
..ATCCTCTTCCCATTGGCGAT	20	0	1	1.00	1	1	0	0	0
...ACCGTGAATGGGATTGGATCC	21	1	1	1.00	1	0	1	0	0
...GTGAATGGGATTGGATCTGCA	21	0	1	1.00	1	1	0	0	0
..AATTCGCTTTGCATCCTCTTCCCATTGGC	29	0	1	1.00	1	1	0	0	0
..GCTTTGCATCCTCTTCCCATTG	22	0	1	1.00	1	1	0	0	0
...CCGTGAATGGGATTGGAA	18	1	1	1.00	1	1	0	0	0
...ACCGTGAATGGGATTGGATCTGCAC	25	1	1	1.00	1	0	1	0	0
...ACCGTGAATGGGATTGGATCTGT	23	1	1	1.00	1	0	1	0	0
..GCATCCTCTTCCCATTGGCGA	21	0	1	1.00	1	1	0	0	0
..CATCCTCTTCCCATTGGCGAC	21	1	1	1.00	1	0	1	0	0
...ACCGTGAATGGGATTGGATCT	21	0	1	1.00	1	1	0	0	0
..AAATTCGCTTTGCATCCTCTTCCCATTG	28	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

AGGACGTTGTGTTAAAATTACGCGTCATGTCGGTCTTTAATTATAACAGTGGCACTTACCCTAACCTAGACGTAACAAACCGTTGTTTAAGCGAAACGTAGGAGAAGGGTAACCGCTATTGAAAATAATTAGTAAATTAAGCCGACATTTTTCAACACCCACATACCCA	Read size	# Mismatch	Hit Count	Total Norm	Total	V039 embryo
..GTAAAAAGTTGTGGGTGTATGG	22	0	1	1.00	1	0	0

Show Alignment With Reads

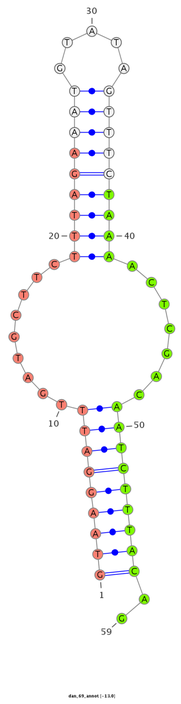
Re-alignment of all predicted orthologs

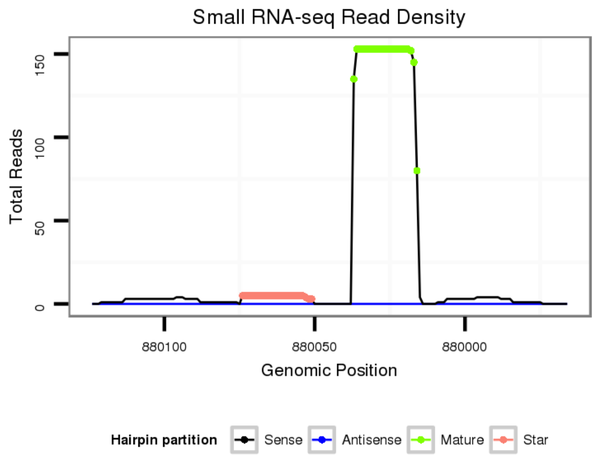
Species	Coordinate	ID	Alignment
droAna3	scaffold_13340:21252181-21252349 +	dan_94	TCC----------TG----------CAACACA-ATTTTAATGCGCAGTACAGCCAGAAATTAATATTG-TC----------ACCGTGAATG----------GGATTGGA-----TCTGCATTG--TT-TGGC-AACAAATTCGCTTTGCATCCTC---TTCCCA-TTGGCGATA---A-----CTTTTATTAATCATTTAATTC-GGCTGTAAAAAG----------TTGTGGG---TGTATGGGT
droBip1	scf7180000396413:1200573-1200741 -		TAC----------TG----------CAACAAA-ATTTTAATGCGCAGTACAGCCTGAAATTAATATTG-TC----------ACCGTGAATG----------GGATCGGA-----TCTGCATTG--TT-TGGC-AACAAATTCGCTTTGCATCCTC---TTCCCA-TTGGTGATA---A-----CTTTTATTAATCATTTAATTC-GGTTGTAAAAAA----------TGGTGGT---TGTGTGGGT
droKik1	scf7180000302390:170899-170986 +		A---
droFic1	scf7180000454106:249482-249642 -		TCT----------TC----------CACTGAA-ATGTTAATGCGCAGTTCAGCCAGAAATTAATATTG-TC----------ACCGTGGAT----------GCGTGGGA-----TCTGCATTG--TT-TGGC-GACAAATTTGAGTTGGTTCCTTC----GCGTTCGGCGATA---A-----CTTTTATTAATCGTTTAATTC-GGGAGTATAAAG----------TGGGGGG---AG------
droEle1	scf7180000491280:2535215-2535377 +		CTT----------TT----------CACCAAA-ATGTTAATGCGCAGTTCAGCCACAAATTAATATTG-TC----------ACCGTGGAT----------GCATGGGA-----TCCGCTTG--TT-TGGC-TACAAATTTGAGTTGGTTCCTTC----GCGTTGGCGATA---A-----CTTTTATTAATCATTTAATTC-GGGAGTATAAAG----------TGGGTGG---AGTGG---GT
droRho1	scf7180000780069:78860-79019 +		CTT----------TT----------CACCAAA-ATGTTAATGCGCAGTTCAGCCAGAAATTAATATTG-TC----------CCGTGGAT----------GCATGGTA-----TCGCTTG--TT-TGGC-GACAAATTTGAGTTGGTTCCTTC----GCGCTTGGCGATA---A-----CTTTTATTAATCATTTAATTC-GGGAGTATAAAG----------TGGGTGG---AGT------
droBia1	scf7180000302113:1148073-1148221 -		AA----------AA----------AAGAAA-ATGTTGATGCGCAGTTCAGCAGAAATTAATACTG--AA----------GAT----------GCTTGCCC-----TCTCGTTG--TT-TGGC-AACAAATTTGAGTTGGTTCCTGC----GTATTTGGCGATA---A-----CTTTTATTAATCATTTAATTC-GGGAGTATAAAC----------TGGGTGG---G------GT
droTak1	scf7180000415765:702487-702640 +		AA----------AA----------AAGAAA-ATGTTAATGCGCAGTTCAACCAGAAATTAATATTG--AA----------GAT----------GCTTGCCA-----TCTCGTTG--TT-TGGC-GACAAATTTGAGTTCCTTCCTC----CCATTGGCGATA---A-----CTTTTATTAATCATTTAATTC-GGGAGTATAATC----------TGGATGG---AGTGGAGGT
droEug1	scf7180000409555:728615-728774 +		CCC----------TG----------AAGAAA-ATGTTAATGCGCAGTTCGGCAGAAATTAATATTG-TC----------ACGAAGGAT----------CCATGGCA-----TCTTGCTTG--TT-TGGC-GACAAATTTGAGTTGGTTCCTTT----GCATTTCACGATA---A-----CTTTTATTAATCATTTAATTC-GGGAGTATAAAG----------TGGGTGG---AGTGG----
dm3	chr3R:26233370-26233536 +		CTC----------AG----------CATCAAAATTGTTAACGCGCAGTTCAGCAGAAATAAATATTG-TCAC----------ACTG-CGAT----------GCATGGGA-----TCACTTTTG--TT-CGGC-GACAAATTTGAGTTGGTTCTTG----CCATT-TGCGATA---A-----CTTTTATTAATCATTTAATTC-GGGAATTATAATC----------TGGCTGG---AGCGCAGAT
droSim2	3r:25552565-25552729 +		CTC----------AG----------CATCAAAATTGTTAATGCGCAGTTCAGCCAGAAATTAATATTG-TC----------ACTG-GGAT----------GCATGGGA-----TCACTTTTG--TT-CGGC-GACAAATTTGAGTTGGTTCCTTG----CCATT-TGCGATA---A-----CTTTTATTAATCATTTAATTC-GGGAGTATAATC----------TGGCTGG---AGCGCAGAT
droSec2	scaffold_4:5058088-5058252 +		CTC----------AG----------CATCAAAATTGTTAATGCGCAGTTCAGCCAGAAATTAATATTG-TC----------ACTG-GGAT----------GCATGGGA-----TCACTTTTG--TT-CGGC-GACAAATTTGAGTTGGTTCCTTG----CCATT-TGCGATA---A-----CTTTTATTAATCATTTAATTC-GGGAGTATAATC----------TGGCTGG---AGTGCAGAT
droYak3	3R:27150412-27150549 +		T----------AA----------AAAAAA-ATGTTAATGCGCAGTTCAGCCAGAAATTAATATTG-TC----------ACCG-GGAT----------GCATGACC-----ACTTTTCTG--TT-TGGC-GACAAATTTGAGTTGGTTCCTTC----GCATTTGGCGATA---A-----CTTTTATTAATCATTTAATTC-GGGAGTATAAATA----------AAAAAA---AAAAAAA
droEre2	scaffold_4820:1779956-1780116 -		CA----------AA----------AAAAAA-TCATAAATTGCTAATGCGCAGTTCAGCCAGAAATTAATATTG-TC----------ACTG-GAAT----------GCAAGGGT-----CGTCGTCTG--TT-TGGC-GACAAATTTGAGTTGGTTCCTTC----GCGTTGCCGATA---G-----CTTTTATTAATCATTTAATTC-GGGAGTATAATG----------TGGCCGG---AGTGCAGAT
dp5	2:1291838-1292033 -		TTC----------TG----------AAAACGA-ATTTTAGTGCGCATTTTA-GCGAAAATTAATATTG-TC----------ACAATGGATGGATGCTGCTGGATGGCTGCATGGCTGGATGGACTGCA-----TCTCGTTG--TT-CGGTTTACAAATTTGAGTTGGTCGC----------GGATTCATGATA---A-----CTTTTATTAATCATTTAATGC-TGTGTCGTGGCAGGGGCAGGAGC----GGGGCTG---TGGT
droPer2	scaffold_7:4092400-4092615 -		TGCCCTGCCTTGCCCTTTGCTTCT----------AAAAAA-ATTTTAGTGCGCATTTTA-GCGAAAATTAATATTG-TC----------ACAATGGATGGATGCTGCTGGATGGCTGCATGGCTGGATGGACTGCA-----TCTCGTTG--TT-CGGTTTACAAATTTGAGTTGGTCGC----------GGATTCATGATA---A-----CTTTTATTAATCATTTAATGC-TGTGTCGTGGCAGGGGCAGGAGC----GGGGCTG---TGGT
droWil2	scf2_1100000004943:9730402-9730540 -		TAT----------TG----------GGGCGTGACTATGCAGTCGTCTGTGTCGCTTAAATTAAAATGC----------TTA----------AC----------ACAATG----------A-----GTTAGTTTA--TT-TCGCAAACAAATTTGATTGGTTCT----------GCATTGATTAGAAATTTGTTTTTATTAATCGTTTAAGAG--T----------AAAAAA---AAAAAAA
droVir3	scaffold_12855:3342792-3342925 +		GGG----------TG----------AAAAAA-CGTGACTATGCAGCACAAATAAGAACA-ACATTTGTTGATAT---GCTAACAAT----------GCAGCC-----CCACGTCTG--TT-CTGC-AACAAATTTGTCTGC----------GAGCTATAATA---AT----ATTTTATTAATCATTTAATC-TCGA-AGTCGCC----------TGC----AAAAAAG
droMoj3	scaffold_6540:9845201-9845303 -		CTA----------TG----------CAAAAA-AAAAAAAAAAAAAAAAAAAAAAAAAA-AA----------AAAAAAA----------AAAAAAAAAAAAAAAAAAAA

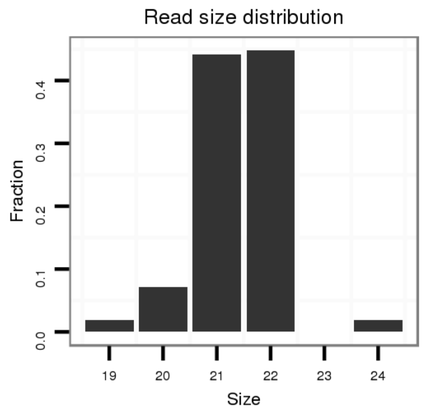
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_69	**scaffold_13340:880016-880074 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

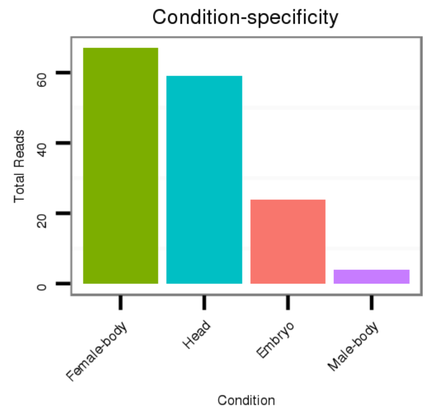
Legend: mature star mismatch in alignment mismatch in read

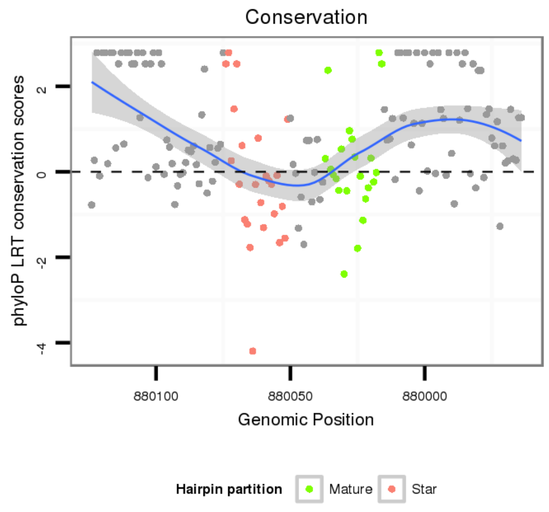
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF17464-in]; CDS [Dana\GF17464-cds]; CDS [Dana\GF17464-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GGTCAACAAGGACAAGGAGACGCAGACTAATAGCCTAAACCTGGCGCCCAGTAAGGATTTGATGCTTCTTTAGAAATGTATAGTTTCTAAAACTCGACAATCTTTACAGACATTTTCAACGTGGAAGAGTTCCTCTTGCAAACGGCCAATGCTGCCAAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	M058 embryo	V055 head	V105 male body	V039 embryo
**********(((((((((.....(((((((((.....)))))))))).....)))))))..**********											
.....TAAAACTCGACAATCTTTACAGT.....	23	1	1	124.00	124	69	9	25	7	10	4
.....AAAACTCGACAATCTTTACAGT.....	22	1	1	94.00	94	48	16	19	3	4	4
.....TAAAACTCGACAATCTTTACAG.....	22	0	1	68.00	68	18	27	14	7	2	0
.....TAAAACTCGACAATCTTTACA.....	21	0	1	59.00	59	19	27	5	6	1	1
.....AAAACTCGACAATCTTTACAG.....	21	0	1	8.00	8	0	6	2	0	0	0
.....AAAACTCGACAATCTTTACA.....	20	0	1	6.00	6	0	4	1	1	0	0
.....TAAAACTCGACAATCTTTAC.....	20	0	1	5.00	5	2	1	1	0	1	0
.....AAAACTCGACAATCTTTACAGC.....	22	1	1	5.00	5	0	0	5	0	0	0
.....TAAAACTCGACAATCTTTACAGC.....	23	1	1	4.00	4	0	0	4	0	0	0
.....GTAAGGATTTGATGCTTCTTTAGA.....	24	0	1	3.00	3	3	0	0	0	0	0
..........ACAAGGAGACGCAGACTAATAGCCT.....	25	0	1	2.00	2	2	0	0	0	0	0
.....AAAACTCGACAATCTTTACAGA.....	22	0	1	2.00	2	0	0	2	0	0	0
.....TAAAACTCGACAATCTTTACAGA.....	23	0	1	2.00	2	0	0	2	0	0	0
.....ACGTGGAAGAGTTCCTCTTGCA.....	22	0	1	2.00	2	2	0	0	0	0	0
.....AAAACTCGACAATCTTTAC.....	19	0	1	2.00	2	1	1	0	0	0	0
.....TAAAACTCGACAATCTTTACAA.....	22	1	1	1.00	1	0	0	1	0	0	0
.....AAAACTCGACAATCTTTACAGTT.....	23	2	1	1.00	1	0	0	1	0	0	0
.....GTTCCTCTTGCAAACGGCCAAT.....	22	0	1	1.00	1	0	1	0	0	0	0
.....GTAAGGATTTGATGCTTCTTT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....AATAGCCTAAACCTGGCGCCC.....	21	0	1	1.00	1	0	0	1	0	0	0
.....AAAACTCGACAATCTTTACACT.....	22	2	1	1.00	1	1	0	0	0	0	0
.....GTAAGGATTTGATGCTTCTTTA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TAAAACTCGACAATCTTTA.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TAAAACTCGACAATCTTTACAC.....	22	1	1	1.00	1	0	0	1	0	0	0
.....AAAACTCGACAATCTTTACAG.....	21	1	1	1.00	1	0	1	0	0	0	0
.....TAAAACTCGACAATCTTTACAGTT.....	24	2	1	1.00	1	0	0	1	0	0	0
.....AAAACTCGACAATCTTTACAGTA.....	23	2	1	1.00	1	0	0	1	0	0	0
.....TCAACGTGGAAGAGTTCCTCT.....	21	0	1	1.00	1	0	0	0	0	1	0
...CAACAAGGACAAGGAGACGCAGACTAAT.....	28	0	1	1.00	1	0	0	0	0	1	0

Anti-sense strand reads

CCAGTTGTTCCTGTTCCTCTGCGTCTGATTATCGGATTTGGACCGCGGGTCATTCCTAAACTACGAAGAAATCTTTACATATCAAAGATTTTGAGCTGTTAGAAATGTCTGTAAAAGTTGCACCTTCTCAAGGAGAACGTTTGCCGGTTACGACGGTTA	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	M058 embryo
**********(((((((((.....(((((((((.....)))))))))).....)))))))..**********							
.....AATAGCCTAAACCTGGCGCCC.....	21	0	1	1.00	1	0	0
.....AAAACTCGACAATCTTTACACT.....	22	2	1	1.00	1	1	0
.....GTAAGGATTTGATGCTTCTTTA.....	22	0	1	1.00	1	1	0
.....TAAAACTCGACAATCTTTA.....	19	0	1	1.00	1	0	0
.....TAAAACTCGACAATCTTTACAC.....	22	1	1	1.00	1	0	0
.....AAAACTCGACAATCTTTACAG.....	21	1	1	1.00	1	0	0
.....TAAAACTCGACAATCTTTACAGTT.....	24	2	1	1.00	1	0	0
.....AAAACTCGACAATCTTTACAGTA.....	23	2	1	1.00	1	0	0
.....TCAACGTGGAAGAGTTCCTCT.....	21	0	1	1.00	1	0	0
...CAACAAGGACAAGGAGACGCAGACTAAT.....	28	0	1	1.00	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13340:879964-880124 -	dan_69	---GGTCAACAAGGACAAGGAGACGCAGACTAATAGCCTAAACCTGGCGCCC---AGTAAGGATTT-GA----T-GCTTCT-------TT--AGAA----------A--TGTATAGTTTCTAAAACTC----GA----CA-A-TCTT--TACAGACATTTTCAACGTGGAAGAGTTCCTCTTGCAAACGGCCAATGCTGCCAATGG
droBip1	scf7180000394085:116610-116765 +		---GGTCAACAAGGACAAGGAGACGCAGACCAATCGGTTGAACCTGGCGTCC---AGTAAGGATTT-CA----T-GCTTCT-------CC--GAAA----------A--TGTATAATTTTAAC----G----A----CA-A-TCTC--TCAGATATTTTCAACGTGGAAGAGTTCCTCCTGCAAACGGCCAATGCTGCCAACGG
droKik1	scf7180000302810:303704-303862 +		---CGTGAACAAGGACAAGGAGACCAGACCAGCGCCATGAACTTGGCTTCC---AGTAGCAACCA-GAT--T-TGGCTTC-------CC--TTAA----------A--AGAG---TTGCTAACCG-----AT----CC-CTCCCT--TGCAGATATATTCAACGTGGAGGAGTTCTTCCTGCAAACGGCAAGTGCTGCCAACGG
droFic1	scf7180000453800:2228526-2228684 -		---CATGAACAAGGATAAGGAGACTCAGACTAGCAGCAGTGAACTTGGCTTCC---AGTCAGGATCC-CC----T-TAATATATA-----AT--TTAA----------A--CTC----CTTTAACAA-----TA----TA-TTCAAT--TACAGATATTTTCAACGTTGAGGAGTTCCTCCTGCAATCGGCCAATGCAGCCAATGG
droEle1	scf7180000491080:82504-82668 +		---CATGAACAAGGACAAGGAGACTCAGACCAGCTCCATGAACTTGGCTTCC---AGTCAGAATCA-AA----TGGGTTA-------AA--ATAA----------A--ATTTTC---ATTTAACAG-----AAGATTTATTTCCTT--TACAGATATTTTCAACGTGGAGGAGTTCTTGCTTGCAGTCGGCCAATGCAGCCAATGG
droRho1	scf7180000768822:56460-56623 +		---TATGAACAAGGACAAGGAGACTCAGACCAGCACCATGAACTTGGCTTCC---AGTCAGGACTA-AA----TAACTTTT-------CT--AA----------TAA-AATGCC---ATTTAACAG-----AATGTTTA-TTCTCC--TACAGATATTTTCAACGTGGAAGAGTTCTTGCTTGCAATCGGCCAATGCAGCCAATGG
droBia1	scf7180000302402:8232790-8232957 -		---CATGAACAAAGACAAGGAGACTCAGACCAGCACTCTGAACATGGCTTCC---AGTCAGGATAC-CC----TAGGTTATACTTTACC--CTAC----------G--TTATATATTTCTAACCA-----AA----TG-TTCCCT--TACAGATATTTTCAACGTGGAGGAGTTCCTCTTGCAATCAGCCAACGCAGCCAATGG
droTak1	scf7180000415811:23564-23721 +		---CATGAACAAAGACAAGGAGACTCAGACCAGCTCCATGAACTTGGCTTCC---AGTAAGGATCC-GC----TATGCTTA-------CA--AA----------TCA-ATTGTC---TTCTTAACCA-----AA----TA--CTCT--TACAGATATTTTCAACGTGGAAGAGTTCTTGCTGCAATCGGCCAATGCAGCCAATGG
droEug1	scf7180000409881:514885-515046 +		---GATGAACAAGGACAAGGAGACTCAGACCAGCACCATGAATATGCCATCC---AGTCAGAAATT-GA----TA-TTCAA-------CA--AA----------TTA-AATTTC---TTTTTACTTATACATA---C--TA--TATT--TTTAGATATTTTCAACGTTGAGGAATTGTTGCTTGCAATCAGCCAATGCCGCTAATGG
dm3	chr3R:6141410-6141567 -		---CATGAACAAGGACAAGGAGACTCAGACCAGCTCAACGAACTTGGCTTCC---AGTCAGTATTC-GC----TAGATTTG-------CC--ATAA----------A--TGCA---TTCTAAACAA-----AA----TA-GTCTCT--TACAGATATATTCAAATGTGGATGAGTTCTTGCTTGCAATCGGCCAATGCCGTTAATGG
droSim2	3r:14924919-14925076 +		---CATGAACAAGGACAAGGAGACTCAAACCAGCTCAACGAACTTGGCTTCT---AGTCAGTATTC-GC----TAGATTT-------CC--ATAA----------A--TGCG---TTATAACAA-----AA----TA-ATCTCT--TACAGATATATTCAACGTAGAGGAGTTCTTGCTTGCAAACGGCCAATGCCGCTAGTGG
droSec2	scaffold_0:15790618-15790775 +		---CATGAACAAGGACAAGGAGACTCAAACCAGCTCAACGAACTTGGCTTCT---AGTCAGTATTC-CC----TAGATTA-------CC--ATAA----------A--TGCG---TTATAACAA-----AA----TA-ATCTCT--TACAGATATATTCAACGTGGAGGAGTTCTTGCTTGCAAACGGCCAATGCCGCTAGTGG
droYak3	3R:10177819-10177977 -		---CATGAACAAGGACAAGGAGACTCAGACCAGCTCAACGAACTTGGCGTCC---AGTCAGTACAC-CC----TAGATATA-------CA--TAAA----------A--TGCA---ATCTAAGCAA-----TA----TA-TTATTATCT--TACAGATATATTCAACGTGGAGGAGTTCTTGCTTGCAATCGGCCAATGCCGCCAATGG
droEre2	scaffold_4770:15465180-15465337 +		---CATGAATAAGGACAAGGAGACTCAGACCAGCTCAACGAACTTGGCTTTC---AGTCAGTACTC-GC----TAGGTTA-------CA--ATAA----------A--TGCA---TTCTAAACAA-----AA----TA-ATCTCT--AATAGATATATTCAACGTGGAGGAGTTCTTGCTGCAATCAGCCAATGCAGCCAATGG
dp5	2:7322480-7322636 +		---CGTTAACAAGGACAAGGAGACGCAGACAACCA------GCTCGACTTCC---AGTAAGTCTCCAAAT--T-CTGGTCA-------CCTTTTGA----------A--CGCC---GTCT--T---TAAATG---GTCTA-TTTTCGTGCTTAGATGTGTTCAATGTCGAGGAGTTTCTGCTGCAATC---GAATTGGTCCAAGAA
droPer2	scaffold_0:1185484-1185640 +		---CGTTAACAAGGACAAGGAGACGCAGACAACCA------GCTCGACTTCC---AGTAAGTCTCCAAAT--T-CTGGTCC-------CCTTTTGA----------A--CACC---GTCT--T---TTAATG---GTCTA-TTTTCGTGCTTAGATGTGTTCAATGTCGAGGAGTTTCTGCTTGCAATC---GAATTGGTCCAAGAA
droWil2	scf2_1100000004943:14963694-14963865 +		ATCTATGAATAAGGATAAGGAAACCAAACCTCCAGTGCAGCTATGAGCGGC---AGTAAGTAGTT-CT----ATGCTTA-------GA--GAAATACCAGTCTATTAAAT--A--AACC---GTTA--T---TTT---A----TA-G-GCTA--TAAAGGTGCGTTCAATATGCAGGACTATGTGCTTCAATCGGCCAATGCAGTCAATGG
droVir3	scaffold_13047:1003814-1003979 +		---AGTTAATAAAGACAAGGAGACCAAACATCAGGGATGCAACTGCTACCCATTAGTCAGTGAAA--TAAATAAACGCA-------CA--TAAA----------T--CGCA---GTC-AAATATAT---T----TA-AAATTATATTTT--TACAGATACGCTTTAATATTGAGGAGTTGCTAGTGCAACGGCCACATGCTGGTATTGG
droMoj3	scaffold_6540:5009550-5009712 +		---CATGAATAAAGACAAGGAGACTCAGACAACAGCTATGCAACTGCTACGTATAAGTAAGTGAAA--TT---T---TTGTAACT--CACATTTA----------C--CATC---GCT--AA---TGAACC--A--TAAATTTTG--CACAGATACCTTCAATATTGAGGAGATTTCTATTGCAAGCTGCGCACGCCGCTCTGG
droGri2	scaffold_14906:5284215-5284376 -		---AGTTAACAAAGACAAGGAGACCAAACAACGGCCACG------TTACCCATTAGTAAGTGCAG--TTATCATGCCGA-------CA-ATTAA----------A--CACA---GCT--AA---CTAATC--ATTTG-CATCCGTTTGCAGACACCTTCAATATTGAGGAGATTTCTGCTGCAAGCAGCGCATACCAGCAATGG

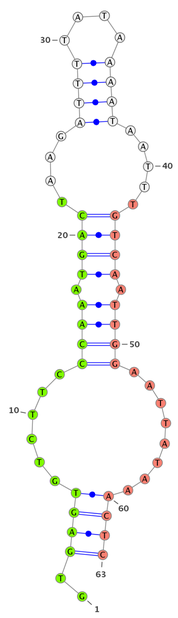
Generated: 09/08/2015 at 07:02 PM

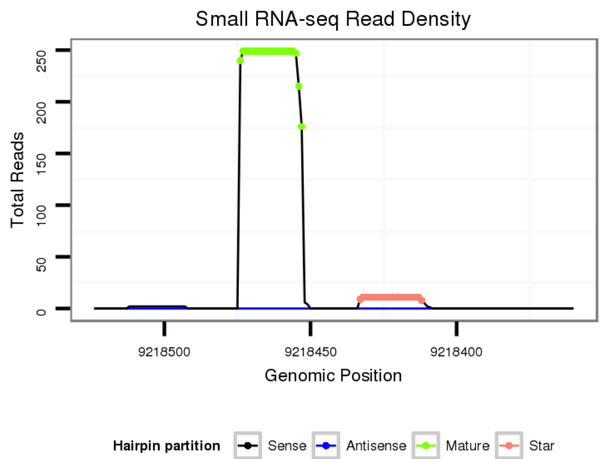
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

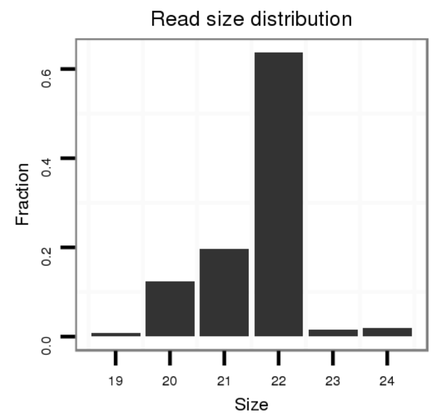
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_1902	**scaffold_13266:9218410-9218474 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

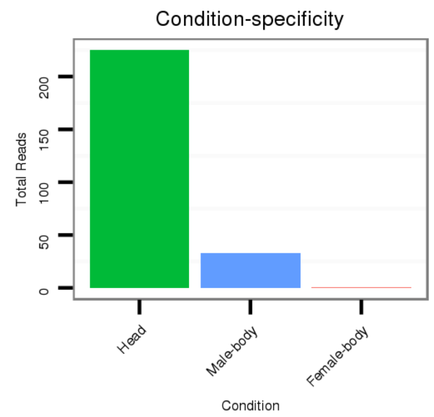
Legend: mature star mismatch in alignment mismatch in read

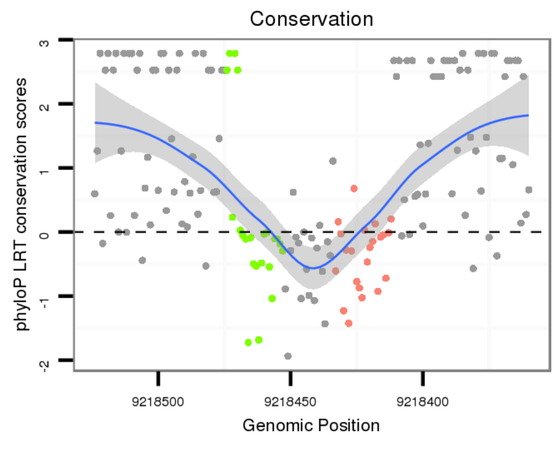
Predicted structure











dan_1902_ensset | 9.2|

Show Alternate Folds

Flybase annnotation

intron [Dana\GF11749-in]; CDS [Dana\GF11749-cds]; CDS [Dana\GF11749-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TCTGCAGCAACTGAACGTGTCTGGTAACCAACTTAGTGAGCTGCCAGTGGGTGAGTGTCTTCCCAAATGACTAAGATTTTATAAAATAATTTGTCAATTGGAATTATAAACTCAGAACTGAGCAGCTTGCGCAATCTGGAGCAGCTGAACATTGCCAAGAATCTG **********..((((.....((((.((((....((((....))))).....)))))..)))))........))))**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	V055 head	M044 female body
.....GTGAGTGTCTTCCCAAATGACT.....	22	0	1	161.00	161	128	22	11	0
.....GTGAGTGTCTTCCCAAATGAC.....	21	0	1	39.00	39	32	3	4	0
.....GTGAGTGTCTTCCCAAATGA.....	20	0	1	32.00	32	22	6	4	0
.....TGAGTGTCTTCCCAAATGACT.....	21	0	1	9.00	9	6	0	2	1
.....GTCAATTGGAATTATAAACTCAGT.....	24	1	1	5.00	5	4	0	0	1
.....GTGAGTGTCTTCCCAAATGACTAA.....	24	0	1	4.00	4	4	0	0	0
.....TGTCAATTGGAATTATAAACTC.....	22	0	1	3.00	3	1	0	2	0
.....TGTCAATTGGAATTATAAACT.....	21	0	1	3.00	3	1	1	1	0
.....TGTCAATTGGAATTATAAACTCAGT.....	25	1	1	3.00	3	2	0	1	0
...........GAACGTGTCTGGTAACCAAC.....	20	0	1	2.00	2	2	0	0	0
.....GTGAGTGTCTTCCCAAATGAA.....	21	1	1	2.00	2	1	0	0	1
.....GTGAGTGTCTTCCCAAATGACTA.....	23	0	1	2.00	2	2	0	0	0
.....TGTCAATTGGAATTATAAACTCA.....	23	0	1	2.00	2	2	0	0	0
.....GTGAGTGTCTTCCCAAATG.....	19	0	1	2.00	2	2	0	0	0
.....GTCAATTGGAATTATAAACTCA.....	22	0	1	1.00	1	1	0	0	0
.....TGTCAATTGGAATTATAAACTCAG.....	24	0	1	1.00	1	0	1	0	0
.....GTCAATTGGAATTATAAACTCAGA.....	24	0	1	1.00	1	1	0	0	0
.....TCAATTGGAATTATAAACTCAGT.....	23	1	1	1.00	1	0	0	0	1
.....TAGTGAGCTGCCAGTGGAAC.....	20	3	8	0.13	1	1	0	0	0

Anti-sense strand reads

AGACGTCGTTGACTTGCACAGACCATTGGTTGAATCACTCGACGGTCACCCACTCACAGAAGGGTTTACTGATTCTAAAATATTTTATTAAACAGTTAACCTTAATATTTGAGTCTTGACTCGTCGAACGCGTTAGACCTCGTCGACTTGTAACGGTTCTTAGAC **********..((((.....((((.((((....((((....))))).....)))))..)))))........))))**********	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
droAna3	scaffold_13266:9218360-9218524 -	dan_1902	TCTGCAGCAACTGAACGTGTCTGGTAACCAACTTAGTGAGCTGCCAGTGGGTGAGTG---TCTTCCCAAATGACTAAGAT-T--------------T-------TATAAAATAATTT----------G--TCA-ATTGGAATTATA-AACTCAGAACTGAGCAGCTTGCGCAATCTGGAGCAGCTGAACATTGCCAAGAATCTG
droBip1	scf7180000396427:364061-364225 -		TCTGCAGCAGCTTAACGTGTCTGGTAACCAACTTAGTGAACTGCCAGTGGGTGAGTT---TATTCGAAAAAGACTATGAT-T--------------C-------TGAATAATGATTC----------C--TTT-TTTCGAATCATA-AACTCAGAACTGAGCAGCTTGCGCAATCTGGAGCAGCTGAACATTGCCAAGAATCGG
droKik1	scf7180000302228:105292-105449 -		CCTCCAGCAGCTAAACGTGGCGGCAACCAGCTTACCGAACTACCAGTGGGTGAGTG---GGACTGCCACTGACTATAAG-CC----------CC-------A----ATGC----------A--TTC-GCTTGT--TCCCCTCCCAGAACTGAGCAGCTTGCGCAATTGGAGCAGTGAATATTGCCAAGAACCAA
droFic1	scf7180000454039:1409973-1410064 +		TCTACAGCAACTAAATGTGTCGGGCAATCAGCTCACCGAACTGCCAGTGGGTAAGA-----TCATTTAC---TGAATG--TTACA---------------------------------------AGAAGTTCTGATAATT----------
droEle1	scf7180000491215:519314-519473 -		TCTCCAGCAGCTGAATGTTCGGGCAATCAACTCCCGAACTGCCAGTGGGTGAGTT---GGACCCATTG-AG-TAGGA--------CCT--TTATGGA----GCTT----------A--CAC-CTTTAC-ATCCC-CTTTCAGAGCTGAGCAACTTGCGCAATCTGGAGCACTGAACATAGCCAAGAACCAA
droRho1	scf7180000779957:365877-366038 -		TCTCCAGCAGCTGAATGTGTCGGGCAATCAACTCACCGAATTGCCAGTGGGTGAGTA---GGATCCTTTAGAGATC----------C-CT-G------CCACCATGGA----GTCT----------A--CCC-GCTTAT--CCCA-CTTTCAGAGCTGAGCAGCTTGCGCAATCTGGAGCACCTAAACATCGCCAAGAACCAA
droBia1	scf7180000302291:3200520-3200670 -		TCTCCAGCAGCTGAATGTGTCGGGCAACCAGCTCACCGAACTTCCAGTGGGTGAGTA---GAG---------GTCC----------GCTTCTTGGA----GTCC----------ATGTCC-GCTTAC--TTCG-CTCCCAGAACTGAGCAGCCTGCGCAATCTGGAGCACTGAACATCGCCAAGAACCAA
droTak1	scf7180000412369:38932-39087 +		TCTCCAGCAGCTGAATGTGTCGGGCAATCAGCTCACCGAACTTCCAGTGGGTGAGTA---GTA------GTGGTCC----------TTATCGCGGGG----TTTC-GT----------A--TCC-TTTCAT--TCCGCTCTTCAGAACTGAGCAGCTTGCGCAATCTGGAGCACTGAACATCGCCAAGAATCAA
droEug1	scf7180000409474:1853846-1853997 -		TCTCCAGCAACTAAATGTCTCGGGCAATCAGCTTACCGAACTTCCAGTGGGTAAGTA---GAACA---------TC----------ATGTCATGGA-GCCATTC----------C--TCT-GCTTAT--TCCA-CTCTTAGAGCTGAGCAGCTTGCGCAATCTGGAGCACTGAATATCGCCAAGAACCAA
dm3	chr2R:16124424-16124581 +		TCTCCAGCAGCTGAATGTGTCGGGCAATCAGCTCACCGAACTACCAGTGGGTGAGTA---GGAAGGTTTACAGTCC----------CCACCATGGA----ATCC----------A--TTC-ACTTGT--ACCG-CTTCCAGAGCTAAGTGGTTTGCGCAATCTGGAGCACTGAACATTCGCAAGAACCAA
droSim2	2r:16704657-16704814 +		TCTCCAGCAGCTGAATGTGTCGGGCAATCAGCTCACCGAACTACCAGTGGGTGAGTA---GGAAGGTTTACAGTCC----------CCACCATGGA----ATCC----------A--TTC-ACTTGT--ACCG-CTTCCAGAGCTCAGTGGTTTGCGCAATCTGGAGCACTGAACATCGCCAAGAACCAA
droSec2	scaffold_1:13690674-13690831 +		TCTCCAGCAGCTGAATGTGTCGGGCAATCAGCTCACCGAACTTCCAGTGGGTGAGTA---GGAAGGTTTACAGTCC----------CCACCATGGA----ATCC----------A--TTC-ACTTGT--ACCG-CTTCCAGAGCCTCAATGGTTTGCGCAATCTGGAGCACTGAACATCGCCAAGAATCAA
droYak3	2R:13079097-13079254 -		TCTCCAGCAGCTGAATGTGTCGGGCAATCAGCTCACCGAACTTCCAGTGGGTGAGTA---CGAAGATTTACAGTTC----------CAACCAAGGA----ATCC----------A--TGC-ACTTCG--ACCG-CTTCCAGAACTCAGTGGTTTGCGCAATCTGGAGCACTGAACATCGCCAAGAACCAA
droEre2	scaffold_4845:10274780-10274937 +		TCTCCAACAGCCTGAATGTGTCGGGCAATCAGCTCACCGAACTTCCCGTGGGTGAGTA---GGAAGGTTTACAGTCT----------CTACCACGGA----ATCC----------A--TCC-ACTTCT--TCCG-CTTCCAGAGCTAAGTGGTTTGCGCAATCTGGAGCACTGAACATCGCCAAGAACCAA
dp5	3:17733385-17733558 -		TCTGCAGCAGCTGAACGTCTCGGGCAATCGGCTGACACAACTACCAAAGGGTAAGATACTAC--------------TAGAACG--CCCCAAGAGCGAC--TTCCG-GTATCCACTGCATTGCCCAC----------CCC-ACTGTC--AACC-CTTTCAGAGATGAGCAACTTGCGCAATTGGAACAGTTGAACATATCCAAGAATCGG
droPer2	scaffold_31:60242-60415 +		TCTGCAGCAGCTGAACGTCTCGGGCAATCGGCTGACACAACTACCAAAGGGTAAGATACTAC--------------TAGAACG--CCCCAAGAGCGAC--TTCCG-GTATCCACTGCATTGCCCAC----------CCC-ACTGTC--AACC-CTTTCAGAGATGAGCAACTTGCGCAATTGGAACAGTTGAACATATCCAAGAATCGG
droWil2	scf2_1100000004514:2630546-2630705 +		TTTGCAACAATTGAATGTATCTGCGAATCAGCTGAGGAATTGCCAGTGGGTAAGTGAATAAAACA--TCGATTGGTCGAT--TTA---------------TCTT----------A--CCC-ATTAGCTATTTC-ATTTTAGAGATGAGCAGTTTGCGCAATTTGGAACAACTGAACATTGCCAAAAATCAA
droVir3	scaffold_12875:3358829-3358993 -		CCTACAGCAGCTGAATGTGAGTGGCAATCAGCTGACCGAGCTACCTATTGGGTAAGAA---GCCACCCACTCAGCCT----------CTACATTGCC---ATTTTACTC----------A--TTT-CTATGTACTCTT-CCTGCAGAGCTGAATACCTTGCGCAATTTGGAGCATCTAAATATTGCCAAAAATCAA
droMoj3	scaffold_6496:21784465-21784629 +		CCTCCACACAGCTGAACGTCAGGGGCAATCAGCTGACGAACTGCCTGTGGGTAAGCGAAC--------------CACGCGG-C---CTGC--CCT--T-TGACCGC----GTTC----------ACACTGTAGATGCCC-ACTGTC--T----TCCTCAGAGCTAAACACCTTGCGCAATTTGGAGCAGCTGAATATAGCCAAAAATCAA
droGri2	scaffold_15112:2790398-2790551 +		TCTGCAGCAGCTGAACGTGAGTGGCAATCAGCTGTGCGAGCTGCCAGTGGGTAAGTG---AGAAAC---ACATT------T----------CATTTTGGC----ATCA----------A--TTCACATTT--TCCTCCAATTAGAGCTGAACACCTTGCGCAATTTGGAGCACTGAACATTGCCAAAAATCAA

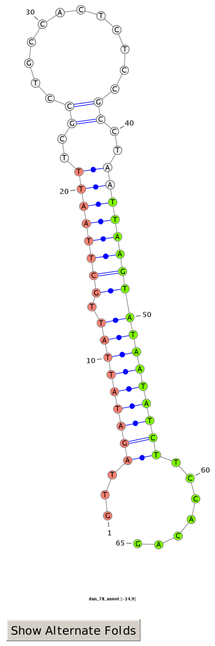
Generated: 09/08/2015 at 10:31 PM

	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

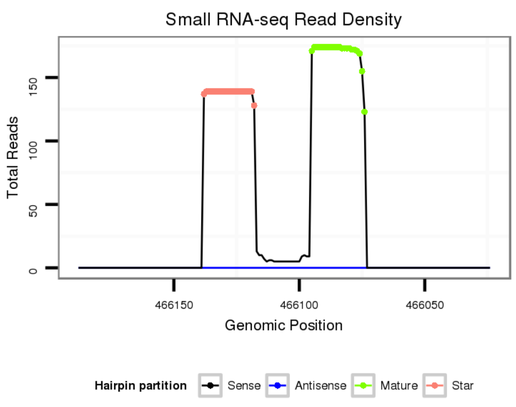
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_78	**scaffold_13248:466074-466138 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

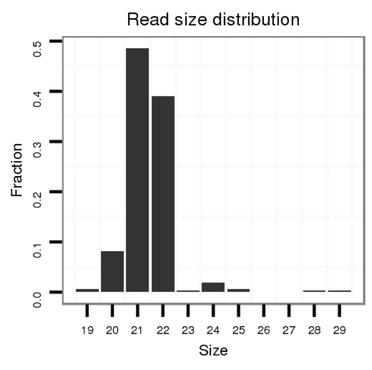
Legend: mature star mismatch in alignment mismatch in read

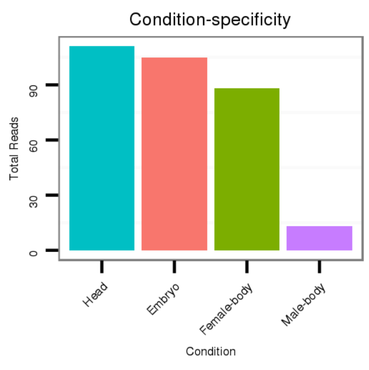
Predicted structure



Show Alternate Folds







Flybase annotation

intron [Dana\GF22450-in]; CDS [Dana\GF22450-cds]; CDS [Dana\GF22450-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GCGTTTATGTACAACCGGGAAGCCGGACACGGCGACAACTGCCGGAGATGGTTAGATATTATTGCTTAATTTCGCCTGCCACTCTCCGCCTAATTAAGTATAATATCTTCCACAGGGCCTACCAGGCCAGGCACCTCATGCCGGAGGTGCCCACCATCGATGACT	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	V106 head	M044 female body	V105 male body	V039 embryo	V055 head
**********...(((((((((.(((((((..((...........)))..)))))))))))))).....**********											
.....TTAAGTATAATATCTTCCACAG.....	22	0	1	120.00	120	59	2	57	0	2	0
.....GTTAGATATTATTGCTTAATT.....	21	0	1	117.00	117	0	97	9	8	2	1
.....TTAAGTATAATATCTTCCACA.....	21	0	1	31.00	31	21	0	10	0	0	0
.....TTAAGTATAATATCTTCCACAGT.....	23	1	1	23.00	23	16	0	5	2	0	0
.....TTAAGTATAATATCTTCCAC.....	20	0	1	12.00	12	12	0	0	0	0	0
.....GTTAGATATTATTGCTTAAT.....	20	0	1	11.00	11	0	7	0	3	0	1
.....TTAAGTATAATATCTTCCACAGC.....	23	1	1	7.00	7	7	0	0	0	0	0
.....GTTAGATATTATTGCTTAATTTCG.....	24	0	1	4.00	4	0	0	2	1	1	0
.....TTAAGTATAATATCTTCCACAGA.....	23	1	1	4.00	4	3	0	1	0	0	0
.....TTAAGTATAATATCTTCCACAA.....	22	1	1	3.00	3	3	0	0	0	0	0
.....CTAATTAAGTATAATATCTTCCAC.....	24	0	1	2.00	2	2	0	0	0	0	0
.....TTAGATATTATTGCTTAATTT.....	21	0	1	2.00	2	2	0	0	0	0	0
.....TTAAGTATAATATCTTCCACAGTA.....	24	2	1	2.00	2	2	0	0	0	0	0
.....TTAAGTATAATATCTTCCACAC.....	22	1	1	2.00	2	2	0	0	0	0	0
.....GTTAGATATTATTGCTTAATTTCGC.....	25	0	1	2.00	2	0	0	2	0	0	0
.....TCGCCTGCCACTCTCCGCCTAA.....	22	0	1	2.00	2	2	0	0	0	0	0
.....GTTAGATATTATTGCTTAATTT.....	22	0	1	2.00	2	0	2	0	0	0	0
.....TAAGTATAATATCTTCCACAG.....	21	0	1	2.00	2	0	0	2	0	0	0
.....GTTAGATATTATTGCTTAATC.....	21	1	1	2.00	2	0	2	0	0	0	0
.....CCTGCCACTCTCCGCCTAATT.....	21	0	1	1.00	1	0	0	1	0	0	0
.....TAAGTATAATATCTTCCACAGTAA.....	24	3	1	1.00	1	0	0	1	0	0	0
.....TAAGTATAATATCTTCCACA.....	20	0	1	1.00	1	0	0	1	0	0	0
.....TGCCACTCTCCGCCTAATTAAGTATAATA.....	29	0	1	1.00	1	0	0	1	0	0	0
.....TTAAGTATAATATCTTCCACAT.....	22	1	1	1.00	1	0	0	1	0	0	0
.....TTAAGTATAATATCTTCCA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....AAGTATAATATCTTCCACAG.....	20	0	1	1.00	1	0	0	1	0	0	0
.....TTAAGTATAATATCTTCCACGT.....	22	2	1	1.00	1	1	0	0	0	0	0
.....GTTAGATATTATTGCTTAATTTCGCCTG.....	28	0	1	1.00	1	0	0	1	0	0	0
.....CTAATTAAGTATAATATCTTCCA.....	23	0	1	1.00	1	0	0	0	1	0	0
.....GTTAGATATTATTGCTTAATG.....	21	1	1	1.00	1	0	1	0	0	0	0
.....CGCCTGCCACTCTCCGCCT.....	19	0	1	1.00	1	0	0	1	0	0	0
.....TAAGTATAATATCTTCCACAGT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TCGCCTGCCACTCTCCGCCA.....	20	1	1	1.00	1	0	0	1	0	0	0
.....CTAATTAAGTATAATATCTT.....	20	0	1	1.00	1	0	0	0	0	0	1
.....TTAAGTATAATATCTTCCACC.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TAATTAAGTATAATATCTTCC.....	21	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

CGCAAATACATGTTGGCCCTTCGGCCTGTGCCGCTGTTGACGGCCTCTACCAATCTATAATAACGAATTAAAGCGGACGGTGAGAGGCGGATTAATTCATATTATAGAAGGTGTCCCGGATGGTCCGGTCCGTGGAGTACGGCCTCCACGGGTGGTAGCTACTGA	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head	M058 embryo	V039 embryo	M044 female body	V106 head
**********...(((((((((.(((((((..((...........)))..)))))))))))))).....**********										
.....TTAAGTATAATATCTTCCACAG.....	22	0	1	120.00	120	59	2	57	0	2	0
.....GTTAGATATTATTGCTTAATT.....	21	0	1	117.00	117	0	97	9	8	2	1
.....TTAAGTATAATATCTTCCACA.....	21	0	1	31.00	31	21	0	10	0	0	0
.....TTAAGTATAATATCTTCCACAGT.....	23	1	1	23.00	23	16	0	5	2	0	0
.....TTAAGTATAATATCTTCCAC.....	20	0	1	12.00	12	12	0	0	0	0	0
.....GTTAGATATTATTGCTTAAT.....	20	0	1	11.00	11	0	7	0	3	0	1
.....TTAAGTATAATATCTTCCACAGC.....	23	1	1	7.00	7	7	0	0	0	0	0
.....GTTAGATATTATTGCTTAATTTCG.....	24	0	1	4.00	4	0	0	2	1	1	0
.....TTAAGTATAATATCTTCCACAGA.....	23	1	1	4.00	4	3	0	1	0	0	0
.....TTAAGTATAATATCTTCCACAA.....	22	1	1	3.00	3	3	0	0	0	0	0
.....CTAATTAAGTATAATATCTTCCAC.....	24	0	1	2.00	2	2	0	0	0	0	0
.....TTAGATATTATTGCTTAATTT.....	21	0	1	2.00	2	2	0	0	0	0	0
.....TTAAGTATAATATCTTCCACAGTA.....	24	2	1	2.00	2	2	0	0	0	0	0
.....TTAAGTATAATATCTTCCACAC.....	22	1	1	2.00	2	2	0	0	0	0	0
.....GTTAGATATTATTGCTTAATTTCGC.....	25	0	1	2.00	2	0	0	2	0	0	0
.....TCGCCTGCCACTCTCCGCCTAA.....	22	0	1	2.00	2	2	0	0	0	0	0
.....GTTAGATATTATTGCTTAATTT.....	22	0	1	2.00	2	0	2	0	0	0	0
.....TAAGTATAATATCTTCCACAG.....	21	0	1	2.00	2	0	0	2	0	0	0
.....GTTAGATATTATTGCTTAATC.....	21	1	1	2.00	2	0	2	0	0	0	0
.....CCTGCCACTCTCCGCCTAATT.....	21	0	1	1.00	1	0	0	1	0	0	0
.....TAAGTATAATATCTTCCACAGTAA.....	24	3	1	1.00	1	0	0	1	0	0	0
.....TAAGTATAATATCTTCCACA.....	20	0	1	1.00	1	0	0	1	0	0	0
.....TGCCACTCTCCGCCTAATTAAGTATAATA.....	29	0	1	1.00	1	0	0	1	0	0	0
.....TTAAGTATAATATCTTCCACAT.....	22	1	1	1.00	1	0	0	1	0	0	0
.....TTAAGTATAATATCTTCCA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....AAGTATAATATCTTCCACAG.....	20	0	1	1.00	1	0	0	1	0	0	0
.....TTAAGTATAATATCTTCCACGT.....	22	2	1	1.00	1	1	0	0	0	0	0
.....GTTAGATATTATTGCTTAATTTCGCCTG.....	28	0	1	1.00	1	0	0	1	0	0	0
.....CTAATTAAGTATAATATCTTCCA.....	23	0	1	1.00	1	0	0	0	1	0	0
.....GTTAGATATTATTGCTTAATG.....	21	1	1	1.00	1	0	1	0	0	0	0
.....CGCCTGCCACTCTCCGCCT.....	19	0	1	1.00	1	0	0	1	0	0	0
.....TAAGTATAATATCTTCCACAGT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TCGCCTGCCACTCTCCGCCA.....	20	1	1	1.00	1	0	0	1	0	0	0
.....CTAATTAAGTATAATATCTT.....	20	0	1	1.00	1	0	0	0	0	0	1
.....TTAAGTATAATATCTTCCACC.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TAATTAAGTATAATATCTTCC.....	21	0	1	1.00	1	1	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13248:466023-466188 -	dan_78	GCGTTTATGTACAACCGGGAAGCCGGACACGGCGACAACTGCCGGAGATGGTTAGATATTA----------TTGCTT-AATTT-------CGCCTGCCACTCTCCGCC----------TAATTAAGTATAATATCTTCCACAGGGCCTACCAGGCCAGGCACCTCATGCCGGAGGTGCCCACCATCGATGACTG
droBipl	scf7180000394734:15700-15864 +		GCGTTCATGTATAACCGGGAAGCCGGACACGGCGACAATTGCCGTCGATGGTTAGATATTC----------TATACTTAATTT-------CGCTCTCGAAT-CCGCC----------TAATTAAGTATAATATCTTCGCAGGGCCTACCAGGCCAAGCACCTAATGCCGGATGTGCCCACCATCGATGCATG
droKik1	scf7180000302517:290431-290595 +		GCATATGTGTTTAACCCGAGAGCGGACATGGCGAGGCCTGTCGCCAGTGGTAAGATTCA----------TCAATTG-AACG-------AAATACCAAGC-TGCTA----------TGA----------TTGATTTTCTCGTTTTTGCAGGGCCTACCAGGCCAATCAGCAGCTTTCGAGCTGACTCAATCGATGCCTG
droFic1	scf7180000454072:627929-628096 -		GCGTTCGTTTTTAACCGGGAGAGGGCACGGCGACAACTGTCGCAGATGGTGAGTTCA----TT--------TT-----AGTGCGTCAA--AATTAAACATTCTCGTGAAAA----------TCACCCAC----------TTTCGTCGACTTGCAGGGCGTACCAGGCAAGCAGCGGCTCCGGAGCTGCCAGGCATCGAGCAGACTG
droEle1	scf7180000488092:612-690 -		GGCCACGTGTATCAACCCTGGAGAGGC----------CAGATAC---------------------CAGTTAG----------CCAGGCAAGCAGCGGCATGCCGCAGCTGCCGGCGATTGCGGACTG
droRho1	scf7180000779467:408864-408934 -		TATT----------CCAGGCAAGCAGCGGCATGCCGCAGCTGCCGGCGATTGCGGACTG
droBia1	scf7180000302126:2737727-2737943 -		GCGTTCGTTTTCAACCCGGAGAGCGGACATGGCGACAACTGCCGCAGATGGTGAGAGCC----GGACCCGTGGGATA--T--GGCTCT---TC----------CTCAAAGGGATA--TTGAGCTTATTAAGTCCC-ATCATTGGTTGCGAATCTATATA----------AGCTTTACTCACCTGTA----------TCCCCACTGCCTAGGGCTCACCAGGCCAAGAGGCGCATGCCGGAGCTTCCGAGCGGTCGAGGACTG
droTak1	scf7180000415366:90211-90267 -		GCATTTCGTGTTCAACCGGGAGAGCGGACACGGCGATGCACTGTCGCAGATGGTAAGAT----------TAGAT---------------------CAGTTAG----------CCAGGCAAGCAGCGGCATGCCGCAGCTGCCGGCGATTGCGGACTG
droEug1	scf7180000409061:131143-131349 +		GCATTCGTGTTTAACCGGGAGGCGGACACGGCGACAATTGTCGTAAATGGTGAGATCA----AGACCATTC-------AT-TTCTCAGC--TTTAAGGACACATATACA----------CATTCTAGACTG----------CTTAGTTATCAAACAGCGTTAATTCTCCATCCTATACTTTGTTTCCAGGGCCTACCAGGCCAGGGGTGCACTGCCGGAGCTTCCGGCGATTGAAGACTG
dm3	chrX:2610689-2610849 +		GCGTTCGTGTTCAACCGGGAGTTGGGTCACGGCGACAACTGCCGCAGATGGTAAGATCA----TTACTTTCTATACATTT-AATG-------CAGTTAG----------TGTCATCACTTATCTC----------TGCCCATTCGTCAGGGACTCTACCAGGCCAAGATGGCGTTTCCGGAGGTGCCGCCCTCATCGAGAGTG
droSim2	x:2412938-2413111 +		GCGTTCGTGTTTAACCGGGAGTTGGGTCACGGCGACAACTGCCGCAGATGGTAAGATCA----CCACTTTCTACACATTG-AATG-------CAGTTAG----------TGCCTTCACTAATCCGTG----------CCCTTCGGTCCTATTCCATTCGTCAGGGCCTACCAGGCCAAGATGGCGTTTCCAAGAGGTGCCGCCATCACGAGAGTG
droSec2	scaffold_10:2372197-2372369 +		GCGTTCGTGTTTAACCGGGAGTTGGGTCACGGCGACAACTGTCGCAGATGGTAAGATCACC-------CTTTTTACACATTG-AATG-------CAGTTAG----------TGCCTTCACTAATCTGTG----------CCCTTCGTTCTATTCCATTCGTCAGGGCCTACCAGGCCAAGATGGCGTTTCCAAGAGGTGCCGCCATCACGAGAGTG
droYak3	X:5739351-5739520 -		GCGTTCGTGTTTAACCGGGAGCTAGGTCACGGCGACAATTGTCGTAGATGGTAAGATTCTA-------CTTGTTTTCCATTG-AATG-------CAGTTAG----------TTCACTTATCTGTG----------CCCTTGTTTATATCCCAATCCACAGGGCCTACCAGGCCAAGATGGCGTTTCCGGAGGTGCCCACCATCGAGGACTG
droEre2	scaffold_4690:37127-37349 +		GCGTTTGTGTTCAACCGGGAGCTAGGTCACGGCGACAATTGTCGCAGATGGTAAGATTCTTGGTCATGA-------CCCC----AC----------TTTTAAGAGACATACTGA----------ATTATTGGCGGGGAACCCTACATAAATGGTTTTGCTCTTGCCGATGGTATTTAATGTGTGTCTCCAG----------TTCCTTTCGTCAGGGCCTACCAGGCCAAGATGGCGTTCCCGGAGATACCCACCATCGAGGACTG
dp5	XL_group1e:2005601-2005762 +		GCGTTTGTGTATAACCGTGAGAAGGACATGGCGACAACTGCCGCAAATGGTAGCGTGG-------CAAGCCTCA-------CTTGCT--TCT-CTTGTTTA----------TG------CCCTA--TCTCTTGTGTATCGTCAGGGCCTACCAAGCAAAGAGCCTGATACGAGAGCTGGCATTGAATAGTGACTG
droPer2	scaffold_18:856039-856200 +		GCGTTTGTGTATAACCGTGAGAAGGACATGGCGACAACTGCCGCAAATGGTAGCGTGG-------CAAGCCTCA-------CTTGCT--TCT-CTTGTTTA----------TG------CCCTA--TCTCTTGTGTATCGTCAGGGCCTACCAAGCAAAGAGCCTGATACGAGAGCTGGCATTGAATAGTGACTG
droWil2	scf2_1100000004909:12239550-12239650 -		GCGTTTGTATTTAATGCCGAAACCGGACACGGCGATAATTGTCGTAAATGGTGT--------------------------CAGTTAG----------CGTATGTAGCCAAATCATTGATGCCGGAATTGCCATTTGTTGGCGATTG
droVir3	scaffold_12472:148259-148422		GCGTTTGTTACAGAGTGAGAGCGGACATGGCGACAATTGTCGCAAATGGTAAGTGAA----CAACA----------TT--GACTTCTCA--GATTAG--ACA-TTAATATA----------TTTCTAA--T---TGATTTAAGGCAGGGGTTATGCGCGCCAAATCAACGATGCCGAGCTGCCAGAGATTGGAGATTG
droMoj3	scaffold_6473:13315507-13315679 +		GCGTTTGATACAGAGCGAGAGCGGCATGGCGATAACTGTCGCAAATGGTAAATGTCC------AATTGGAGATCA--T--GACAATACT--TATAAG----------CATTTATCATTATAAATAATATT----------CATTAAGTGCAGGGGTTATGCGCGCCAATCGATGATGCCGAGCTGCCGGAATATAGTGGATTG
droGri2	scaffold_15203:8905141-8905209 +		GCGTTTACCTACAGAGCGAGATAGGACACGGCGACAACTGTCGCAAGTGGTGAGTGTTCG----------CTGTTT-AA---------------------CAGTTAG----------

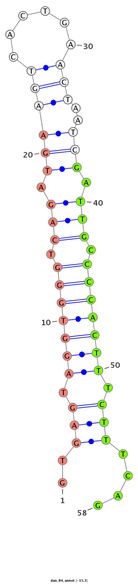
Generated: 09/08/2015 at 10:31 PM

	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

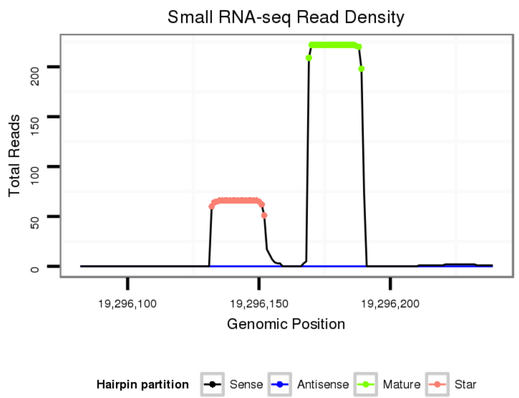
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_84	**scaffold_13340:19296132-19296189 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

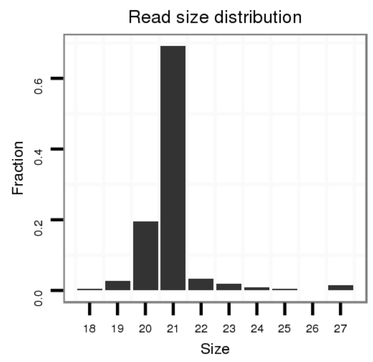
Legend: mature star mismatch in alignment mismatch in read

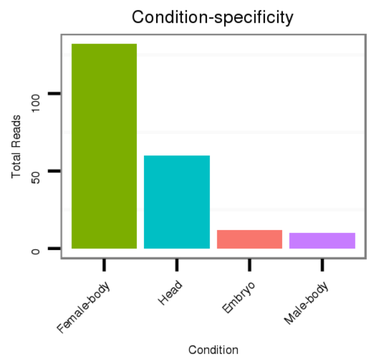
Predicted structure

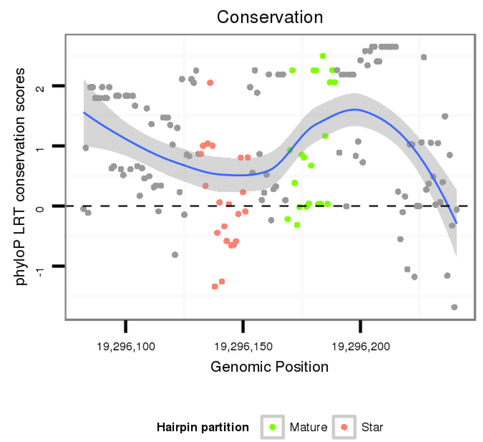


Show Alternate Folds









Flybase annnotation

intron [Dana\GF18705-in]; CDS [Dana\GF18705-cds]; utr5 [utr5_minus_10448]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GAGATCCCTCCACTAAACAATACAAGCAACAAACAAACAAACAAGCACAGGTGAGTAGGTGGGTCAGATGAAGTCACTGAACTAATCGATTGCCCCACTTTCTTTCAGTGTACATACAACTGTAACGAATTTAAACAAAAATCCAAAGCAGAAGCAAG	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V106 head	M058 embryo	V105 male body	V055 head	V039 embryo
**********..(((.(((((((.(((.((((((.....)))..)))).)))))))).)))....**********											
.....GATTGCCCCACTTTCTTTCAG.....	21	0	1	113.00	113	92	10	8	1	2	0
.....GATTGCCCCACTTTCTTTCAGT.....	22	0	1	70.00	70	44	16	7	2	0	1
.....GATTGCCCCACTTTCTTTCAGA.....	22	1	1	49.00	49	40	0	8	0	1	0
.....GTGAGTAGGTGGGTCAGATGA.....	21	0	1	33.00	33	3	22	0	2	4	2
.....GATTGCCCCACTTTCTTTCA.....	20	0	1	20.00	20	17	1	0	0	2	0
.....GTGAGTAGGTGGGTCAGATG.....	20	0	1	11.00	11	1	8	0	1	1	0
.....ATTGCCCCACTTTCTTTCAG.....	20	0	1	9.00	9	9	0	0	0	0	0
.....ATTGCCCCACTTTCTTTCAGA.....	21	1	1	5.00	5	5	0	0	0	0	0
.....GTGAGTAGGTGGGTCAGAT.....	19	0	1	3.00	3	0	3	0	0	0	0
.....GTGAGTAGGTGGGTCAGATGAAG.....	23	0	1	3.00	3	1	1	0	1	0	0
.....GTGAGTAGGTGGGTCAGATGAA.....	22	0	1	3.00	3	0	2	0	1	0	0
.....ATTGCCCCACTTTCTTTCAGT.....	21	0	1	3.00	3	3	0	0	0	0	0
.....GATTGCCCCACTTTCTTTCAGTT.....	23	1	1	3.00	3	3	0	0	0	0	0
.....GTGAGTAGGTGGGTCAGATGAAGTCAC.....	27	0	1	3.00	3	0	3	0	0	0	0
.....GTGAGTAGGTGGGTCAGATGAAGT.....	24	0	1	2.00	2	0	0	1	1	0	0
.....GATTGCCCCACTTTCTTTCAGC.....	22	1	1	2.00	2	0	0	2	0	0	0
.....CGATTGCCCCACTTTCTTTCAG.....	22	0	1	2.00	2	1	1	0	0	0	0
.....GATTGCCCCACTTTCTTTCAGAA.....	23	2	1	2.00	2	1	0	1	0	0	0
.....GATTGCCCCACTTTCTTTA.....	19	1	1	1.00	1	1	0	0	0	0	0
.....GTGAGTAGGTGGGTCAGATGAT.....	22	1	1	1.00	1	0	0	0	1	0	0
.....TCGATTGCCCCACTTTCTTTCAGT.....	24	0	1	1.00	1	0	0	1	0	0	0
.....AGTAGGTGGGTCAGATGAA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TCGATTGCCCCACTTTCTTTCA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....GATTGCCCCACTTTCTTTC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TGAGTAGGTGGGTCAGATGA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TGAGTAGGTGGGTCAGATGAA.....	21	0	1	1.00	1	0	0	0	1	0	0
.....AATCCAAAGCAGAAGCAAG	19	0	1	1.00	1	0	0	1	0	0	0
.....ATTGCCCCACTTTCTTTCA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TGAGTAGGTGGGTCAGATGACC.....	22	2	1	1.00	1	1	0	0	0	0	0
.....TTTAAACAAAAATCCAAAGCAG.....	22	0	1	1.00	1	0	0	0	1	0	0
.....GAGTAGGTGGGTCAGATGAAG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TGAGTAGGTGGGTCAGATGAAG.....	22	0	1	1.00	1	0	0	0	1	0	0
.....TGAGTAGGTGGGTCAGATGAAGT.....	23	0	1	1.00	1	0	0	0	0	0	1
.....GTGAGTAGGTGGGTCAGATGAAGTC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....GTGAGTAGGTGGGTCAGA.....	18	0	1	1.00	1	0	0	0	1	0	0
.....GTGAGTAGGTGGGTCAGATT.....	20	1	1	1.00	1	0	1	0	0	0	0
.....TCGATTGCCCCACTTTCTTT.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GTGAGTAGGTGGGTCAGATGT.....	21	1	1	1.00	1	0	0	0	1	0	0

Anti-sense strand reads

CTCTAGGGAGGTGATTTGTTATGTTCGTTGTTTGTTTGTTTGTTCGTGTCCACTCATCCACCCAGTCTACTTCAGTGACTTGATTAGCTAACGGGGTGAAAGAAAGTCACATGTATGTTGACATTGCTTAAATTTGTTTTTAGGTTTCGTCTTCGTTC	Read size	# Mismatch	Hit Count	Total Norm	Total	V039 embryo	V055 head
**********..(((.(((((((.(((.((((((.....)))..)))).)))))))).)))....**********							
.....GAGTAGGTGGGTCAGATGAAG.....	21	0	1	1.00	1	1	0
.....TGAGTAGGTGGGTCAGATGAAG.....	22	0	1	1.00	1	0	1
.....TGAGTAGGTGGGTCAGATGAAGT.....	23	0	1	1.00	1	0	0
.....GTGAGTAGGTGGGTCAGATGAAGTCAC.....	27	0	1	1.00	1	0	0
.....GTGAGTAGGTGGGTCAGATGAAGT.....	24	0	1	1.00	1	0	0
.....GTGAGTAGGTGGGTCAGATGAA.....	22	0	1	1.00	1	0	0
.....GTGAGTAGGTGGGTCAGATGAAG.....	23	0	1	1.00	1	0	0
.....GTGAGTAGGTGGGTCAGATGA.....	21	0	1	1.00	1	0	0
.....GTGAGTAGGTGGGTCAGATGT.....	21	1	1	1.00	1	0	0
.....GTGAGTAGGTGGGTCAGATGAAG.....	22	0	1	1.00	1	0	0
.....GTGAGTAGGTGGGTCAGATGAAGT.....	23	0	1	1.00	1	0	0
.....GTGAGTAGGTGGGTCAGATGAAGTC.....	25	0	1	1.00	1	0	0
.....GTGAGTAGGTGGGTCAGA.....	18	0	1	1.00	1	0	0
.....GTGAGTAGGTGGGTCAGATT.....	20	1	1	1.00	1	0	0
.....GTGAGTAGGTGGGTCAGATGT.....	21	1	1	1.00	1	0	0

Show Alignment With Reads

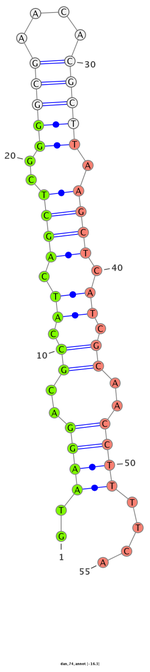
Re-alignment of all predicted orthologs

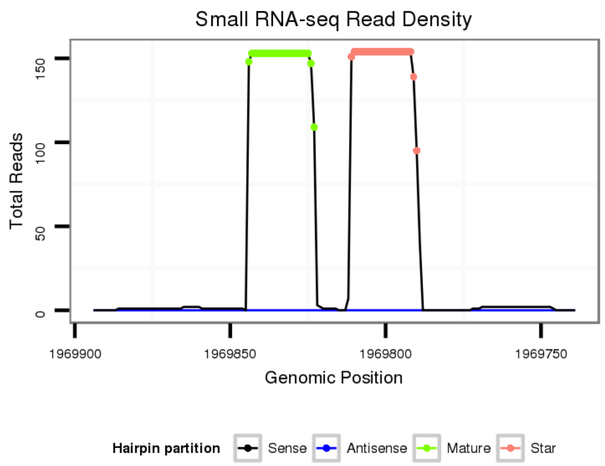
Species	Coordinate	ID	Alignment
droAna3	scaffold_13340:19296082-19296241 +	dan_84	GAG----------ATCCCTCCACTAAACAATA--CAAG---CAACAA----------ACAAAC--AAA---------CA-A--GCACAGGTGAGTAG----------GTG----------GGT---CAGATG-AAGTCAC--TG--AACTAATCGATTGCCC----------CACTTT--CTTTCAGTGTACA----TACAACTGT-AACGAATTTAAAC--AAA--AATCCAAAG---C---AGA------AGCAAGAA
droBip1	scf7180000396413:3069672-3069857 -		GAGAG--TC----------GATGCAACAATCCCTCCAGTAAACAATA--CAAACAGTAACCA--GAA---------ACCT-ACGGA-----AATCGAACCAA-GAAGCACAGGTGAGTCT--------CTAGA--CACGACTA--TAG-GAAG---GTGATA-AAGTCAC--------TCACCC----------CCACGTTT--ATTTCAGTGTACA----TACAACTGT-AACGAATTTAAAA--ACC--AAA--TAGC---------AG-C-----GCA
droKik1	scf7180000302697:662109-662249 -		AAGAG--TAAGGCGCATCGCAAATGCAACAATCCCTCCAG---------------------------------------CAGTGAGTGC----------GAGTGTGATG---AGT-GGGTGAAGTGATG-AAGTCAC--GG--AGCTAATTACTTGTCC----------CACTTT--ATTCCAGTGTACA----TACAACTGT-AACGAATTTAAAC----------------------
droFic1	scf7180000453826:322538-322721 +		AAGAG--TAAGGCGCATCGCAAATGCAACAATCCCTCCAGTAAACAATA--CAAAAAG------AACC---------------G-----AA-G--AAACAGGTGAGTTG----------TCCACTGATA---AATTGAGC--CCATG-AAGTCAGCGTG--ATTTAATTATTGCCC----------CACTTC--ATTCCAGTGTACA----TACAACTGT-AACGAATTTAAAC--CAA---------AGG---------AC-A-----GCAAGAA
droEle1	scf7180000491261:1882234-1882426 -		AAGAG--TCAGGCGCATCGCAAATGCAACAATCCCTCCAGTAAACAATA--CAAAATCCAACAA---ACAAGAAGC---------------G-----AA-G--AAACAGGTGAGTGG----------CTGATA---AATTGGC---GACG-AAGTCAGCCGTG--AACTAATTGATTGCCC----------CACTTT--ATTCCAGTGTACA----TACAACTGT-AACGAATTTAAAA--TCC---------AAGCAAG---CGG-T-----TAGCG
droRho1	scf7180000778847:4906-5080 +		---------AGGCGCATCGCAAATACAACAATCCCTCCAGTAAACAATA--CAAAATCCAAC---ACAAGAAGC---------------G-----AA-G--AAACAGGTGAGTGG----------CTGATA---AATTGGA---GTGTG-AAGTCAGAGA--AGCTAATTGATTGCCC----------CACTTT--ATTCCAGTGTATA---TATAACTGT-AACGAATTTAAAA--TCC---------AAGCAAG---CG----------
droBia1	scf7180000302075:1536432-1536632 +		---------GCAAATGCAACAATCCCTCCAGTAAACAATA--CAAAAATCAACAA---AC---------AAGT-ACAGCAAAC--AAA---------AAGA--AAACAGGTGAGTTG----------CTGCCGCCGACTGATA---AATTGACC---CCATG-AAGTCAGCGTG--AGCTAATTGATTGCCC----------TCCACTTT--ATTCCAGTGTACA----TACAACTGT-AACGAATTTAAGC--AGC--AACC--AAGCAA--------AGCGGTTC
droTak1	scf7180000413872:268937-269110 -		CACAGAGTAAGGCGCATCGCAAATGCAACAATCCCTCCAGTAAACAATA--CAAAATCAACAA----------------GAGCAAAC--AAA---------AA-G--AAACAGGTGAGTTG----------TG--TTGATG---AATTGA---TTATG-AAGTCAGCGTGAAAGCTAATTGATTGCCC----------CACTTT--ATTGCAGTA----------AACGAATTTAAGAAGCAA---------AAGG----------
droEug1	scf7180000409770:875063-875268 -		CAGAG--TAAGGCGCATCGCAAATGCAACAATCCCTCCAGTAAACAATA--CAAAAACCAA---------GCA-AAGT-ACAGCAAACA--G-----AA-G--AAACAGGTGAGTTATTACCGTTGTTGTTGTTGACT----------------GATG-GAGTCGGTGTG--AGCTAATTGATTACCC----------CACTTT--ATTCCAGTGTACATATATACAACTGT-AACGAATTTAAGC--AAC---------AAGC---------T-GAAGAA
dm3	chr3R:23393890-23394085 -		CAGAGTGTAAGGCGCATCGCATATGCAACAATCCCTCCAGTAAACAATA--CAGAAAG------------A-AAGT-ATAGCAAACACAAA---------AA-G--AAACAGGTGAGTAG----------TTGCACTGATAATTAATGACGC--GTGATG-AAGTCAGCGTG--AGCTAATTGATTGGC----------CACTTA--ATTCCAGTGTACA----TACAACTGT-AACGAATTTAAGC--AAG---------AAGCAAG----------
droSim2	3r:22818955-22819145 -		CAGAGTGTAAGGCGCATCGCAAATGCAACAATCCCTCCAGTAAACAATA--CAGAAAG------------A-AAGT-ATAGCAAACACAAA---------AA-G--AAACAGGTGAGTAG----------TTGCACTGATA---AATTGACC--GTGATG-AAGTCAGCGTG--AGCTAATTGATTGCCC----------CACTTA--ATTCCAGTGTACA----TACAACTGT-AACGAATTTAAGC--AGC---------AAGC----------
droSec2	scaffold_22:27664-27854 -		CAGAGTGTAAGGCGCATCGCAAATGCAACAATCCCTCCAGTAAACAATA--CAGAAAG------------A-AAGT-ATAGCAAACACAAA---------AA-G--AAACAGGTGAGTAG----------TTGCACTGATA---AATTGACC--GTGATG-AAGTCAGCGTG--AGCTAATTGATTGCCC----------CACTTA--ATTCCAGTGTACA----TACAACTGT-AACGAATTTAAGC--AAC---------AAGC----------
droYak3	3R:23095113-23095320 +		CAGAG--TAAGGCGCATCGCAAATGCAACAATCCCTCCAGTAAACAATA--CAAAAATCAACAA---CACAAGAAGCA-AAGT-ATAGCAAAC--AAA---------AA-G--AAACAGGTGAGTAG----------TAGTTAACTGATA---AATTAACC--GTGATTATAAGTCAGCAGTG--AGCTAATTGATTGCCC----------CACTTT--ATTCCAGTGTACA----TACAACTGT-AACGAATTTAAGC--AAC---------AAGCAA---------
droEre2	scaffold_4820:4643885-4644080 +		CAGAG--TAAGGCGCATCGCAAATGCAACAATCCCTCCAGTAAACAATA--CAAAAATCAACAA---CACAAGAAGCA-AAGT-ATAGCAAACA-G-----AA-G--AAACAGGTTTGTAG----------TTCACTGATA---AATTGACC--GTGATG-AAGTCAGCAGTG--AGCTAATTGATTGCCC----------CACTTG--ATTCCAGTGTACA----TACAACTGT-AACGAATTTAAAC--AA---------AGC----------
dp5	2:9040934-9041143 -		CACAAGAGAAGGCGCAAC---AGTGCAACAATCCCTCCAGGCAACAAGAAGCTGAAAGCAGCAGCAG-A-CAGCAGCAGAAGTGGCAGCAAACA-GAACGTAAATCTA-G--AAACAGGTGAGTGC----------CATTCTAAAA---CGT-TTTCAAGGGGAGA-AAGT---------AATGAATATATTCTCA----------TGTTTT-CTGGCAGTGTAAA----TACAACTGT-AACGAATTTAAAG-GAAA---------AAGC----------
droPer2	scaffold_0:2854418-2854644 -		CACAAGAGAAGGCGCAAC---AGTGCAACAATCCCTCCAGGCAACAAGAAGCTGAAAGCAGCAGCAGCAGCAGAAGTGGCAACAAACA-GAACGTAAATCTA-G--AAACAGGTGAGTGC----------CATTCTAAAA---CGT-TTTCAAGGGGAGA-AAGT---------AATGAATATATTCTCA----------TGTTTT-CTGGCAGTGTAAA----TACAACTGT-AACGAATTTAAAC-GAAACAAAA-AAGC---------AG-A-----CAACA
droWil2	scf2_1100000004902:3632585-3632643 -		---------------------------------------

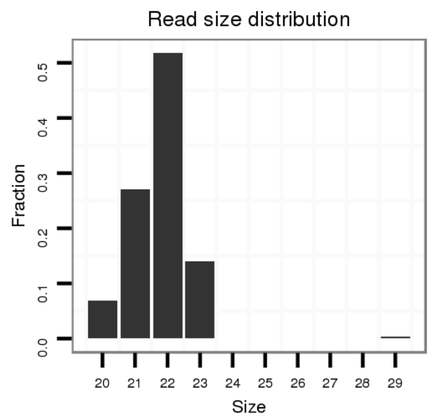
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_74	**scaffold_13117:1969789-1969844 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

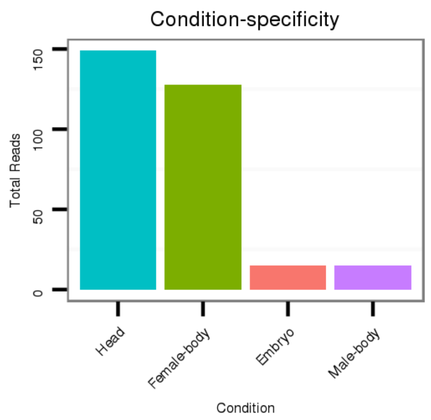
Legend: mature star **mismatch in alignment** mismatch in read

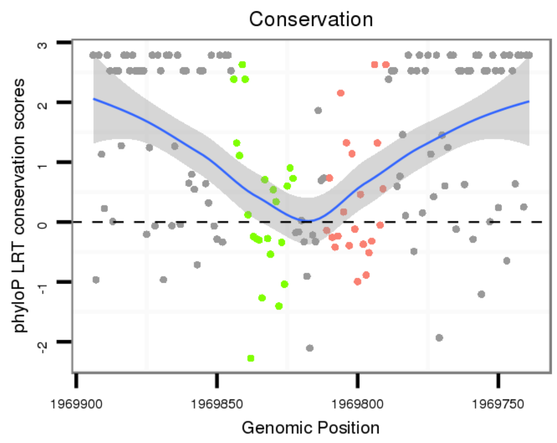
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF20998-in]; CDS [Dana\GF20998-cds]; CDS [Dana\GF20998-cds]; utr3 [utr3_plus_7527]; utr3 [utr3_plus_7526]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TAACTAGCGCCATGTGGCCGAAGACCAACCTGCGCTCAGGCATCGTCAAGGTAAGGACGCCATCAGCTCGGGGCGAACACGCTTAAGCTCATCGCAACCTTTTCAGGCCGTCACTGAGCAGCTCTCCTACGGACCCTTCGCTTGCGTCAGCTTCTT **********..((((..((.((.((((..(((((....)))))).))))).)).))..))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V106 head	V055 head	M058 embryo	V105 male body	V039 embryo
.....GTAAGGACGCCATCAGCTCGGG.....	22	0	1	103.00	103	21	77	2	0	1	2
.....TAAGCTCATCGCAACCTTTTCA.....	22	0	1	51.00	51	29	3	13	3	3	0
.....TAAGCTCATCGCAACCTTTTCAG.....	23	0	1	40.00	40	25	6	6	1	1	1
.....TAAGCTCATCGCAACCTTTTC.....	21	0	1	39.00	39	21	3	13	2	0	0
.....GTAAGGACGCCATCAGCTCGG.....	21	0	1	37.00	37	10	18	3	3	3	0
.....TAAGCTCATCGCAACCTTTT.....	20	0	1	14.00	14	10	1	1	1	1	0
.....GTAAGGACGCCATCAGCTCG.....	20	0	1	6.00	6	1	0	0	0	5	0
.....TTAAGCTCATCGCAACCTTTTC.....	22	0	1	5.00	5	4	0	0	1	0	0
.....TAAGCTCATCGCAACCTTTTCAA.....	23	1	1	4.00	4	1	0	0	1	0	2
.....AAGCTCATCGCAACCTTTTCA.....	21	0	1	3.00	3	3	0	0	0	0	0
.....TAAGGACGCCATCAGCTCGGG.....	21	0	1	3.00	3	2	1	0	0	0	0
.....GTAAGGACGCCATCAGCTCGGGT.....	23	1	1	2.00	2	1	1	0	0	0	0
.....TAAGCTCATCGCAACCTTTTCAGA.....	24	1	1	2.00	2	2	0	0	0	0	0
.....GTAAGGACGCCATCAGCTCGGT.....	22	1	1	2.00	2	2	0	0	0	0	0
.....TAAGCTCATCGCAACCTTTTCAAA.....	24	2	1	2.00	2	0	0	0	2	0	0
.....TAAGCTCATCGCAACCTTTTCG.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TTAAGCTCATCGCAACCTTTTCA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TCTCCTACGGACCCTTCGCTTGCGTCA.....	27	0	1	1.00	1	0	1	0	0	0	0
.....TTAAGCTCATCGCAACCTTTTCAGC.....	25	1	1	1.00	1	1	0	0	0	0	0
.....TAAGCTCATCGCAACCTTTTCAGT.....	24	1	1	1.00	1	1	0	0	0	0	0
.....CTGCGCTCAGGCATCGTCAA.....	20	0	1	1.00	1	0	1	0	0	0	0
.....CCTACGGACCCTTCGCTTGCGTC.....	23	0	1	1.00	1	0	0	0	1	0	0
.....TAAGCTCATCGCAACCTTTTCTT.....	23	2	1	1.00	1	1	0	0	0	0	0
.....TAAGGACGCCATCAGCTCGG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GTAAGGACGCCATCAGCTCGGGG.....	23	0	1	1.00	1	0	0	0	0	1	0
.....TAAGGACGCCATCAGCTCGGGGC.....	23	0	1	1.00	1	0	0	0	1	0	0
.....GTAAGGACGCCATCAGCTCGT.....	21	1	1	1.00	1	0	0	1	0	0	0
.....TTAAGCTCATCGCAACCTTTT.....	21	0	1	1.00	1	0	0	1	0	0	0
.....GTAAGGACGCCATCAGCTCGGGGCGAACA.....	29	0	1	1.00	1	0	1	0	0	0	0
.....TAAGCTCATCGCAACCTTTTT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....GTAAGGACGCCATCAGCTCGGAT.....	23	2	1	1.00	1	0	1	0	0	0	0
.....CCGTCACTGAGCAGCTCTCCTAT.....	23	1	1	1.00	1	1	0	0	0	0	0
........GCCATGTGGCCGAAGACCAACCTGCGC.....	27	0	1	1.00	1	0	0	0	1	0	0
.....GTAAGGACGCCATCAGCTCGGGA.....	23	1	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

ATTGATCGCGGTACACCGGCTTCTGGTTGGACGCGAGTCCGTAGCAGTTCCATTCCTGCGGTAGTCGAGCCCCGCTTGTGCGAATTCGAGTAGCGTTGGAAAAGTCCGGCAGTGACTCGTCGAGAGGATGCCTGGGAAGCGAACGCAGTCGAAGAA **********..((((..((.((.((((..(((((....)))))).))))).)).))..))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head	V105 male body
.....CGTAGGACGCCATCAGCTCGTT.....	21	1	1	1.00	1	0	0	0
.....CGTAGGACGCCATCAGCTCGGT.....	21	1	1	1.00	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13117:1969739-1969894 -	dan_74	TAACTAGCGCCATGTGGCCGAAGACCAACCTGCGCTCAGGCATCGTCAAGGTAAGGACGCC---A----------TCAGCTCGGGGCC--GAAC----------ACGCTTAAGCTC---ATCG----------C---AACCTTTTCAGGCCGTCACTGAGCAGCTCTCCTACGGACCCTTCGCTTGCGTCAGCTTCTT
droBip1	scf7180000396425:97407-97563 +		TCACCAGCGCCATGTGGCCGAAGACCAACCTGCGCTCGGCATCATCAAGGTAAGGCCGCC---ATCAGC----------TCGGGGCG--AAAC----------AAGCTTAAGCTC---ATCG----------C---AACATTTTCAGGCCGTCACTGAGCAGCTCTCCTACGGACCCTTGCTTGCGTTAGCTTCTT
droKik1	scf7180000302469:1014380-1014540 -		TAACCAGCGCCATGTGGCCACACACAACCTGCGCACGGGTATAGTCAAGGTAAGTTAAAGG-G-GA----------A-CA--GCAGC--AGCTTCTGGC----------AGAG------ATC---AACCTTG----------C---CCCCATTGCAGGCCATCACGAGCAGCTATCCTACGGACCCTTTGCCTGCGTCAGCTTCTT
droFic1	scf7180000454072:1743085-1743235 -		TAACCAGCGCCATGTGGCCACACAGAAATCTGCGCACTGGCGTCATAAAGGTAAGAAGTGCCACTTAACCCG------CCGCCCGAGCT------------TC---AACG----------A---CCGTTTTGCAGGCCATCAGAGCAGCTCTCCTATGGACCCTTCGCCTGCGTCAGCTTCTT
droEle1	scf7180000491024:11312-11411 +		TCACCAGCGCCATGTGGCCACAGACCAATCTGCGCACGGCATCGTTAAG----------A----------A----------A--CA----------TC---AACG----------A---CCGTTTTGCAGGCCATCAGCGAGCAGCTATCCTACGGACCTTTCGCCTGCGTTAGCTTATT
droRho1	scf7180000776645:11913-12012 -		TCACCAGCGCTATGTGGCCGCAGACCAATCTCGGCACGGCATCGTCAAG----------A----------A----------A--CA----------TC---AACG----------A---CCGTTTTGCAGGCCATCAGCGAGCAGCTGTCCTACGGACCTTTTGCCTGTGTCAGCTTATT
droBia1	scf7180000301760:3950321-3950491 +		TCACCAGATGCCATGTGGCCGCAGACCAATCTGCGCACGGCATCGTCAAGGTAAGATGTGTA-GTTCCCAACG-------CTGCTTCAGCTTCAGCGG--GACT----------GAGCTCACCCTC---AAAC----------G---CCCCTTTGCAGGCCATCAGCGAGCAGCTTCCTACGGGCCCCTTTGCCTGCGTAAGCTTCTT
droTak1	scf7180000415704:959498-959650 +		TCACCAGCGCCATGTGGCCGCAGACCAACCTGCGCACGGCATCGTCAAGGTAAGAGTCC---TCCATCCGACTTCGGGCTCCCGC---------A--G------CTC---ACCC----------G---CTCCCTTGCAGGCCATCAGCGAGCAGCTGTCCTACGGACCCTTCGCCTGCGTCAGCTTCTT
droEug1	scf7180000408994:71097-71262 +		TAACCAGCGCCATGTGGCCACAGACCAATCTGCGCTACCGGCATCGTTAAGGTAAGATGTGTGGACTCAATCTG------GCGCTTCAGTTACAGCGG--AGTC----------AAG------TTG---ATCC----------A---CTCCTTTGTAGGCCTATCAGCGAACAGCTGTCATATGGACCTTTTGCCTGCGTAAGCTTCTT
dm3	chrX:1362169-1362333 +		TCACCAGCGCCATGTGGCCGCAGACTAATCTGCGCACGGCATCGTTAAGGTAAGGACTGAGACTCAATCCG-------GCTCCTCAGTCGCAGCGG--GACC----------AAG------CTC---AACC----------G---CCTCTTTGCAGGCCATCAGCGAACAGCTTCCTACGGACCCATTCGCTTGCGTAAGCTTATT
droSim2	x:1242195-1242359 +		TCACCAGCGCCATGTGGCCGCAGACCAATCTGCGCACGGCATCGTTAAGGTAAGGGCTGAGACTGAATCCG-------GCTCCTCAGCCGCAGCGG--GACC----------AAG------CTC---AACC----------G---CCTATTTGCAGGCCATCAGCGAACAGCTTCCTACGGACCCTTCGCTTGCGTAAGCTTATT
droSec2	scaffold_10:1189148-1189312 +		TCACCAGCGCCATGTGGCCGCAGACCAATCTGCGCACGGCATCGTTAAGGTAAGGGCTGAGACTGAATCCG-------GCTCCTTAGCCGCAGCGG--GACG----------AAG------CTC---AACC----------G---CCTATTTGCAGGCCATCAGCGAACAGCTTTCTACGGACCCTTCGCTTGCGTAAGCTTATT
droYak3	X:1266942-1267106 +		TCACCAGCGCCATGTGGCCGCAGACCAATCTGCGCTCCGGCATCATTAAGGTAAGGGCTGAGACTCAATCCG-------GCACCTCAGTCGCAGCGG--GATT----------AAG------CTC---AACC----------G---CCTCTTTGCAGGCCATCAGCGGAGCAGCTTTCCTACGGACCCTTCGCTTGCGTAAGCTTCTT
droEre2	scaffold_4644:1351711-1351875 +		TCACCAGCGCCATGTGGCCGCAGACCAACCTTCGGCATCGGCATCGTAAAGGTAAGGGCTGAGACTCATTCCG-------GCACCTCAGTCGCAGCGG--GACC----------ATG------CTC---AACC----------G---CCCCTTTGCAGGCCATTAGCGAACAGCTTTCCTACGGACCCTTCGCTTGCGTAAGCTTATT
dp5	XL_groupla:4655661-4655830 -		TCACCAGATGCCATGTGGCCGCAGACCAACCTGCGCACGGTGTCGTCAAGGTAAGTTGAAG----A----------A------CACGGGAG--CTCAC----------AGCGT---------GATTAGCGCTTGACTTA----------CTTCGGCAACAA---ACCACTTGCAGGCCATCAGAGCAGCTCTCCTACGGACCCTTGCTTGCGTCAGCTTCTT
droPer2	scaffold_11:1244515-1244684 -		TCACCAGATGCCATGTGGCCGCAGACGAACCTGCGCACGGTGTCGTCAAGGTAAGTTGAAG----A----------A------CAGCGGGAG--CTCAC----------AGCGT---------GATTAGCGCTTGACTTA----------CTTCGGCCACAA---ACCACTTGCAGGCCATCAGAGCAGCTCTCCTACGGACCCTTGCTTGCGTCAGCTTCTT
droWil2	scf2_1100000004909:8926999-8927160 +		TCACTAGTGCCATGTGGCCACAGACTAATTTTCGCATAGGCATAATTAAGGTGAGTGTGTGA-AG---ATGTG-------A----CGATTCGCATGC--GACA----------ATG------GTC---AACAATTT----------T---GCTGTTTGTTAGGCCATAACGAACACAATATCCTATGGACCTTTTGCCTGTGTTAGTTTCTT
droVir3	scaffold_13042:4769311-4769465 -	dvi_14791	TGACCAGCGCCATGTGGCCGCAACACAATCTGCGCATCGGCATTGTCAAGGTCAGTAGAGGG-A-----------A------CACAG--GAAG----------AGG------CTAGGTCATCAATTG----------ATATATGCTTTCCAGGCGATAACGAGCAAATGCAGCTACGGCCCGTTCGCCTGTGTCAGCTTCTT
droMoj3	scaffold_6328:4015167-4015333 -		TCACCAGATGCCATGTGGCCGCAGAGCAATCTGCGCATTGGCCTGCTCAAGGTGAGTAA---GAGTGCTGCC----------A----------GG--ATCGA----------CAT---------GGCTGAC---------AGGTTGCCAAACTTCTTAACT-G---AA-CATTCCAGGCCGCAACGGAGCAACTGTCCTATGGCCCCTTTGCCTGCGTTAGCTTCTT
droGri2	scaffold_14853:316863-317041 +		TAACTAGCGCCATGTGGCCGCAAAGAATCTACGTATTGGCATTGTCAAGGCCAGTATCGAG-AGTGC----------A----------A----CC---ACCTTCTCACCATCATCATTATCGT---------CATCATCATTTGCCTGACTGCTT----------AT-A---ACACATTTCAGGCCATTAGCGAGCAATCTCCTATGGACCCTTCGCTTGCGTCAGTTTCTT

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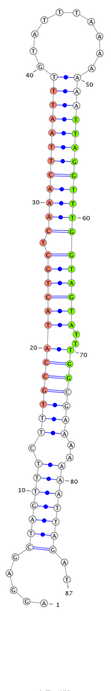
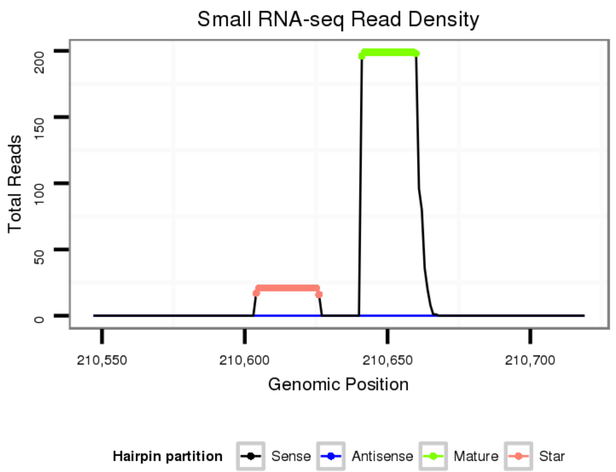
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

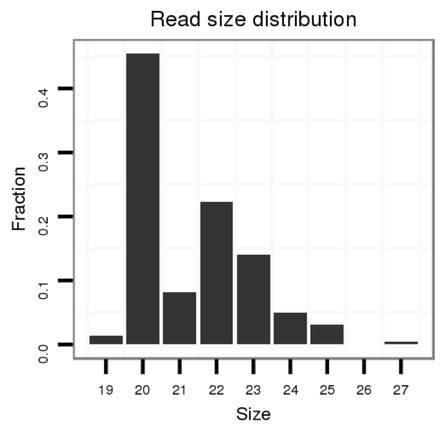
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_221	**scaffold_13335:210597-210669 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

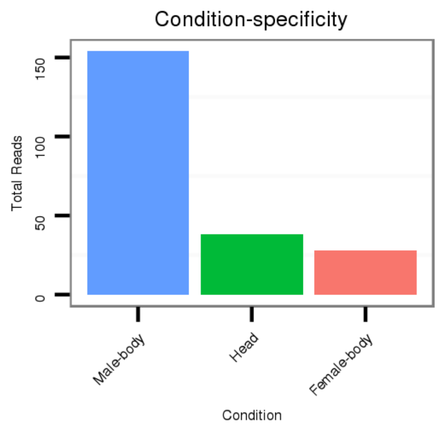
Legend: mature star mismatch in alignment mismatch in read

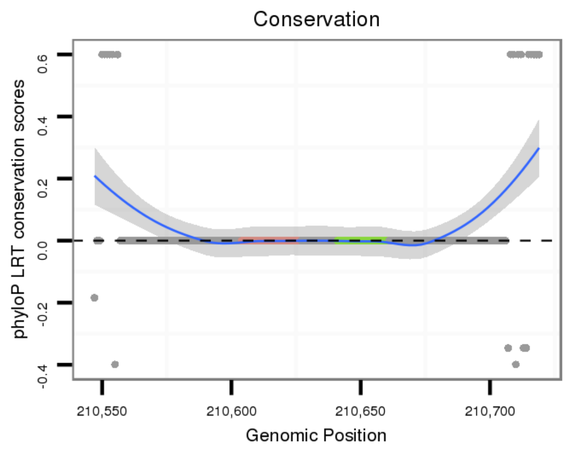
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTAATTTAATTAGTTTAAAATATTATAGACGCAGAAAAAAAGAGGAGCTAGTTTCTTTGCCATACTGCTCAAACTTAATTTGTATTTAAAAAAATTAGGTTTGGTAGTATTTGGCGAAAAAAATTAGATTCCGAAGCTACGGAGAGTAATTTTTTAGTGCGAAAATGCATATT **********.....(((((((.(((((((((((((.(((((((((((.........)))))))))))))))))))..)))))))..)))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	M044 female body	V106 head	V055 head	M058 embryo
.....TTAGGTTTGGTAGTATTTGG.....	20	0	1	100.00	100	82	1	13	4	0
.....TTAGGTTTGGTAGTATTTGGCG.....	22	0	1	44.00	44	34	1	3	6	0
.....TTAGGTTTGGTAGTATTTGGC.....	21	0	1	16.00	16	11	1	4	0	0
.....TTAGGTTTGGTAGTATTTGGCGA.....	23	0	1	16.00	16	10	2	3	1	0
.....TGCCATACTGCTCAAACTTAATT.....	23	0	1	14.00	14	0	14	0	0	0
.....TTAGGTTTGGTAGTATTTGGCGAA.....	24	0	1	11.00	11	7	0	3	1	0
.....TTAGGTTTGGTAGTATTTGGCGAAA.....	25	0	1	7.00	7	7	0	0	0	0
.....TGCCATACTGCTCAAACTTAAT.....	22	0	1	3.00	3	0	3	0	0	0
.....TTAGGTTTGGTAGTATTTGT.....	20	1	1	3.00	3	2	0	1	0	0
.....TGCCATACTGCTCAAACTTAATTA.....	24	1	1	2.00	2	0	2	0	0	0
.....TAGGTTTGGTAGTATTTGG.....	19	0	1	2.00	2	0	2	0	0	0
.....GCCATACTGCTCAAACTTAATT.....	22	0	1	2.00	2	0	2	0	0	0
.....GCCATACTGCTCAAACTTAAT.....	21	0	1	2.00	2	0	2	0	0	0
.....TTAGGTTTGGTAGTATTTGGCGAAAT.....	26	1	1	1.00	1	1	0	0	0	0
.....TTAGGTTTGGTAGTATTTGGT.....	21	1	1	1.00	1	1	0	0	0	0
.....TTAGGTTTGGTAGTATTTG.....	19	0	1	1.00	1	1	0	0	0	0
.....TTAGGTTTGGTAGTATTTGGCGAAAAA.....	27	0	1	1.00	1	1	0	0	0	0
.....TAGGTTTGGTAGTATTTGGCGAA.....	23	0	1	1.00	1	1	0	0	0	0
.....TTAGGTTTGGTAGTATTTGGA.....	21	1	1	1.00	1	1	0	0	0	0
.....TTAGGTTTGGTAGTATTTGGCGT.....	23	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

AATTAAATTAATCAAATTTTATAATATCTGCGTCTTTTTTTCTCCTCGATCAAAGAAACGGTATGACGAGTTTGAATTAAACATAAATTTTTTTAATCCAAACCATCATAAACCGCTTTTTTTAATCTAAGGCTTCGATGCCTCTCATTAAAAAATCACGCTTTTACGTATAA **********.....(((((((.(((((((((((((.(((((((((((.........)))))))))))))))))))..)))))))..)))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	M058 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13335:210547-210719 +	dan_221	TTAATTTAATTAGTTTAAAATATTATAGACGCAGAAAAAAAGAGGAGCTAGTTTCTTTGCCATACTGCTCAAACTTAATTTGTATTTAAAAAAATTAGGTTTGGTAGTATTTGGCGAAAAAAATTAGATTCCGAAGCTACGGAGAGTAATTTTTTAGTGCGAAAATGCATATT
droBip1	scf7180000394803:11922-11922 +		T----------
droKik1	scf7180000302610:1796865-1796885 +		A--ATTTATTT----------A-AA-A-AT-ATATT

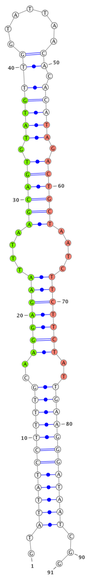
Generated: 09/08/2015 at 08:00 PM

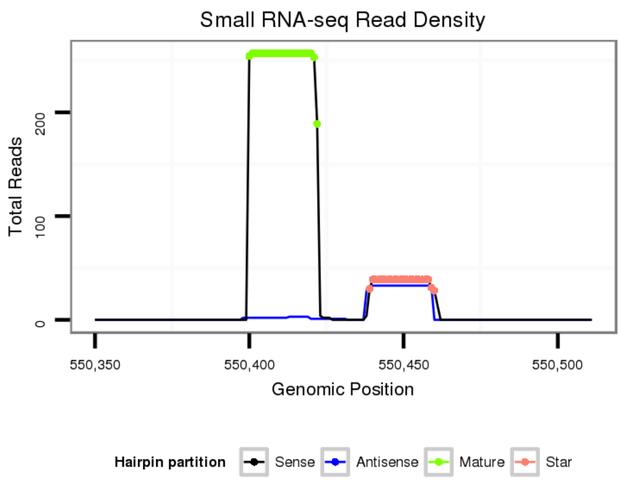
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

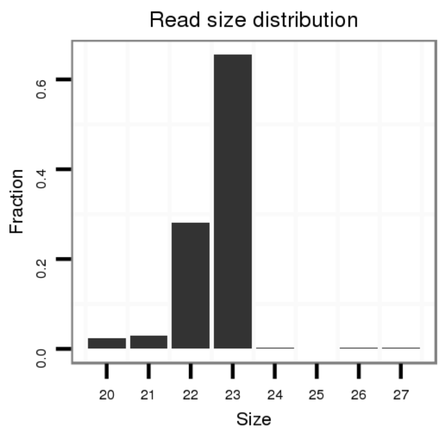
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_57	**scaffold_12903:550400-550461 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

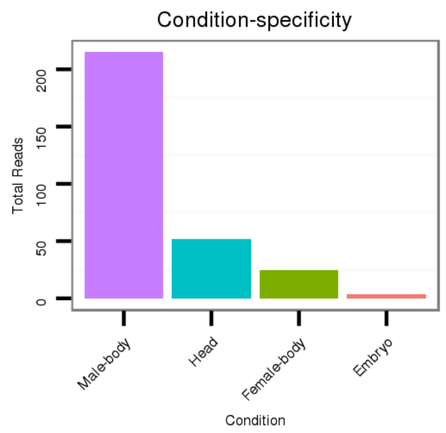
Legend: mature star mismatch in alignment mismatch in read

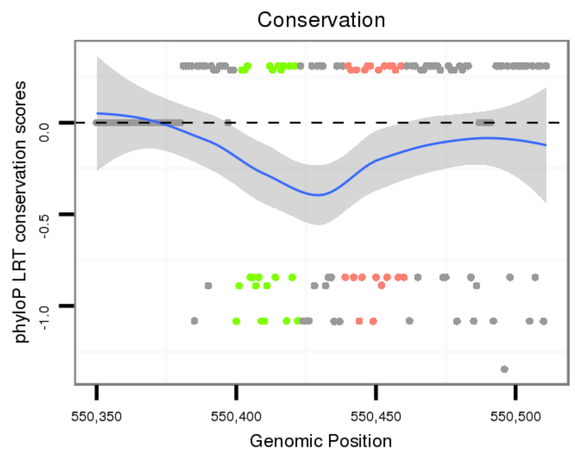
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dana\GF15947-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CGATCATCACAACTTCATAAATCACATCCAGAAAAGTATTATCCTTTTGCAAGGAGAATTTAAGCAGTGTATGTTGGTATTAACACACATAGACTGCTAATCTTCTTCTATTGAAGGGATAATCGGAGCAACAAGTAGGTATTTTTGATAAAAAATTTTTAA **********..(((((((((((..(((((((....(((((((.(((((((.......)).)))))).)))))))....)))))))..)))))))))))...**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V105 male body**	**V055 head**	**V106 head**	**female body**	**M058 embryo**	**V039 embryo**
.....AAGGAGAATTTAAGCAGTGTATG.....	23	0	1	184.00	184	154	11	17	2	0	0
.....AAGGAGAATTTAAGCAGTGTAT.....	22	0	1	64.00	64	51	7	4	2	0	0
.....TAGACTGCTAATCTTCTTCTAT.....	22	0	1	10.00	10	2	1	0	5	0	2
.....TAGACTGCTAATCTTCTTCTATT.....	23	0	1	8.00	8	0	0	3	4	1	0
.....TAGACTGCTAATCTTCTTCT.....	20	0	1	7.00	7	2	1	1	2	1	0
.....AGACTGCTAATCTTCTTCTATT.....	22	0	1	6.00	6	0	1	0	5	0	0
.....AAGGAGAATTTAAGCAGTGTA.....	21	0	1	4.00	4	2	0	2	0	0	0
.....AAGGAGAATTTAAGCAGTGTATGA.....	24	1	1	4.00	4	3	1	0	0	0	0
.....AGACTGCTAATCTTCTTCTAT.....	21	0	1	3.00	3	0	0	0	3	0	0
.....ATAGACTGCTAATCTTCTTCTA.....	22	0	1	2.00	2	0	0	2	0	0	0
.....AAGGAGAATTTAAGCAGTGTATT.....	23	1	1	2.00	2	2	0	0	0	0	0
.....AGGAGAATTTAAGCAGTGTATGTTGG.....	26	0	1	1.00	1	1	0	0	0	0	0
.....CAAGGAGAATTTAAGCAGTGTATGA.....	25	1	1	1.00	1	1	0	0	0	0	0
.....ATAGACTGCTAATCTTCTTCT.....	21	0	1	1.00	1	0	0	0	1	0	0
.....TAGACTGCTAATCTTCTTCTAG.....	22	1	1	1.00	1	0	0	0	0	1	0
.....AAGGAGAATTTAAGCAGTGTATGT.....	24	0	1	1.00	1	0	1	0	0	0	0
.....AAGGAGAATTTAAGCAGTGTATA.....	23	1	1	1.00	1	1	0	0	0	0	0
.....AAGGAGAATTTAAGCAGTGTATGTAT.....	26	2	1	1.00	1	0	1	0	0	0	0
.....ATAGACTGCTAATCTTCTTCTAT.....	23	0	1	1.00	1	0	0	0	1	0	0
.....AGGAGAATTTAAGCAGTGTATG.....	22	0	1	1.00	1	1	0	0	0	0	0
.....AAGGAGAATTTAAGCAGTGTATGC.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TAGACTGCTAATCTTCTTCTATA.....	23	1	1	1.00	1	0	1	0	0	0	0
.....TAGACTGCTAATCTTCTTCTA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....AAGGAGAATTTAAGCAGTGTATGTTGG.....	27	0	1	1.00	1	1	0	0	0	0	0
.....AGGAGAATTTAAGCAGTGTATGT.....	23	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

GCTAGTAGTGTTGAAGTATTTAGTGTAGGTCTTTTCATAATAGGAAAACGTTCCTCTTAAATTCGTCACATACAACCATAATTGTGTGTATCTGACGATTAGAAGAAGATAACTTCCCTATTAGCCTCGTTGTTCATCCATAAAAACTATTTTTTAAAAATT **********..(((((((((((..(((((((....(((((((.(((((((.......)).)))))).)))))))....)))))))..)))))))))))...**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V105 male body**	**V106 head**	**V055 head**	**M044 female body**	**V039 embryo**	**M058 embryo**
.....TATCTGACGATTAGAAGAAGAT.....	22	0	1	28.00	28	13	9	3	2	1	0
.....TCTGACGATTAGAAGAAGAT.....	20	0	1	5.00	5	5	0	0	0	0	0
.....CGTTCCTCTTAAATTCGTCACA.....	22	0	1	2.00	2	0	0	0	2	0	0
.....TTATCTGACGATTAGAAGAAGAT.....	23	1	1	2.00	2	0	2	0	0	0	0
.....CGTCACATACAACCATAAT.....	19	0	1	1.00	1	0	0	0	0	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:550350-550511 +	dan_57	CGATCATCACAACTTCATAAATCACATCCAGAAAAGTATTATCCTTTTGCAAGGAGAATTTAAGCAGTGTATGTTG-GTATTAACACACATAGACTGCTAATCTTCTTCTATTGAAGGGATAATCGGAGCAACAAGTAGGTATTTTTGATAAAAAATTTTTAA
droBip1	scf7180000395912:18990-19115 +		----------AAAATTATTTCCTTT-GGCTGGAAGTCGGTAGTAGTTTGTTGTATTTTTATTGAAACAGGCGACTACCCATTTCCACTTAAAGGATAATCAAAGCCACAAAGT-----GTTTCACAAAAAACGTCTTCA

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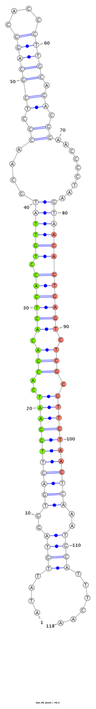
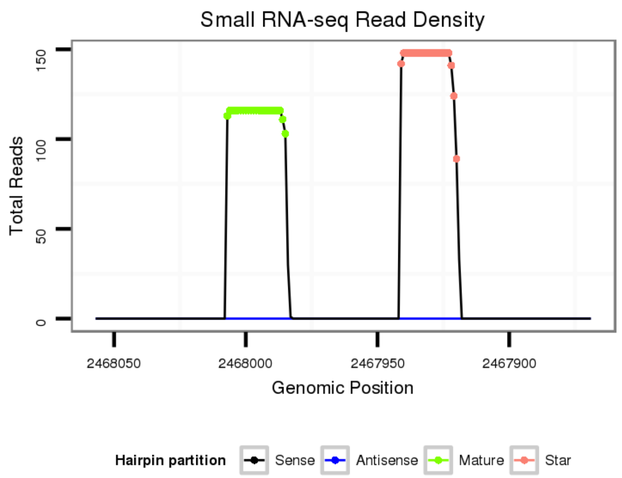
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

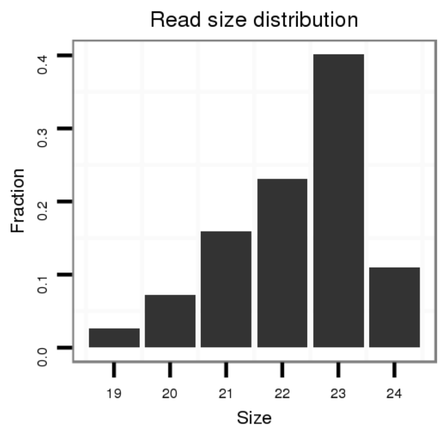
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_68	**scaffold_13417:2467919-2468007 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

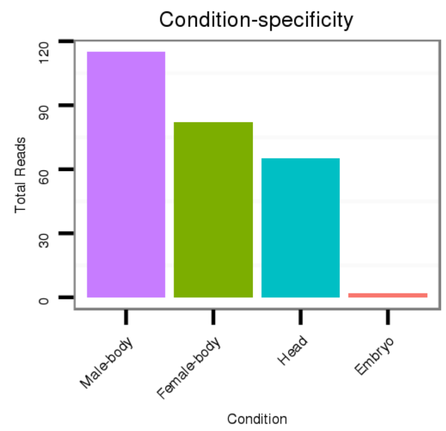
Legend: mature star mismatch in alignment mismatch in read

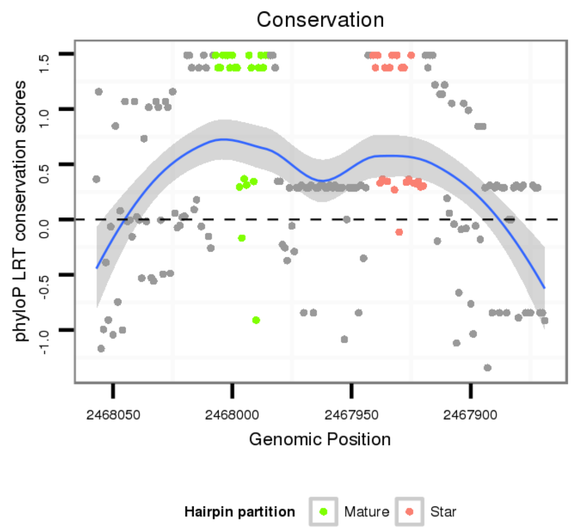
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

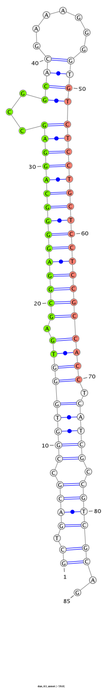
hide 3p reads | show mid mismatch reads

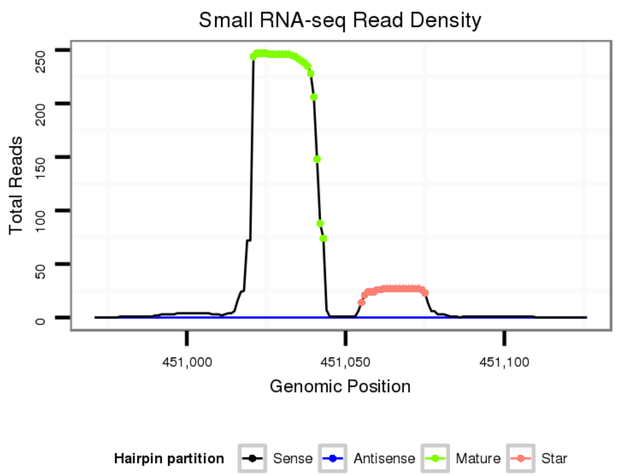
| | | |

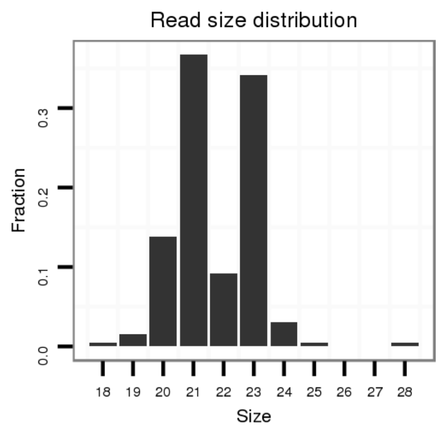
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_63	**scaffold_13337:451021-451076 +**	**confident**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

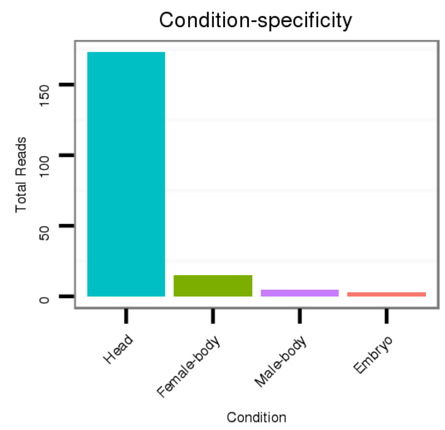
Legend: mature star mismatch in alignment mismatch in read

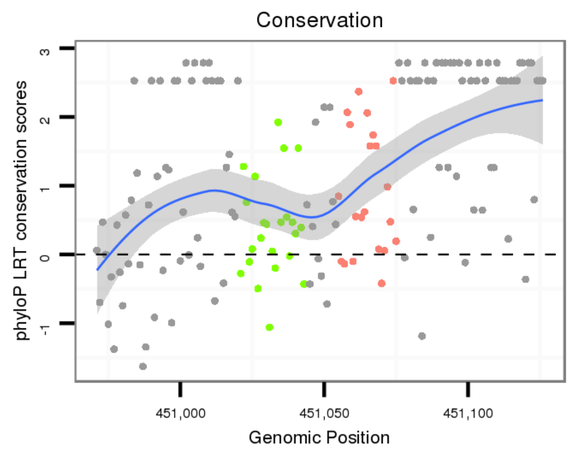
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dana\GF24918-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GTCGTCACCACCTCGGGCTCTCCACCACCTCTGCAGCTGACGCCGGTGGGTGAGCGGAGGGGCAGGAGCCGGCACGAAAGGGGTGTCTCCTGCTCCTCCGCCACCTCATCGCCGTCGCAGTACAACTCCAGCGAGGAGCTGGCCGCCATCTTTGGC **********************************((.(((((.(((((((((.(((((((((((((((((...((((.....)))))))))))))))))))))).)))))).))))))..**********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	M058 embryo	V055 head	V105 male body	V039 embryo
..........TGAGCGGAGGGGCAGGAGCCGGC..........	23	0	1	67.00	67	64	0	1	0	2	0
..........TGAGCGGAGGGGCAGGAGCCG..........	21	0	1	59.00	59	52	1	0	3	3	0
..........GGTGAGCGGAGGGGCAGGAGCC..........	22	0	1	32.00	32	32	0	0	0	0	0
..........TGAGCGGAGGGGCAGGAGCC..........	20	0	1	25.00	25	24	0	0	1	0	0
..........GGTGAGCGGAGGGGCAGGAGC..........	21	0	1	15.00	15	15	0	0	0	0	0
..........TGAGCGGAGGGGCAGGAGCCGG..........	22	0	1	13.00	13	12	1	0	0	0	0
..........TGAGCGGAGGGGCAGGAGCCGGCA..........	24	0	1	6.00	6	6	0	0	0	0	0
..........GTCTCCTGCTCCTCCGCCACC..........	21	0	1	6.00	6	5	1	0	0	0	0
..........TCTCCTGCTCCTCCGCCACCT..........	21	0	1	5.00	5	0	5	0	0	0	0
..........TGGGTGAGCGGAGGGGCAGGAGC..........	23	0	1	5.00	5	5	0	0	0	0	0
..........GTGGGTGAGCGGAGGGGCAGGAG..........	23	0	1	4.00	4	4	0	0	0	0	0
..........TGGGTGAGCGGAGGGGCAGGAG..........	22	0	1	3.00	3	2	1	0	0	0	0
..........CTCCTGCTCCTCCGCCACCTCA..........	22	0	1	3.00	3	1	1	0	1	0	0
..........GTGGGTGAGCGGAGGGGCAGGA..........	22	0	1	3.00	3	3	0	0	0	0	0
..........TGTCTCCTGCTCCTCCGCCACC..........	22	0	1	3.00	3	2	1	0	0	0	0
..........TGTCTCCTGCTCCTCCGCCAC..........	21	0	1	2.00	2	0	2	0	0	0	0
..........GTCTCCTGCTCCTCCGCCACCT..........	22	0	1	2.00	2	0	1	1	0	0	0
..........GTGGGTGAGCGGAGGGGCA..........	19	0	1	2.00	2	2	0	0	0	0	0
..........GGTGAGCGGAGGGGCAGGAGCCA..........	23	1	1	2.00	2	2	0	0	0	0	0
..........GGTGAGCGGAGGGGCAGGAGCCC..........	23	1	1	2.00	2	2	0	0	0	0	0
..........GGTGGGTGAGCGGAGGGGCAG..........	21	0	1	2.00	2	2	0	0	0	0	0
..........TGAGCGGAGGGGCAGGAGCCGGT..........	23	1	1	2.00	2	2	0	0	0	0	0
..........ACCTCTGCAGCTGACGCCG..........	19	0	1	1.00	1	1	0	0	0	0	0
..........TGAGCGGAGGGGCAGGAGCCT..........	21	1	1	1.00	1	1	0	0	0	0	0
..........CTGCTCCTCCGCCACCTCATCG..........	22	0	1	1.00	1	0	1	0	0	0	0
..........GGGTGAGCGGAGGGGCAGGAGCCGG..........	25	0	1	1.00	1	0	1	0	0	0	0
..........CGCAGTACAACTCCAGCGAGGAGCC..........	25	1	1	1.00	1	0	0	1	0	0	0
..........CTGCTCCTCCGCCACCTCATCGC..........	23	0	1	1.00	1	0	1	0	0	0	0
..........CTCCACCACCTCTGCAGC..........	18	0	1	1.00	1	0	0	1	0	0	0
..........GAAAGGGGTGTCTCCTGCTCCTCCGCCA..........	28	0	1	1.00	1	0	0	1	0	0	0
..........TGAGCGGAGGGGCAGGAGC..........	19	0	1	1.00	1	1	0	0	0	0	0
..........CCGGTGGGTGAGCGGAGGGGCAGG..........	24	0	1	1.00	1	1	0	0	0	0	0
..........GTGGGTGAGCGGAGGGGCAGGAT..........	23	1	1	1.00	1	1	0	0	0	0	0
..........GCCGGTGGGTGAGCGGAGGGG..........	21	0	1	1.00	1	0	0	0	0	0	1
..........GAGCGGAGGGGCAGGAGC..........	18	0	1	1.00	1	0	1	0	0	0	0
..........TGAGCGGAGGGGCAGGAGCCGGCAC..........	25	0	1	1.00	1	1	0	0	0	0	0
..........TCTCCTGCTCCTCCGCCAC..........	19	0	1	1.00	1	0	1	0	0	0	0
..........CCACCACCTCTGCAGCTGA..........	19	0	1	1.00	1	0	0	0	0	1	0
..........CACCTCGGGCTCTCCACCACCTCTGC..........	26	0	1	1.00	1	0	0	1	0	0	0
..........AGCTGACGCCGGTGGGTGAGC..........	21	0	1	1.00	1	0	0	1	0	0	0
..........GAGCGGAGGGGCAGGAGCCG..........	20	0	1	1.00	1	1	0	0	0	0	0
..........TCTCCTGCTCCTCCGCCACC..........	20	0	1	1.00	1	0	1	0	0	0	0
..........GTGGGTGAGCGGAGGGGCAGGTT..........	23	2	1	1.00	1	1	0	0	0	0	0
..........GTGGGTGAGCGGAGGGGCAGG..........	21	0	1	1.00	1	0	1	0	0	0	0
..........GTCTCCTGCTCCTCCGCCACCC..........	22	1	1	1.00	1	0	0	1	0	0	0
..........TGAGCGGAGGGGCAGGAGCCA..........	21	1	1	1.00	1	1	0	0	0	0	0
..........TGAGCGGAGGGGCAGGAGCCGC..........	22	1	1	1.00	1	1	0	0	0	0	0
..........TGGGTGAGCGGAGGGGCAGGAGCT..........	24	1	1	1.00	1	1	0	0	0	0	0
..........GAGCGGAGGGGCAGGAGCC..........	19	0	1	1.00	1	1	0	0	0	0	0
..........TCTCCTGCTCCTCCGCCACCTT..........	22	1	1	1.00	1	0	1	0	0	0	0
..........GCAGTACAACTCCAGCGAGGAGC..........	23	0	1	1.00	1	0	0	1	0	0	0
..........GTGGGTGAGCGGAGGGGC..........	18	0	1	1.00	1	1	0	0	0	0	0
..........TGAGCGGAGGGGCAGGATT..........	19	2	2	0.50	1	0	1	0	0	0	0

Anti-sense strand reads

CAGCAGTGGTGGAGCCCGAGAGGTGGTGGAGACGTCGACTGCGGCCACCCACTCGCCTCCCCGTCCTCGGCCGTGCTTTCCCCACAGAGGACGAGGAGGCGGTGGAGTAGCGGCAGCGTCATGTTGAGGTCGCTCCTCGACCGGCGGTAGAAACCG **********************************((.(((((.(((((((((.(((((((((((((((((...((((.....)))))))))))))))))))))).)))))).))))))..**********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V039 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13337:450971-451126 +	dan_63	GTCGTCA------CC-------ACCTCG----------GGCTCTCCACCACCTCTGCAGCTGACGCCGGTGGGTGAGCGGAGGGGCAGGAGCCGGCACGAAAGGGGTGTCTCCTGCTCCTCCGCC---------ACCTCATCGCCGTCGCAGTACAACTCCAGCGAGGAGCTGGCCGCCATCTTTGGC
droBip1	scf7180000395155:308335-308496 -		GTCACGTCTGCCACC-------ACCTCG----------GGCTCACCACCACCGCTGCAGCTGACACCGGTGGGCGAGCGGAGGGGCAGGAGCCGGCACGATAGGGGTGCCTCCTGCTCCTCTGCC---------ACCTCATCGCCGTCGCAGTACAACTCCAGCGAGGAGCTGGCCGCCATCTTTGGC
droKik1	scf7180000302441:1351240-1351388 -		-------------CA-ACC---GCCTCGGGTGGTGGATCATTATGCGCGCCGCCGCTGCAGCTGACGCCGGTGGGCGAGCGTAGGA----------AGCGTGGAGCTTGATGCTCCTCCGCC---------ACCTCATCGCCGTCACAGTACAACTCCAGCGAGGAGCTGGCCGCCATCTTTGGC
droFic1	scf7180000454105:733820-733965 +		-------------CC-------TCCTCG----------GGATGCGCGCCTCGCGCTGCAGCTGACCCGCGTGGGCAACGGAGGAGCAGGATCCGGGAGCAGCGGGGCCGGCTCCTGCTCCTC---C---------GCCTCCTCGCCGTCGCAGTACAACTCCAGCGAGGAGCTGGCCGCCATCTTCGGC
droEle1	scf7180000491249:3020365-3020520 -		-------------CCAACCGATTGCTCG---------GGTTCGTCACCACCACCGCTGCAGTTGACACCAGTGGGTGAGCGGCGGAGGA------------AGAGGGGAGCCTCTTGCTCCTCCTCGCTCCTCCTCGACATCCTCGCCGTCGCAGTACAACTCCAGCGAGGAGCTGGCCGCCATTTTTGGC
droRho1	scf7180000780275:77328-77463 +		CA-----------CC-------TCATCG----------GGATGGCCACCGCCGTTGCAGTTGACGCCAGTGGGTGAGCGGAGGAGGA--------------GGGGAGTCTCCTGTTCCTCCTCC---------ACATCCTCACCATCGCAGTACAACTCCAGCGAGGAGCTGGCCGCCATTTTTGGC
droBia1	scf7180000302428:9166896-9167038 +		-------------TC-------TCCTCG----------GGTTGCCCACCACCGCTGCAGTTGACGCCGGTGGGTGAGCGGCGGGGCAGGAACCGGCGGGAGAGGGGAGTCTCCTGCTCCTC---C---------ACATCCTCACCATCGCAGTACAACTCCAGCGAGGAGCTGGCCGCCATTTTTGGC
droTak1	scf7180000415857:146452-146585 +		-------------TT-------TCCACG----------GATTGACCACCACCGCTTCAACTGACACCGGTGGGTGAGAGGAGGATTA--------------GAGGAGCCTCCTGCTCCTCCAGC---------ACATCCTCACCATCGCAGTACAACTCCAGCGAGGAGCTGGCCGCCATTTTTGGC
droEug1	scf7180000409466:134458-134599 +		-------------T-------TCCTCG----------GGCTCGCCACCACCGCTTCAGTTGACCCAGTGGGTGAGCGGAGGGGCAGGAACCGGGGAGAGAGGAGCCTCCTGCTCCTC---C---------ACATCCTCACCATCGCAGTACAACTCCAGCGAGGAGCTGGCCGCCATTTTTGGC
dm3	chr3L:2406402-2406544 +		-------------CC-------CCGTCG----------GTATGCCCACCACCGCTGCAGTTGACGCCAGTGGGTGATCGGAGGGGCAGGAACCGGGGAGGCGGGGAGCTTCCTGCTCCTC---C---------ACATCCTCACCTTGACAGTACAACTCCGAGCGAGGAGCTGGCCGCCATTTTTGGC
droSim2	3L:2303352-2303494 +		-------------CC-------CCGTCG----------GTATGCCCACCACCGCTGCAGTTGACGCCAGTGGGTGATCGGAGGTGCAGGAACCGGGGAGGCGGGGAGCTTCCTGCTCCTC---C---------ACATCCTCACCTTGACAGTACAACTCCGAGCGAGGAGCTGGCCGCCATTTTCGGC
droSec2	scaffold_2:2430740-2430882 +		-------------CC-------CCGTCG----------GTATGCCCACCACCGCTGCAGTTGACGCCAGTGGGTGATCGGAGGGGCAGGAACCGGGGAGGCGGGGAGCTTCCTGCTCCTC---C---------ACATCCTCACCTTGACAGTACAACTCCGAGCGAGGAGCTGGCCGCCATTTTCGGC
droYak3	3L:9529533-9529675 -		-------------CC-------CCATCG----------GTATGCCCACCGCCGCCTGCAGTTGACGCCAGTGGGTGATCCAAGGGGCAGGAACCGGGGAGGCGAGGAGCTTCCTGCTCCTC---C---------ACATCCTCACCGTGACAGTACAACTCCAAGCGAGGAGCTGGCCGCCATTTTTGGC
droEre2	scaffold_4784:2421991-2422133 +		-------------GC-------CCCTCG----------GTATGCCCACCACCGCTGCAGTTGACGCCAGTGGGTGATCGGAGGGGCAGGAACCGGGGAGGCGAGGAGCTTCCTGCTCCTC---C---------ACATCCTCACCTTGACAGTACAACTCTAGCGAGGAGCTGGCCGCCATTTTTGGC
dp5	XR_group6:12367350-12367464 +		GACG-----------------ACC---GCCTCG-----TGC-TCTGTGTGCCCAGAGCCGCTGCAGCTGACGCCCGTGCGGAGG---CAG------C---------TCCTCATCGCGATCGCAGTACAACTCCAGCGAAGAGCTGGCTGCCATTTTTGGC
droPer2	scaffold_33:388491-388605 +		GACG-----------------ACC---GCCTCG-----TGC-TCTGTGTGCCCAGAGCCGCTGCAGCTGACGCCCGTGCGAGG---CAG------C---------TCCTCATCGCCATCGCAGTACAACTCCAGCGAAGAGCTGGCTGCCATTTTTGGC
droWil2	scf2_1100000004729:1965453-1965596 +		GCCAAAA------GA-------GAGCCG----------GCTTCTTCTCCCCTGCAATTGACGCCGAAAAGTGAAAGAAAATCAAAGGATGCT---GAAAGGGCATCGTGCGGGAGG------A---------TCATCATCGCCATCGCAATATAATTCTAGTGAAGAATTGGCTGCCATATTTGGC
droVir3	scaffold_10322:182200-182329 +		GCCGTCG------CCGACC---TCGTCG-----TCA-TCCGCCTCATCCCCGCCGTTGCAATTGACGCCAGTGGGGAACCCAGAG----------------------C---ACG---------C---------TCTTCGTCGCCGTCGCAGTACAATTCCGAGCGAGGAGCTGGCCGCCATCTTTGGC
droMoj3	scaffold_6680:2236159-2236288 +		ATCGCCT------------ACGTCC-----TCG-ACCTGCTCGTCGCCGCCGTTGCAGCTGACACCGGTGGGTGGCGATGCGA----------------GTGGAGC---ACGCT--------------------CCTCTTCTCCCTCGCAGTACAATTCCGAGCGAGGAGCTGGCCGCCATATTTGGC
droGri2	scaffold_15110:318187-318309 -		GTTGCCCT------CC-------CCGTCG---------CCATCACGATCACCTCCGTTGCAGTTGACGCCGGTGGGTGAGCGGAGAG----------------------C---ACGCT--------------------CCTCCTCGCCATCTCAGTACAATTCCAGCGAGGAGCTGGCAGCCATTTTTGGC

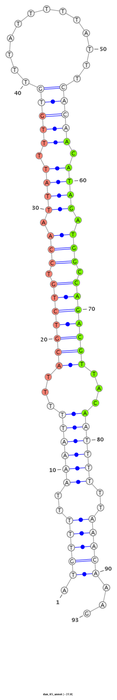
Generated: 09/08/2015 at 07:46 PM

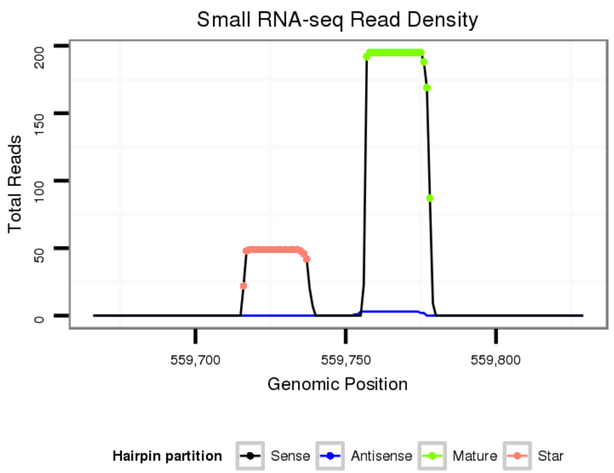
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

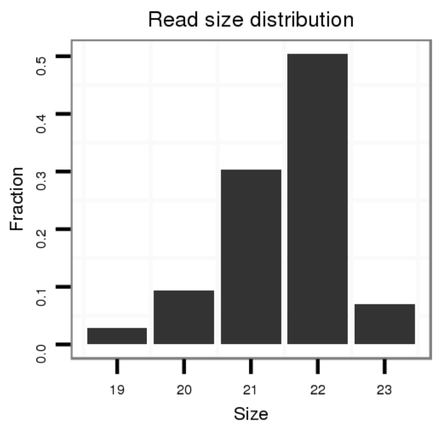
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_65	**scaffold_12903:559716-559779 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

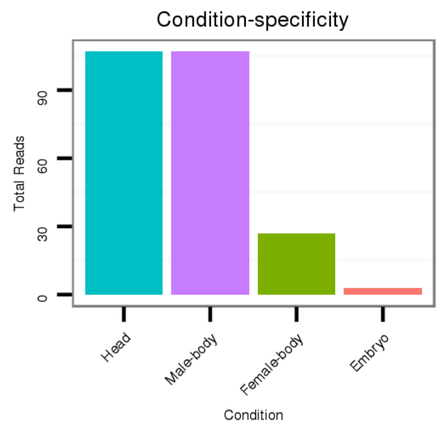
Legend: mature star mismatch in alignment mismatch in read

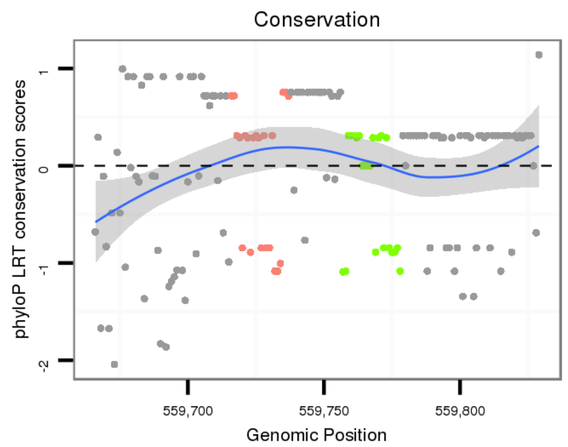
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AACAATTTAAAAAATATATATTGCCTGAAATATGTATGTTTTTAAAATTTTTACGTCTGTCCAATTATTTTGTGTTTATTTTTATTTCACAACATAGATGGCCAGACGTTACAATTTTTTAAACAAAGCGGCTGTGAAGGAAAGTGTTACTAAAACTCAAATCA **********.(((((..(((((((...(((((((.(((.((((.(((((.....)))))).))))).))).)))))))...))))))..))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V106 head	M044 female body	V055 head	M058 embryo	V039 embryo
.....ACATAGATGGCCAGACGTTACA.....	22	0	1	76.00	76	37	26	8	5	0	0
.....ACATAGATGGCCAGACGTTAC.....	21	0	1	61.00	61	25	31	3	1	0	1
.....AACATAGATGGCCAGACGTTAC.....	22	0	1	20.00	20	7	11	1	0	1	0
.....ACATAGATGGCCAGACGTTA.....	20	0	1	17.00	17	10	5	0	2	0	0
.....TTACGTCTGTCCAATTATTTTG.....	22	0	1	15.00	15	8	2	5	0	0	0
.....TACGTCTGTCCAATTATTTTGT.....	22	0	1	12.00	12	8	2	1	0	1	0
.....ACATAGATGGCCAGACGTTACAA.....	23	0	1	9.00	9	0	9	0	0	0	0
.....TACGTCTGTCCAATTATTTTGTG.....	23	0	1	7.00	7	3	0	3	1	0	0
.....TACGTCTGTCCAATTATTTTG.....	21	0	1	6.00	6	0	2	3	1	0	0
.....ACATAGATGGCCAGACGTT.....	19	0	1	6.00	6	2	3	0	1	0	0
.....ACATAGATGGCCAGACGTTT.....	20	1	1	5.00	5	1	2	1	1	0	0
.....ACATAGATGGCCAGACGTTAT.....	21	1	1	3.00	3	3	0	0	0	0	0
.....TTACGTCTGTCCAATTATTTT.....	21	0	1	3.00	3	0	1	1	1	0	0
.....TTACGTCTGTCCAATTATTT.....	20	0	1	2.00	2	0	2	0	0	0	0
.....ACATAGATGGCCAGACGTTAG.....	21	1	1	2.00	2	1	0	0	1	0	0
.....CATAGATGGCCAGACGTTACA.....	21	0	1	2.00	2	2	0	0	0	0	0
.....ACATAGATGGCCAGACGTTAA.....	21	1	1	2.00	2	1	1	0	0	0	0
.....AACATAGATGGCCAGACGTTA.....	21	0	1	2.00	2	2	0	0	0	0	0
.....TTACGTCTGTCCAATTATTTTGAA.....	24	2	1	1.00	1	0	1	0	0	0	0
.....TTACGTCTGTCCAATTATTTG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....CATAGATGGCCAGACGTTAC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....AACATAGATGGCCAGACGTTAA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....CATAGATGGCCAGACGTTACT.....	21	1	1	1.00	1	0	0	1	0	0	0
.....AACATAGATGGCCAGACGTT.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TTACGTCTGTCCAATTATTTTT.....	22	1	1	1.00	1	0	0	0	1	0	0
.....ACGTCTGTCCAATTATTTTG.....	20	0	1	1.00	1	0	0	1	0	0	0
.....TTACGTCTGTCCAATTATTTTTA.....	23	2	1	1.00	1	0	0	0	1	0	0
.....ACATAGATGGCCAGACGTTACAT.....	23	1	1	1.00	1	0	1	0	0	0	0
.....ACATAGATGGCCAGACGTTACC.....	22	1	1	1.00	1	0	0	0	1	0	0
.....TACGTCTGTCCAATTATTTT.....	20	0	1	1.00	1	0	0	1	0	0	0
.....TTACGTCTGTCCAATTATTTGT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TTACGTCTGTCCAATTATTTGA.....	23	1	1	1.00	1	0	0	1	0	0	0
.....ACATAGATGGCCAGACGTTC.....	20	1	1	1.00	1	0	1	0	0	0	0
.....TTACGTCTGTCCAATTATT.....	19	0	1	1.00	1	0	0	0	1	0	0

Anti-sense strand reads

TTGTTAAATTTTTTATATATAACGGACTTTATACATACAAAAATTTTAAAAATGCAGACAGGTTAATAAAACACAAATAAAAATAAAGTGTTGTATCTACCGGTCTGCAATGTTAAAAAATTTGTTTCGCCGACACTTCCTTTCACAATGATTTTGAGTTTAGT **********.(((((..(((((((...(((((((.(((.((((.(((((.....)))))).))))).))).)))))))...))))))..))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V039 embryo	M058 embryo	V055 head	V105 male body
.....GTTGTATCTACCGGTCTGCAAT.....	22	0	1	2.00	2	2	0	0	0	0	
.....GTGTTGTATCTACCGGTCTGCA.....	22	0	1	1.00	1	1	0	0	0	0	

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:559666-559829 +	dan_65	AACA--ATTTAAAAAATATATATTGCCTGAAATATGTATGTTTTTAAAATTTTTACGTCTGTCCAATTATTTTGTGTTTATTTT-----TATTTCACAACATAGATGGCCAGACGTTACAATTTTTTAAACAAAGCGGCTGTGAAGGAAAGTGT--------TACTAAAACTCAAATCA
droBip1	scf7180000395925:48566-48733 -		AAAA--ACAAATAAAATGT-CATAGTGTCTGGAAATTATAATTT-AAAACTGTTACATCAGTCTAGCTCGGTTGTGTTTTTTTTTTAATATTTCACATATAGA----CTGATCCATTCA-TTTTTAACTAAAGCAACGATCAAGCGGAAGTATTTGGTGTTTAATAAATACTCAAA--A
droEle1	scf7180000491278:1072167-1072180 -		TAGA--GGTCAAAC--AA
droRho1	scf7180000778082:74467-74520 -		AAAGCAATTTTAAGAGTAAAGATTGGGTTGGATAATCATATTTTTAAGATTTTT---
droTak1	scf7180000415857:724844-724855 +		AAAA--TAAAAT--TA
droYak3	2R:7536018-7536057 +		GACA--TTTCAAAAAGTATATATTTTCTAATTAATATATGTT---
dp5	3:13547608-13547637 -		TTTAT--TTTGTTTTATTTT-----TATCTCTCAC--CA

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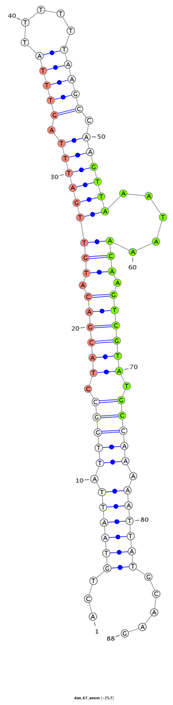
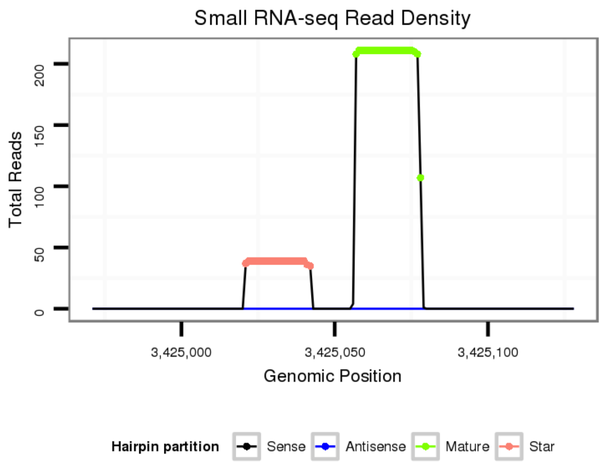
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

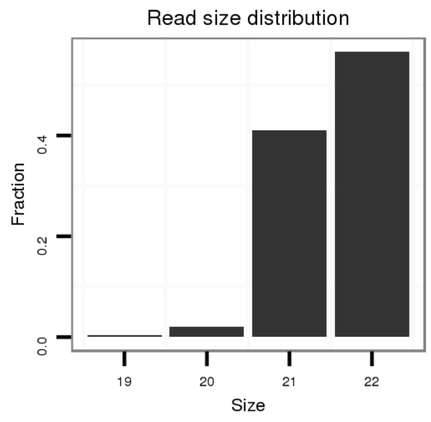
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_67	**scaffold_13117:3425021-3425078 +**	**confident**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

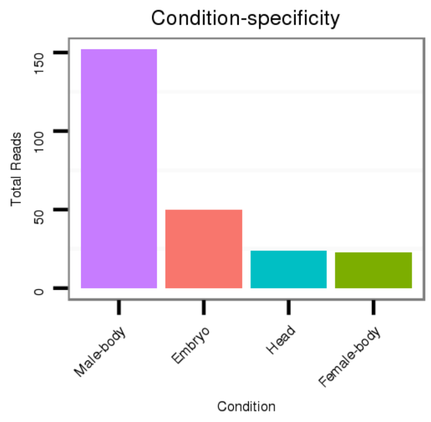
Legend: mature star **mismatch in alignment** mismatch in read

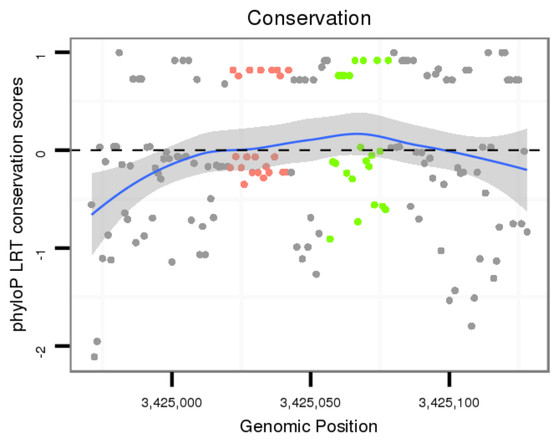
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dana\GF20896-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTGAAATAATTGTTAAATTAATTGGAGTTAAAAATACTGTAATTATTGGCCTACGACATGTTGATTTAGTTTATTTTTTAAGCCAAGTTAAATAAACAAGTCGTATGCCAAAAATTATGCAAGCCACAAGATCGATTCCATAAAAAAAAATATTTTTA	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	M058 embryo	M044 female body	V055 head	V106 head	V039 embryo
**********...(((((((.(((((.(((((((.(((((((((.(((((.....)))))...)))))))...)))))))...)))))).)))))).....**********											
.....GTTAAATAAACAAGTCGTATGC.....	22	0	1	104.00	104	47	36	3	6	7	5
.....GTTAAATAAACAAGTCGTATG.....	21	0	1	97.00	97	89	2	2	3	1	0
.....CTACGACATGTTGATTTAGTTT.....	22	0	1	33.00	33	9	4	14	2	3	1
.....GTTAAATAAACAAGTCGTATGCT.....	23	1	1	7.00	7	7	0	0	0	0	0
.....AGTTAAATAAACAAGTCGTATG.....	22	0	1	4.00	4	3	0	0	0	1	0
.....CTACGACATGTTGATTTAGT.....	20	0	1	3.00	3	0	0	2	0	1	0
.....GTTAAATAAACAAGTCGTATGCA.....	23	1	1	3.00	3	0	2	0	0	0	1
.....TTAAATAAACAAGTCGTATGC.....	21	0	1	2.00	2	1	1	0	0	0	0
.....TACGACATGTTGATTTAGTTT.....	21	0	1	2.00	2	1	0	1	0	0	0
.....GTTAAATAAACAAGTCGTAT.....	20	0	1	2.00	2	2	0	0	0	0	0
.....GTTAAATAAACAAGTCGTATGT.....	22	1	1	2.00	2	2	0	0	0	0	0
.....AGTTAAATAAACAAGTCGTATGT.....	23	1	1	1.00	1	0	0	1	0	0	0
.....TTAAATAAACAAGTCGTATGCCT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....CTACGACATGTTGATTTAGTTTT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....GTTAAATAAACAAGTCGTA.....	19	0	1	1.00	1	0	1	0	0	0	0
.....TTAAATAAACAAGTCGTATGCC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....CTACGACATGTTGATTTAGTT.....	21	0	1	1.00	1	0	0	1	0	0	0
.....GTTAAATAAACAAGTCGTATT.....	21	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

CACTTTATTAACAATTTAATTAACCTCAATTTTTATGACATTAATAACCGGATGCTGTACAACTAAATCAAATAAAAAATTCGGTTCAATTTATTTGTTCAGCATACGGTTTTTAATACGTTCGGTGTTCTAGCTAAGGTATTTTTTTTTATAAAAAT	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	M058 embryo
**********...(((((((.(((((.(((((((.(((((((((.(((((.....)))))...)))))))...)))))))...)))))).)))))).....**********							
.....CGAATTAACCTCAATTTT.....	18	2	20	0.05	1	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13117:3424971-3425128 +	dan_67	GTGAAATAATTGTTAAATTAA-TTGG----------AGTTAAAAATA---------CTGTAATTATTGGCCTACGACATGTTGA-TTTAGTTTATTTTTTAAGCCAAGTTAAATAAACA--AGTCGTATGCCAAAAATTATGCAAGCCAC----------AAGATCGATTC-CA--TA-------AAAAAAAATATT-----TTT-A
droBip1	scf7180000395895:128435-128590 -		GAAATACTATT-------AA-TTGGAATCTTA----------AGTCTAAAATA---------TTGCTGTGGTTGGCCTACGACATGTTGA-TTTAGTTTATGTCTGGAA-CAATTAAATAAATA--AGTCGTTTGCCAAAAATTATGCAAA----------AACAACGATTT-AA--AA-------AAA-TAAATAATAAAAATAA-A
droEle1	scf7180000491023:198326-198491 +		TGCAA-TAAATATATAATTTA-AAAG---------ATTCATTAAAGA----------G----------------------AATACAAGTCTTCGCTAAAAT--ATCAGTTTTTTTATTAACAACAA--------TATT------AGTCCAATAATGAAAT--GTCATACACCTTT--TAACTCGTTATACAATTTCAAACCGATTGACATTCA--------AACCAGAATATT-----TTTAT
droRho1	scf7180000779985:163806-163966 -		ATAGG-TTTTTACTTACTTCC-TTAT-----AAGATTAATATTGTATTTATATGTAACACCTACAAACATACAAAGAATT----------TTTCAATATATTTTTTCAGACTA----------CACC--ACACATAAGCCACA----------AACATATGTAAATGGC----------A---TTTGTTC-TT--TGTTATAAAATAATTTAA-----------T-A
droYak3	X:6797531-6797649 +		ACGAAGGAATT-------AAATCG-----------CATACGCATCAACTGGAAATTTAGATTTT----------TCAAGCAAAGAAACATTATTTTATATCTAAAAATAACTTAGCCAGGAATCTTT--AAATTG----------------------T--TA-------TAAATAAA-----------T-C

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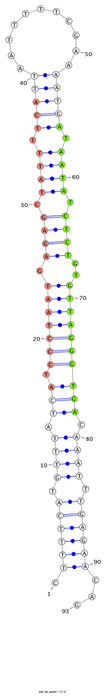
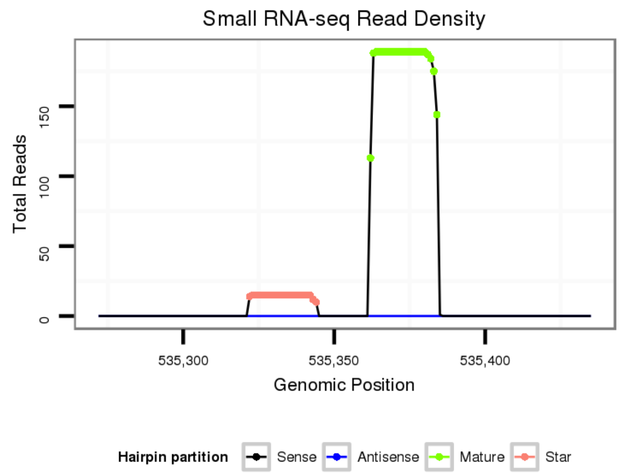
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

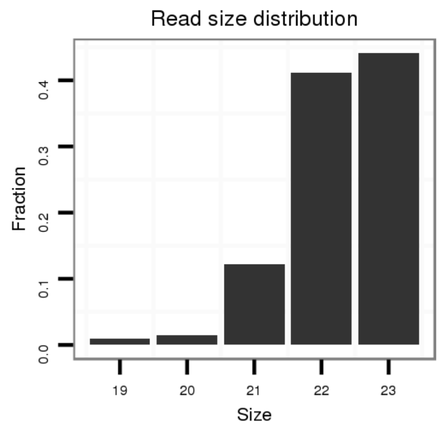
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_66	**scaffold_12903:535322-535385 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

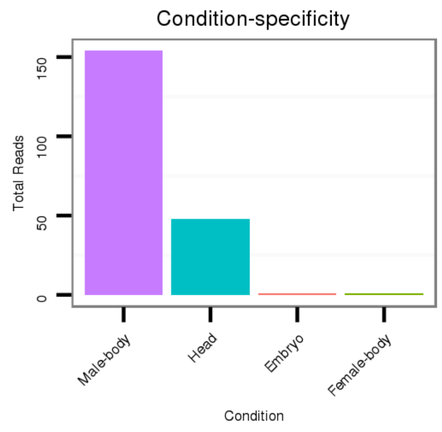
Legend: mature star mismatch in alignment mismatch in read

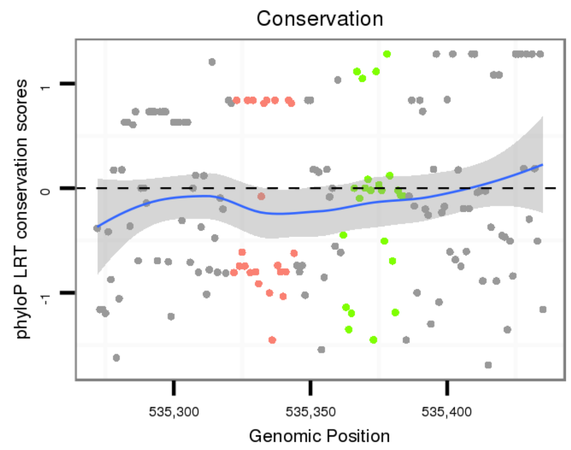
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTTTTTATTGAATCTTTTATTTTTTAGTTATCTTCCTTTTCATGTTTATCATCCCTAATGAGAGCTATTTTCATTAATTTTTCGAAAATGATAATATCTCTGTGTTAGGGTGACAAATTTGAGAACAGTCTACAAAATAAAGTGGTGTTTATATATATTTTTAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V055 head	V106 head	M044 female body	M058 embryo	V039 embryo
***********************************.(((((((.((((.(((.(((((((.((((.((((.(((((..........)))))).)))).))))..))))))))))).))))).)))))...***********************************											
.....ATAATATCTCTGTGTTAGGGTGA.....	23	0	1	80.00	80	64	12	3	1	0	0
.....TAATATCTCTGTGTTAGGGTGA.....	22	0	1	62.00	62	53	6	3	0	0	0
.....ATAATATCTCTGTGTTAGGGTG.....	22	0	1	19.00	19	11	0	8	0	0	0
.....TAATATCTCTGTGTTAGGGTG.....	21	0	1	12.00	12	9	2	1	0	0	0
.....ATCCCTAATGAGAGCTATTTTCA.....	23	0	1	9.00	9	2	0	7	0	0	0
.....ATAATATCTCTGTGTTAGGGT.....	21	0	1	9.00	9	6	2	1	0	0	0
.....TAATATCTCTGTGTTAGGGTGT.....	22	1	1	5.00	5	5	0	0	0	0	0
.....ATCCCTAATGAGAGCTATTTT.....	21	0	1	3.00	3	2	1	0	0	0	0
.....ATAATATCTCTGTGTTAGGGTGAA.....	24	1	1	3.00	3	3	0	0	0	0	0
.....ATAATATCTCTGTGTTAGGG.....	20	0	1	3.00	3	3	0	0	0	0	0
.....ATCCCTAATGAGAGCTATTTTC.....	22	0	1	2.00	2	0	1	0	0	1	0
.....ATAATATCTCTGTGTTAGG.....	19	0	1	2.00	2	2	0	0	0	0	0
.....TAATATCTCTGTGTTAGGGTGAC.....	23	0	1	1.00	1	1	0	0	0	0	0
.....AATATCTCTGTGTTAGGGTGA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TCCCTAATGAGAGCTATTTTCA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....ATAATATCTCTGTGTTAGGGTGG.....	23	1	1	1.00	1	0	1	0	0	0	0
.....ATCCCTAATGAGAGCTATTTTCT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TAATATCTCTGTGTTAGGGTGG.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TAATATCTCTGTGTTAGGGTGAT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....ATAATATCTCTGTGTTAGGGTGT.....	23	1	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

AAAAAATAACTTAGAAAATAAAAAATCAATAGAAGGAAAAGTACAAATAGTAGGGATTACTCTCGATAAAAGTAATTAAAAAGCTTTTACTATTATAGAGACACAATCCCACTGTTTAAACTCTTGTCAGATGTTTTATTTCACCACAAATATATATAAAAATA	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V039 embryo	M058 embryo	V055 head
***********************************.(((((((.((((.(((.(((((((.((((.((((.(((((..........)))))).)))).))))..))))))))))).))))).)))))...***********************************									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:535272-535435 +	dan_66	TTTTTTATTGAATCTTTTATTTTTTAGTTATCTTCCTTTTCATGTTTATCATCCCTAATGAGAGCTATTTTCATTAATTTTTCGAA----------AATGATAATATCTCTGTGT---TAGGGTGACAAATTTGAGAACAGT----------CTACAAAATAAAGTGGTGT-TTATATATATTTTTAT
droBip1	scf7180000395952:1943-2080 -		TAACTAAAAA----TC--ATTTCTTAAG----------TTTTCTTTTTTTAATAGAAGTGAGATCGCAGTTTCTTTCAA----------A----GGCTATCTCACTGAAATTACAAAGAGAAACT---TGACA----------ACCTGTCAAATAATAACATATCAACTGTATTTTTATAA
droKik1	scf7180000302798:211533-211619 -		GGGAAAGGTA----------TGGTGTTTGAGA----------TCGGTGAGTTATATTC----------GATTT----------AAATAAT----------TTTGTAAGATAATAATAATTTTAAGATATATCTTTGAG
droTak1	scf7180000415843:977999-978130 -		TTTTCTACGAAAACTT--GTTTTTTAAATATTTTG-AAGCACTTAAGT----------TTTAGAGAATTATATTTATGTTCTCGAAGCACTTTAT---AATTAT----------AATTGTTTGAATAACGCTGTATATTTTA---------TATATTATATTTTTAAT
droGri2	scaffold_14822:226493-226630 -		ATTATTAGTA----------TTTTCATATTTATGTTTGTTTATGTGATTTATTTTCGTTACTTTTTTTAA----------ATTAAATGTATCTTTCTGT---TATTGTATTTACATTATTAATG----------GTTTATTTTTTAAAATTTATTTT-ATTTATATATTTTAT

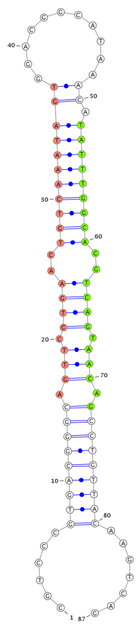
Generated: 09/08/2015 at 08:01 PM

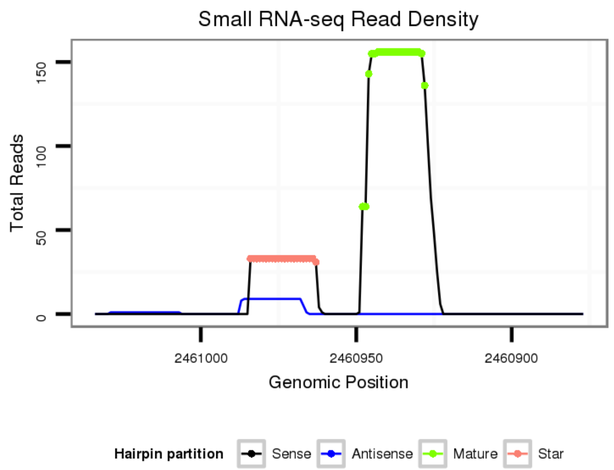
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

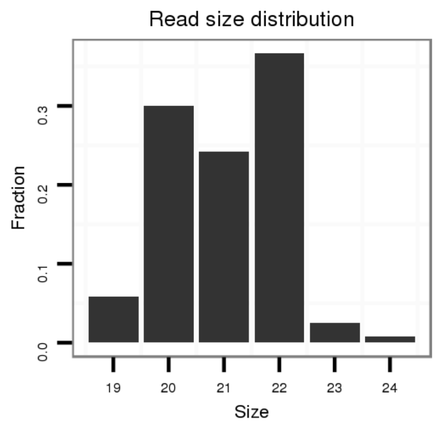
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_75	**scaffold_13417:2460927-2460984 -**	**confident**	**Testes-restricted**	**antisense_to_CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

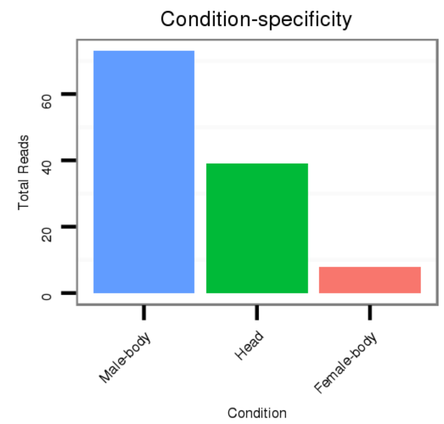
Legend: mature star mismatch in alignment mismatch in read

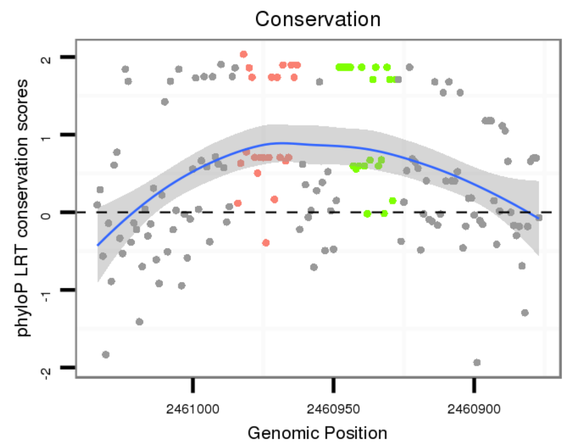
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to CDS [Dana\GF20485-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TCACACCAAGTGAGATCCGGCCCCTGCAGACGTCGCGTCCCGTGACGGGCAGTTCCTGAACTGTCAAATAGTGGACGGCATAAACATATTTGGCACGTCAGTAACAGCCTGTTACAAGTCAGCGCACGACCAGCACTACCGGCCACCCTCGGCGGAAG **********.....(((((((((.(((.((((..((((((((((((.....)).)))))))))..))))).)))).)))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	M044 female body	V055 head	V106 head	M058 embryo	V039 embryo
.....TATTTGGCACGTCAGTAACAG.....	21	0	1	27.00	27	19	2	1	5	0	0
.....AGTTCCTGAACTGTCAAATAGT.....	22	0	1	27.00	27	9	2	4	12	0	0
.....TTTGGCACGTCAGTAACAGCCT.....	22	0	1	21.00	21	9	7	4	0	1	0
.....TTTGGCACGTCAGTAACAGCC.....	21	0	1	20.00	20	11	2	5	2	0	0
.....TATTTGGCACGTCAGTAACA.....	20	0	1	19.00	19	14	0	2	3	0	0
.....TTTGGCACGTCAGTAACAGC.....	20	0	1	17.00	17	14	1	1	1	0	0
.....TATTTGGCACGTCAGTAACAGC.....	22	0	1	16.00	16	11	1	2	2	0	0
.....TTTGGCACGTCAGTAACAGCCTG.....	23	0	1	12.00	12	0	12	0	0	0	0
.....TTTGGCACGTCAGTAACAG.....	19	0	1	6.00	6	4	0	2	0	0	0
.....TTGGCACGTCAGTAACAGCCTG.....	22	0	1	6.00	6	1	4	1	0	0	0
.....AGTTCCTGAACTGTCAAATAGTGT.....	24	1	1	4.00	4	2	1	0	1	0	0
.....TTTGGCACGTCAGTAACAGCCTGT.....	24	0	1	3.00	3	0	3	0	0	0	0
.....AGTTCCTGAACTGTCAAATAGTG.....	23	0	1	3.00	3	0	2	0	1	0	0
.....TTGGCACGTCAGTAACAGCCTGT.....	23	0	1	3.00	3	1	1	1	0	0	0
.....AGTTCCTGAACTGTCAAATAGTT.....	23	1	1	2.00	2	0	2	0	0	0	0
.....TTTGGCACGTCAGTAACAGT.....	20	1	1	2.00	2	2	0	0	0	0	0
.....TATTTGGCACGTCAGTAACAGT.....	22	1	1	2.00	2	1	0	1	0	0	0
.....AGTTCCTGAACTGTCAAATAG.....	21	0	1	2.00	2	1	0	0	1	0	0
.....TTGGCACGTCAGTAACAGCCT.....	21	0	1	2.00	2	0	2	0	0	0	0
.....TATTTGGCACGTCAGTAACAGCT.....	23	1	1	2.00	2	2	0	0	0	0	0
.....TATTTGGCACGTCAGTAAC.....	19	0	1	1.00	1	0	0	0	1	0	0
.....TATTTGGCACGTCAGTAACAGTTT.....	23	2	1	1.00	1	1	0	0	0	0	0
.....TTTGGCACGTCAGTAACAGCA.....	21	1	1	1.00	1	0	1	0	0	0	0
.....TATTTGGCACGTCAGTAACAT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....GGCACGTCAGTAACAGCCTG.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TTTGGCACGTCAGTAACAGCT.....	21	1	1	1.00	1	0	0	1	0	0	0
.....AGTTCCTGAACTGTCAAATAGTGG.....	24	0	1	1.00	1	0	0	0	1	0	0
.....TTTGGCACGTCAGTAACAGAG.....	21	2	1	1.00	1	1	0	0	0	0	0
.....ATATTTGGCACGTCAGTAACAG.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TTGGCACGTCAGTAACAGCC.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TTTGGCACGTCAGTAACAGA.....	20	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

AGTGTGGTTCACTCTAGGCCGGGGACGTCTGCAGCGCAGGGCACTGCCCGTCAAGGACTTGACAGTTTATCACCTGCCGTATTTGTATAAACCGTGCAGTCATTGTCGGACAATGTTCAGTCGCGTGCTGGTCGTGATGGCCGGTGGGAGCCGCCTTC **********.....(((((((((.(((.((((..((((((((((((.....)).)))))))))..))))).)))).)))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	M058 embryo	V105 male body	V055 head
.....CCGTCAAGGACTTGACAGTTT.....	21	0	1	4.00	4	3	0	0	1	0
.....CCGTCAAGGACTTGACAGTT.....	20	0	1	3.00	3	2	1	0	0	0
.....CCGTCAAGGACTTGACAGTTTA.....	22	0	1	1.00	1	1	0	0	0	0
.....GGTTCACTCTAGGCCGGGGACGT.....	23	0	1	1.00	1	0	1	0	0	0
.....CGTCAAGGACTTGACAGTT.....	19	0	1	1.00	1	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13417:2460877-2461034 -	dan_75	TCACACCAAGTGAGATCC------GGCCCC----------TGCAGACG------TCGCGTCCCGTGACGGGCAGTTCCTGAACTGTCAAATAGTGGACGGCATA----------A-ACATATTTGGCACGTCAGTAACAGCCTGTTACAAGTCAGCGCACG-ACCAGCACTACCGGCCACCCTCGGCGGAAG
droBip1	scf7180000395874:32892-33048 -		TCACACCAAGTGAGATCC------GGCCCC----------TGCAAACG------TCGCGTCCCGTGACGGGCAGTTCCTGAACTGTCAAATAGTGGACGGCATA----------A-ACATATTTGGCACGTCAGTAACAGCCTGTTACAAGACAGCGCACG-ACCAGCAATACCGGCCACC-TCGATGGAAG
droKik1	scf7180000302517:1186181-1186300 +		GC----------------------------TGTCCCGTGACAGGCAGTTCCTGAACTGTCAAATAGTGGATGACATG----------A-GAATATTTGGCACCCAGAGACAGCCTGTTACTGGCAGCCAACG-ACC---CATCCCGGACACC-CAAAGAGAAA
droFic1	scf7180000453342:708297-708306 +		TCGGCGGAA---------------------------TGTCCCGTGACAGGCAGTTCCTGAACTGTCAAATAGTGGATGACATG----------A-ACATATTTGGCACGTCAGTAACAGCCTGTTACTGGCAGCCAACG-ACC---CATCCCGGACACC-CAAAGAGAAA
droRho1	scf7180000777310:10109-10138 +		TCAGAGCAAATGAGAGAC------AGCTGC----------TGCAGA--------TGTCCCGTGACAGGCAGTTCCTGAACTGTCAAATAGTGGATGACATG----------A-ACATATTTGGCACGTCAGTAACAGCCTGTTACTGGCAGCCAACG-ACC---CATCCCGGACACC-CAAAGAGAAA
droBia1	scf7180000296918:1593-1629 +		ATAA----------------------------TGTCCCGTGACAGGCAGTTCCTGAACTGTCAAATAGTGGATGACATG----------A-ACATATTTATTAGTCAATAACTGCACGTTCCA----------CAAAGAGAAA
droEug1	scf7180000408987:110777-110831 +		TCGCAACTGCTGCGCCAC------AGCCTC----------TGCTGACG------TCGCTGCCGGCGAAAGGCACTTC----------A-ACATATTTATTAGTCAATAACTGCACGTTCCA----------CAAAGAGAAA
droYak3	2L:18553215-18553275 -		TCACACCAGGTGAGATTC------AGCTCC----------TTCAGATG------CCTC----------CAGTGCCACAATCAGGACCAGTGG----------A-ACATATTTATTAGTCAATAACTGCACGTTCCA----------CAAAGAGAAA
droWil2	scf2_1100000004909:7960701-7960896 +	dwi_143	TCACTTCATGTGCCGAATAGAGTCAACGCAGAACAAGCTAAAATTGTTATTGTGT----------TATACCAGAATCAAGAGCTACT-AAT------TGGCGTCTTGTGACGGGCAGTTCCTGAACTGTCAAATAGTAGATACACTGATAA----------TTAGTATCTATTTGGCACGTCAGTAACAGCCTTTACAATTAAATGCAAATGCGGCGAGA----------G
droVir3	scaffold_13042:902989-903199 -	dvi_45	TTGGCTCAGATGCAAACA------CAGCG------ATAACGATAACGATAACGATAACAATAACGATAACTTAAGC---GATA-AGG-ATAACGATAAGCGGCATCTGGTGACTAGCCGTTCCTGAAGTGTCAAATAGTAGGTACTACTCGTAAGAAAATGTACGTTCGATTTTTATTTGGCACATCAGTGACAGCATGTTACGAGTAATTGCACA-AGAGCCAGCAGCCGG----------
droMoj3	scaffold_6328:2897593-2897725 -	dmo_206	G----------------------------TGTCCCGTGACAGGCAGTTCCTGAACTGTCAAATAGTGAGTACTACTCGTAAGAAAATGTACGTTCGATTTTTATTTGGCACATCAGTGACAGCATGTCACGAGTAATTGCACA-AGGACCAGACGCCGATAAG----------
droGri2	scaffold_15081:2041135-2041301 -	dgr_20	TCCTCTCAAATGACGCAC------G---G------GCAACAGCATTCGTGGCGG----------GGAATCTGAGT---GAGC-CGG-AGG------ATGCATCTGGTAACTAGGCGTTCCTGTGTAGCCAAATAGTTGGTAGCACG----------ATTGTTATTTGGCACATCAGTGACTGCTGGTTAACGGTGAGCGCACA-ACAACGCCA----------

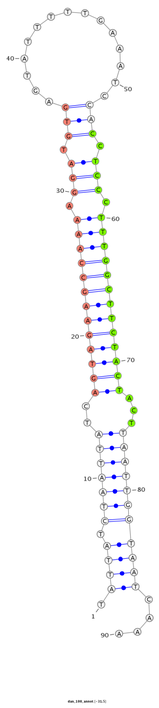
Generated: 09/08/2015 at 08:01 PM

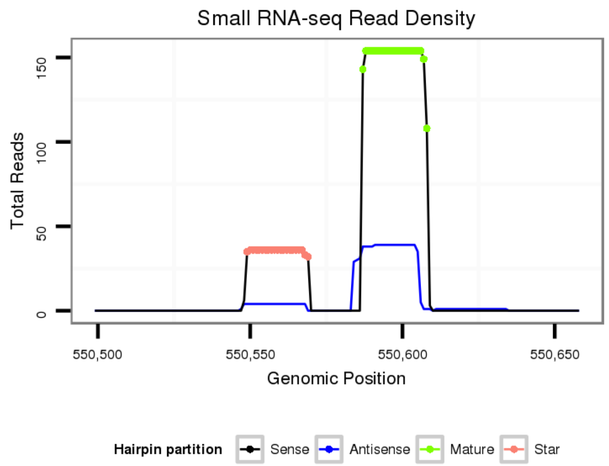
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	4
rescue.candidate	1

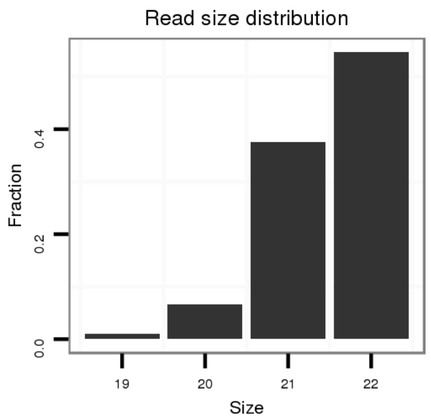
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_100	**scaffold_12903:550549-550608 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

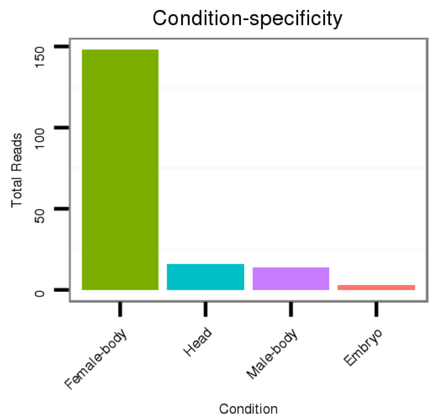
Legend: mature star mismatch in alignment mismatch in read

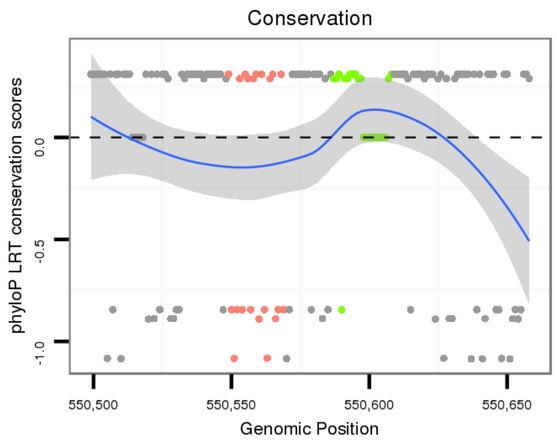
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dana\GF15947-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAAAAATTTTTAAAAAGTGATAATAATTCTTGGAGTATTATCTAATTATCAGTAGAAGCCAAAAGGATGTGAGTATTTTTGAAATCCACCTCCCTTTGGCTTCTACTACTTAATTGGTAATCAAAACTGCTTCAAAAACAGTCTAAAACTAACTGAAAAG **********.(((((.(((((((..(((((((((((((.(((.(((.....)))).)))).)))))))))))))...)))))))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V105 male body	V106 head	V055 head	M058 embryo
..CCTCCCTTTGGCTTCTACTACT..	22	0	1	99.00	99	96	1	0	0	2
..CCTCCCTTTGGCTTCTACTAC..	21	0	1	36.00	36	32	1	2	1	0
..AGTAGAAGCCAAAAGGATGTG..	21	0	1	26.00	26	4	11	9	1	1
..CTCCCTTTGGCTTCTACTACT..	21	0	1	6.00	6	6	0	0	0	0
..CTCCCTTTGGCTTCTACTAC..	20	0	1	5.00	5	5	0	0	0	0
..CCTCCCTTTGGCTTCTACTA..	20	0	1	5.00	5	4	0	1	0	0
..CAGTAGAAGCCAAAAGGATGTG..	22	0	1	5.00	5	0	4	1	0	0
..CCTCCCTTTGGCTTCTACTACTT..	23	0	1	3.00	3	3	0	0	0	0
..AGTAGAAGCCAAAAGGATG..	19	0	1	2.00	2	0	1	1	0	0
..CCTCCCTTTGGCTTCTACTACTA..	23	1	1	2.00	2	2	0	0	0	0
..AGTAGAAGCCAAAAGGATGTGTT..	23	2	1	2.00	2	0	1	1	0	0
..AGTAGAAGCCAAAAGGATGTC..	21	1	1	2.00	2	0	0	1	1	0
..GTAGAAGCCAAAAGGATGTG..	20	0	1	1.00	1	1	0	0	0	0
..CCTCCCTTTGGCTTCTACTACC..	22	1	1	1.00	1	0	0	0	0	1
..AGTAGAAGCCAAAAGGATGTA..	21	1	1	1.00	1	0	1	0	0	0
..CAGTAGAAGCCAAAAGGATG..	20	0	1	1.00	1	0	0	1	0	0
..AGTAGAAGCCAAAAGGATGT..	20	0	1	1.00	1	0	0	0	1	0

Anti-sense strand reads

TTTTTTAAAAATTTTTCACTATTATTAAGAACCTCATAATAGATTAATAGTCATCTTCGGTTTTCCTACACTCATAAAAACTTTAGGTGGAGGGAAACCGAAGATGATGAATTAACCATTAGTTTTGACGAAGTTTTTGTCAGATTTTGATTGACTTTTC **********.((((.(((((((..(((((((((((((.(((.(((.....)))).)))).)))))))))))))...)))))))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	M044 female body	M058 embryo	V055 head
..GGTGGAGGGAAACCGAAGATGA..	22	0	1	24.00	24	11	9	4	0	0
..GGTGGAGGGAAACCGAAGATG..	21	0	1	4.00	4	1	1	2	0	0
..GGAGGGAAACCGAAGATGA..	19	0	1	4.00	4	2	2	0	0	0
..TGAGGGAAACCGAAGATGA..	19	1	1	4.00	4	3	1	0	0	0
..GTCATCTTCGGTTTTCCTACA..	21	0	1	3.00	3	0	0	2	1	0
..GGAGGGAAACCGAAGATGAT..	20	0	1	3.00	3	0	3	0	0	0
..TGTGGAGGGAAACCGAAGATGA..	22	1	1	2.00	2	1	0	0	0	1
..GTGGAGGGAAACCGAAGATGA..	21	0	1	1.00	1	0	1	0	0	0
..GGAAACCGAAGATGATGAA..	19	0	1	1.00	1	0	0	0	1	0
..TGGAGGGAAACCGAAGATGA..	20	0	1	1.00	1	0	0	1	0	0
..AGTCATCTTCGGTTTTCCTACA..	22	0	1	1.00	1	0	0	1	0	0
..GGTGGAGGGAAACCGAAGATGAT..	23	0	1	1.00	1	1	0	0	0	0
..TAACCATTAGTTTTGACGAAGTTT..	24	0	1	1.00	1	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:550499-550658 +	dan_100	AAAAAATTTTTAAAAAGTGATAATAATTCTT----------GGAGTATTATCTAATTAT--CAGTAGAAGCCAAAAGGATGTGAGTATTTTTGAAATCCA----------CCTCCCTTTGGCTTCTACTACTTAATTGGTAATCAAAACTGCTTCAAAAACAGT----------CTAAAACTAACTGAAAAG
droBip1	scf7180000395912:19103-19310 +		AAAAAAGTCTTCAAA-----TTAAAGTTCAAAGAGAAGAAAAGTGTTAAAATACAAAAAAAAAGTATTATCTAATTACTACAAGGCGAGTCATAGTGAAATACATATTTTTAAAAGTATTACATTATACCTTCCTTTGG---------CTTAATTGATAATCAAATCTTCAACAAAAAAATAATAATAATAATAATAATAATAAAGTGAAAATGAAG

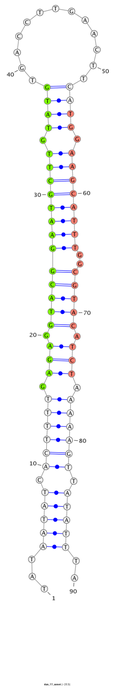
Generated: 09/08/2015 at 08:01 PM

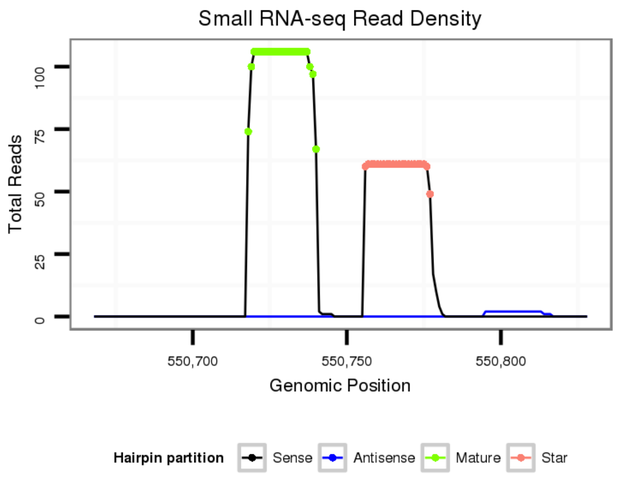
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

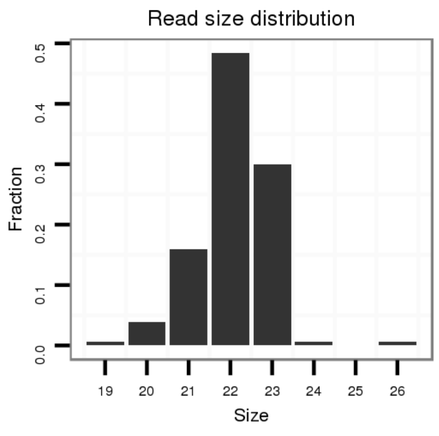
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_77	**scaffold_12903:550718-550778 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

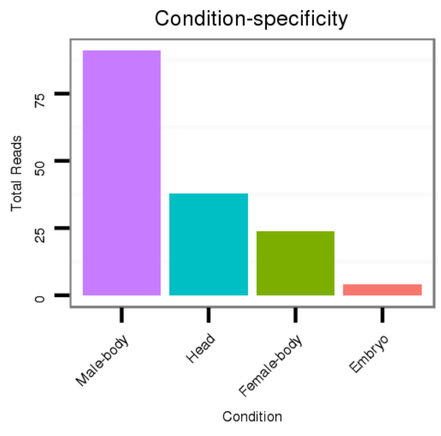
Legend: mature star mismatch in alignment mismatch in read

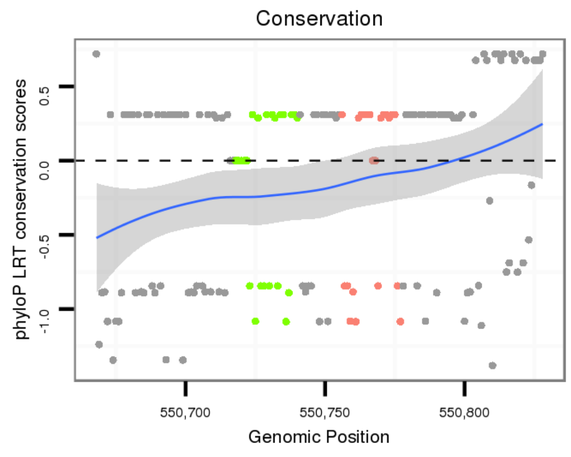
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dana\GF15947-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACTATTCATTATAATAATATCTTATGAATATCTTATATAATATCACTTTTGAGAGGTACGGAATGCTTGTATGTGACCTTGAACTTCATGGAAGCATTTGGCGTACATCTAAAAAGTTATATTTATTTCCCAATATCCCTCAGAACTTTCAAACCGCCCT	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	M044 female body	V106 head	V055 head	M058 embryo
**********...(((((.(((((((.(((.((((((((((((((.((((.............)))).)))))))))..)))))).))).)))))).))).)))))..**********										
.....GAGAGGTACGGAATGCTTGTATG.....	23	0	1	40.00	40	29	1	7	3	0
.....TGGAAGCATTTGGCGTACATCT.....	22	0	1	31.00	31	11	15	0	4	1
.....GAGAGGTACGGAATGCTTGTAT.....	22	0	1	25.00	25	17	1	7	0	0
.....AGAGGTACGGAATGCTTGTATG.....	22	0	1	20.00	20	13	1	3	3	0
.....TGGAAGCATTTGGCGTACATC.....	21	0	1	11.00	11	5	2	0	1	3
.....TGGAAGCATTTGGCGTACATCTA.....	23	0	1	7.00	7	5	2	0	0	0
.....TGGAAGCATTTGGCGTACATCTAA.....	24	0	1	6.00	6	4	2	0	0	0
.....AGAGGTACGGAATGCTTGTAT.....	21	0	1	5.00	5	1	0	3	1	0
.....GAGGTACGGAATGCTTGTATG.....	21	0	1	5.00	5	5	0	0	0	0
.....GAGAGGTACGGAATGCTTGT.....	20	0	1	5.00	5	2	0	2	1	0
.....TGGAAGCATTTGGCGTACATCTAAA.....	25	0	1	3.00	3	0	0	1	0	2
.....GAGAGGTACGGAATGCTTGTA.....	21	0	1	3.00	3	2	0	0	1	0
.....TGGAAGCATTTGGCGTACATCTT.....	23	1	1	2.00	2	0	1	0	1	0
.....AGAGGTACGGAATGCTTGT.....	19	0	1	1.00	1	0	1	0	0	0
.....TGGAAGCATTTGGCGTACATCTAT.....	24	1	1	1.00	1	1	0	0	0	0
.....TGGAAGCATTTGGCGTACATCTAC.....	24	1	1	1.00	1	1	0	0	0	0
.....GAGAGGTACGGAATGCTTGTATGT.....	24	0	1	1.00	1	0	0	1	0	0
.....GAGGTACGGAATGCTTGTATGTGACC.....	26	0	1	1.00	1	1	0	0	0	0
.....GAGAGGTACGGAATGCTTGTATA.....	23	1	1	1.00	1	1	0	0	0	0
.....TGGAAGCATTTGGCGTACATCTAAAA.....	26	0	1	1.00	1	1	0	0	0	0
.....GGAAGCATTTGGCGTACATCT.....	21	0	1	1.00	1	0	1	0	0	0
.....GAGAGGTACGGAATGCTTGTG.....	21	1	1	1.00	1	1	0	0	0	0
.....TGGAAGCATTTGGCGTACAT.....	20	0	1	1.00	1	0	0	0	1	0

Anti-sense strand reads

TGATAAGTAATATTATTATAGAATACTTATAGAATATATTATAGTGAAAACTCTCCATGCCTTACGAACATACACTGGAACTTGAAGTACCTTCGTAAACCGCATGTAGATTTTTCAATATAAATAAAGGGTTATAGGGAGTCTTGAAAAGTTTGGCGGGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	V055 head	M044 female body	V039 embryo
**********...(((((.(((((((.(((.((((((((((((((.((((.............)))).)))))))))..)))))).))).)))))).))).)))))..**********									
.....AGGGTTATAGGGAGTCTTGAAA.....	22	0	1	1.00	1	1	0	0	0
.....AGGGTTATAGGGAGTCTTG.....	19	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:550668-550828 +	dan_77	ACTATTCATTATAATAATATCTTATGAATATCTTATATAATATCACTTTTGAGAGGTACGGAATGCTTGTATGTGACCTTGAACTTCATGGAAGCATTTGGCGTACATCTAAAAAGTTATATTTATT----------TCCCAATATCCCTCA----------GAACTTTTCAAACCGCCCT
droBip1	scf7180000395912:19320-19551 +		AAATGTGCGAATAAAAATAATTATGTCAATATGTATAGTGTTTTCTGAT------ATCCAAAGTGTTTTAATGTATTTTTTAAATTCATAACTTCATTT--TGTACATTGGAAAAATTCTATATATTAAACCTATGTTAAAGAGTTAAAGTTGAGTTGAGTTCCCACATTGATTCAATGTGATATTTCCAAATGGGGTATTAACATCTTGGCATTGGTATATAACTACTGTAGCTGCCCT
droRho1	scf7180000778091:424734-424760 +		AT----------CCATCC----------CAACTTTTCAAACCACCCT

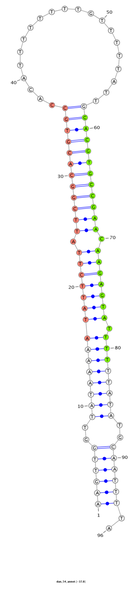
Generated: 09/08/2015 at 08:01 PM

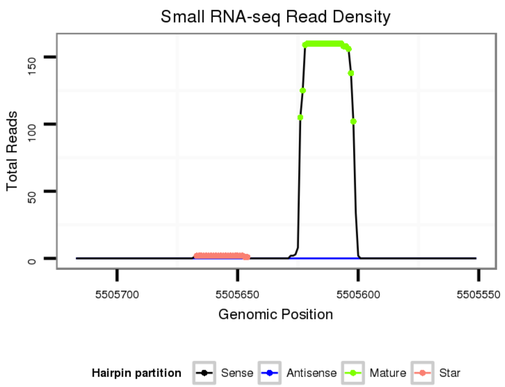
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

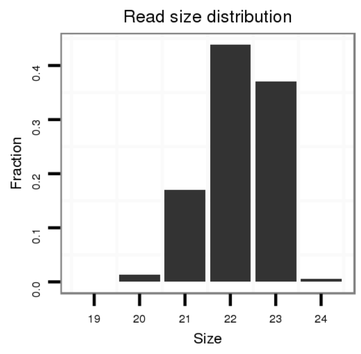
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_54	**scaffold_13417:5505601-5505667 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

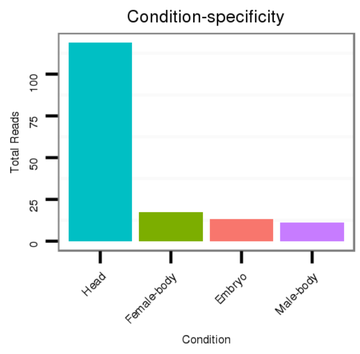
Legend: mature star mismatch in alignment mismatch in read

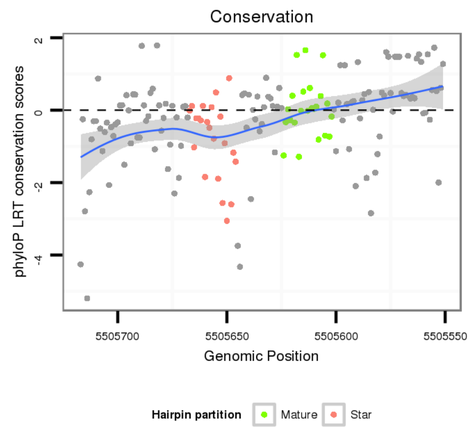
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
	1. scaffold_1799:718-739 - 2. dan_3842 scaffold_5374:3752-3773 - 3. scaffold_12413:6913-6934 - 4. dan_3559 scaffold_12984:484764-484785 - 5. scaffold_13010:38421-38442 - 6. scaffold_13045:115422-115443 - 7. scaffold_13045:1082635-1082656 - 8. scaffold_13045:1409242-1409263 - 9. scaffold_13099:928740-928761 - 10. scaffold_13099:1596592-1596613 - 11. scaffold_13099:2263467-2263488 - 12. scaffold_13099:2994218-2994239 - 13. scaffold_13111:42113-42134 - 14. dan_4034 scaffold_13169:153-174 - 15. dan_3800 scaffold_13239:158193-158214 - 16. dan_3482 scaffold_13258:231621-231642 - 17. scaffold_13258:662118-662139 - 18. scaffold_13258:1490530-1490551 - 19. scaffold_13337:21588305-21588326 - 20. scaffold_13417:3022525-3022546 - 21. scaffold_3748:3188-3209 + 22. dan_3542 scaffold_8626:8513-8534 + 23. dan_3993 scaffold_12913:87261-87282 + 24. scaffold_12944:105366-105387 - 25. dan_3549 scaffold_12984:311059-311080 - 26. dan_3456 scaffold_13099:847093-847114 + 27. scaffold_13339:3072579-3072600 + 28. dan_54 scaffold_13417:5505646-5505667 - 29. dan_3507 scaffold_13417:6151276-6151297 + 30. scaffold_13499:325605-325626 - 31. scaffold_13499:1520243-1520264 +

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATCAATTTTGGTAACGAAAATATGCTATTATATACAAGTTGGTTATAAAAATATTCTATTTTTTTGTTTTTATTGCACGTGCCGAACAAGAGTATTTTTTATATGCAATTTTATACATCAACAGTGGCGAGCACATGTGGATACATGTT						V106	M044 female	V105	M058	V039	V055
***********************************(((((((..(((((((((((((((((.(((((((((((.....................)))))))))))).)))))))).)))))))))..))))))..***********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	head	body	male body	embryo	embryo	head
..........CACGTGCCGAACAAGAGTATTTT..	23	0	1	51.00	51	39	5	3	2	1	1
..........CACGTGCCGAACAAGAGTATTT..	22	0	1	30.00	30	24	0	1	1	3	1
..........CGTGCCGAACAAGAGTATTTTT..	22	0	1	25.00	25	16	7	2	0	0	0
..........CACGTGCCGAACAAGAGTATT..	21	0	1	15.00	15	10	1	3	0	1	0
..........ACGTGCCGAACAAGAGTATTTT..	22	0	1	9.00	9	6	1	0	0	1	1
..........CGTGCCGAACAAGAGTATTTT..	21	0	1	7.00	7	4	1	1	0	1	0
..........ACGTGCCGAACAAGAGTATTTTT..	23	0	1	6.00	6	5	1	0	0	0	0
..........ACGTGCCGAACAAGAGTATTT..	21	0	1	4.00	4	3	1	0	0	0	0
..........GCACGTGCCGAACAAGAGTATT..	22	0	1	2.00	2	0	0	0	1	0	1
..........GCACGTGCCGAACAAGAGTATTT..	23	0	1	2.00	2	2	0	0	0	0	0
..........CGTGCCGAACAAGAGTATTTTTT..	23	0	1	2.00	2	0	1	1	0	0	0
..........ATTGCACGTGCCGAACAAGAGT..	22	0	1	2.00	2	2	0	0	0	0	0
..........ATATTCTTATTCGGCACGTGCC..	22	0	20	1.30	26	11	0	0	15	0	0
..........AATATTCTTATTCGGCACGTG..	21	0	20	1.15	23	4	19	0	0	0	0
..........GCACGTGCCGAACAAGAGTATTTT..	24	0	1	1.00	1	1	0	0	0	0	0
..........ACGTGCCGAACAAGAGTATT..	20	0	1	1.00	1	1	0	0	0	0	0
..........GCACGTGCCGAACAAGAGTATTC..	23	1	1	1.00	1	0	0	0	1	0	0
..........GTGCCGAACAAGAGTATTTTT..	21	0	1	1.00	1	0	0	1	0	0	0
..........CACGTGCCGAACAAGAGTAT..	20	0	1	1.00	1	0	0	0	0	0	1
..........TGCACGTGCCGAACAAGAGTAT..	22	0	1	1.00	1	0	0	0	1	0	0
..........AATATTCTTATTCGGCACGTGC..	22	0	20	0.95	19	14	0	4	0	1	0
..........AAATATTCTTATTCGGCACGTG..	22	0	20	0.60	12	8	0	2	0	0	2
..........CGTGCCGAACAAGAGTATTTTC..	22	1	2	0.50	1	0	0	0	1	0	0
..........ATATTCTTATTCGGCACGTGCCA..	23	0	8	0.50	4	0	2	0	2	0	0
..........CACGTGCCGAACAAGAGTATTAA..	23	2	5	0.20	1	0	0	0	0	1	0
..........AAATATTCTTATTCGGCACG..	20	0	20	0.15	3	0	0	0	3	0	0
..........ATATTCTTATTCGGCACGTG..	20	0	20	0.15	3	3	0	0	0	0	0
..........TATTCTTATTCGGCACGTGCC..	21	0	20	0.15	3	0	3	0	0	0	0
..........ATATTCTTATTCGGCACGTGC..	21	0	20	0.10	2	0	0	0	0	0	2
..........ATATTCTTATTCGGCACGTGCT..	22	1	20	0.10	2	0	2	0	0	0	0
..........AAAATATTCTTATTCGGCACGT..	22	0	20	0.05	1	0	1	0	0	0	0
..........ATTCTTATTCGGCACGTGC..	19	0	20	0.05	1	0	0	0	1	0	0
..........AAAAATATTCTTATTCGGCACG..	22	0	20	0.05	1	0	0	1	0	0	0
..........AAATATTCTTATTCGGCACGT..	21	0	20	0.05	1	0	0	0	1	0	0
..........ATATTCTTATTCGGCACGT..	19	0	20	0.05	1	0	1	0	0	0	0

Anti-sense strand reads

TAGTTAAAACCATTGCTTTTATACGATAATATATGTTCAACCAATATTTTTATAAGAATAAGCCGTGCACGGTGTAAAAAAAACAAAAATAACGTGCACGGCTTGTTCTCATAAAAAATATACGTTAAAATATGTAGTTGTCACCGCTCGTGTACACCTATGTACAA						V105 male body	M044 female body	M058 embryo
**********************************(((((((..(((((((((((((((((.(((((((((((.....................)))))))))))).)))))))).)))))))))..))))))..**********************************	Read size	# Mismatch	Hit Count	Total Norm	Total				

Show Alignment With Reads

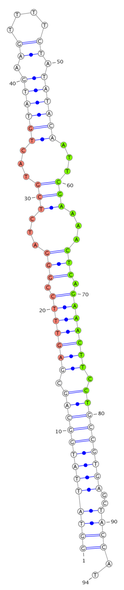
Re-alignment of all predicted orthologs

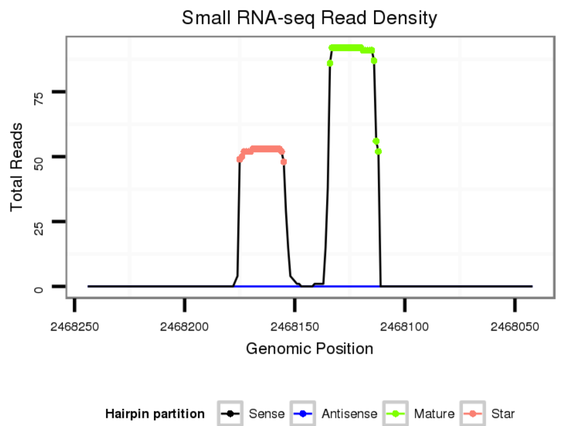
Species	Coordinate	ID	Alignment
droAna3	scaffold_13417:5505551-5505717 -	dan_54	ATCAAT-TT----------TGGTAAC-----GAA--AATATGCTATTA--TA------TA----CAAGTTGGTTATAAAAATATTC----------T----T-ATTCGGCACGTGCCACAT----------T----------T---------TTTTTGTTTTTATTGC-ACGTGCCGAACAAG-AGTATTTT--TTATATGCAATTTTATACATCAACAGT---GGCGAGCACATGTGGATACATGTT
droBip1	scf7180000396580:847081-847223 +		ATCCTT-TT----------TGTGAC-----GAA--AAA-AA------T--------T------TAATATAGCTTTTTAAAACTATTAAAAAATGTTCGTACGCTGTACGT--------GT-G--TG-TG----------T----------T---------TTTTAGTTTTTGTTGC-ACGTGCCGATAAAG-ATAGTGTT-TAATATGTAACTTTATATAAG------T-TATA
droKik1	scf7180000302485:17852-17960 +		GTAAAT-GT----------TGTAAG-----TAA--AGA-AA---AGTT--------CA---GAAAAACAAAAAAAAATTGTTT----------T----G-AATCGCGGT-A--TTTT----------T----------T---------TTTATTTTTTATTAA-TGATACTAAACAAG-AACATT--T----------T---------T-TT
droFic1	scf7180000452149:20428-20462 -		ATACAT--T----------T-------T-----T---T----------T--------T-----T---T----------T----T-T----------T----T-----------T----------T---------T----------T---------T----------T---------ACAGT---GGCGAGCACATGTGGATACATGTT
droEle1	scf7180000490359:18227-18355 -		ATCAAT-TT----------TGGTGAC-----GAA--AATGAATT---ATGCATTCGAGTAAATGTTATCCATCTA--AAATGTTT----------TCATTCGGACTTCAT-------GA-G--CG-AG----------GTATTTAA----------T---------T---------T---

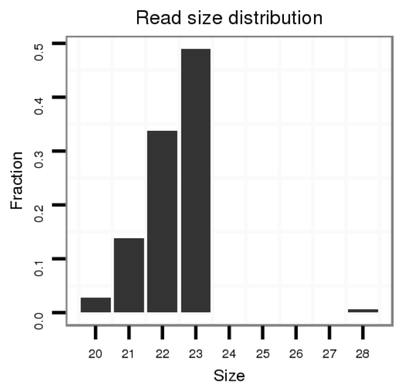
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_229	**scaffold_13417:2468092-2468194 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

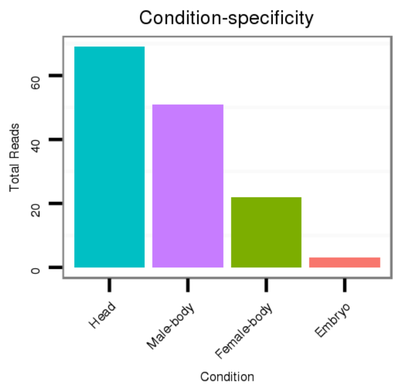
Legend: mature star mismatch in alignment mismatch in read

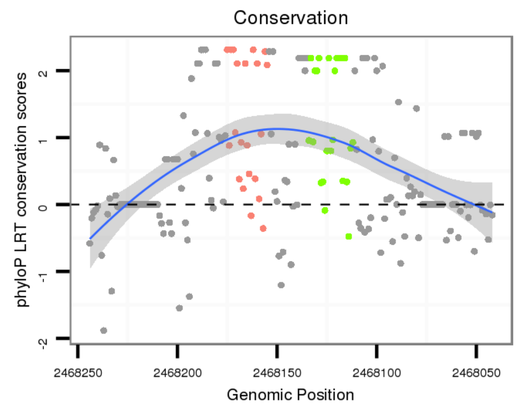
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTCCCCGCACTGAGACAGCTCCTGTGCGACAACCACGGGGTGCGGGGAGTACCTGGTATTATGGCAGCGAGTTTCCGGGATCTCGTACTGTATGAAGTTTTCTATATACAATTCGAAAACTCAGAAACTTCCTGCCGTGAGCTACCATTGATCAACGGCTGAGTATGCGACCGGAAAGGGGACGCGAATGCGAGGACTAAAGG	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	V055 head	M044 female body	M058 embryo
**********(((((((((((((.(((((((.(((...(((...(((((((.((....)).)))))))...)))...)))).)))))))..)))))..)))))..**********										
..ATTCGAAAACTCAGAAACTTCCT..	23	0	1	46.00	46	29	8	5	3	1
..AATTCGAAAACTCAGAAACTTC..	22	0	1	20.00	20	7	4	4	4	1
..AGTTTCCGGGATCTCGTACTG..	21	0	1	17.00	17	1	13	0	3	0
..AGTTTCCGGGATCTCGTACTGT..	22	0	1	14.00	14	0	8	1	5	0
..AGTTTCCGGGATCTCGTACTGTA..	23	0	1	11.00	11	1	4	2	4	0
..CAATTCGAAAACTCAGAAACTTC..	23	0	1	10.00	10	3	2	4	0	1
..TTCGAAAACTCAGAAACTTCCT..	22	0	1	6.00	6	4	1	1	0	0
..CAATTCGAAAACTCAGAAACTT..	22	0	1	4.00	4	2	2	0	0	0
..AGTTTCCGGGATCTCGTACT..	20	0	1	3.00	3	2	1	0	0	0
..AATTCGAAAACTCAGAAACTTCC..	23	0	1	3.00	3	1	1	0	1	0
..ATTCGAAAACTCAGAAACTTCCTT..	24	1	1	2.00	2	1	0	0	1	0
..ATTCGAAAACTCAGAAACTTC..	21	0	1	1.00	1	0	1	0	0	0
..CGAGTTTCCGGGATCTCGTACTGTATGA..	28	0	1	1.00	1	0	0	0	1	0
..TTTCCGGGATCTCGTACTGTAT..	22	0	1	1.00	1	0	1	0	0	0
..ATTCGAAAACTCAGAAACTTCCC..	23	1	1	1.00	1	1	0	0	0	0
..AGTTTCCGGGATCTCGTACTT..	21	1	1	1.00	1	0	1	0	0	0
..AATTCGAAAACTCAGAAACTTT..	22	1	1	1.00	1	0	0	0	1	0
..AGTTTCCGGGATCTCGTACTGTAAA..	25	2	1	1.00	1	0	0	1	0	0
..AATTCGAAAACTCAGAAACTTCA..	23	1	1	1.00	1	0	0	0	1	0
..ATTCGAAAACTCAGAAACTTCC..	22	0	1	1.00	1	1	0	0	0	0
..GAGTTTCCGGGATCTCGTACT..	21	0	1	1.00	1	0	1	0	0	0
..AGTTTCCGGGATCTCGTACTA..	21	1	1	1.00	1	0	1	0	0	0
..GTTTCCGGGATCTCGTACTG..	20	0	1	1.00	1	0	0	1	0	0
..GAGTTTCCGGGATCTCGTACTG..	22	0	1	1.00	1	0	1	0	0	0
..AGTTTCCGGGATCTCGTACTGTAA..	24	1	1	1.00	1	0	1	0	0	0
..TTTCCGGGATCTCGTACTGTATG..	23	0	1	1.00	1	0	0	0	1	0
..CGGGATCTCGTACTGTATGAAG..	22	0	1	1.00	1	0	1	0	0	0
..ATATACAATTCGAAAACTCAGA..	22	0	1	1.00	1	0	1	0	0	0
..GTTTCCGGGATCTCGTACTGTT..	22	1	1	1.00	1	0	0	0	1	0
..CGAGTTTCCGGGATCTCGTAC..	21	0	1	1.00	1	0	1	0	0	0
..GAGTTTCCGGGATCTCGTACTGA..	23	1	1	1.00	1	0	1	0	0	0

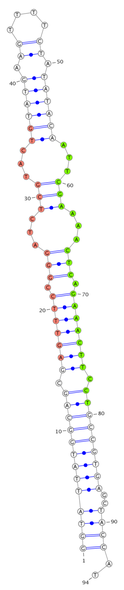
Anti-sense strand reads

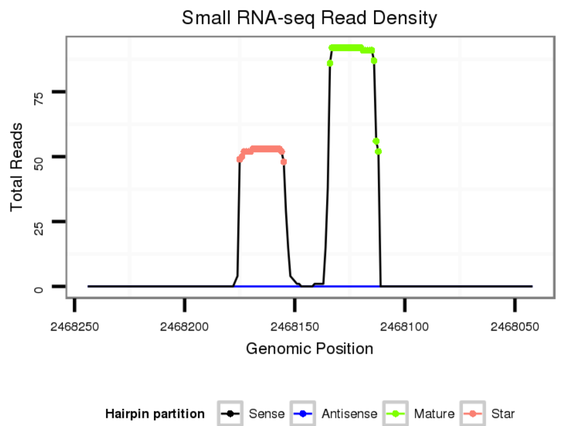
AAGGGGCGTGACTCTGTCGAGGACACGCTGTTGGTGCCCCACGCCCCTCATGGACCATAATACCGTCGCTCAAAGGCCCTAGAGCATGACATACTTCAAAAGATATATGTTAAGCTTTTGAGTCTTTGAAGGACGGCACTCGATGGTAACTAGTTGCCGACTCATACGCTGGCCTTTCCCCTGCGCTTACGCTCCTGATTTCC	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V105 male body	M058 embryo	V039 embryo	V106 head
**********(((((((((((((.(((((((.(((...(((...(((((((.((....)).)))))))...)))...)))).)))))))..)))))..)))))..**********										
..CCTGGTATAGCCGCAGAAAGTTTCCGAGTTTCGTAATGTATGGTTA...TATTTGAAAT..	22	0	1	14.00	14	0	8	1	5	0
..CCTGGTATTATCGCAGCAAGTTTCCGGGACTTCGTACTGTATGAA-G...AATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..AG...TC..CTCGAAGAC-AA..CAAGTCGTTGGTATTATCGCAGCAAGTTTCCGGGATTTCGTACTGTATGAC-A...AATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..CCTGGTATTATCGCAGCAAGTTTCCGGGATTTCGTACTGTATGAC-A...AATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..CCTGGTATTATCGCAGCAAGTTTCCGGGATTTCGTACTGTATGACTA...GATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..CCTGGTATTATCGCAGCAAGTTTCCGGGATTTCGTACTGTATGCT-G...AATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..TA..CCCTGATAGAGG..CGACATCGTGGTATTATCGCAATAAGTTCCTGGGATTTCCCACTGTATTAC-G...ATTTTTACAT..	23	0	1	10.00	10	3	2	4	0	1
..GGCTTTCCGGGATCTCGTACTT..	21	0	1	1.00	1	0	1	0	0	0
..GTTTCCGGGATCTCGTACTGTAT..	22

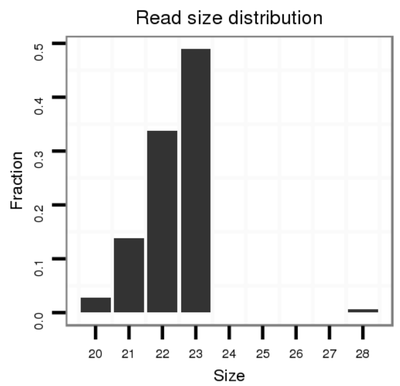
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_229	**scaffold_13417:2468092-2468194 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

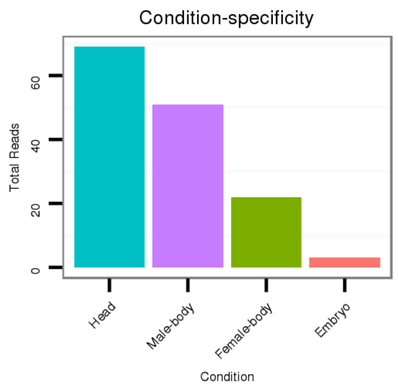
Legend: mature star mismatch in alignment mismatch in read

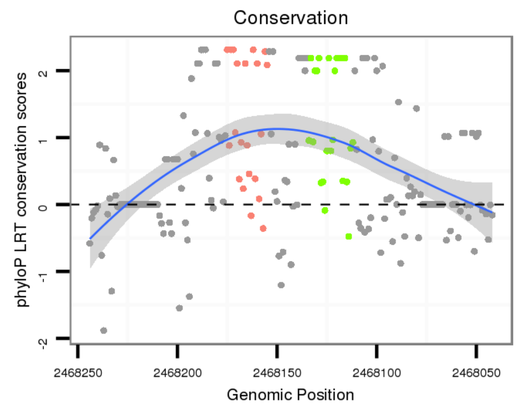
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTCCCCGCACTGAGACAGCTCCTGTGCGACAACCACGGGGTGCGGGGAGTACCTGGTATTATGGCAGCGAGTTTCCGGGATCTCGTACTGTATGAAGTTTTCTATATACAATTCGAAAACTCAGAAACTTCCTGCCGTGAGCTACCATTGATCAACGGCTGAGTATGCGACCGGAAAGGGGACGCGAATGCGAGGACTAAAGG	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	V055 head	M044 female body	M058 embryo
**********(((((((((((((.(((((((.(((...(((...(((((((.((....)).)))))))...)))...)))).)))))))..)))))..)))))..**********										
..ATTCGAAAACTCAGAAACTTCCT..	23	0	1	46.00	46	29	8	5	3	1
..AATTCGAAAACTCAGAAACTTC..	22	0	1	20.00	20	7	4	4	4	1
..AGTTTCCGGGATCTCGTACTG..	21	0	1	17.00	17	1	13	0	3	0
..AGTTTCCGGGATCTCGTACTGT..	22	0	1	14.00	14	0	8	1	5	0
..AGTTTCCGGGATCTCGTACTGTA..	23	0	1	11.00	11	1	4	2	4	0
..CAATTCGAAAACTCAGAAACTTC..	23	0	1	10.00	10	3	2	4	0	1
..TTCGAAAACTCAGAAACTTCCT..	22	0	1	6.00	6	4	1	1	0	0
..CAATTCGAAAACTCAGAAACTT..	22	0	1	4.00	4	2	2	0	0	0
..AGTTTCCGGGATCTCGTACT..	20	0	1	3.00	3	2	1	0	0	0
..AATTCGAAAACTCAGAAACTTCC..	23	0	1	3.00	3	1	1	0	1	0
..ATTCGAAAACTCAGAAACTTCCTT..	24	1	1	2.00	2	1	0	0	1	0
..ATTCGAAAACTCAGAAACTTC..	21	0	1	1.00	1	0	1	0	0	0
..CGAGTTTCCGGGATCTCGTACTGTATGA..	28	0	1	1.00	1	0	0	0	1	0
..TTTCCGGGATCTCGTACTGTAT..	22	0	1	1.00	1	0	1	0	0	0
..ATTCGAAAACTCAGAAACTTCCC..	23	1	1	1.00	1	1	0	0	0	0
..AGTTTCCGGGATCTCGTACTT..	21	1	1	1.00	1	0	1	0	0	0
..AATTCGAAAACTCAGAAACTTT..	22	1	1	1.00	1	0	0	0	1	0
..AGTTTCCGGGATCTCGTACTGTAAA..	25	2	1	1.00	1	0	0	1	0	0
..AATTCGAAAACTCAGAAACTTCA..	23	1	1	1.00	1	0	0	0	1	0
..ATTCGAAAACTCAGAAACTTCC..	22	0	1	1.00	1	1	0	0	0	0
..GAGTTTCCGGGATCTCGTACT..	21	0	1	1.00	1	0	1	0	0	0
..AGTTTCCGGGATCTCGTACTA..	21	1	1	1.00	1	0	1	0	0	0
..GTTTCCGGGATCTCGTACTG..	20	0	1	1.00	1	0	0	1	0	0
..GAGTTTCCGGGATCTCGTACTG..	22	0	1	1.00	1	0	1	0	0	0
..AGTTTCCGGGATCTCGTACTGTAA..	24	1	1	1.00	1	0	1	0	0	0
..TTTCCGGGATCTCGTACTGTATG..	23	0	1	1.00	1	0	0	0	1	0
..CGGGATCTCGTACTGTATGAAG..	22	0	1	1.00	1	0	1	0	0	0
..ATATACAATTCGAAAACTCAGA..	22	0	1	1.00	1	0	1	0	0	0
..GTTTCCGGGATCTCGTACTGTT..	22	1	1	1.00	1	0	0	0	1	0
..CGAGTTTCCGGGATCTCGTAC..	21	0	1	1.00	1	0	1	0	0	0
..GAGTTTCCGGGATCTCGTACTGA..	23	1	1	1.00	1	0	1	0	0	0

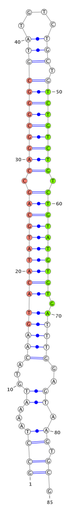
Anti-sense strand reads

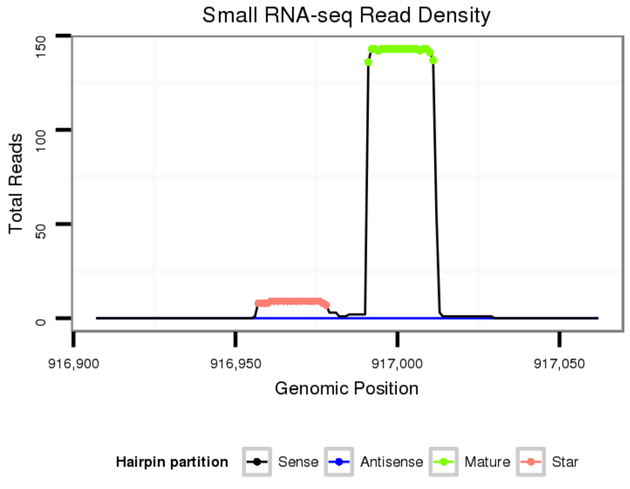
AAGGGGCGTGACTCTGTCGAGGACACGCTGTTGGTGCCCCACGCCCCTCATGGACCATAATACCGTCGCTCAAAGGCCCTAGAGCATGACATACTTCAAAAGATATATGTTAAGCTTTTGAGTCTTTGAAGGACGGCACTCGATGGTAACTAGTTGCCGACTCATACGCTGGCCTTTCCCCTGCGCTTACGCTCCTGATTTCC	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V105 male body	M058 embryo	V039 embryo	V106 head
**********(((((((((((((.(((((((.(((...(((...(((((((.((....)).)))))))...)))...)))).)))))))..)))))..)))))..**********										
..CCTGGTATAGCCGCAGAAAGTTTCCGAGTTTCGTAATGTATGGTTA...TATTTGAAAT..	22	0	1	14.00	14	0	8	1	5	0
..CCTGGTATTATCGCAGCAAGTTTCCGGGACTTCGTACTGTATGAA-G...AATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..AG...TC..CTCGAAGAC-AA..CAAGTCGTTGGTATTATCGCAGCAAGTTTCCGGGATTTCGTACTGTATGAC-A...AATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..CCTGGTATTATCGCAGCAAGTTTCCGGGATTTCGTACTGTATGAC-A...AATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..CCTGGTATTATCGCAGCAAGTTTCCGGGATTTCGTACTGTATGACTA...GATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..CCTGGTATTATCGCAGCAAGTTTCCGGGATTTCGTACTGTATGCT-G...AATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..TA..CCCTGATAGAGG..CGACATCGTGGTATTATCGCAATAAGTTCCTGGGATTTCCCACTGTATTAC-G...ATTTTTACAT..	23	0	1	10.00	10	3	2	4	0	1
..GGCTTTCCGGGATCTCGTACTT..	21	0	1	1.00	1	0	1	0	0	0
..GTTTCCGGGATCTCGTACTGTAT..	22

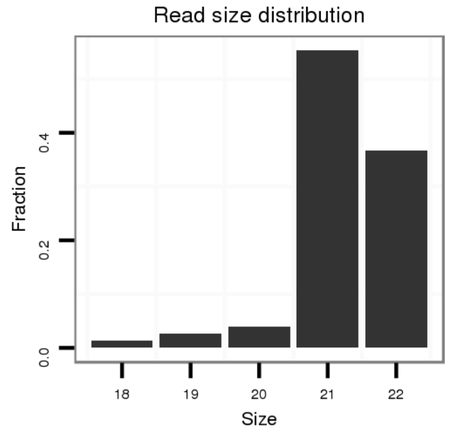
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_288	**scaffold_13334:916957-917012 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

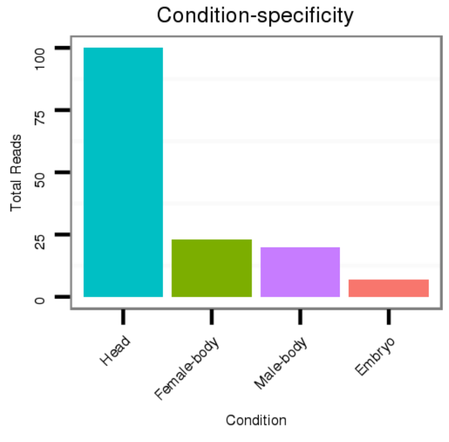
Legend: mature star mismatch in alignment mismatch in read

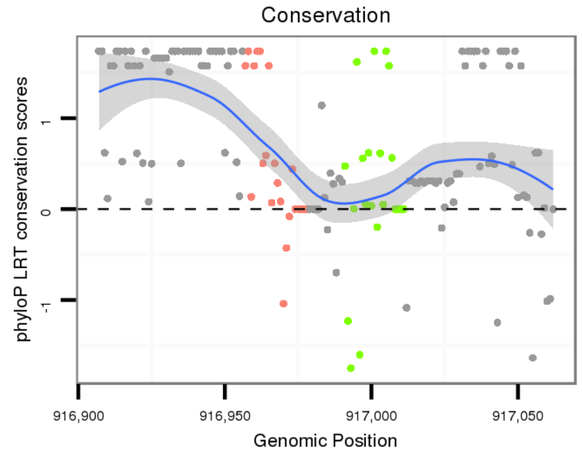
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTAACCAACACTGACCAGCATTAAGAAAATAATTTGCCTAAAATGTACAAGTACATATGCAGCCAGGCGGGCGTATGTCTGCTGTCTGTCTGTCTGTATGTGTGATTTGGAGTAAGTGCGAAAAAGTTTTCTTCGCAATGCAGCTTACTTTTCA **********************************((((...((...((((((((((((((.((((((((((((....)))).))))))))).))))))))))).))))..))).))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	V105 male body	M058 embryo	V055 head	V039 embryo
..........TCTGTCTGTCTGTATGTGTGA..........	21	0	1	79.00	79	68	4	4	1	2	0
..........TCTGTCTGTCTGTATGTGTGAT..........	22	0	1	50.00	50	17	9	13	5	6	0
..........GTACATATGCAGCCAGGCGGGC..........	22	0	1	4.00	4	1	1	0	1	1	0
..........TCTGTCTGTCTGTATGTGTG..........	20	0	1	3.00	3	3	0	0	0	0	0
..........CTGTCTGTCTGTATGTGTGAT..........	21	0	1	2.00	2	0	0	1	0	1	0
..........CTGTCTGTCTGTATGTGTGA..........	20	0	1	2.00	2	0	1	1	0	0	0
..........CTGTCTGTCTGTATGTGTGATT..........	22	0	1	2.00	2	1	0	0	1	0	0
..........TCTGTCTGTCTGTATGTGT..........	19	0	1	2.00	2	0	1	1	0	0	0
..........GCGTATGTCTGCTGTCTGTCC..........	21	1	1	1.00	1	0	0	0	1	0	0
..........GTACATATGCAGCCAGGCG..........	19	0	1	1.00	1	0	1	0	0	0	0
..........TCTGTCTGTATGTGTGAT..........	18	0	1	1.00	1	1	0	0	0	0	0
..........GTACATATGCAGCCAGGCGG..........	20	0	1	1.00	1	0	1	0	0	0	0
..........TCTGTCTGTCTGTATGTGTGAC..........	22	1	1	1.00	1	0	0	0	1	0	0
..........CTGCTGTCTGTCTGTCTGTATG..........	22	0	1	1.00	1	0	1	0	0	0	0
..........GTACATATGCAGCCAGGCGGG..........	21	0	1	1.00	1	0	1	0	0	0	0
..........AGTACATATGCAGCCAGGCGGGCGTA..........	26	0	1	1.00	1	1	0	0	0	0	0
..........GGCGTATGTCTGCTGTCT..........	18	0	1	1.00	1	0	1	0	0	0	0
..........ATATGCAGCCAGGCGGGCGTA..........	21	0	1	1.00	1	0	1	0	0	0	0
..........CTGTCTGTCTGTATGTGTG..........	19	0	1	1.00	1	0	1	0	0	0	0
..........GTGATTTGGAGTAAGTGCGAAA..........	22	0	1	1.00	1	0	0	1	0	0	0
..........TCTGTCTGTCTGTATGTGTGT..........	21	1	17	0.06	1	1	0	0	0	0	0

Anti-sense strand reads

Show Alignment With Reads

AATTGGTTGTGACTGGTCGTAATTCTTTTATTAAACGGATTTTACATGTTCATGTATACGTCGGTCCGCCCGCATACAGACGACAGACAGACAGACATACACACTAAACCTCATTCACGCTTTTTCAAAAAGAAGCGTTACGTCGAATGAAAAAGT **********************************((((...((...((((((((((((((.((((((((((((....)))).))))))))).))))))))))).))))..))).))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	female body	embryo	head	embryo	head
..........GTCTGTCTGTCTGTATGTGTGT..........	21	1	17	0.06	1	1	0	0	0	0
..........GTACATATGCAGCCAGGCGGG..........	21	0	1	1.00	1	0	1	0	0	0
..........GTACATATGCAGCCAGGCGG..........	20	0	1	1.00	1	0	1	0	0	0
..........GTACATATGCAGCCAGGCG..........	19	0	1	1.00	1	0	1	0	0	0
..........GCGTATGTCTGCTGTCTGTCC..........	21	1	1	1.00	1	0	0	0	1	0	0
..........TCTGTCTGTCTGTATGTGT..........	19	0	1	2.00	2	0	1	1	0	0	0
..........CTGTCTGTCTGTATGTGATT..........	22	0	1	2.00	2	1	0	0	1	0	0
..........CTGTCTGTCTGTATGTGA..........	20	0	1	2.00	2	0	1	1	0	0	0
..........CTGTCTGTCTGTATGTGTGAT..........	21	0	1	2.00	2	0	0	1	0	1	0
..........GTACATATGCAGCCAGGCGGGC..........	22	0	1	4.00	4	1	1	0	1	1	0
..........TCTGTCTGTCTGTATGTGTGAT..........	22	0	1	50.00	50	17	9	13	5	6	0
..........TCTGTCTGTCTGTATGTGTGA..........	21	0	1	79.00	79	68	4	4	1	2	0

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13334:916907-917062 +	dan_288	TTAACCAACACTGACCAGCATTAAGAAAA------TAATTTGCCTAAAATGTACAAG---TACATATGCAGCCAGGCGGGCGTATGTCTGCT-G----------TCTGTCTG----------TCT---GTATGTGTGATTTGGAGTAAGTGCGAAAAAGTTTT-TCTTCGC---AATGCAGCTTA-CTTTT---------TC----------A
droBip1	scf7180000396733:558455-558625 +		TTAACCAACACTGACCAGCATTAAGAAAA------TAATTTGCCTAAAATGTACAAG---TACATATGCAGCAACG---------GCGTAT--G--------ATATATATATATATATACATATATGTTTGTGTGTGTGTGTGA----GTTGGAGTAAGTGCGAAAAAGTTTTTCCTTCGC---AATGCAGCTTA-TTTTT---T----TAC----------A
droKik1	scf7180000302344:1693666-1693800 +		TTAACCAACACTGACCAACATTAAGAAAGTGT---TAATTTGCCTAAAATGTACAAG---TTCATGCGTG-GGTGT----------ATGTGGG-----------------TGCGTGTG----------TGT---GTGTGT----------AG--TAAAGTTTT-CCTCTAGAAAAATGCATCTTCAGTT-G---C----TTG----------A
droFic1	scf7180000451789:254181-254301 +		TTAACCAACACTGACCAGCATTAAGAAAGTGT---TAATTTGCCTAAAATGTACAAG---TACATGTGCG-TGATG----------CT-G----------TCTG----------TGT---GTATGT----------GC--GGGAGTTTT-CCTCTGCCA-AATGCAACTTA-CTTGT---------T-----------
droEle1	scf7180000491006:1902484-1902612 +		TTGACCAACACTGACCAGCATTAAGAAAGTGT---TAATTTGCCTAAAATGTACAAG---TACATGTGTG-CCATG----------TT-G----------CCTATGTG----------TGT---GTGTGT----------GC--GGGAGTTTT-CCTCTGTCAAAATGCAACTTA-ATTTG---------TA----------A
droRho1	scf7180000779514:140737-140858 -		TTAACCAACACTGACCAGCATTAAGAAAGTGT---TAATTTGCCTAAAATGTACAAG---TACATGTGCG-GAGTG----------T----------TGTG----------CGT---ATGTGT----------GC--GGGAGTTTT-CCTCTGCCAAAATGCAACTTA-ATTTG---------TA----------A
droBia1	scf7180000302069:974124-974253 -		TTAACCAACACTGACCAGCATTAAGAAAGTGT---TAATTTGCCTAAAATGTACAAG---TACATGTGCG-GGGTG---------GCCTGCTTG-----CA----------TGAA--TG----------TGT---ATGTGT----------GT--GGGAGTTTT-CCTCTGCCA-AATGCAACTGA-ATTT----------T-----------
droTak1	scf7180000414549:171624-171752 +		TTAGCCAACACTGACCAGA------AAAGTGTTGTTAATTTGCCTAAAATGTACCAG---TACATGTGCG-G--TG---------GCCGCTTC----------TGTATGTG----------TGT---GTGTGT----------GC--GGGAGTTTT-CCTCTGCCA-AATGCAACTTA-ATTCT---------TA----------A
droEug1	scf7180000408744:70405-70555 +		TTAACCAACACTGACCAGCATTAAGAAAGTGT---TAATTTGCCTAAAACGTATAAG---TACATGTGCG-C--TG---------GCCTGT-G-CTTTGTATATATATATATATAGATATA----------TAT---ATGTGT----------AC--GGGAGTTTT-CCTCTGTCA-AATGAAACATT-TACTT---T----TAA----------G
dm3	chrX:8455709-8455859 +		TTAGCCAACACTGGCGAACATTAAGAAAGTGT---TAATTTGCCTAAAATGTACAAG---TACATGTGCG-GCATG---------GCCTGCT-G----------TAAATGTG----------TGT---GGGTGT----------AC--GGGAGTTTT-CCTCTGTCA-AATGCAACTAA-GTTTTTTTT----TACCGAAAATTCAGCCA
droSim2	x:8026609-8026741 +		TTAGCCAACACTGCCCAACATTAAGAAAGTGT---TAATTTGCCTAAAATGTACAAG---TACATGTGCG-GCATG---------GCCTGCT-G----------TAAATATG----------TGT---GGGTGT----------AC--GGGAGTTTT-CCTCTGCCA-AATGCAACTAA-GTTTT---------GT----------A
droSec2	scaffold_35:304277-304409 +		TTAGCCAAATACTGCCCAACATTAAGAAAGTGT---TAATTTGCCTAAAATGTACAAG---TCCATGTGCG-GCATG---------GCCTGCT-G----------TAAATATG----------TGT---GGGTGT----------AC--GGGAGTTTT-CCTCTGCCA-AATGCAACTAA-GTTTT---------T----------A
droYak3	X:12856253-12856391 -		TTAGCCAACACTGACCAACATTAAGAAAGTGT---TAATTTGCCTAAAATGTACAAG---TACATGTGCG-GCATG---------GCCTGCTTG----------TACATGTG----------TGT---GTGTGT----------GC--GGGAGTTTT-CCTCTGTCA-AATGCAACTAA-GTTTATTTTT----TAC----------C
droEre2	scaffold_4690:6656907-6657044 -		TTAGCCAACACTGACCAACATTAAGAAAGTGT---TAATTTGCCTAAAATGTAGCAGTTGTACATGTGCG-A----------CTGCTTG----------TGCA--TG----------TGT---GTGTGT----------GC--GGGAGTTTT-CCTCTGCCG-AATGCAACCAA-GTTTTTTTTTTGTAC----------C

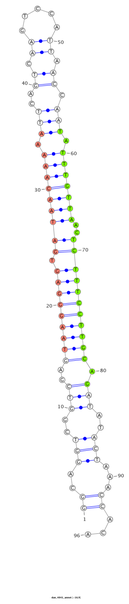
Generated: 09/08/2015 at 07:46 PM

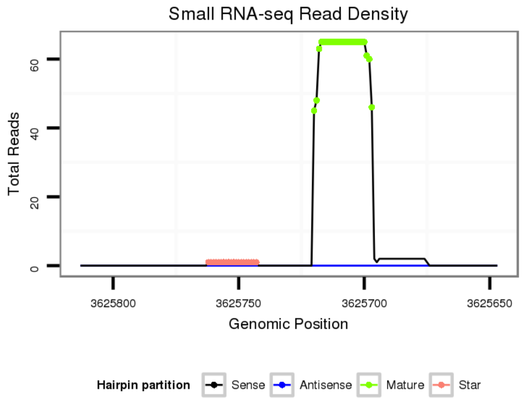
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

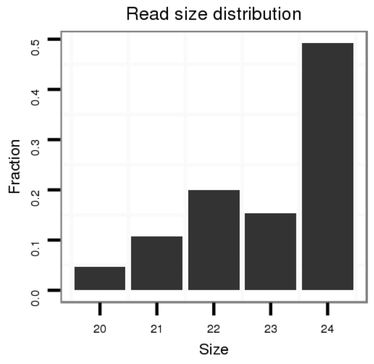
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_4041	**scaffold_12943:3625697-3625763 -**	**confident-exception**	**MiRNA**	**5pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

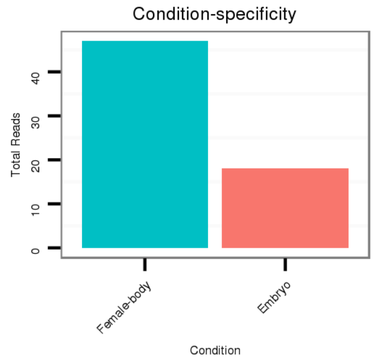
Legend: mature star mismatch in alignment mismatch in read

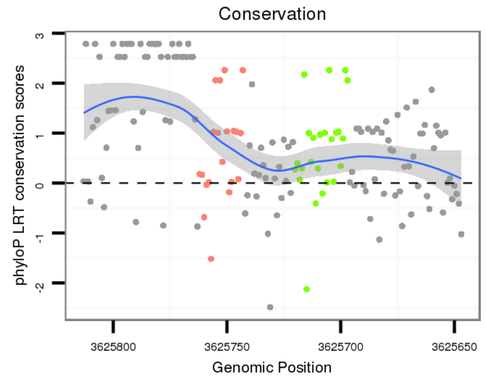
Predicted structure











Show Alternate Folds

Flybase annnotation

utr5 [utr5_plus_2731]; utr5 [utr5_plus_2732]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATTTGTGGGTTTTAACCAGTTTCAATCGGTTATTGCGGCAGGTCGGTCGAGTAAGGGAGTGATAACAAAAATTCAGTCAAGTCCATTAACCAATATTTGTTAACTCTTTCCTTGCAGATATACTAAACCACACAAAGAGAAGTAACCAAAAAAAAAAGAGTAAATCATA						M044	M058	V105	V039
************************************((..(((..(((..(((((((((.(((((((((.(((..((.((.....)).)).))).)))))))..)))))))))).)))..))))...))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	female body	embryo	male body	embryo
.....TTTGTTAACTCTTTCCTTGCAGT.....	23	1	1	45.00	45	16	25	4	0
.....TATTTGTTAACTCTTTCCTTGCAG.....	24	0	1	32.00	32	18	13	0	1
.....TTTGTTAACTCTTTCCTTGCAG.....	22	0	1	11.00	11	10	1	0	0
.....TATTTGTTAACTCTTTCCTTGCA.....	23	0	1	9.00	9	6	3	0	0
.....TTTGTTAACTCTTTCCTTGCAGC.....	23	1	1	5.00	5	0	5	0	0
.....TTTGTTAACTCTTTCCTTGCA.....	21	0	1	3.00	3	3	0	0	0
.....TATTTGTTAACTCTTTCCTTGCAGT.....	25	1	1	3.00	3	1	1	1	0
.....TTTGTTAACTCTTTCCTTGCAGT.....	22	1	1	2.00	2	2	0	0	0
.....TTGTTAACTCTTTCCTTGCAG.....	21	0	1	1.00	1	1	0	0	0
.....ATACTAAACCACACAAAGAGA.....	19	0	1	1.00	1	0	1	0	0
.....TATTTGTTAACTCTTTCCTTGC.....	22	0	1	1.00	1	1	0	0	0
.....TAAGGGAGTGATAACAAAAA.....	20	0	1	1.00	1	1	0	0	0
.....ATTTGTTAACTCTTTCCTTGCA.....	22	0	1	1.00	1	1	0	0	0
.....TTTGTTAACTCTTTCCTTGCAGA.....	23	0	1	1.00	1	1	0	0	0
.....TTGTTAACTCTTTCCTTGCA.....	20	0	1	1.00	1	1	0	0	0
.....ATTTGTTAACTCTTTCCTTG.....	20	0	1	1.00	1	1	0	0	0
.....ATATACTAAACCACACAAAGAGAA.....	22	0	1	1.00	1	0	1	0	0
.....ATTTGTTAACTCTTTCCTTGCAG.....	23	0	1	1.00	1	1	0	0	0
.....AAGTAACCAAAAAAAAAA.....	18	0	4	0.25	1	0	1	0	0

Anti-sense strand reads

TAAACACCCAAAATTGGTCAAAGTTAGCCAATAACGCCGTCCAGCCAGCTCATTCCCTCACTATTGTTTTTAAGTCAGTTCAGGTAATTGGTTATAAACAATTGAGAAAGGAACGTCTATATGATTTGGTGTTTCTCTTCATTGGTTTTTTTTTTCTCATTTAGTAT						V055	M058	V039
************************************((..(((..(((..(((((((((.(((((((((.(((..((.((.....)).)).))).)))))))..)))))))))).)))..))))...))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	head	embryo	embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12943:3625647-3625813 -	dan_4041	ATTTGTGGGTTTTAACCAGTTTCAATCGGTTATTGCGGCAGGTCGGTCGAGT----------AAGGGAGTGATAACAAAAATT---CAGTC-------AAG-TCCATTAA----------CCAAT-------AT--TTGTTA--ACTCTTTCCTTGCAGATA----------TA------CTA----AACCACAAAG----------AGAAGTAACCAAAAA----------AAAAA----GAGTAAATCATA
droBip1	scf7180000396433:509893-510052 -		ATTGGTGGGATTTAACCAGTTTCAATTGGTTATTGCGGCAGGTCGGTCGAGT----------AAGGGAGTGATAACAAAAATT---AAGTC-------AAGACGA-ATAA----------CCAAT-------AT--TTGTTA--ACTCTTTCCTTGCAGATACCAA----------ACGG--A----------TA------CTA---ACCCA----------AAAAACAAA----------AAAGA---------ATAACA
droKik1	scf7180000302643:149840-150014 +		ATTCGTGGGTTTTAACCAGTTTCAATTGGTTATTGCGGCAGGTCGGTCGAGT---------GAGAGGCGCTGTGTAATAAAAATC---AAGTCAAAAATCGA---A--AATAA----------ACATT-------AT--TTTTAA--ACTCTTTCCTTGCAGACA----------TA------CCC---AACCAAACAG----------CAAACCGGAATAGAAAGGCAA---GAGAAACTAACC
droFic1	scf7180000453842:593641-593799 +		GTTCGTGGGTTTTAACCAGTTTCATTGGTTATTGTGGCAGGTCGGTCGACC----CC-------CAGAGAGTGATGATAAAAATA---AAGTC-------AAAAAGAGTTTA----------GTTAT-ATGATACTAC--TTTTT--CTCTTCTCCTTGCAGTTAACAAAA----C----AG----------H-------H---H---------H---AGCTACTAA---------H--AAAGG---------TGACTG
droEle1	scf7180000491186:1152331-1152462 +		ATTTGTGGGCTTTAACCAGTTTCAATTGGTTATTGCGGCAGGTCGGTCGATT----------TTGGCAGTGATAATAAAAAAG--GAAGGC-------AAGCCAAATATA----------GTAAT-------AT--TTATTT--ACCATCTCATTGCAGTTAACTAAT----C----AC----------H-------H---H---------H---------H---------H-----H---------A
droRho1	scf7180000771933:31906-32060 +		ATTTGTGGCTTTTAACCAGTTTCAATTGGTTATTGCGGCAGGTCGGTCGATT----------TTGGAAGTGATACTAAAAAA---AAGGC-------AAGCCGAATGTA----------GTCAT-AATATAT-T--CTGCTT--ATTTTCCTTGCAGTTAACCAAA----C----AC----------H-------H---H---------H---AGTAACTAA---------H--CAAGG---------AAACTG
droBia1	scf7180000302422:6989065-6989211 -		GTTCGTGGGTTTTAACCAGTTTCATTGGTTATTGTGCAGGTCGGTCGACT----------TGAAGAGTGCTAATAACAACA---AATGT-------AAAACGATTAA----------GTTAT-------AT--TTGTTTACTCTCTCCTTGCAGTTAAAAAG----AGG-------GC----------H-------H---H---------H---AGCAACTAA---------H--CAAG-----------
droTak1	scf7180000415708:336728-336880 -		TTCCGTTGGATTTAACCAGTTTCGATTGGTTATTGCGGCAGGTCGGTCGACT----------TGAACAGTGATATTAAAAAG---AAGGC-------TCGATGATTTCA----------GTAAC-------TC--TTATTT--AC-CTTTGATTGCAGTTACAAAAACCAAGG----------AC----------H-------H---H---------H---ATGAACTTA---------H--AAAGG---------AAACTG
droEug1	scf7180000409767:196154-196324 -		ATTCGTGGGTTTTAACCAGTTTCGATTGGTTATTGCGGCAGGTCGGTCGATC----T------CATTCCCAGTGATAATAAACAAA---AAATCTCAGTT----ACGA-GTTG----------GTAAT-------AT--CTATTACTCTCTTCCTTGCAGTTACACAA----------H-------H---H---------H---------H-------AACAACAACTAACAACCATAACTAAAAAGGGT---------AAACTG
dm3	chr2L:21114459-21114603 +		ATCCGTGGGTTTTAACCAGTTTCAATTGGTTATTGCGGCAGGTCGGTCGACT----------TGAAGAGTGATGATAATAAAAA---AAGGC-------AAGATGACTTAAACATGAACAAAATTGACT----T---------ACTCT--TTCTT--CTTTTCTCCTGGCAGGTGAAGAAA----C----H-------H---H---------H---------H---------H-----H----------
droSim2	2L:20546295-20546433 +		ATCCGTGGGCTTTAACCAGTTTCAATTGGTTATTGTGGCAGGTCGGTCGACT----------TGAAGAGTGATGATGTACAAAA---AAGGC-------AAGATTAACTTA------ACAAAATTGACT----T---------ACTCCTTTCTTT--TTTCTCTTGGCAGGTGAAGAAA----C----H-------H---H---------H---------H---------H-----H----------
droSec2	scaffold_18:1032810-1032948 +		ATCCGTGGGTTTTAACCAGTTTCAATTGGTTATTGTGGCAGGTCGGTCGACT----------TGAAGAGTGATGATGTACAAAA---AAGGC-------AAGATTAACTTA------ACAAAATTGACT----T---------ACTCCTTTCTTT--TTTCTCTTGGCAGGTGAAGAAA----C----H-------H---H---------H---------H---------H-----H----------
droYak3	2R:1654720-1654860 -		ATTCGTGGGTTTTAACCAGTTTCAATTGGTTATTGTGGCAGGTCGGTCGACT----------TGAAGAGTGATAGCAATAAAAAGGAAGGC-------AAGATTAACTTA------TTAAAATTGGA-T----T---------ACTC-----TT----TTTTCCTTGCAGGTCAAGAAA----C----A----------H-------H---H---------H---------H---------H-----H---------TACA
droEre2	scaffold_4845:3378453-3378608 -		ATCCGTGGGTTTTAACCAGTTTCAGTTGGTTATTGTGGCAGGTCGGTCGACT----------TGAAGAGTGATAGTGCTAAGAATTAAGGC-------A-GATTAACTTA------TCGAAACTGGTC----T---------ACTCT-------T---TTATTCCTTTTAGGTAAAGAAA----C----ATAACAGCTG----H-------H---H---------H---------H---------H-----H---------AACAGCTG
dp5	4_group1:4971425-4971623 -	dps_3834	ATGTGTGGGTTTAATCCAGTTTCGATTGGTTATTGTGGAAGGTCGGTCGACC----GGCGTGTGTAAGGGAGTGATAACAAAAATT---AAGAAAAAA-TCGA----A--------AAAAAATAAT----TCAATT-------AT--TTGTTA--ACTCTTTCCTTGCAGAA----A----CTAAGCGAACA----H-------H---H---------H---------H---------H-----H---------AGAAGGAGGCTTTAAGCAGTAACCAACAACCTATGCCTATGCCTA----TGC-------AGTA
droPer2	scaffold_5:245788-245986 +	dpe_116	ATGTGTGGGTTCAATCCAGTTTCGATTGGTTATTGTGGAAGGTCGGTCGACC----GGCGTGTGTAAGGGAGTGATAACAAAAATT---AAGAAAAAA-TCCA----A--------AAAAAATAAT----TCAATT-------AT--TTGTTA--ACTCTTTCCTTGCAGAA----A----CTAAGCGAACA----H-------H---H---------H---------H---------H-----H---------AGAAGGAGGCTTTAAGCAGTAACCAACAACCTATGCCTATGCCTA----TGC-------AGTA
droWil2	scf2_1100000004585:4878979-4879186 -	dwi_5418	ATTTCTGGGAATTTAACCAGTTTCAATTGGTTATTGTGGCAGGTCGGTCGATTAACCACAGTG-GTATGGAAGTGATGACAAAAA----------GGTTCAA-TTAAAAATGTACAATCTTGACTAAATCAAC-------AT--TTGTTA--ACTCTTCCTTATAGGACACA----------ACTGAACATAACCGCAGAAAATAGCAACAACTATCAACAACTACAAA----------H-------H---H---------H---------H---------H-----H---------GAGAGATAACT
droVir3	scaffold_13246:2198392-2198445 -		TTTACTGGATATTAACCAGTTTCGGTTGGTTATTGCGGCAGGTCGGTCGTTT----------AA----------H-----H-------H---H-------H---------H-----H-------H---H-------H---H---------H-------H---H---------H---H---------H---------H-----H---------H---------H-----H----------
droMoj3	scaffold_6500:26320843-26320892 -		TTTACTGGGATTTAACCAGTTTAAGTTGGTTATTGCGGCAGGTCGGTCGA----------H---------H-----H-------H---H-------H---------H-----H-------H---H-------H---H---------H-------H---H---------H---H---------H---------H-----H---------H---------H-----H----------
droGri2	scaffold_15126:3759879-3759927 +		TTTTCTGGGATGTTAACCAGTTTCGGTTGGTTATTGTGGCAGGTCGGTCG----------H---------H-----H-------H---H-------H---------H-----H-------H---H-------H---H---------H-------H---H---------H---H---------H---------H-----H---------H---------H-----H----------

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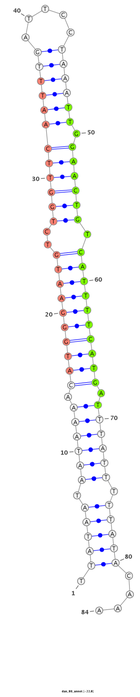
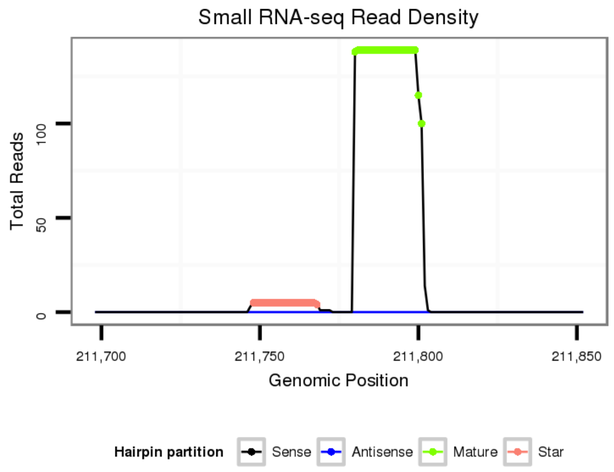
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	2
rescue.candidate	2

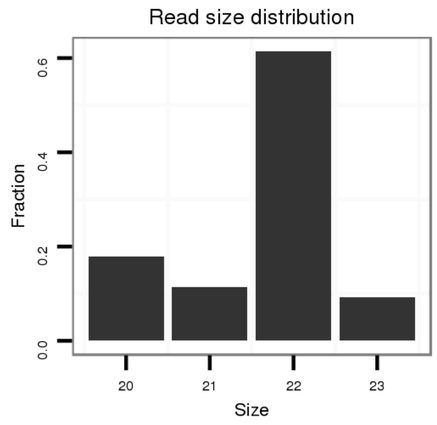
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_80	**scaffold_13335:211748-211802 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

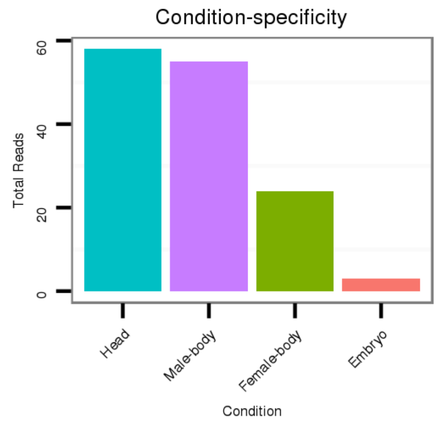
Legend: mature star mismatch in alignment mismatch in read

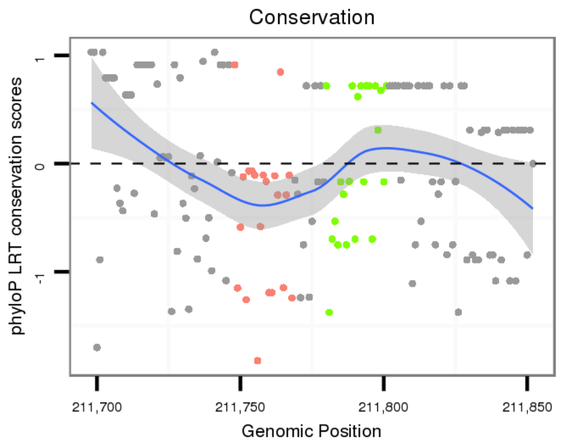
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAAAAAAAACAATAAATAAAATATAATAGTCTTACTTATAATAATAAAACATGGGAATGTCTGGTTCAATTTGATTCCTAAATTGGAACTGTCATTTTCATGATTTATTTTTATACAAAATCATCATCATTAAAAACAAAGTGATAGTGTATCTA **********.(((((.(((((((.((((((((((..((((((((((((.....))))))).))))))).))))))))))).))))))).))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V106 head	V055 head	M044 female body	M058 embryo	V039 embryo
.....TTGGAACTGTCATTTTCATGAT.....	22	0	1	86.00	86	26	21	17	19	3	0
.....TTGGAACTGTCATTTTCATG.....	20	0	1	24.00	24	13	5	5	1	0	0
.....TTGGAACTGTCATTTTCATGA.....	21	0	1	14.00	14	5	7	0	2	0	0
.....TTGGAACTGTCATTTTCATGATT.....	23	0	1	13.00	13	9	3	0	1	0	0
.....TTGGAACTGTCATTTTCATGATA.....	23	1	1	6.00	6	2	3	0	0	0	1
.....ATGGGAATGTCTGGTTCAATT.....	21	0	1	2.00	2	2	0	0	0	0	0
.....TTGGAACTGTCATTTTCATGAA.....	22	1	1	2.00	2	2	0	0	0	0	0
.....TTGGAACTGTCATTTTCATGAC.....	22	1	1	1.00	1	0	0	1	0	0	0
.....TTGGAACTGTCATTTTCATGT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....ATGGGAATGTCTGGTTCAAA.....	20	1	1	1.00	1	1	0	0	0	0	0
.....CATGGGAATGTCTGGTTCAAT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CATGGGAATGTCTGGTTCAATTTGAT.....	26	0	1	1.00	1	1	0	0	0	0	0
.....CATGGGAATGTCTGGTTCAATT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TGGAACTGTCATTTTCATGA.....	20	0	1	1.00	1	0	0	0	1	0	0
.....TTGGAACTGTCATTTTCATGATTT.....	24	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

TTTTTTTTTGTTATTTATTTTATATTATCAGAATGAATATTATTATTTTGTACCCTTACAGACCAAGTTAAACTAAGGATTTAACCTTGACAGTAAAAGTACTAAATAAAAATATGTTTTAGTAGTAGTAATTTTTGTTTCACTATCACATAGAT **********.(((((.(((((((.((((((((((..((((((((((((.....))))))).))))))).))))))))))).))))))).))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13335:211698-211852 +	dan_80	AAAAAAAAACAATAAATAAAATAT--AATAGTC----------TTACTTATAATAATAAAACATGGGAATGTCTGGTTCAATTTGAT-TCCTAAATT--GGAACTGTCATTTTCATGATTTATTTTTATACAAAATCATCATCATTAAAAACAAAGTGATAGTGTATCTA
droBip1	scf7180000395973:671577-671718 +		AATTA---------ATAAAATATAGAATATTTATTTT---------AATTT----AAAATATAA-AAAACTATCCCTGTAAATGCA-TATTAAATGC--AATACAGTT-TTTTTATGATTTATTTTTGAATAAAACATAAACTTTAGTTCAAGAGCTTATTTTATTT-
droRho1	scf7180000779965:5736-5871 +		AAAAAAAAACAA----------T--TTAAAT-TCAGATAACATTCAATTTTTTTTATCAATAATACATTATAATTAGAAATGCACTCCTTTGTTCTTATTCATAGATATATTATATTTAAGTTTTATCTTTTTACAAATTATTCATTGTT----------
droBia1	scf7180000302262:6589-6633 -		AACTAAAAATGTTAACTAAAATGT--ATTTGTC----------TCACCAATACCCAT----------]---------]--]
droEre2	scaffold_4929:435989-436049 +		AATTA---------ATAAAATG--CAATATTTATGAT---------]----AACATTATAAAACACGAAGTTGCCTAATTCGATT----]---------]--]

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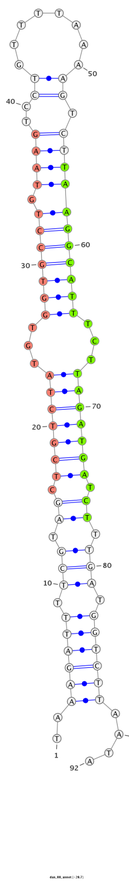
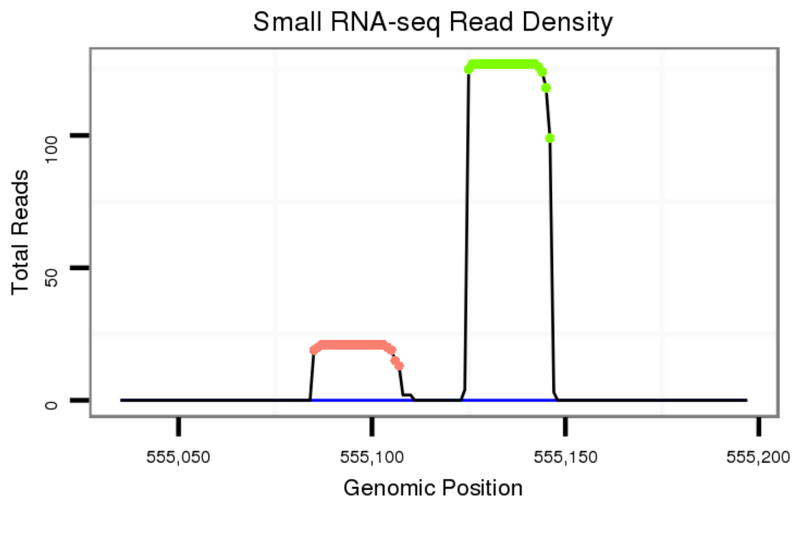
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

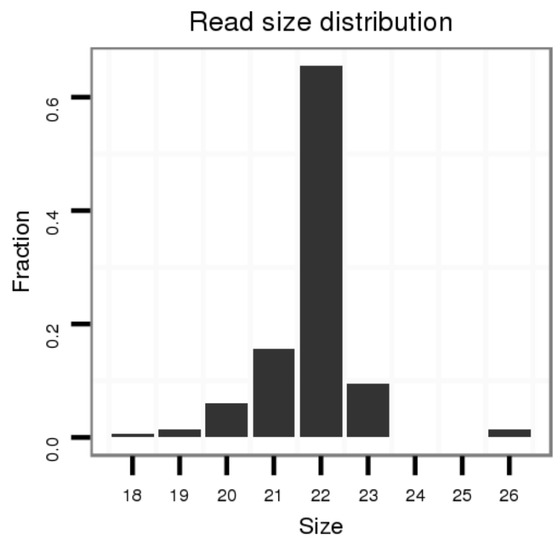
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_88	**scaffold_12903:555085-555147 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

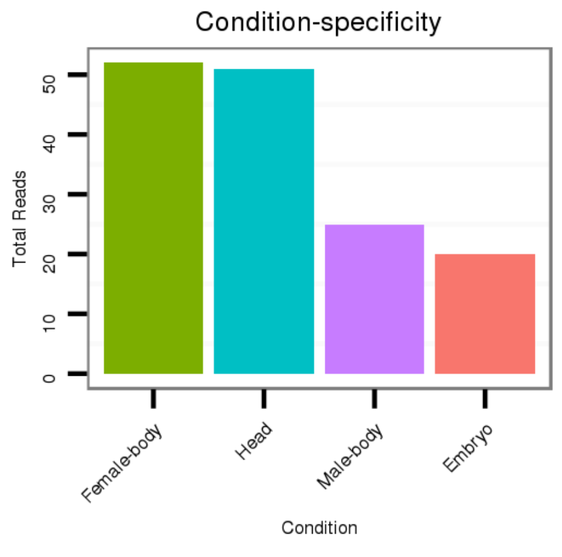
Legend: mature star **mismatch in alignment** mismatch in read

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

ATTTTTATTTAATTTTTTGTGAGGAGAGTCGATCTTAAAGATTTTCGTAGCTCGTCTATGTGGTGCCTGTAAGTCCTGTTTTAAAAGTCTTAAGGCATTTCTTAGATGATCTTTGATGGTCTTAATAGCTTCATGATAATAATCATATTACTTCGAATTATTT **********..((((((.(((.((.(((((((...(((((((.((((..((........))).)))))))))))...)))))))..)).)))..))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V055 head	V106 head	V105 male body	M058 embryo	V039 embryo
..........TAAGGCATTTCTTAGATGATCT..........	22	0	1	93.00	93	23	19	22	19	10	0
..........TAAGGCATTTCTTAGATGATC..........	21	0	1	17.00	17	5	1	1	2	8	0
..........CTCGTCTATGTGGTGCCTGTAAG..........	23	0	1	9.00	9	6	0	3	0	0	0
..........TAAGGCATTTCTTAGATGAT..........	20	0	1	6.00	6	2	0	2	0	2	0
..........CTCGTCTATGTGGTGCCTGTA..........	21	0	1	4.00	4	4	0	0	0	0	0
..........TAAGGCATTTCTTAGATGATCTT..........	23	0	1	3.00	3	3	0	0	0	0	0
..........CTCGTCTATGTGGTGCCTGTAAGTCC..........	26	0	1	2.00	2	1	0	1	0	0	0
..........CTCGTCTATGTGGTGCCTGTAA..........	22	0	1	2.00	2	0	0	1	1	0	0
..........TTAAGGCATTTCTTAGATGATCT..........	23	0	1	2.00	2	0	0	0	2	0	0
..........TAAGGCATTTCTTAGATGATCTTGAG..........	26	3	1	1.00	1	1	0	0	0	0	0
..........CTCGTCTATGTGGTGCCTGT..........	20	0	1	1.00	1	1	0	0	0	0	0
..........TAAGGCATTTCTTAGATGATCTA..........	23	1	1	1.00	1	0	0	0	1	0	0
..........TAAGGCATTTCTTAGATGA..........	19	0	1	1.00	1	0	0	1	0	0	0
..........AAGGCATTTCTTAGATGATCT..........	21	0	1	1.00	1	1	0	0	0	0	0
..........CGTCTATGTGGTGCCTGTAAG..........	21	0	1	1.00	1	1	0	0	0	0	0
..........TCGTCTATGTGGTGCCTGTAAG..........	22	0	1	1.00	1	1	0	0	0	0	0
..........AAGGCATTTCTTAGATGATC..........	20	0	1	1.00	1	1	0	0	0	0	0
..........TTAAGGCATTTCTTAGATGATC..........	22	0	1	1.00	1	0	0	0	1	0	0
..........TAAGGCATTTCTTAGATG..........	18	0	1	1.00	1	1	0	0	0	0	0
..........TTAAGGCATTTCTTAGATGA..........	20	0	1	1.00	1	1	0	0	0	0	0
..........CTCGTCTATGTGGTGCCTG..........	19	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

TAAAAATAAATTAAAAAACACTCCTCTCAGCTAGAATTTCTAAAAGCATCGAGCAGATACACCACGGACATTCAGGACAAAATTTTCAGAATTCCGTAAAGAATCTACTAGAAACTACCAGAATTATCGAAGTACTATTATTAGTATAATGAAGCTTAATAAA **********..((((((.(((.((.(((((((...(((((((.((((..((........))).)))))))))))...)))))))..)).)))..))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	V039 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:555035-555197 +	dan_88	ATTTTTATTTAATTTTTTGTGAGGAGAGTCGATCTTAAAGATTTTCGTAGCTCGTCTATGTGGTGCCTGTAAGTCCTGTTTTAAAAGTCTTAAGGCATTTCTTAGATGATCTTTGATGGTCTTAATAGCTTCATGATAATAATCATATTACTTCGAATTATTT

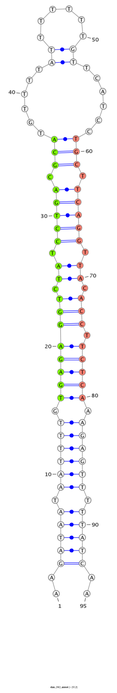
Generated: 09/08/2015 at 08:02 PM

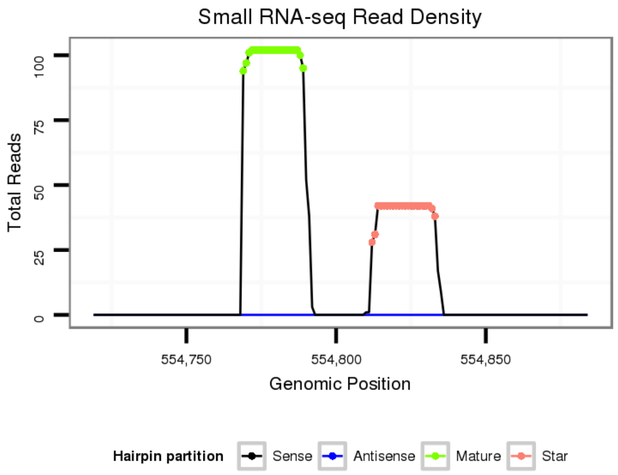
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

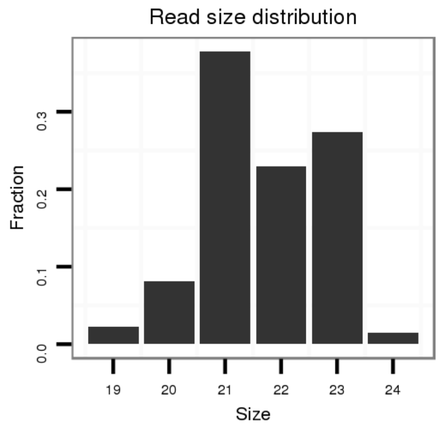
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_242	**scaffold_12903:554769-554834 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

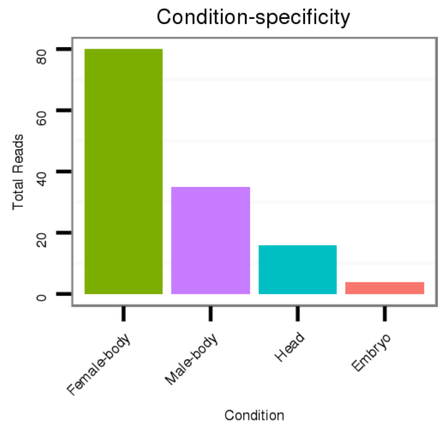
Legend: mature star mismatch in alignment mismatch in read

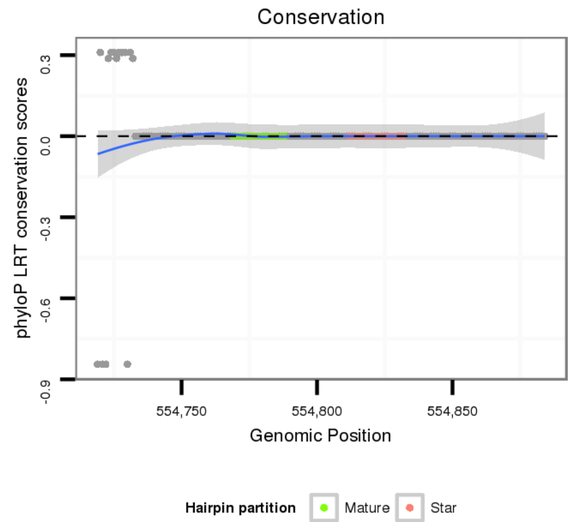
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CAGTCATCATAGTGGTTTTTTTCAGTGTTTTTTTTAAGATAATAATTTTGTGAGAGGTCTATCCTGACGCATGTTTTATTTTTTTGTTCATCCTGCTTCAGGTTACACCTTCTCAAAGAGTTTTTATCAAAGCCTCGTTTATTTATATTTTAATTTTAAAATGAAA	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V105 male body	V106 head	V055 head	M058 embryo	V039 embryo
**********..(((((.(((((((.(((((((((.((.(((((.(((.....((.....)).....))).))))))).)).))).))))))).)))))).)))))..**********											
.....TGAGAGGTCTATCCTGACGCA.....	21	0	1	40.00	40	18	15	4	2	1	0
.....TGAGAGGTCTATCCTGACGCATG.....	23	0	1	31.00	31	19	9	1	1	1	0
.....TGCTTCAGGTTACACCTTCTCA.....	22	0	1	17.00	17	15	1	0	0	0	1
.....TGAGAGGTCTATCCTGACGCAT.....	22	0	1	14.00	14	2	7	4	1	0	0
.....TGAGAGGTCTATCCTGACGC.....	20	0	1	5.00	5	2	0	1	2	0	0
.....TGCTTCAGGTTACACCTTCTCAA.....	23	0	1	5.00	5	5	0	0	0	0	0
.....CTTCAGGTTACACCTTCTCAAA.....	22	0	1	5.00	5	3	0	2	0	0	0
.....AGAGGTCTATCCTGACGCATG.....	21	0	1	4.00	4	4	0	0	0	0	0
.....CTTCAGGTTACACCTTCTCA.....	20	0	1	3.00	3	2	0	0	0	1	0
.....TGCTTCAGGTTACACCTTCTCAAA.....	24	0	1	3.00	3	3	0	0	0	0	0
.....CTTCAGGTTACACCTTCTCAA.....	21	0	1	3.00	3	3	0	0	0	0	0
.....GAGAGGTCTATCCTGACGCA.....	20	0	1	3.00	3	3	0	0	0	0	0
.....TGAGAGGTCTATCCTGACGCATGT.....	24	0	1	2.00	2	1	1	0	0	0	0
.....TGCTTCAGGTTACACCTTCTC.....	21	0	1	2.00	2	2	0	0	0	0	0
.....TGAGAGGTCTATCCTGACG.....	19	0	1	2.00	2	1	1	0	0	0	0
.....GCTTCAGGTTACACCTTCTCT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TGAGAGGTCTATCCTGACGT.....	20	1	1	1.00	1	0	0	0	1	0	0
.....GCTTCAGGTTACACCTTCTCAAA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....CCTGCTTCAGGTTACACCTTCTC.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TGAGAGGTCTATCCTGACGCATGA.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TGAGAGGTCTATCCTGACGCAA.....	22	1	1	1.00	1	0	1	0	0	0	0
.....TGAGAGGTCTATCCTGACGCATT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....GCTTCAGGTTACACCTTCT.....	19	0	1	1.00	1	1	0	0	0	0	0
.....GCTTCAGGTTACACCTTCTCA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GAGGTCTATCCTGACGCATGT.....	21	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

GTCAGTAGTATCACCAAAAAAAGTCACAAAAAAAATTCTATTATTAAAACACTCTCCAGATAGGACTGCGTACAAAATAAAAAAACAAGTAGGACGAAGTCCAATGTGGAAGAGTTTCTCAAAAATAGTTTCGGAGCAAATAAATATAAAATTAAAATTTTACTTT	Read size	# Mismatch	Hit Count	Total Norm	Total	V039 embryo	M058 embryo	V105 male body
**********..(((((.(((((((.(((((((((.((.(((((.(((.....((.....)).....))).))))))).)).))).))))))).)))))).)))))..**********								

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:554719-554884 +	dan_242	CAGTCATCATAGTGGTTTTTTTCAGTGTTTTTTTTAAGATAATAATTTTGTGAGAGGTCTATCCTGACGCATGTTTTATTTTTTTGTTCATCCTGCTTCAGGTTACACCTTCTCAAAGAGTTTTTATCAAAGCCTCGTTTATTTATATTTTAATTTTAAAATGAAA
droBip1	scf7180000395912:23739-23752 +		TAACCATCATAATG----------

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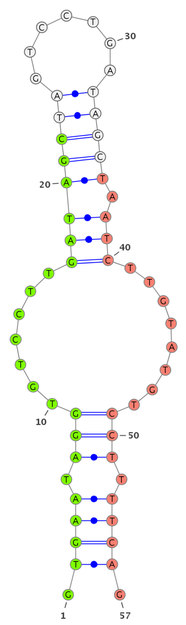
miRNAfail

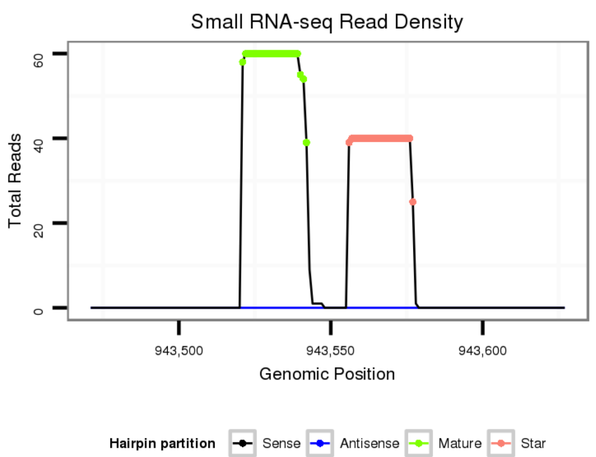
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

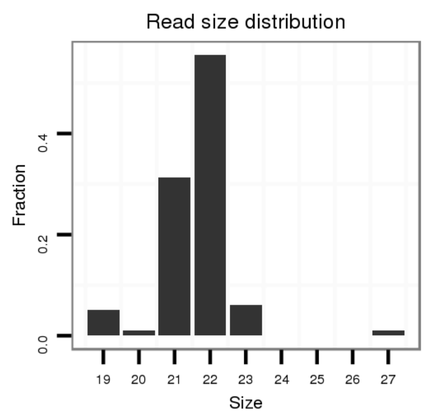
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_3291	**scaffold_13417:943521-943577 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

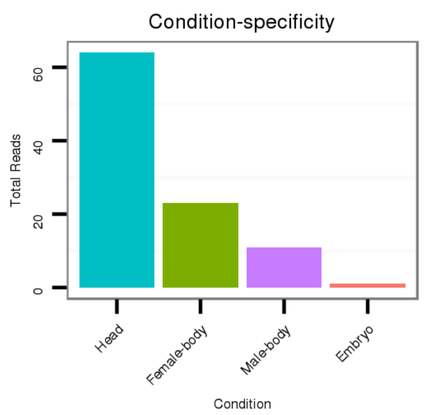
Legend: mature star mismatch in alignment mismatch in read

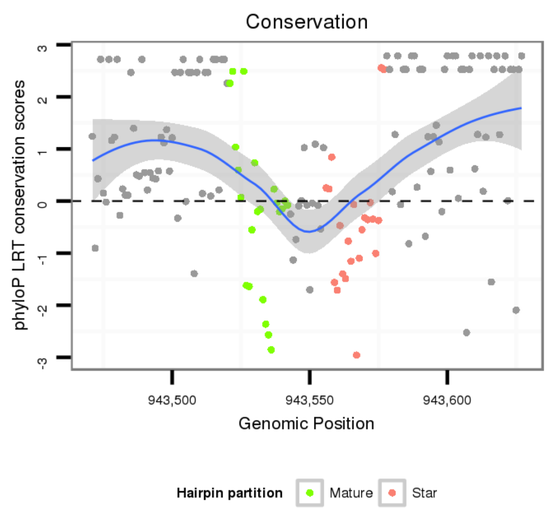
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF20397-in]; CDS [Dana\GF20397-cds]; CDS [Dana\GF20397-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GACAACTGCAAACCGAGGACTCCAAGGAGCCGCAGCGTGTGGCCATCAAGGTGAATAGGTGTCCTTGATAGCTAGTCCTGATAGCTAATCTTGTATGTCCTTTTCAGAGCCTGCGGAAAGGCGCCAGCGAGTTTGCGGAGCTCCTCCAGGAGGCTCA	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	V105 male body	V055 head	V039 embryo	M058 embryo
**********.(((((.(((.......(((((((((.......)))))).)))........))).)))))..**********											
.....TAATCTTGTATGTCCTTTTCAGT.....	23	1	1	41.00	41	17	18	2	4	0	0
.....GTGAATAGGTGTCCTTGATAGC.....	22	0	1	30.00	30	21	1	8	0	0	0
.....TAATCTTGTATGTCCTTTTCAG.....	22	0	1	23.00	23	12	9	1	0	1	0
.....TAATCTTGTATGTCCTTTTCA.....	21	0	1	15.00	15	2	12	0	1	0	0
.....GTGAATAGGTGTCCTTGATAG.....	21	0	1	15.00	15	13	0	2	0	0	0
.....GTGAATAGGTGTCCTTGATAGCT.....	23	0	1	6.00	6	6	0	0	0	0	0
.....GTGAATAGGTGTCCTTGAT.....	19	0	1	5.00	5	5	0	0	0	0	0
.....AATCTTGTATGTCCTTTTCAGT.....	22	1	1	2.00	2	0	2	0	0	0	0
.....TAATCTTGTATGTCCTTTTCAGTT.....	24	2	1	2.00	2	0	2	0	0	0	0
.....GTGAATAGGTGTCCTTGATAGA.....	22	1	1	2.00	2	2	0	0	0	0	0
.....TGAATAGGTGTCCTTGATAGCT.....	22	0	1	2.00	2	2	0	0	0	0	0
.....GTGAATAGGTGTCCTTGATAGCTT.....	24	1	1	1.00	1	0	0	1	0	0	0
.....GTGAATAGGTGTCCTTGATAGCTAGTC.....	27	0	1	1.00	1	1	0	0	0	0	0
.....TAATCTTGTATGTCCTTTTCATT.....	23	2	1	1.00	1	0	0	0	0	1	0
.....GTGAATAGGTGTCCTTGATT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....TAATCTTGTATGTCCTTTTCAGC.....	23	1	1	1.00	1	1	0	0	0	0	0
.....AATCTTGTATGTCCTTTTCAG.....	21	0	1	1.00	1	0	1	0	0	0	0
.....GTGAATAGGTGTCCTTGATA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TAATCTTGTATGTCCTTTTCAGA.....	23	0	1	1.00	1	0	1	0	0	0	0
.....GTGAATAGGTGTCCTTGATAT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....GTGAATAGGTGTCCTTGATAC.....	21	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

CTGTTGACGTTTGGCTCCTGAGGTTCCTCGGCGTCGCACACCGGTAGTTCCACTTATCCACAGGAACTATCGATCAGGACTATCGATTAGAACATACAGGAAAAGTCTCGGACGCCTTTCCGCGGTCGCTCAAACGCCTCGAGGAGGTCCTCCGAGT	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	V055 head	V039 embryo
**********.(((((.(((.......(((((((((.......)))))).)))........))).)))))..**********								

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13417:943471-943627 +	dan_3291	GACAACTGCAAACCGAGGACTCCAA------GGAGCCGCAGCGTGTGGCCATCAAGGTGAATAGGTG--------TCCTTG---ATA--GCTAG----------TCCTGATAGC---TAAT------C----------T-------T-GTATGTCCT--------TTTCAGAGCCTGCGGAAAGGCGCCAGCGAGTTTGCGGAGCTCCTCCAGGAGGCTCA
droBip1	scf7180000396362:250497-250580 -		AG--TCCACCTAGCTAA---T-----G----------T-------A-GTGTTTCCT--------TTTCAGAGCCTGCGGAAAGGAGCCAGCGAGTTTGCGGAACTCCTCCAGGAGGCCA
droKik1	scf7180000302724:153247-153409 -		GCCAGCTGCAGACGGAGGATGCCAA------GGAACCACAGCGGGTTGCCATCAAGGTGTGTTA---------TGTCCG---GTT--TCTAGCAAGGTG----------TAGGT----------------------G-GGTCTAAACCCT-------A-GCTCATCCC-------CCACAGAGTCTGCGCAAGGGCGCCAGCGAGTTCGCGGAGCTGCTCCAGGAGGCCA
droFic1	scf7180000453882:910999-911160 -		GTCAGTTGCAGACGGAGGACTCCGG------GGAGCCCAGCGAGTGGCCATCAAGGTGAGTCA---------CTCTG---T---------GAAGTGGGG-----CATCCGCAA----------TGGATTA----------TTGGA------A----------C-------C-CTTCAA-T-------CCTCAGAGGTTGCGGAAAGGAGCCAGCGAATTCGCCGAGTTGCTGCAGGAAGGCCA
droEle1	scf7180000490214:338333-338496 +		GTCAGCTGCAGACGAGCACTCCGA------GGAGCCGCAGCGGTGGCCATCAAGGTGAGTCA---------TCTGG---------CGAAAATACAA----------TCATTCCATCA----------ATGACTCCC--T----------C-------G-ATCCGAATC-------CTCTAGAGCCTGCCAAGGGAGCCAGTGAATTTGCTGAGCTGCTGCAGGAGGCTCA
droRho1	scf7180000779189:1783-1946 +		GTCAGCTGCAGACGAGGACTCCGA------GGAGCCCAAGGAGTGGCCATTAAGGTGAGTAG---------TCCTAG---------GCAGAAACGTGG------AG--------TCACCGCCCGACTA----------ATGAC------C----------C-------C-CTC-TTATC-------CCCCAGAGCCTGCGAAAGGGAGCCAGCGAATTTGCAGAGCTGCTGCAGGAGGCCA
droBia1	scf7180000302126:3958274-3958426 -		GTCAGTTGCAGACGGAGGACTCCGA------GGAGCCGCAGCGGTGGCCATTAAGGTGAGTTG---------TGTG---------GCGGAAGAGTGG-----CAACCTCAA----------T----------TC---A----------T-------C-CG-TGCATC-------CCCTAGAGCCTGCGAAAGGGAGCCAGCGAGTTCGCGGAGCTGCTCCAGGAGGCCA
droTak1	scf7180000415394:852176-852334 -		GTCATTTGCAGACGAGGACTCCGA------GGAGCCGCAACGAGTGGCCATCAAGGTGGGTTC---------TGATT---T-AC-TTTGTATGTGG-----CACTTTTAA----------T----------A------AAATC-C-------CCG--TAATTC-------CTCTAGAGCCTGCGAAAGGGAGCCAGCGAGTTTGCCGAGCTTCTGCAAGAGGCCA
droEug1	scf7180000409631:100358-100521 -		GTCAGCTGCAAACAGAGGACTCCGA------AGAGCCACAGCGAGTGGCCATCAAGGTGAGTTA---------TGTCA---------TGGAAACCAGG-----CAC---------GTTTCTATTGACAG----------TTGAT------C----------T-------G-CC-TTAAGC-------CTATAGAGCCTGCGAAAAGGTGCCAGCGAATTTGCAGAGCTGCTTCAGGAAGCACA
dm3	chrX:10966781-10966939 -		GTCAGTTGAAGACGGAGGACTCCGA------GGAGCCGCAAGGAGTGGCCATCAAGGTGAGTAG---------TGTCG---GTA--GCCGCGAAAAGGGG----------CAACTT----------TTGAA------C----------T-------G-CTTCGATC-------CTCCAGAGCCTGCGCAAGGGAGCCAGTGAATTTGCCGAGCTGCTTCAGGAGGCTCA
droSim2	x:10423157-10423315 -		GTCATTTGAAGACGGAGGACTCCGA------GGAGCCGCAAGGAGTGGCCATCAAGGTGAGTAG---------TGTGCG---GTA--GCCGCGAAAAGGGG----------CCACTA----------TTGAC------C----------T-------G-GTTTCGATC-------CTCCAGAGCCTGCGCAAGGGAGCCAGTGAATTTGCCGAGCTGCTCCAGGAAGCTCA
droSec2	scaffold_15:1678080-1678238 -		GTCATTTGAAGACGGAGGACTCCGA------GGAGCCGCAAGGAGTGGCCATCAAGGTGAGTAG---------TGTGCG---GTA--GCCGCGAAAAGGGG----------CCACTA----------TTGAC------C----------T-------G-GTTTCGATC-------CTCCAGAGCCTGCGCAAGGGAGCCAGTGAATTTGCCGAGCTGCTCCAGGAAGCTCA
droYak3	X:11151146-11151308 +		GTCAGTTGAAAACGGAGGACTCCGA------GGAGCCGCAAGGAGTGGCCATCAAGGTGAGTCA---------GTGAGTCTG-C-G--CGGAAAAGGG----------AGGG-------CAACTA----------TTGAT------C----------CT-------G-GTCTTGATA-------CTCCAGAGCCTTCGCAAGGGCGCCAGTGAATTTGCGGAGCTGCTCCAGGAGGCCA
droEre2	scaffold_4690:4158582-4158735 +		GCCAGTTGAATACGGAGGACTCCGA------GGAGCCGCAAGGAGTGGCCATCAAGGTGAGTAG---------TGTACG---------CGGCAAAGGGG----------CAACTA----------TTGAC------T----------T-------G-GCT-TGATC-------CTCTAGAGCCTGCGCAAGGGAGCCAGCGAATTTGCGGAGCTGCTCCAGGAGGCTCA
dp5	XL_grouple:869188-869350 -		GAGATCTTGCATTCCGAGGACAAGAA------GGATTCGCAGCGCGTGGCTATAAAGGTGATTAA---------AGAAGCCT-T-AG-TCTTAA--GAT----------A----------TAGAA------AGCATTCTAAACCCT-------T-G---CTTAT-------ACACAGAGCCTGCGTAAGGGTGCCAGCGAGTTTGCGGAGCTGTTGCAGGAGGCCA
droPer2	scaffold_30:334332-334494 +		GAGATCTGCATTCCGAGGACAAGAA------GGATTCGCAGCGCGTGGCTATCAAGGTGATTAA---------AGTAGCAA-C-AG-TCTTAA--GAT----------A----------TAGAA------AGCATTCTAAGCCCT-------T-G---CTAAT-------ACACAGAGCCTGCGTAAGGGTGCCAGCGAGTTTGCGGAGCTTCTGCAGGAGGCCA
droWil2	scf2_1100000004515:1025942-1026041 -		GTGAACTTCAGCTTGAGCAGCAGAA------GGAGCCGCAAGGTGTTGCGATCAA--GAGTCTCGCAAGGGAGAAGTCTGAGTTTGCCGAACTGCTGCAGGAGGCTCA
droVir3	scaffold_13042:3133208-3133367 +		GTCAGCTGCAGGCCGAGGAGGAGGC------GCAGCCGCAGCGTGTTGCCATCAAGGTGAGTGG---------AGCAG----C-AG-TTTTT--TT-TTTGCCACAATT----------CA----------AGGAT------T----------C-------T-CC-TCGCCT-------TTACAGAGTCTGCGCAAGGGCGCCAGCGAGTTCGCGGAGCTGCTGCAGGAAGGCCA
droMoj3	scaffold_6328:3578537-3578703 +	dmo_521	GCCAGCTGCAGGGCGAAGACGAGGC------GCAGCCGCAGCGTGTGGCCATCAAGGTGAGTGT---------TAGAG----G-CTGG----------TCACCTACCTCA----------GGCCCAAACTGAAGCACCGT-C-------CCCATCCACTTGCAGAGTCTGCGCAAGGGCGCCAGCGAGTTTGCAGAGCTGCTGCAGGAGGCGCA
droGri2	scaffold_15081:3113544-3113713 -		GCCAGCTGCAGGGCCGGCGAGGGCGACAATTCGCGCCACAGCGCGTGGCAATCAAGGTAAATGACTACCTGGATTGATTG----------ACCAACTGACTGATGATATTTG-T----------T-------A-CTTGCATTC-------GTTTAGAGCCTGCGCAAGGGCTACAGTGAGTTTGCCGAGCTGCTCCAGGAGGCGCA

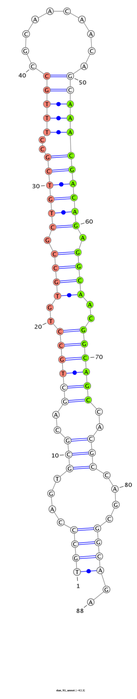
Generated: 08/18/2015 at 04:01 PM

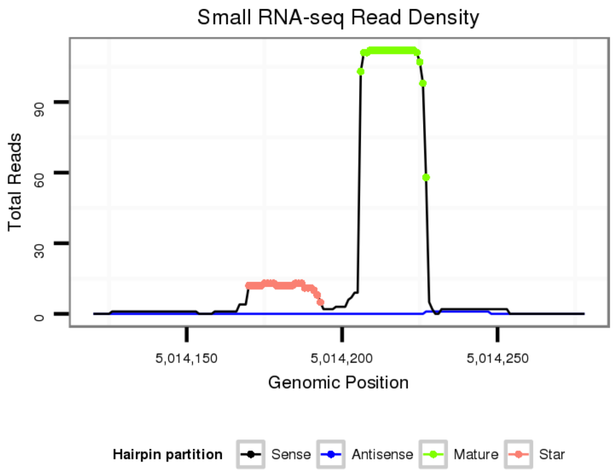
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

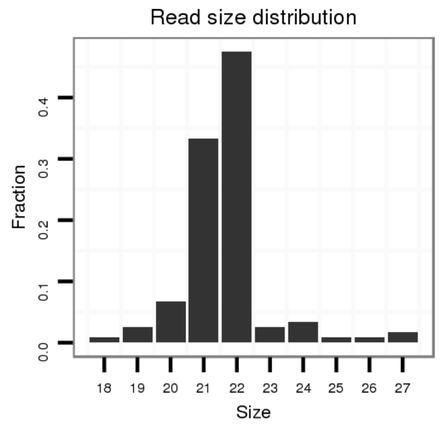
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_91	**scaffold_13266:5014170-5014228 +**	**confident**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

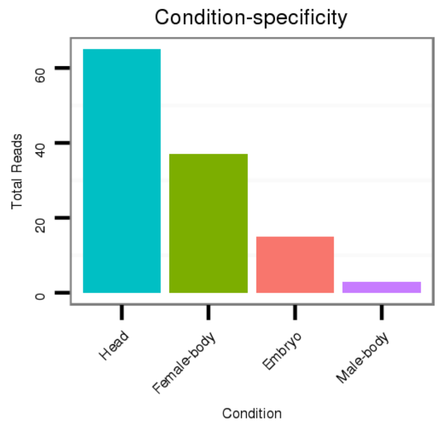
Legend: mature star mismatch in alignment mismatch in read

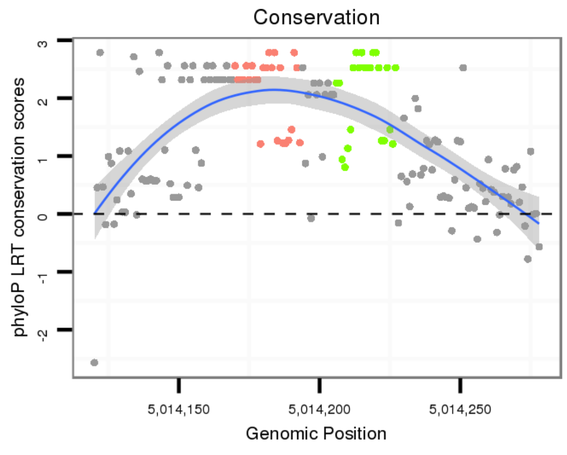
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dana\GF12812-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACAGCAGGCCAACCAACAGCAGCAGAAGCCCCAGCTGCCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCTTTGCCGCAACAACAGCAAACGACAGAGGCAACGGCAGCCACGCCAGCGGCAGAGACACCCGCCCAAGCATCAACTTCCACCTCCACCAG	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	M058 embryo	V105 male body	V055 head	V039 embryo
********************************((((....(((..((((((..((((.((((((..(((((..........)))))))))))).))))..))))))..)))....)))))..********************************	**size**	**Mismatch**	**Count**	**Norm**	**Total**	**head**	**body**	**embryo**	**body**	**head**	**embryo**
..........AAACGACAGAGGCAACGGCAGC..........	22	0	1	52.00	52	35	9	5	0	2	1
..........AAACGACAGAGGCAACGGCAG..........	21	0	1	37.00	37	23	12	1	1	0	0
..........AAACGACAGAGGCAACGGCA..........	20	0	1	4.00	4	2	1	1	0	0	0
..........TGCCTGTGCCGCTGTCGCCTTTGC..........	24	0	1	3.00	3	2	1	0	0	0	0
..........AACGACAGAGGCAACGGCAG..........	20	0	1	3.00	3	0	3	0	0	0	0
..........AGCTGCCTGTGCCGCTGTCGC..........	21	0	1	2.00	2	0	2	0	0	0	0
..........TGCCTGTGCCGCTGTCGCCTTTG..........	23	0	1	2.00	2	0	2	0	0	0	0
..........AACGACAGAGGCAACGGCA..........	19	0	1	2.00	2	0	2	0	0	0	0
..........TGCCTGTGCCGCTGTCGCCTTT..........	22	0	1	2.00	2	0	2	0	0	0	0
..........CCAGCGGCAGAGACACCCGCCC..........	22	0	1	2.00	2	0	1	1	0	0	0
..........AAACGACAGAGGCAACGGC..........	19	0	1	1.00	1	0	0	1	0	0	0
..........AAACGACAGAGGCAACGGCAGCA..........	23	1	1	1.00	1	0	0	1	0	0	0
..........CAGCAAACGACAGAGGCAACGGCA..........	24	0	1	1.00	1	0	0	0	1	0	0
..........AGCAAACGACAGAGGCAACGGC..........	22	0	1	1.00	1	0	0	1	0	0	0
..........AAACGACAGAGGCAACGGCAGTT..........	23	2	1	1.00	1	1	0	0	0	0	0
..........ACAGCAAACGACAGAGGCAACGGCA..........	25	0	1	1.00	1	0	1	0	0	0	0
......GGCCAACCAACAGCAGCAGAAGCCCCAG..........	28	0	1	1.00	1	0	1	0	0	0	0
..........AAACGACAGAGGCAACGGCAT..........	21	1	1	1.00	1	1	0	0	0	0	0
..........CGCCTTTGCCGCAACAAC..........	18	0	1	1.00	1	0	0	1	0	0	0
..........GTGCCGCTGTCGCCTTTGCCGCAACA..........	26	0	1	1.00	1	0	1	0	0	0	0
..........TGCCTGTGCCGCTGTCGCCTTTGG..........	24	1	1	1.00	1	0	1	0	0	0	0
..........GCAAACGACAGAGGCAACGGCAGCCA..........	26	0	1	1.00	1	0	1	0	0	0	0
..........AACGACAGAGGCAACGGCAGC..........	21	0	1	1.00	1	0	0	1	0	0	0
..........AGCAAACGACAGAGGCAACGGCA..........	23	0	1	1.00	1	0	0	0	1	0	0
..........TGCCTGTGCCGCTGTCGCCTT..........	21	0	1	1.00	1	0	1	0	0	0	0
..........CGACAGAGGCAACGGCAGCC..........	20	0	1	1.00	1	0	1	0	0	0	0
..........AGCTGCCTGTGCCGCTGTCGCCTTTG..........	26	0	1	1.00	1	0	1	0	0	0	0
..........TGCCTGTGCCGCTGTCGCCTTTGA..........	24	1	1	1.00	1	0	1	0	0	0	0
..........AACGACAGAGGCAACGGCAGCC..........	22	0	1	1.00	1	0	0	1	0	0	0
..........CAGCAAACGACAGAGGCAACGG..........	22	0	1	1.00	1	0	0	1	0	0	0
..........AACGACAGAGGCAACGGCAGCCA..........	23	0	1	1.00	1	0	0	1	0	0	0
..........GCAAACGACAGAGGCAACGGC..........	21	0	1	1.00	1	0	0	1	0	0	0
..........CAGCAAACGACAGAGGCAACGGCAGCC..........	27	0	1	1.00	1	1	0	0	0	0	0
..........CAGTGCGCAGCTGCCTGTGC..........	20	0	1	1.00	1	0	0	1	0	0	0
..........ACAACAGCAAACGACAGAGGCAACGGC..........	27	0	1	1.00	1	0	1	0	0	0	0
..............CAACAGCAGCAGAAGCCCCAGC..........	22	0	2	0.50	1	0	1	0	0	0	0
..............ACAGCAGCAGAAGCCCCAGC..........	20	0	3	0.33	1	0	1	0	0	0	0

Anti-sense strand reads

TGTCGTCCGGTTGGTTGTCGTCGTCTTCGGGGTCGACGGGTCACGCGTCGACGGACACGGCGACAGCGGAAACGGCGTTGTTGTCGTTTGCTGTCTCCGTTGCCGTCGGTCGCCGTCTCTGTGGGCGGGTTCGTAGTTGAAGGTGGAGGTGGTC	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head	M044 female body	V105 male body
********************************((((....(((..((((((..((((.((((((..(((((..........)))))))))))).))))..))))))..)))....)))))..********************************	**size**	**Mismatch**	**Count**	**Norm**	**Total**	**head**	**body**	**body**
..........GGTGCGGTCGCCGTCTCTGTG..........	21	0	1	1.00	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13266:5014120-5014278 +	dan_91	ACA---GC---AGGCCAACC------AACAGCAGCAGAAGCCCCAGCTGCCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCTTTGCCGCAAC------AACAGCAAACGACAGAGGCAACGGCAGC------C---ACGCCAGCGGCAGAGACAC---CCGCCCAAG--------------CA---TCAAC----------------TTCCAC------CTCCACCAG
droBip1	scf7180000395751:823810-823965 +		ACAACAGC---AGGCCAACCAAC---AGC------AGAAGCCCCAGCTGCCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCTTTGCCGCTAC------ATCAGCAAACGACAGAGGCAACGGCAGC------C---ACGCCAGCGGCAGAGACTC---CCGCCCAAA--------------CA---CCC--------------------ACCAC------CTCGTCCAG
droKik1	scf7180000302411:441463-441636 +		GCATCAGCACCAGC------ACAGCAGCAGAAG---CAGCTGCCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCTTGCCGCCAC------AACAGCAAACGACAGAGGCAACGGCAGC------C---ACGCCAGCAGCAGC---ACTGCCCGCCCAC-----TT----C-CACT---CCACTTCTACAAGT--TTA-AATTCTGC------CTCCACCAC
droFic1	scf7180000453811:56738-56884 -		T-A---G----C-----A------AAC------AGAAA---CAGCTGCCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCTTGCCGCAAGAACAACAACAGCAAACGACAGAGGCAACGGCAGCAGCA--------------GCAGC---AC---CCGCCCAC---TCAGC----T-TACT---CCAATCC--------------ATCCGC------CTCATCTAA
droEle1	scf7180000491232:161904-162042 -		GCA---GC---AGC-----A------AAC------AGAAG---CATCTGCCCAGTGCGCAGCTGCCTGTGCCGCTTGCCGCAACA---ACAACAGCAAACGACAGAGGCAACGGCAGCAGCA--------------GCAGC---AT---CCGCC-----------------CACA---CCAACCC--------------ATCCGC------CTCGTCCAG
droRho1	scf7180000780265:156508-156648 -		T-A---G----C-----A------AAC------AGAAG---CAGCTACCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCTTGCCGCAACA---ACAACAGCAAACGACAGAGGCAACGGCAGCAGCA--------------GCAGCAGCAGC---AA---CCGCC-----------------CACA---CCAACCC--------------ATCCGC------CTCCACCAG
droBia1	scf7180000302143:1194624-1194789 -		GCAGCAGCAGTAGC-----A------AGC------AGAAG---CAACTGCCCAGTGCGCAGCTGCCTGTGCCGCTGTCGCCTTGCCGCAACA---ACAACAGCAAACGACAGAGGCAACGGCAGCAGCAGCAGTAGCACTAGCAGTAGC---AC---CCGCC-----------------CACT---CCAACCC--------------ATCCGCCTCCGCCGCGTCCTAG
droTak1	scf7180000415722:103172-103284 +		GTA---C----G-----A------AAC------AGAAA---CAACTGCCAGTGCGCAGCTGCCTGTGCCGCTTGCCGCAACA---ACAACAGCAAACGACAGAGGCAACGGCAGCAGCA--------------GCAGCAGTAGC---AC---CCGCC-----------------CA---CCC-----CCC--------
droEug1	scf7180000409474:730397-730537 -		C-ACCAGT---AGC-----A------AAC------AGAAG---CAACTGCCCAGTGCGCAGCTGCCTGTGCCGCTTGCCGCAACA---ACAACAGCAAACGACAGAGGCAACGGCAGCAGCA--------------GCAACC---AA---CCGCC-----------------CACT---GTAATCC--------------ATCCAC------CGGACCTAG
dm3	chr2R:17211923-17212054 +	dme_419	C-A---GC---AGC-----AAAC---AAC------AGAAG---CAACTGCCAGTGCGCAGCTGCCTGTGCCGCTTGCCGCAACA---ACAACAGCAAACGCGAGAGGCAACGGCAGCAGCA--------------GCAGC---AC---CCGCC-----------------CACT---CCAAGGT--------------ATC---------------GGT
droSim2	2r:17766345-17766482 +	dsi_32456	C-A---GT---AGC-----AAAC---AAC------AGAAG---CAACTGCCAGTGCGCAGCTGCCTGTGCCGCTTGCCGCAACA---ACAACAGCAAACGCGAGAGGCAACGGCAGCAGCA--------------GCAGC---AC---CCGCC-----------------CACT---CCAAGGT--------------ATCCAC------C---TCGGT
droSec2	scaffold_9:543283-543420 +	dse_1843	C-A---GT---AGC-----AAAC---AAC------AGAAG---CAACTGCCAGTGCGCAGCTGCCTGTGCCGCTTGCCGCAACA---ACAACAGCAAACGCGAGAGGCAACGGCAGCAGCA--------------GCAGC---AC---CCGCC-----------------CACT---CCAAGGT--------------ATCCAC------C---TCGGT
droYak3	2R:11976255-11976398 -	dya_1795	C-A---A----C-----AAAC---AAC------AGAAG---CAACTGCCAGTGCGCAGCTGCCTGTGCCGCTTGCCGCAACA---ACAACAGCAAACGCGAGAGGCAACGGCAGCAGCA--------------GCAGC---AC---CCGCC-----------------CACT---CCAAGGT--------------ATCAAGCTCCGTTTCGTCCAG
droEre2	scaffold_4845:11355711-11355845 +	der_1520	T-A---G----C-----AAGC---AAC------AGAAG---CAACTGCCAGTGCGCAGCTGCCTGTGCCGCTTGCCGCAACA---ACAACAGCAAACGCGAGAGGCAACGGCAGCAGCA--------------GCAGC---AC---CCGCC-----------------CACT---CCAAGGT--------------ATCCAC------C---TCGCGG
dp5	3:9802172-9802321 -	dps_3826	C-A---GT---AGC-----AACACC-AAC------AGCAG---CAGCTGCCCAGTGCGCAGCTGCCTGTGCCGCTTGCCGCCAC------AACAGCAAACGACAGAGGCAACGGCAGC------C---ACGCCAGTAGCAGC---ACCACGTAGAACCA------CAACCAC--------------ACTGGT------CTCATCCGC
droPer2	scaffold_4:5118146-5118304 -	dpe_2480	C-A---GT---AGAC-----AACACC-AAC------AGCAG---CAGCTGCCCAGTGCGCAGCTGCCTGTGCCGCTTGCCGCCAC------AACAGCAAACGACAGAGGCAACGGCAGC------C---ACGCCAGTAGCAGC---ACCACGTAGAACCA------CAAACACAGT---CGTCTC--------------ATCCGC------CCACTCCGC
droWil2	scf2_1100000004510:1465991-1466101 +	dwi_5424	T-A---GC---AGTTGGTCCAAT---AAC------A----------------------------AGCTGTTGCCCTGCCACAACAAAAACAACAGCAACACACAGAGGCAACAAGTTGTGGA---------ACTGC---CG---TCACC---CCATCATC----C-CAA-----------------------------TCCACTAA
droVir3	scaffold_12875:18068736-18068879 -		ACAACAAC---CAC-----A------ACG------AGCAG---CAGCTGCTCAGTGCGCAGCTGCCTGTGCCGCTGTGAACTTGTC-----------GACAGAGGCAACGGCAGCAGCA--------ACGCCAGCAGCAGC---TT---CCAGA-----------------TACT---CCAATACAGCAACAGCAGAAACCTCCGCCTC---GG-
droMoj3	scaffold_6496:11689370-11689486 -		ACAACAAC---------AAC---AAC------AGCAG---CAGCTGCTCAGTGCGCAGCTGCCTGTGCCGCTGTGAACTTGTC-----------GACAGAGGCAACGGCAGCGCA--------ACGCCAGCAGCAGC---TT---CCAGA-----------------TAC---------------------------TCCTCCAA
droGri2	scaffold_15245:4197257-4197401 -	dgr_473	C-A---GA---AACCAACAAACACCAAC------AGCAG---CAGCTGCCCAGTGCGCAGCTGCCTGTGCCGCTGTGAACTTGTC-----------GACAGAGGCAACGGCAGCGGCAGCA--------ACGCCAGCAGCTGC---TT---CCAGC---ACATCATC-A---TCATCATCCAA-----------------TCCATCAA

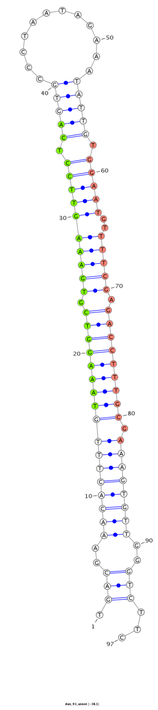
Generated: 09/08/2015 at 07:47 PM

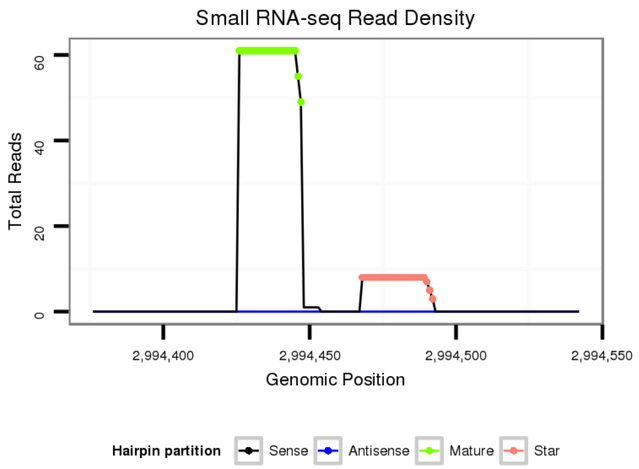
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	7

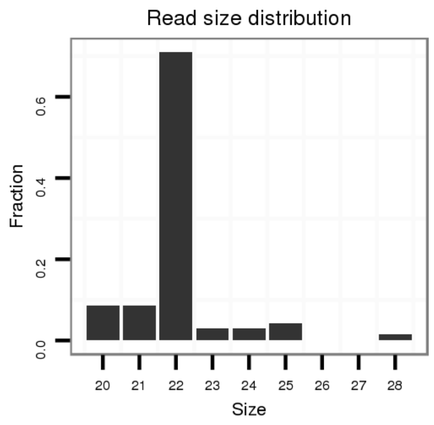
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_93	**scaffold_13117:2994426-2994492 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

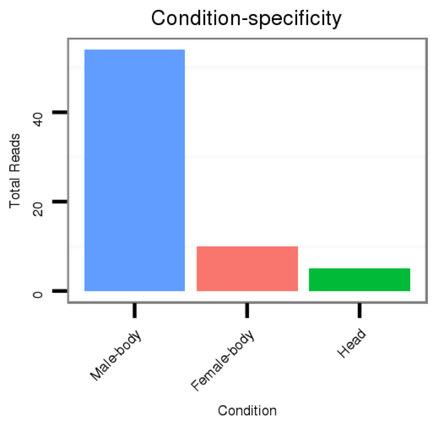
Legend: mature star mismatch in alignment mismatch in read

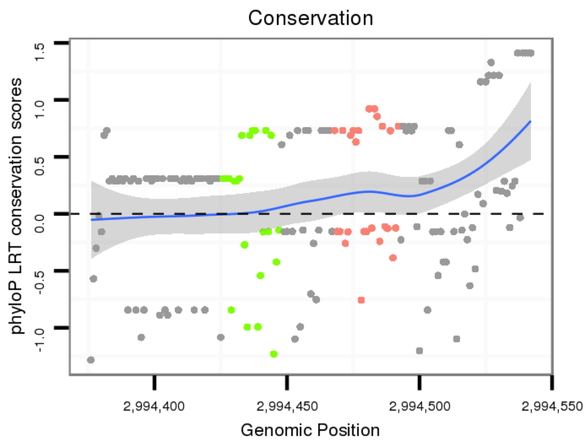
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTTTTGTGACGAGAGGACGGAAAGAATAGAATTCGTGACGAAACACTTTGTAAAGGTCGTGAAAGTTCCTCAGTGCCCTAATAGAAATATTGTGGAATGTTTTCGAGACCTTTGCGAAAGTGTTGGGTCTTCGCCATCGGAAAGTTATTAGTGGCTCTCGGATTAAT **********.(((..(((((((((((((((((.((((((((((.(((((.....)))))).)))))..)))))).)))))))))).))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	M044 female body	V055 head	M058 embryo	V106 head	V039 embryo
..........TAAAGGTCGTGAAAGTTCCTCA..........	22	0	1	48.00	48	41	3	4	0	0	0
..........TAAAGGTCGTGAAAGTTCCT..........	20	0	1	6.00	6	5	0	1	0	0	0
..........TAAAGGTCGTGAAAGTTCCTC..........	21	0	1	6.00	6	6	0	0	0	0	0
..........TGGAATGTTTTCGAGACCTTTGCGA..........	25	0	1	3.00	3	0	3	0	0	0	0
..........TGGAATGTTTTCGAGACCTTTGCG..........	24	0	1	2.00	2	1	1	0	0	0	0
..........TGGAATGTTTTCGAGACCTTTGC..........	23	0	1	2.00	2	0	2	0	0	0	0
..........TAAAGGTCGTGAAAGTTCCTCT..........	22	1	1	1.00	1	1	0	0	0	0	0
..........TGGAATGTTTTCGAGACCTTTG..........	22	0	1	1.00	1	0	1	0	0	0	0
..........TAAAGGTCGTGAAAGTTCCTCAAC..........	24	2	1	1.00	1	1	0	0	0	0	0
..........TAAAGGTCGTGAAAGTTCCTCAGTGCCC..........	28	0	1	1.00	1	1	0	0	0	0	0
..........TAAAGGTCGTGAAAGTTCCTCAG..........	23	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

CAAAACACTGCTCTCCTGCCTTTCTTATCTTAAGCACTGCTTTGTGAAACATTTCCAGCACTTTCAAGGAGTCACGGGATTATCTTTATAACACCTTACAAAAGCTCTGGAAACGCTTTCACAACCCAGAAGCGGTAGCCTTTCAATAATCACCGAGAGCCTAATTA **********.(((..(((((((((((((((((.((((((((((.(((((.....)))))).)))))..)))))).)))))))))).))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13117:2994376-2994542 +	dan_93	GTTTTGTGACGAGAG---GACGGAAAGAATAGAATTCGTGAC---GAAACACTTTGTAAAGGTCGTGAAAGTTCCTCAGTGCC-CTAATAG-AAATATTGTGGAATGTTTTCG--------------------AGACCTTTGCGAAAGTGTTGGGTCTTCGCCATCGGAAAGTTATTAGTGGCTCTCGGATTAAT
droBip1	scf7180000396696:140582-140752 -		ATTTTGTGACGAGAAGTTGATGTGAAGAAAAATATTTGTGACTTAAAAATACTTTTATAAGGGTCGGAACATTCCGCA-TGCCGTTCATAA-AATATTGTGGAATGT-TACG--------------------AGACCTTTGCGAAAGTGTTTGGCGTTTGCCATCA-AAAGTTATTAGTGGCTCGCGGATTAAT
droFic1	scf7180000453926:397083-397100 -		A--GTGTACGTGTGAAGTAAT
droBia1	scf7180000302432:101620-101626 +		G--AATAAT
droTak1	scf7180000415769:352777-352894 -		TGGAAGT---CTTGAAACATTCAGGGAAACT-ATAGTAAGCAGTATTAATAAACAGTTTTTAATGCACACGCAGTCATTTTGAAAC--------------------AACAGGATTTGTGTTCTTCAGTGGCGTGTAAAATAAT
droEug1	scf7180000408193:46357-46416 +		TATA--TAATCATTTTGAGAGCATCAGGAACAGTGTCA--------------------GCCTTTCAGTGGCGTGGGAAAATAAT
dm3	chrX:21442760-21442786 -		A--AAGCATTCAGTGGCGTGTGAAATAAT
droSim2	x:20141185-20141211 -		A--AAGCATTCAGTGGCGTGTGAAATAAT
droSec2	scaffold_8:3725489-3725515 -		A--AAGCATTCAGTGGCGTGTGAAATAAT
droYak3	X:20580479-20580505 -		A--AAGCATTCAGTGGCGTGTGAAATAAT
droEre2	scaffold_4690:17924206-17924223 -		A--GTGGCGTGTGAAATAAT

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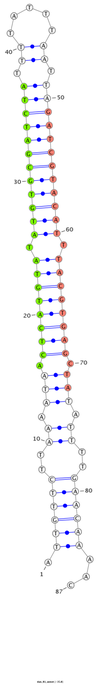
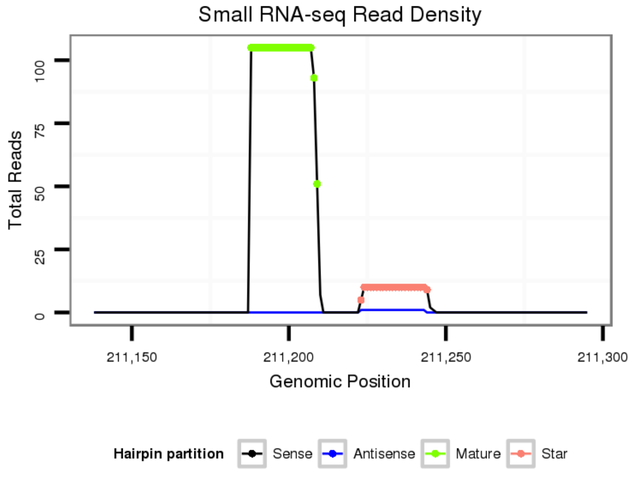
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

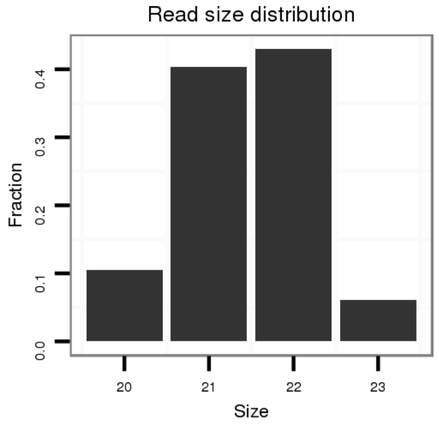
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_81	**scaffold_13335:211188-211245 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

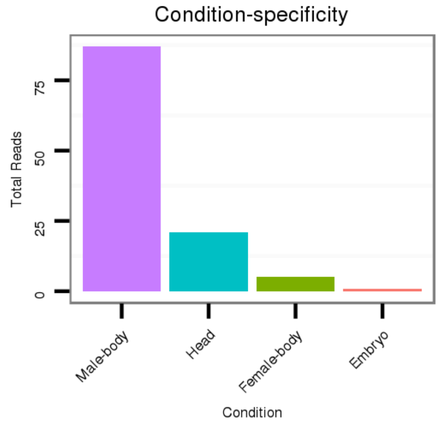
Legend: mature star mismatch in alignment mismatch in read

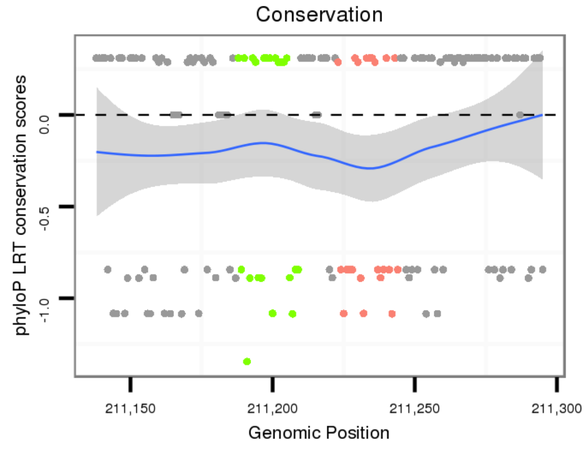
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AATTGTGAAATATAAATATATTCTTCAAATCGGAGATTGTTCTTAAAATAACTCATGTATATGTGCGATCTATTTTATTTAATTAGATCGTACATTTACGTGAGCTATATTTTGAACAAAACTTAACAACAAATTTAATTCAACAATATTAAATTTTC **********.((((((..((.(((.(((((((((.((((((((((((.((.....)).)))))))))))).)))))))).)))).))..))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V055 head	M044 female body	M058 embryo	V106 head	V039 embryo
....ACTCATGTATATGTGCGATCTA....	22	0	1	44.00	44	35	6	1	0	2	0
....ACTCATGTATATGTGCGATCT....	21	0	1	42.00	42	31	9	1	1	0	0
....ACTCATGTATATGTGCGATC....	20	0	1	12.00	12	11	1	0	0	0	0
....ACTCATGTATATGTGCGATCTAT....	23	0	1	7.00	7	5	1	1	0	0	0
....GATCGTACATTTACGTGAGCTA....	22	0	1	4.00	4	3	0	1	0	0	0
....ACTCATGTATATGTGCGATCTAA....	23	1	1	4.00	4	4	0	0	0	0	0
....ATCGTACATTTACGTGAGCTA....	21	0	1	3.00	3	2	1	0	0	0	0
....ATCGTACATTTACGTGAGCTATA....	23	0	1	1.00	1	0	1	0	0	0	0
....ACTCATGTATATGTGCGATCTATA....	24	1	1	1.00	1	1	0	0	0	0	0
....ATCGTACATTTACGTGAGCTAT....	22	0	1	1.00	1	0	1	0	0	0	0
....ACTCATGTATATGTGCGATCC....	21	1	1	1.00	1	1	0	0	0	0	0
....GATCGTACATTTACGTGAGCT....	21	0	1	1.00	1	0	0	1	0	0	0
....ATGTATATGTGCGATCTAAA....	20	2	2	0.50	1	1	0	0	0	0	0

Anti-sense strand reads

TTAACACTTTATATTTATATAAGAAGTTTAGCCTCTAACAAGAATTTTATTGAGTACATATACACGCTAGATAAAATAAATTAATCTAGCATGTAAATGCACTCGATATAAAACTTGTTTTGAATTGTTGTTTAAATTAAGTTGTTATAATTTAAAAG **********.((((((..((.(((.(((((((((.((((((((((((.((.....)).)))))))))))).)))))))).)))).))..))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	M058 embryo
....CTAGCATGTAAATGCACTCGA....	21	0	1	1.00	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13335:211138-211295 +	dan_81	AATTGTGAAATATAAATATATTCTTCAAATCGGAGATTGTTCTTAAAATAACTCATGTATATGTGCGATCTATTTTATTTAATTAGATCGTACATTTACGTGAGCTAT--------------ATTTTGAACAAAACTTAACAACAAATTTAATTCAACAATATTAAATTTTC
droBip1	scf7180000396431:1453190-1453352 +		AATTAATTCAAGTTAATTGGCATCTGCC---AAGAGAGTGCTCA----GTTATTGTTGATTATTTGCGAAACGTTTTA--TAACAAGGGTACACTGTTACAAAAAATGTAAAACATTTAAATTAACACTAAAAAAGCCCTAACAACAAATTTAACTTATTAACAT-AATCTTTT

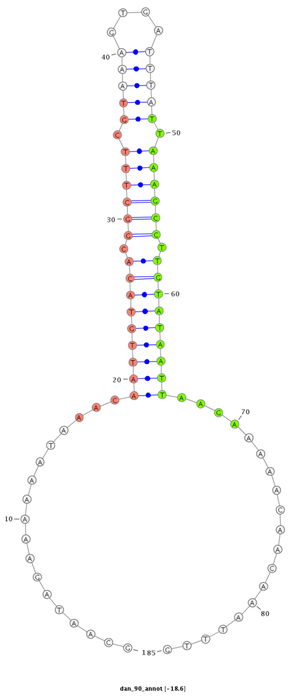
Generated: 09/08/2015 at 07:12 PM

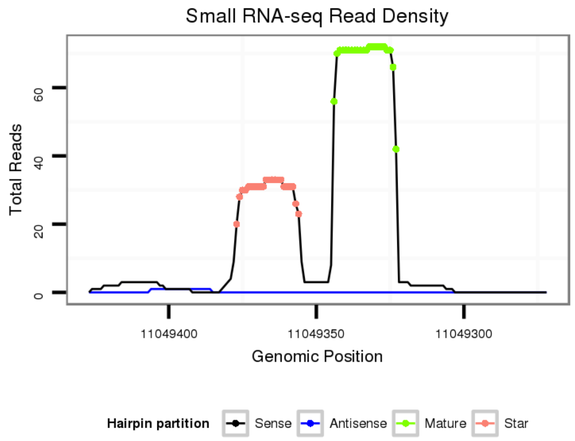
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

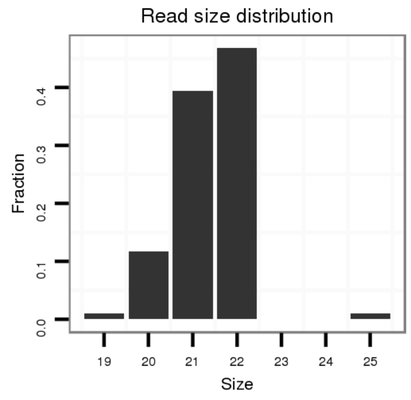
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_90	**scaffold_13340:11049322-11049377 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

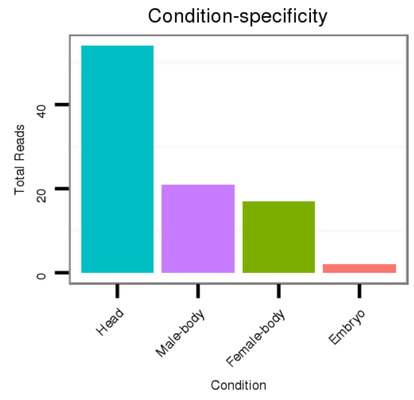
Legend: mature star mismatch in alignment mismatch in read

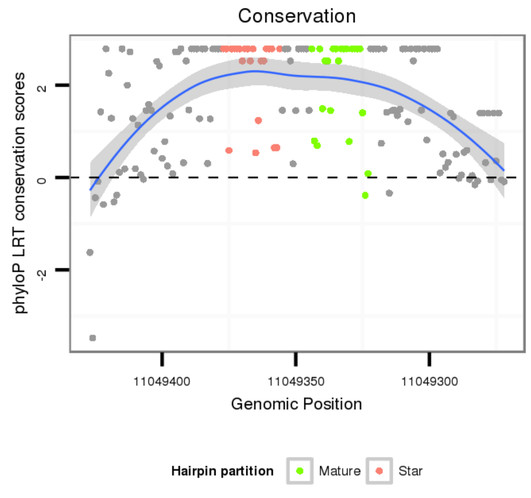
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTTGAAAAAGAAATCAACCCTCAACCAACCACAAAGCAATAGAAAAAATAAACAATTGTACACGGCTTTCGTAAAGTGATTTATTAAAGCCTTGTATAATTAAGAAAAACAACAAATTTGTGTTTTTATTTTCCATTAGAATCGCAATCTAATTAC	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	M044 female body	M058 embryo	V055 head	V039 embryo
**********.....((((((((.(((((((.(((((....))))).)))))).)))))))).....**********											
.....TTAAAGCCTTGTATAATTAAGA.....	22	0	1	30.00	30	19	10	0	0	1	0
.....TTAAAGCCTTGTATAATTAAG.....	21	0	1	17.00	17	13	1	3	0	0	0
.....TAAAGCCTTGTATAATTAAGA.....	21	0	1	8.00	8	6	1	0	0	1	0
.....AACAATTGTACACGGCTTTCGT.....	22	0	1	7.00	7	0	2	4	0	0	1
.....TTAAAGCCTTGTATAATTAAGT.....	22	1	1	5.00	5	3	1	0	0	1	0
.....TAAAGCCTTGTATAATTAAG.....	20	0	1	5.00	5	5	0	0	0	0	0
.....ATTAAAGCCTTGTATAATTAA.....	21	0	1	4.00	4	3	0	0	0	1	0
.....ACAATTGTACACGGCTTTCGTA.....	22	0	1	4.00	4	0	1	2	0	1	0
.....ACAATTGTACACGGCTTTCGT.....	21	0	1	4.00	4	0	2	2	0	0	0
.....AAACAATTGTACACGGCTTTC.....	21	0	1	3.00	3	0	0	0	3	0	0
.....AACAATTGTACACGGCTTTCG.....	21	0	1	2.00	2	0	1	0	0	1	0
.....AACAATTGTACACGGCTTTC.....	20	0	1	2.00	2	0	0	1	1	0	0
.....ATTAAAGCCTTGTATAATTAAG.....	22	0	1	2.00	2	0	1	1	0	0	0
.....AACAATTGTACACGGCTTTCGTT.....	23	1	1	1.00	1	0	0	1	0	0	0
.....CACGGCTTTCGTAAAGTGATTT.....	22	0	1	1.00	1	0	1	0	0	0	0
.....AAAGCCTTGTATAATTAAGA.....	20	0	1	1.00	1	1	0	0	0	0	0
..........AATCAACCCTCAACCAACCACAAA.....	24	0	1	1.00	1	0	0	0	1	0	0
.....TAAACAATTGTACACGGCTTTCGT.....	24	0	1	1.00	1	0	1	0	0	0	0
.....CACGGCTTTCGTAAAGTGATT.....	21	0	1	1.00	1	0	0	1	0	0	0
.....ATAATTAAGAAAAACAACAAATTTGTGTT.....	29	0	1	1.00	1	0	1	0	0	0	0
.....AAACAATTGTACACGGCTTTCGT.....	23	0	1	1.00	1	0	0	1	0	0	0
.....TATTAAAGCCTTGTATAATT.....	20	0	1	1.00	1	1	0	0	0	0	0
.....AACAATTGTACACGGCTTTCGC.....	22	1	1	1.00	1	0	0	0	1	0	0
.....ATAAACAATTGTACACGGC.....	19	0	1	1.00	1	0	0	0	1	0	0
.TTGAAAAAGAAATCAACCCTCAACC.....	25	0	1	1.00	1	0	0	0	1	0	0
.....AAATAAACAATTGTACACGGC.....	21	0	1	1.00	1	0	0	0	1	0	0
.....TAAAGCCTTGTATAATTAAGTT.....	22	2	1	1.00	1	1	0	0	0	0	0
.....CAATTGTACACGGCTTTCGT.....	20	0	1	1.00	1	0	0	1	0	0	0
.....ATTGTACACGGCTTTCGTA.....	19	0	1	1.00	1	0	0	1	0	0	0
.....ATAATTAAGAAAAACAACAAATTTGT.....	26	0	1	1.00	1	0	0	0	1	0	0
.....TAAAGCCTTGTATAATTAAGT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TTAAAGCCTTGTATAATTAA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TTAAAGCCTTGTATAATTAAC.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TAAAGCCTTGTATAATTAAGAAAAA.....	25	0	1	1.00	1	0	0	1	0	0	0
.....AAACAATTGTACACGGCTTTCG.....	22	0	1	1.00	1	0	1	0	0	0	0
.....AATAAACAATTGTACACGGCTTTC.....	24	0	1	1.00	1	0	0	0	1	0	0
.....AAAAGAAATCAACCCTCAA.....	19	0	1	1.00	1	0	0	1	0	0	0
.....TAAAGCCTTGTATAATTAAGAT.....	22	1	1	1.00	1	1	0	0	0	0	0
.....CAATTGTACACGGCTTTCGTA.....	21	0	1	1.00	1	0	0	1	0	0	0
.....GTAAAGTGATTTATTAAAGCCTTGT.....	25	0	1	1.00	1	0	1	0	0	0	0
.....GATTTATTAAAGCCTTGC.....	18	1	2	0.50	1	0	0	0	1	0	0

Anti-sense strand reads

AAACTTTTTCTTTAGTTGGGAGTTGGTTGGTGTTTCGTTATCTTTTTTATTTGTTAACATGTGCCGAAAGCATTTCACTAAATAATTTCGGAACATATTAATTCTTTTTGTTGTTTAAACACAAAAATAAAAGGTAATCTTAGCGTTAGATTAATG	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V039 embryo
**********.....((((((((.(((((((.(((((....))))).)))))).)))))))).....**********							
.....GTTGGTTGGTGTTTCGTTATC.....	21	0	1	1.00	1	1	0

Show Alignment With Reads

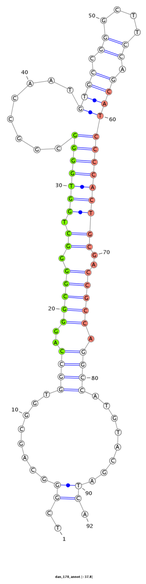
Re-alignment of all predicted orthologs

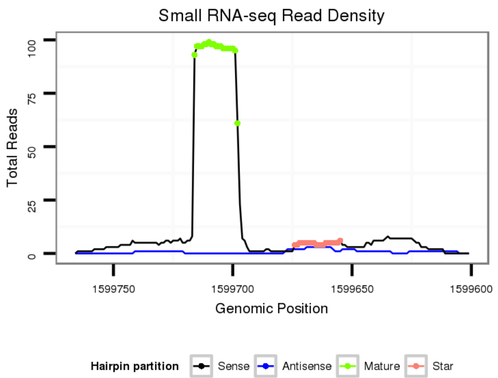
Species	Coordinate	ID	Alignment
droAna3	scaffold_13340:11049272-11049427 -	dan_90	TTT------GAAAAAG--------AAA-TCAA-CC-CTCA--ACC------AACCACAAAGCAATAGAAA----------------AAATAAA-CAATTGTACACGGCTTTCGTAAAGTGATTTATTAAAGCCTTGTATAATTAAGAAAAACAA--------CAAA-TTTGTGTTTTTATTTTCCAT----------TAGAATCGCAATCTAATTAC----------
droBip1	scf7180000396374:34264-34410 +		AA-------AGAA--------A-T---GCCTCA--ACC------AACCACAAAGCAATAGAAA----------------AAATAAA-CAATTGTACACGGCTTTCGTAAAGTGATTTATTAAAGCCTTGTATAATTAACAAAAACAA--------CAAA-TTTGTGTTTTTATTTTCCATAA----------GAATCTGAATCTAATTGC----------
droKik1	scf7180000302247:250347-250529 +		GAA-A-CCCCAGAA--------AACCAA-C-----CAACC------ATCAACAAAACAATAGAAGA-A----A-AAAAACAAAATAAA-CAATTGTACATGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAAAAAAAGAAC---AACCAAAA-TTTGTGTTTTTATTTGCCTTATCACGTACACTTTTTCGTTGGCGATTTTATTTT----------
droFic1	scf7180000454106:2527577-2527750 +		CC-----CCAGAA--------AGCCAA-C-CACCA--ACC------AACCACAAAACAATAGAAA----------AACAAATAA-CAATTGTACACGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACAAAAAAA----ACCTTCCAA-ATTGTGTTTTTATTTGCCTTATCACGTACCATTTTTCGTTTGTAATTTTATTTT----------
droEle1	scf7180000491212:1154179-1154309 +		CCC------AGAA--------AAGCAT-GCACCA--ACC------AGC-----AACAATAAA-----------AAAACAAATAAA-CAATTGTACACGGCTTTCGTAAAGTAATTTATTAAAGCTTTGTATAATTAACAAAAAAGA---ACCCCAAA-TTTGTGTTTTTATTT-----------------------

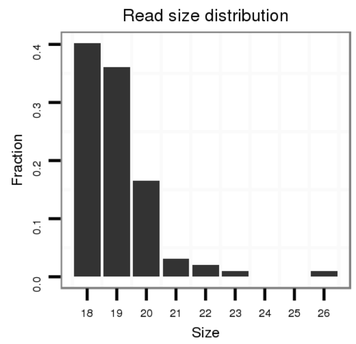
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_170	**scaffold_13335:1599651-1599716 -**	**confident**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

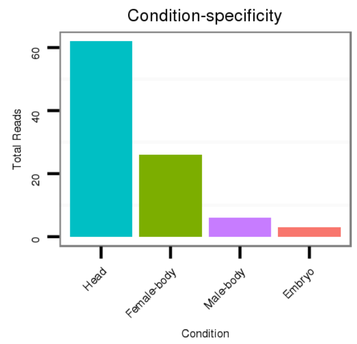
Legend: mature star mismatch in alignment mismatch in read

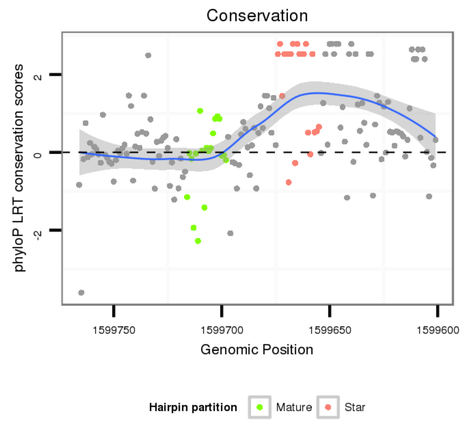
Predicted structure











Show Alternate Folds

Flybase annotation

CDS [Dana\GF19373-cds]; intron [Dana\GF19373-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAATGAGCAATCAGCCTCGGGGATCGCGGGACAGCTCGGGCAGCGGTGGCCAGGGCGGGGCTGGTGGGGCGGCCAATGTGCCGGGCTTCCAGCATCCCCACTGCGACCGCCAGGCCATGTACGATCAGCCAGTTCGCAAGCAGAGGACCAAGGGAGGTAAGTTTGG	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	V105 male body	M058 embryo	V039 embryo	V055 head
**********..((.....((((..(((((.((.(((((((.....((((.((....)).)))))))))))..)))))..)))).....)).**********											
.....CAGGGCGGGGCTGGTGGGG.....	19	0	1	34.00	34	24	7	2	1	0	0
.....CAGGGCGGGGCTGGTGGG.....	18	0	1	34.00	34	26	5	3	0	0	0
.....CAGGGCGGGGCTGGTGGGGC.....	20	0	1	14.00	14	7	6	1	0	0	0
.....AGGGCGGGGCTGGTGGGG.....	18	0	1	4.00	4	2	2	0	0	0	0
.....CAGGGCGGGGCTGGTGGGGCGGA.....	23	1	1	2.00	2	1	1	0	0	0	0
.....CGCGGGACAGCTCGGGCAGCG.....	21	0	1	2.00	2	0	1	1	0	0	0
.....CATCCCCACTGCGACCGCCA.....	20	0	1	2.00	2	2	0	0	0	0	0
.....GATCAGCCAGTTCGCAAGCAGAGGAC.....	26	0	1	1.00	1	1	0	0	0	0	0
.....TCCCCACTGCGACCGCCAGGC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....GGGGCTGGTGGGGCGGCCAATGTGCC.....	26	0	1	1.00	1	0	1	0	0	0	0
.....CAGGGCGGGGCTGGTGGGGA.....	20	1	1	1.00	1	1	0	0	0	0	0
.....AGGGCGGGGCTGGTGGGGC.....	19	0	1	1.00	1	0	1	0	0	0	0
.....AGCGGTGGCCAGGGCGGG.....	18	0	1	1.00	1	1	0	0	0	0	0
.....AGGCCATGTACGATCAGCCAG.....	21	0	1	1.00	1	0	1	0	0	0	0
.....GTTCGCAAGCAGAGGACCAAGGGA.....	24	0	1	1.00	1	0	0	1	0	0	0
.....GGCCAGGGCGGGGCTGGTGGGGCGGC.....	26	0	1	1.00	1	0	0	0	1	0	0
.....GCGGGGCTGGTGGGGCGG.....	18	0	1	1.00	1	1	0	0	0	0	0
.....CATCCCCACTGCGACCGCCAGG.....	22	0	1	1.00	1	0	1	0	0	0	0
.....CAGGGCGGGGCTGGTGGGGCGGC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....GGGATCGCGGGACAGCTCGGG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CGGGCAGCGGTGGCCAGGGCG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....AATCAGCCTCGGGGATCGC.....	19	0	1	1.00	1	0	0	0	1	0	0
.....CAGCCAGTTCGCAAGCAGAG.....	20	0	1	1.00	1	0	1	0	0	0	0
.....GATCAGCCAGTTCGCAAGCAGAG.....	23	0	1	1.00	1	0	1	0	0	0	0
.....GGCAGCGGTGGCCAGGGCGGGGCT.....	24	0	1	1.00	1	0	1	0	0	0	0
.....CAGGGCGGGGCTGGTGGGA.....	19	1	1	1.00	1	0	0	0	0	1	0
.....CCAGGGCGGGGCTGGTGGGGC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....CAGGGCGGGGCTGGTGGGGCG.....	21	0	1	1.00	1	0	0	0	0	1	0
.....AGTTCGCAAGCAGAGGACCAAGGGA.....	25	0	1	1.00	1	0	0	0	1	0	0
.....CAGGGCGGGGCTGGTGGGGCGGCA.....	24	1	1	1.00	1	1	0	0	0	0	0
.....CCAGGGCGGGGCTGGTGGGGCGG.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GGTGGCCAGGGCGGGGCTGGTGG.....	23	0	1	1.00	1	1	0	0	0	0	0
.....CATGTACGATCAGCCAGTTCGCAAGCA.....	27	0	1	1.00	1	0	0	0	1	0	0
.....CAGGGCGGGGCTGGTGGGGCGG.....	22	0	1	1.00	1	0	1	0	0	0	0
.....ACCGCCAGGCCATGTACGA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....CCGGGCTTCCAGCATCCCCAC.....	21	0	1	1.00	1	0	0	0	1	0	0
.....CAGGGCGGGGCTGGTGGGGCA.....	21	1	1	1.00	1	1	0	0	0	0	0
.....AAGCAGAGGACCAAGGGAGGC.....	21	1	1	1.00	1	0	0	0	1	0	0
.AATGAGCAATCAGCCTCGGGGATC.....	24	0	1	1.00	1	0	0	1	0	0	0
.....GGGACAGCTCGGGCAGCGGTGGCC.....	24	0	1	1.00	1	0	0	0	1	0	0
.....GCCTCGGGGATCGCGGGACAGC.....	22	0	1	1.00	1	0	1	0	0	0	0
.....CAGCCAGTTCGCAAGCAG.....	18	0	1	1.00	1	0	1	0	0	0	0
.....AGGGCGGGGCTGGTGGGGT.....	19	1	2	0.50	1	0	0	1	0	0	0

Anti-sense strand reads

TTTACTCGTTAGTCGGAGCCCCTAGCGCCCTGTCGAGCCCGTCGCCACCGGTCCCGCCCCGACCACCCCGCCGGTTACACGGCCCGAAGGTCGTAGGGGTGACGCTGGCGGTCCGGTACATGCTAGTCGGTCAAGCGTTCGTCTCCTGGTTCCCTCCATTCAAACC	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V055 head	V039 embryo	M058 embryo
**********..((.....((((..(((((.((.(((((((.....((((.((....)).)))))))))))..)))))..)))).....)).**********									
.....GGTGACGCTGGCGGTCCGGTA.....	21	0	1	1.00	1	1	0	0	0
.....GTCGTAGGGGTGACGCTGG.....	19	0	1	1.00	1	1	0	0	0
.....CGCCCTGTCGAGCCCGTCGCC.....	21	0	1	1.00	1	1	0	0	0
.....GTCGTAGGGGTGACGCTGGC.....	21	0	1	1.00	1	1	0	0	0
.....CCGGTACATGCTAGTCGGTCA.....	21	0	1	1.00	1	1	0	0	0
.....GTCTCCTGGTTCCCTCCATTC.....	21	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13335:1599601-1599766 -	dan_170	AAA--TGA----------G----------CAA---TCAGCCTCG----------GGGATCGCGGGA----------CAGCTCGGGCAGCGGTGGCCAGGGCGGGG------C---------TG----------GTGGGGC---GGCCAAT---GTGCCGGGCTTCCAGCATCCCCACTGCGACCGCCAGGCCATGTACGATCAGCCA---GTTCGCAAGCAGAGGACCAAGGGAGGTAAGTTTGG
droBip1	scf7180000395454:68618-68782 +		AAA--TGA----------G----------CAA---TCAGCCGCG----------AGGTTCGAGGGA----------CAGTAGCGGCAGCTCCGGTCCAACGGGTG------C---------TG----------GTGGGGC---GGCCAAT---GTGCCGGGCTTCCAGCATCCCCACTGCGATGGCGACAGCCATGTACGATCAGCCA---GTGCGCAAGCAGAGGACCAAGGGAGGTAAGTTGGG
droKik1	scf7180000302696:1733044-1733204 +		CCA--TGA----------G----------CTCCGCTGCAGCTTG---GACGTC----------AASATGGCGGGA----------CA----------CAGTCCGG----GG---G------C---AGCAC---CT----------CCGG----GGGGGCGAGGGT---GTGCCGCCTTCAAGCATCCCCACTGCGACCGCCAGGCCATGTACGCCAGCCG---GTGCGACAGATCAGGAACAAGGAGGTGAG-----
droFic1	scf7180000454077:1850378-1850544 -		CAA--TGA----------G----------CTCCACTGGAAGAGCG----------AGGATCGCGCGA----------TAGCTGTGGAAACCCATGGCC------G----------CA----------CG---GGG---TGGGGGG---GTGCGTCCTTCCAGCATCCCCATTGCGACCGCAGGCTATGTACGACAACCG---GTGCGAAAATGAGGACCAAAGGAGGTGAG-----
droEle1	scf7180000491006:1659097-1659266 +		ACA--TGA----------G----------TTC---GGGAGTGCG----------AGGATCGCGCGA----------CAGTTCTGGAAGTTCAGGGTCTCG----GG---G----------A------ATCAGC----TGGAACGG----CGG---GGGC---GGGCGGT---CGATCCCTTCCAGCATCGTCACTGCGACCGGGCGGCCATGTACGACAACCG---GTGCGAAGATGAGGACCAAACGAGGTGAG-----
droRho1	scf7180000779675:15537-15697 -		CCA--TGA----------G----------CTC---GGGAGACGG----------AGGATCGCGCGA----------TAGTTGTGGAAGTCCAGGCGCGCGTGGAG------C---------CG----------CGG---GGGT---TGGCGGT---CGCGCCCCTTCCAGCATCCCCATTGCGACCGGGCTGCCATGTACGACAACCG---GTGCGAAGATGAGGACCAAGGAGGTGAG-----
droBia1	scf7180000302421:2077801-2077976 +		CGA--TGA----------G----------CTC---TGGAGAGCG----------AGGATCGCGCGA----------CAGCGCTGGAAACCAGTGGCGCGCGGG------C---------TG------CTG---------GAACGGGCTTGGG---GGCGGGCTCGAGT---GCGCCCCTTCCAGCATCGCATTGCGACCGGGCGGCCATGTACGACAGCCG---GTGCGAAGATAAGGACCAAGGAGGTGAG-----
droTak1	scf7180000415141:219447-219608 +		ATG--TC----------------------------GGGTCAAAG----------AGGATCGCGCGA----------CAGCGGTGGAAGTCCAGGGCGCCG----GG---G------C---TCAG------TGC----------AACCG---GGAA---GGTAGT---GCACGCCCTTCCAGCATCCCCACTGCGACCGGGCGGCCATGTACGACAGCCG---GTGCGAAGATGAGGACCAAGGAGGTGAG-----
droEug1	scf7180000409064:217890-218059 +		CAA--TGA----------G----------CTCGGCGGGACAGCG----------AGGATCGCGCGA----------CAGCTATGGAAGCCTGGGGCG-------G------G---GGAG---CTG-GGCAATCTGGAA----------CGGC---GGGAAGT---GGTACCCCTTCCAGCATCCCCATTGCGACCGGCGGCCATGTACGACAGCCG---GTGCGAAGATGAGGACCAAGGAGGTGAG-----
dm3	chrX:8137926-8138102 +		AACTATGA----------A----------CTTGACGGGACAGCG----------AGGATCACGCGA----------CAGTATTGGAGCTACGGT----------G------G---GGAATGCTCCAGC----CG------GATC-CGGTGC----GGCGCACCAGCACCTTCCAGCATCGACATGCGAGAGGCGGCCATGTACGCCAACCG---GTGCGAAGATGAGCACCAAGGAGGTGAGCATGG
droSim2	x:7709596-7709770 +		CGA--TGA----------A----------CTCGACGGGAAAGCG----------AGGATCACGCGA----------CAGTATTGGAGCTCCGGT----------G------G---GGAGTGCTCCAGC----CG------GATC-CGGTGC----GGCGCACCAGCACCTTCCAGCATCGACATGCGAGAGGCGGCCATGTACGCCAACCG---GTGCGAAGATGAGCAACAAGGAGGTGAGCGTGG
droSec2	scaffold_44:229019-229195 +		AACGATGA----------A----------CTCGACGGGCGCAGCG----------AGGATCACGCGA----------CAGTATTGGAGCTCCCGGT----------G------G---GGAGTGCTCCAGC----CG------GATC-CGGTGC----GGCGCACCAGCACCTTCCAGCATCGACATGCGAGAGGCGGCCATGTACGCCAACCG---GTGCGAAGATGAGCAACAAGGAGGTGAGCGTGG
droYak3	X:13176092-13176261 -		CGA--TGA----------A----------CTCGACGGGAAAGCG----------AGGATCACGCGA----------CAGGAGTGGAGCTCCCGGTGCT-------G------G---GGGGCTTCAGG----TG------GATC-CGGTGG----GGGGCACCGCGACCTTCCAGCATCGACATGCGAGAGGAGCGGCATGTACGCCAACCG---GTGCGAAGATGAGCACCAAGGAGGTGAGCGTGG
droEre2	scaffold_4690:10504692-10504866 +		CCA--TGA----------A----------CTCGCCGGGGCAGCG----------AGAGTCACGCGA----------CAGCAGTGGAACTCCCAGT----------G------G---GGGGTTCCTCAAT----AG------GATC-TAGTGG----GGGGTGCAACAGCACCTTCCAGCATCCACATGCGAGAGACGGCCATGTACGCCAGCCG---GTGCGAAAGCTGAGCACCAAGGAGGTGAGCGTGG
dp5	XL_group3a:1965381-1965560 -		AAC--TCTAT----------A----------CACGA-TGCAGAGGA----------ATCGTCAGGGAAATCACAAATGACTGATACGAAGGATTCTCCAAATATGGCGGTATAGG----------
droPer2	scaffold_11:2713563-2713742 +		AAC--TCTAT----------A----------CACGA-TGCAGAGGA----------ATCGTCAGGGAAATCACAAATGACCGATACGAAGGATTCTCCAAATATGGCGGTATAGG----------
droWil2	scf2_1100000004909:12001882-12002069 -		AGT--AAA----------G----------GAA-GCGGATTAG---GGT----------CCCAGAGCCGTGGCTCGGATGA----------CAGCGGCAATAGCCTAGCAACAGG------GGAGGAGGTGTTGGTGTAG----------TTC---AACCAAT---GTACGCCCTTTACCATCGACATTGCGATGGCGACGCATACCATGTACGCTCAGCCG---GCACGAATGTTTAGGCGTACCAGAGGTGAGTACGA
droVir3	scaffold_12928:1253311-1253490 -		AGA--CGA----------A----------CTTCGC---AATCAGTAACCGCAATCCTGGCAAAACATTGCCACAGGGTCGCAACTCAATCGA----------AAG---CTC-AACCAC----------CGA----TTGTGGCATTAAT---GTGCCGCCTTTAATCACCCATTGCGATAGCGACGGCCATGTATCGACGCCG---GTGCGAAGGTTAACGCACTAGGAGGTAAG-----
droMoj3	scaffold_6473:13736553-13736728 +		TAA--TGC----------A----------ACAAGGGCGCTCGACGTATTCGC---AASAGTCTGGACGCAATCCGGGCAAAACTTTGCAGACCGGCCGCAGCTCGGCGCGA----------AG---GAG-CTC-AACCAC----------CGA----CAGCGGCTTAAT---GTGCCGCCTTTAACATCGCACTGCGATCGCGACGGCCATGTACGAACAGCCG---GTGCGCAAG----------AAGCTCGGAGGTAAGCGT---
droGri2	scaffold_15203:8457790-8457981 +		AAA--TCTAACAACAATGAAGCCAACTAATACTGC----------TGT---CGCAGAGAA----------GGCCACGACCG----------CAGTTCGCGTATCTCCGCGCGA-------G------G---TGG-CTC-GACCAC----------TGC----AACCGGCATCAAT---GTGCGACCGTTTAATCATCCCCACTGCGATAGCGACGGCCATGTATCGACGCCG---GTGCGCAAGATTAAAACACTCGGAGGTAAGCGT---

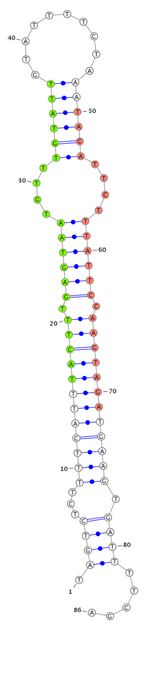
Generated: 09/08/2015 at 07:51 PM

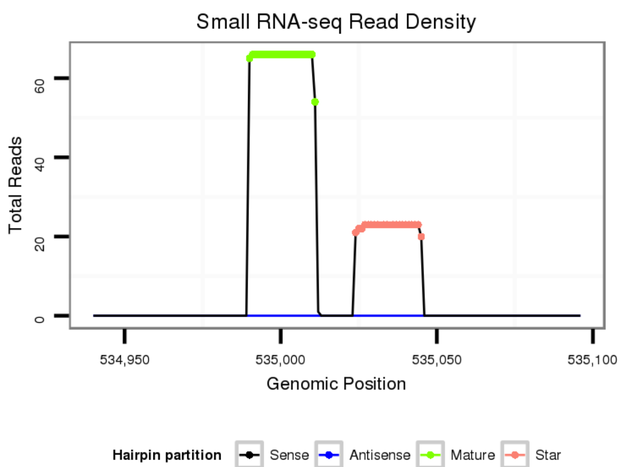
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

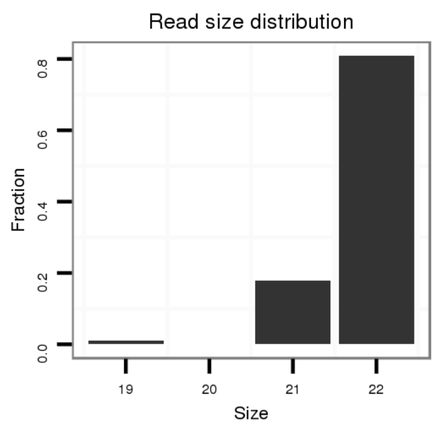
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_86	**scaffold_12903:534990-535046 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

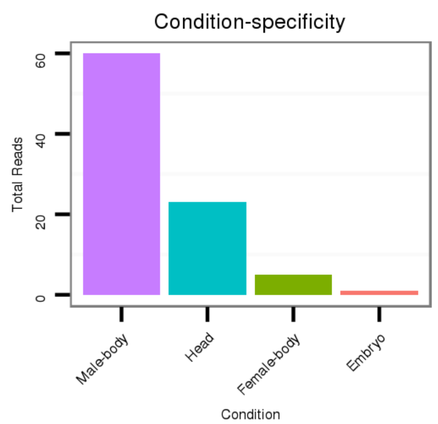
Legend: mature star mismatch in alignment mismatch in read

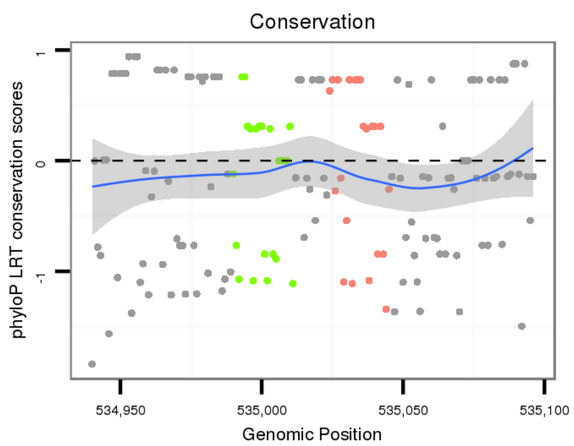
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AATAAATATCATAAAAATAAATATTAAATATTACTTAGTCTCTTTTCATTTACTTTGAGTAATGTTTGTATTGTATTTTCTAAATACATTCTTTATTCCAAGTAGATGAAGTGATTTTCGATCATCAGTTGAAATAAAAAAAATAAATATAACAACT	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V106 head	M044 female body	V055 head	M058 embryo
***********************************.((((...((((((((((((.((((((....((((((..........))))))....))))))..))))))))))))).))))).....***********************************										
.....TACTTTGAGTAATGTTTGTATT.....	22	0	1	53.00	53	41	8	3	1	0
.....TACATTCTTTATTCCAAGTAGA.....	22	0	1	18.00	18	5	11	2	0	0
.....TACTTTGAGTAATGTTTGTAT.....	21	0	1	12.00	12	12	0	0	0	0
.....TACTTTGAGTAATGTTTGTATTA.....	23	1	1	4.00	4	1	3	0	0	0
.....TACATTCTTTATTCCAAGTAG.....	21	0	1	3.00	3	1	2	0	0	0
.....TACTTTGAGTAATGTTTGTATTT.....	23	1	1	3.00	3	2	0	0	1	0
.....TACTTTGAGTAATGTTTGTATTGA.....	24	1	1	1.00	1	0	1	0	0	0
.....TACTTTGAGTAATGTTTGTAA.....	21	1	1	1.00	1	1	0	0	0	0
.....ACTTTGAGTAATGTTTGTATTG.....	22	0	1	1.00	1	1	0	0	0	0
.....ATTCTTTATTCCAAGTAGA.....	19	0	1	1.00	1	0	0	0	0	1
.....ACATTCTTTATTCCAAGTAGA.....	21	0	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

TTATTTATAGTATTTTTATTTATAATTTATAATGAATCAGAGAAAAGTAAATGAAACTCATTACAAACATAACATAAAAGATTTATGTAAGAAATAAGGTTCATCTACTTCACTAAAAGCTAGTAGTCAACTTTATTTTTTTTATTTATATTGTTGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	V039 embryo	V055 head
***********************************.((((...((((((((((((.((((((....((((((..........))))))....))))))..))))))))))))).))))).....***********************************									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:534940-535096 +	dan_86	AATA----AATATCATAAAAATAAAT--------ATTAAATA----------TTACTTAGTCTCTTTTCATTTACTTTGAGTAATGTTTGTATTGTAT---TTTCTAAATAC----ATTCTTTATTCCAAGTAGATGA-AGTGATTTTCGAT----CATCAGTTGAAATA---AAAAAAAT--AAATATAACAACT
droBip1	scf7180000395952:2268-2439 -		CCTA----GGC----------------------ATCTAATAAAATCTTTAAAAATGTGTACAAATACATATTTTCTATTTTGGTGTTTTTTCGTAGGGCA----TAGTACTTTTTTTAA--AC----ATCTTATTGCAAAATGCATTAAAACGGCGTTGACTCAGTGTTAGTGT---TAAAAAATATAATAAATATATAAAATTT
droRho1	scf7180000778091:407267-407291 +		CAGC----AATATAATAACAAT--ATAATAT--
droTak1	scf7180000415843:978318-978480 -		TATTTTTTAACATGATAAGAAAGGCTATTTAATTCTTTACGAATATTTAATAAAAATATTCAATGCTGCATTTAAAC----------CATAT---AGTCTATGTAATCCAAAACTCTAT---------CCCAATTTGGGACCTAATTAAAT---TAGGC---TAATTTATTTATCCAAAACGTAGAATGC
droEre2	scaffold_4690:9432332-9432380 +		AAAA----AAA------AAAAGTGGC---------TTTGACCA----------TTATTTAATCTAGTTTCTCTCAATT----------

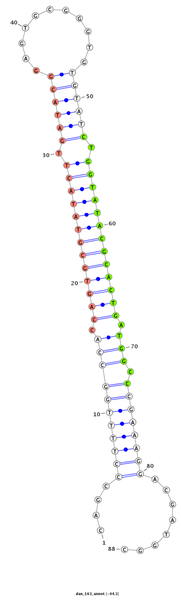
Generated: 09/08/2015 at 08:07:21 PM

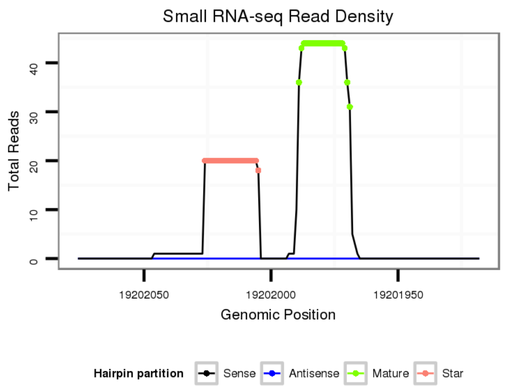
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

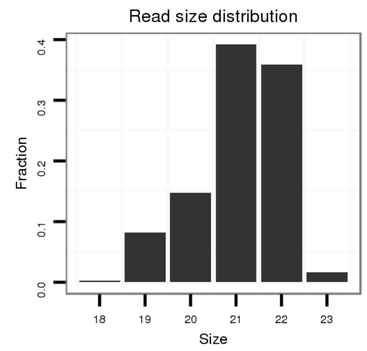
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_163	**scaffold_13340:19201968-19202026 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

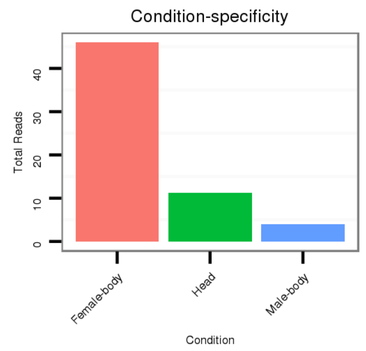
Legend: mature star mismatch in alignment mismatch in read

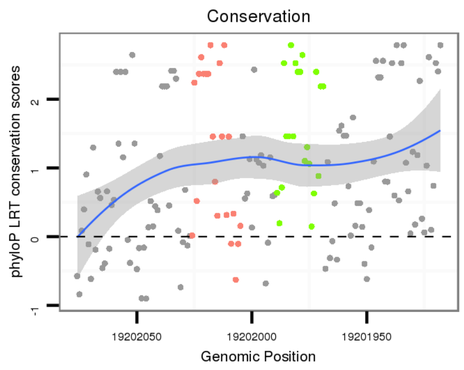
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CACTATGAATGCCAGAGCACCCTCTAAATGTCAAGCAGCCCTTTTGGCCACCAGTGCGTATACTTGATACGGAGTGCGGGTGTGTATCTGGTATACGCACTGATGGCCCGAAAGGACGATGGCGGCGCCGAGGATAACAACGACAGGGAGCCCAGAGCT	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V106 head	V105 male body	V055 head	M058 embryo
**********....((((((((((.(((((((((((.(((((((.....))))))).)))))))))))).)))).))))).....**********										
.....CTGGTATACGCACTGATGGCC.....	21	0	1	20.00	20	17	2	0	1	0
.....CCAGTGCGTATACTTGATACGG.....	22	0	1	18.00	18	10	5	3	0	0
.....TCTGGTATACGCACTGATGG.....	20	0	1	4.00	4	3	1	0	0	0
.....CTGGTATACGCACTGATGG.....	19	0	1	3.00	3	3	0	0	0	0
.....TCTGGTATACGCACTGATGGCC.....	22	0	1	3.00	3	2	0	1	0	0
.....TGGTATACGCACTGATGGCC.....	20	0	1	3.00	3	3	0	0	0	0
.....CTGGTATACGCACTGATGGCCCA.....	22	1	1	2.00	2	2	0	0	0	0
.....CCAGTGCGTATACTTGATACG.....	21	0	1	2.00	2	0	2	0	0	0
.....CTGGTATACGCACTGATGGC.....	20	0	1	2.00	2	2	0	0	0	0
.....TGGTATACGCACTGATGGC.....	19	0	1	2.00	2	2	0	0	0	0
.....TCTGGTATACGCACTGATGGCA.....	22	1	1	1.00	1	1	0	0	0	0
.....CTGGTATACGCACTGATGGCCCG.....	23	0	1	1.00	1	1	0	0	0	0
.....GGTATACGCACTGATGGCCCG.....	21	0	1	1.00	1	1	0	0	0	0
.....TCTGGTATACGCACTGATGGC.....	21	0	1	1.00	1	1	0	0	0	0
.....GTATCTGGTATACGCACTGATG.....	22	0	1	1.00	1	1	0	0	0	0
.....TCAAGCAGCCCTTTTGGCCA.....	20	0	1	1.00	1	1	0	0	0	0
.....TCTGGTATACGCACTGATGGCCC.....	23	0	1	1.00	1	1	0	0	0	0
.....TGGTATACGCACTGATGGCCCGA.....	23	0	1	1.00	1	1	0	0	0	0
.....TGGTATACGCACTGATGGCCC.....	21	0	1	1.00	1	1	0	0	0	0
.....CAGTGCGTATACTTGATACGGT.....	22	1	2	0.50	1	1	0	0	0	0
.....CCAGTGCGTATACTTGAT.....	18	0	5	0.20	1	0	0	0	1	0

Anti-sense strand reads

GTGATACTTACGGTCTCGTGGGAGATTTACAGTTCGTCGGGAAAACCGGTGGTCACGCATATGAACTATGCCTCACGCCCACACATAGACCATATGCGTGACTACGGGCTTTCCTGCTACCGCCGCGGCTCCTATTGTTGCTGTCCCTCGGGTCTCGA	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head	V106 head
**********....((((((((((.(((((((((((.(((((((.....))))))).)))))))))))).)))).))))).....**********								

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13340:19201918-19202076 -	dan_163	CACTAT------GAATGCCAGAGCACCCTCT---------AAAT--GTCAAGCAGCCCTTTTGGCC----ACCAGTGCGTATACTTGATACGGAGTGCGGGTGT----------GTATCTGGTATACGCACTGATGGC----------CG----------AAAGGACGATGGCGGCGCCGAGG----ATAACAACGACAGGGAGCCCAGAG----------CT
droBip1	scf7180000396413:3162407-3162567 +		CGCAAT------AAATGCCAGAACACCCTCT---------AAAT--CCCAAGCAGCCCTTTTGGCC----ACCAGTGCGTATACTTAACACAGAGTGCGGGTGTGT----------ATATCTGGTATACGCACTGATGGC----------CG----------AAAGGACGATGGCGGTGCCGAGG----ATAACAACGACAGGGAGCCCAGAG----------CT
droKik1	scf7180000302697:760627-760864 +		GTTAAT------AACGCAAAGACACCGATTCAT-----AAATGCCGAGCGCAGCCCTTTTGGCA----TGCCAGTGCGTATACTTGATATGGAGTGCGGGTGCTTGTGGTCCTGTGTGGGA-GC--CTCTCTGTGTGTGT----ATGTGTGT----------GTATCCTGTATACGCACTGCTGGC----------TGCTGCTGTCGGCATTGGAAACGATGGCGAAC-GGAGGACGACGGCGGCAGCGAGG----ATAACAACGACAGGGAGCTCAGAG----------CT
droFic1	scf7180000453826:226434-226646 -		GACAAC------AACTAAAACGACTCCCTCT---------GCAC--TCAGAGCAGCCCTT-----------CAGTGCGTATACTTAATACGAAGTGCGGGTGTTGC----------A--GTG-GCTCTCAGGGTGTTT---GTGCGCTC---CCC-CACAAAATATCCTGTATACGCACTGCTGGC----------TGCTGCTGTCGGCATTGGAAACGATGG------AAGACGACGGCGGCAGCGAGG----ATAACAACGACAGGGAGCTCAGAG----------CT
droEle1	scf7180000491261:1985856-1986086 +		GATAAT------AACTGCCAGGACACCGACT---------ATGC--GGAGAGCAGCCCTTTTGCCC----GGCCAGTGCGTATACTTATATGGAGTGTGGGTGTAATA----------TGCCTTCTCTCTTTGTTTGT-------TTTGCTCCACCAACGAAATATCCTGTATACGCACTGCTGGC----------TGCTGCTGTCGGCATTGGAAACGATGGCGAATTGCGAGACGACGGCGGCAGCGAGG----ATAACAACGACAGGGAGCTCAGAG----------CT
droRho1	scf7180000779416:4024-4253 +		GATAAT------AACTGCAAAGGACACCGACT---------ATGT--GGAGAGCAGCCCTTTTGCCC----GGCCAGTGCGTATACTTAATACGGAGTGCGGGTGCTTA----------TGTCTGCTCTCTGTGTTTGT-----GTGCTC---CTCCAACAAAATATCCTGTATACGCACTGCTGGC----------TGCTGCTGTCGGCATTGGAAACGATGGCGAATTGGGAGACGAGGGCGGCAGCGAGG----ATAACAACGACAGGGAGCTCAGAG----------CT
droBia1	scf7180000302075:1432376-1432574 -		AATAAC------TAGTGCCAGGACACCCTCT---------AAGA--GAAGAGCAGCCTTTTCAGCC--CCAGCCGCGTGCGTATACTTAACGTGGAGTGCGGGTGGTTA----------AGTC-GCT----------CTC-CGGCAAAATGTCCTGTATACGCACTGCTGGC----------CGCAGCTGTCGGCATGGCAAACGATGGCGAATTG---C---------ACGAGAGG----ATAACAACGACAGGGAGCCCAGAG----------CT
droTak1	scf7180000413872:386549-386760 +		AATAAC------AACTGAAAGGACACCCTCT---------AAGC--GAAGAGCAGCCTTTTACCC--CCTGCCAGTGCGTATACTTAATATGGAGTGCGGGTGGTTA----------AGTC-CTCT----------CTC-CGGCAAAATATCCTGTATACGCACTGCTGGC----------TGCTGCTGTCGGCATTGAAACGATGGCGAA--GGAAGACGAGGGCGGAAGCCGAGGAGAGCATAACGACGACAAGGAGCTCATAG----------CT
droEug1	scf7180000409770:972510-972727 +		C-----------AACTGCAGGAGACACCCTCT---------AAGT--GGAGAGCAGCCTTTTTACC----CCAGTGCGTATACTTAATATTGAGTGCGGGTGGTTA----------TGC-CTCTCAGTGTTTGT-------GTTT---CTC-CGGCAAAATATCCTGTATACGCACTGCTGGC----------CGCTGCTGTCGGCATTGAAAACGATGGCGAA--GGAAGACGAGGGCGGAAGCCGAGGAGAGCATAACGACGACAAGGAGCTCATAG----------CT
dm3	chr3R:23487904-23488136 +		CATAAC------AACTGCAAGGACACCCCTT---------ACAC--GGAGAGCAGCCTTTTTGCCCGTCCATTCAGTGCGTATACTTAATACTGAGTGCGGGTGTTT----------GTACGA--CTCTCTGCGTTTGT----GTGTGTTT---CTC-GGCAAAATATCCTGTATACGCACTGCTGGC----------TGCTGCTGTCGGCATTGGAAACGATGGCAAAC-GGAGGACGCGCGCGGCTGAGAGG----ATAACAACGACGGGAGCTCAGAG----------CT
droSim2	3r:22912979-22913211 +		CATAAC------AACTGCAAGGACACCCCTT---------ACAC--GGAGAGCAGCCTTTTTGCCCGTCCATTCAGTGCGTATACTTAATACTGAGTGCGGGTGTT--G---------GCACGA--CTCTCTGCGTTTGT----GTGTGTTT---CTC-GGCAAAATATCCTGTATACGCACTGCTGGC----------TGCTGCTGTCGGCATTGGAAACGATGGCAAAC-GGAGGACGCGCGCGGCTGAGAGG----ATAACAACGACGGGAGCTCAGAG----------CT
droSec2	scaffold_22:131137-131369 +		CATAAC------AACTGCAAGGACACCCCTT---------ACAC--GGAGAGCAGCCTTTTGCCCGTCCATTCAGTGCGTACTTAATACTGAGTGCGGGTGTT--G---------GCACGA--CTCTCTGCGTTTGT----GTGTGCTT---CTC-GGCAAAATATCCTGTATACGCACTGCTGGC----------TGCTGCTGTCGGCATTGGAAACGATGGCAAAC-GGAGGACGCGCGCGGCTGAGAGG----AAAACAACGACGGGAGCTCAGAG----------CT
droYak3	3R:22999027-22999246 -		CCTAAC------AACTGCAAGGACACCCCGT---------ACAC--GGAGAGCAGCCTTTTTGT-GCCCATTCAGTGCGTATACTTAATACCGAGTGCGGGTGTT--G---------CGGTATGA--CTCTCTGCGCTTGTGTGTGTGTTT---CTC-GGCAAAATATCCTGTATACGCACTGCTGGC----------TGCTGCTGTCGGCATTGGAAACGATGGCCAAC-----------------GGAGG----ATAACAACGACGGGCGAGCTCAGAG----------CT
droEre2	scaffold_4820:4549210-4549440 -		CATAAC------CAGTGCAAGGACACGCCGT---------ACCC--GGGGAGGTGCCCTTTTATGT-GCCCATTCAGTGCGTATACTTAATATTGAGTGCGGGTGTT--G---------GCATGA--CGCTCTGCGCTTGT----GTGTGTTT---CTC-GGCAAAATATCCTGTATACGCACTGCTGGC----------TGCTGCTGTCGGCATTGGAAACGATGGCGAAT-GGAGGACGCGG-GCGGCTGAGAGG----ATGACAACGACGGGAGTTCAGAG----------CT
dp5	2:3843000-3843215 +		CATAAATGGCAGCCCCTGCAAAGACACCCTCT---------ATGT--GG-GGCAGCCCTTTTCGGA--A--------TTCCCATAGCATGGAGCGCGGGTGTT--G---------GT-------TCTGTATGTATG----------GGAATATCCTGTATACGCACTGCTGCCTCTTCTTCTG--CTGCTGCTGCTGCTGTCGTCGGCACTGGCAACGACGG------------------ATACGAGG----ATAACAACGACGGGAGCAC--GCCCAGAGACCAGAGTCCT
droPer2	scaffold_7:507716-507934 -		CATAAATGGCAGCCCCTGCAAAGACACCCTCT---------ATGT--GG-GGCAGCCCTTTTCGGA--A--------TCCCATAGCATGAAGCGCGGGTGTT--G---------GT-------TCTGTATGTATG----------GGAATATCCTGTATACGCACTGTTCCTCTTCTTCTGCTGCTGCTGCTGTCGTCGGCACTGGCAACGACGG------------------ATACGAGG----ATAACAACGACGGGAGCAC--GCCCAGAGACCAGAGTCCT
droWil2	scf2_1100000004902:3729448-3729584 +		CCTTGT--GCATAGAATAGATAAACACCCTCT---------AAAC--GGGGGTG-------------AACAGTGCGTATACTTAACTTGGAGTGAGGGTGTC----------TTTGTGTATGTT----------ATATTATCCTGTATACGCATATGTCC---CAG-GAGGAGGAGAGAGAACAGAG----------CT
droVir3	scaffold_12855:2127459-2127651 -		AGCT--------AACAGAAAGCACCCCTTATATATCTGTATAT--ATAGAACACGCCCTTTATGGC--GGTGGCAGTGCGTATGCTTAATATGC-A---------GTCTGTGTGTTTGT---GT---T----TT-GC----CTGTGTATACGCACCCCAGGC-----GTGCC---CTG---TGCTGCTCCTGTCGCTGGCAACGACGAACAAC----------GAGAAGG----ATAACGACGATGTGA-----ACAG----------CT
droMoj3	scaffold_6540:32422928-32423041 -		--TTGT---GTGT----------GCAAAGGGGAAGCGTGC----------CTGCTGCTGCCGCTGGCAACGACGAGCAGC----------GAGAAGG---ACATCACGACGATGTGA-----ATAG----------CT
droGri2	scaffold_15074:2128468-2128644 -		ATCT--------AACTGACTGAGCACCCTGT---------ATAA--GCAT--AAGCCTTTTAGGG--GGTGGCTGTGCGTATACTTAACGGGGAATGTGTATACA----------C--ATATATGCATTGGT---ATGTG----------CACTG----TCTGTATACGCACTCCTGGC----------GCAACGACG------GAGCAGCAGAGAGG----ATAACGATGAGGATGAGAATAGCG----------T

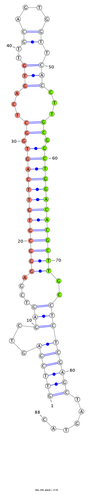
Generated: 09/08/2015 at 07:51 PM

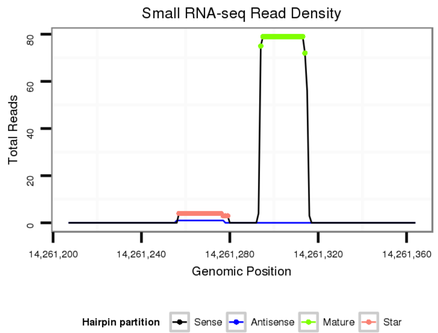
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

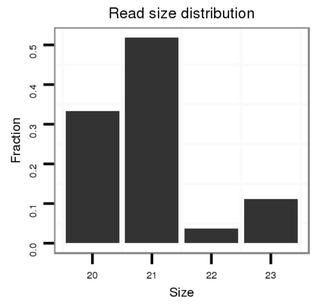
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_196	**scaffold_13337:14261257-14261314 +**	**confident**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

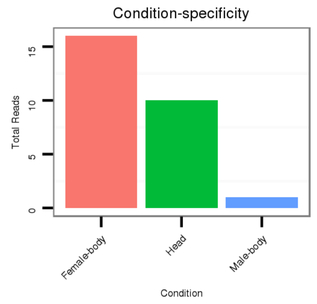
Legend: mature star mismatch in alignment mismatch in read

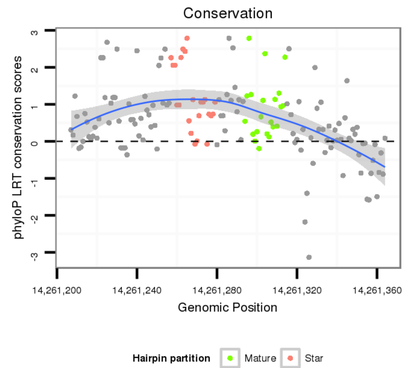
Predicted structure











Show Alternate Folds

Flybase annotation

Antisense to intron [Dana\GF23901-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACGAAACGGAGCGAAATTAGCAATCAATCGAAGTGGTTCGAGTCGAGTCGAGGGCGTGTTCAGTGGCTCAGTGTTGCAGTGGTTCACCTTGCGGCTGGACACGCTTGCCTCTCGAGCTAGTACACTCAACAAAAATATGAGTGAAAAAGATATTCAAT	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V055 head	V106 head	M058 embryo	V105 male body
**********(((((((...(((....(((((((((((((.(((...(((..((....)).)))...)).)))))))))))..)))))))))).....**********										
.....CTTGCGGCTGGACACGCTTGCC.....	22	0	1	47.00	47	47	0	0	0	0
.....CTTGCGGCTGGACACGCTTGCC.....	21	0	1	14.00	14	11	2	1	0	0
.....CTTGCGGCTGGACACGCTTG.....	20	0	1	7.00	7	2	2	2	0	1
.....CCTTGCGGCTGGACACGCTTGCC.....	23	0	1	3.00	3	2	0	0	1	0
.....TTGCGGCTGGACACGCTTGCC.....	21	0	1	3.00	3	3	0	0	0	0
.....AGGGCGTGTTCAGTGGCTCAGTG.....	23	0	1	3.00	3	1	1	1	0	0
.....CTTGCGGCTGGACACGCTTGCCT.....	23	0	1	3.00	3	3	0	0	0	0
.....TTGCGGCTGGACACGCTTGC.....	20	0	1	1.00	1	1	0	0	0	0
.....CCTTGCGGCTGGACACGCTTGC.....	22	0	1	1.00	1	1	0	0	0	0
.....AGGGCGTGTTCAGTGGCTCAGTGA.....	24	1	1	1.00	1	0	1	0	0	0
.....AGGGCGTGTTCAGTGGCTCA.....	20	0	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

TGCTTTGCCTCGCTTTAATCGTTAGTTAGCTTCACCAAGCTCAGCTCAGCTCCCGCACAAGTCACCGAGTCACAACGTCACCAAGTGGAACGCCGACCTGTGCGAACGGAGAGCTCGATCATGTGAGTTGTTTTATACTCACTTTTCTATAAGTTA	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head	V106 head	M044 female body
**********(((((((...(((....(((((((((((((.(((...(((..((....)).)))...)).)))))))))))..)))))))))).....**********								
.....CTCCCGCACAAGTCACCGAGTC.....	22	0	1	1.00	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13337:14261207-14261364 +	dan_196	ACG----------AAAC-------G-------GAGC----------GAAATTAGCAATCAATCGAAGT----------GG---TTCGA-GTCGAGTCGAGGGCGT---GTTCAGTGGCTCAGTGTTGCAGTGGTTCACCTTGCGGCT----------GGACACGCTTGCCTCT----CG---AGC-TAGTACACTCAACAAAA-A------TATGAG----TG----------AAAAA---GATATT-------CAAT
droBip1	scf7180000396641:1026767-1026919 -		ACG----------A---G-AG-------G---------------------GAATTAGCAATC----GATAGGACGT---GGTGCAGTGGCTCAGTGTTGCAGTGGTTCACCTTGCGGCT----------GGACACGCTTGCCTCT----CG---AGCTGAATGCACTCACGAAAA-A------TATGAGACTTA----------AA---GCATT-------CGAT
droKik1	scf7180000302351:355541-355725 -		ACG----------AAA-AAGAA-AA-------G---------------------GAATTAGCAATC----GATATGGACAT--GAATATACAT----ATACAAGTATAAGGA-ATCGAGTCGAGGGCGT---GTGG----------AGTGGTTCACTTGCGTGT----------GGACACGGTGGCTGA----CA---ACTTCGGTGCACTGTAAATAATACGGAAACTAGATGC---A----------CCTTTTTT-A---A-AGGTTGCTTAAA-------AAAT
droFic1	scf7180000454107:1131246-1131370 +		ACG----------AGCAGGAAAAAA-------G---------------------GAATTAGCAATC----GATAT----------GG---CTCGA-ATCGAGTCGAGGGCGT---GTGG----------AGTGGTTGTCTTGCAGT----------GGACACGGTGGCTGACTCAGT---ACTTGCCTGCACTCGAAGAAA-A------CG----------AAT
droEle1	scf7180000490993:481475-481640 +		ACGGGACATGGCGACGCAAAGCGAGGACGAGCAGGAA-AA-------G---------------------GAATTAGCAATC----GATAT----------GG---CTCGA-AGCGAGTCGAGGGCGT---GTGG----------AGTGGTTCACTTGCTTGCT----------GGACACGGTGGCTGA----GT---ACTTCGTTACACTCGAAAAT-AA------CGTGATCTCTT----------AAT---CATT
droRho1	scf7180000779956:242778-242929 +		ACG----------AGCAGAAA-AA-------G---------------------GAATTAGCAATC----GATATATGCAT----------GG---CTCGA-ATTGAGTCGAGGGCGT---GTGG----------AGTGGTTCACTTGCTTGCT----------GGACACGGTGGCTGA----GT---ACTTCGCTACACTCGAGAAA-A------CGTGATCTCTT----------AGCATTTAGTTAAT
droBia1	scf7180000302193:854035-854242 +		ACG----------AGCAGG-A-GA-------G---------------------GAATTAGCAATC----GATAT----------GG---CTCGA-AGCGAGTCGAGGGCGT---GTGCAGCGGCTCAGTGGTGCAGTGGTTCACTTGCTTGCT----------GGACACGGTGGCTGA----CA---ATCAGTTACACTCGAAAAA-A------CGTGATCTGTTTGATATTACATGGATATGGTTGCAACTATTTCTGCCCTTTCTGGCATGTTAA---AATCAG----------CATT
droTak1	scf7180000415409:316577-316711 +		GCG---------GCGCGGAGCGAGGACGAGCAAGAA-AA-------G---------------------GCTATTAGCAATC----GATAT----------GG---CTCGA-ATCGAGTCGAGGGCGT---GTGG----------AGTGGTTCACTTGCTGCG----------GGACACGGTGGCTGA----CT---ATCAGTTACACTCGAAAAA-A------CG----------AAT
droEug1	scf7180000409471:2011579-2011726 -		ACG----------AGCAAGAAAAA-------G---------------------GAATTAGCAATC----GATAT----------GG---CTCGA-ATTGAGTCGAGGGCGT---GTGG----------AGTGGTTCACTTGCTAAT----------GGACACGGTGGCTGA----CT---ACTTAGTTACACTCAAAGAAA-AA------CTTGATAATTTT----------A-CAA---TTAAGT---------TGGC
dm3	chr3L:17557993-17558111 +		ACG----------AGCAAGAA-AA-------G---------------------GAATTAGCAATC----GATAT----------GG---CTCGA-ATCGAGTCGAGGGCGT---GTGG----------AGTGGTTCACTTGCTTGCT----------GGACACGGTGGCTGA----CT---ACTTCGATGCACTCGAAAAA-A------CG----------AAT
droSim2	3L:17148593-17148711 +		ACG----------AGCAAGAA-AA-------G---------------------GAATTAGCAATC----GATAT----------GG---CTCGA-ATCGAGTCGAGGGCGT---GTGG----------AGTGGTTCACTTGCTTGCT----------GGACACGGTGGCTGA----CT---ACTTCGATGCACTCGAAAAA-A------CG----------AAT
droSec2	scaffold_0:9604880-9604998 +		ACG----------AGCAAGAA-AA-------G---------------------GAATTAGCAATC----GATAT----------GG---CTCGA-ATAGAGTCGAGGGCGT---GTGG----------AGTGGTCCACTTGCTTGCT----------GGACACGGTGGCTGA----CT---ACTTCGATGCACTCGAAAAA-A------CG----------AAT
droYak3	3L:16501498-16501594 -		ACG----------AGCAAGAA-AA-------G---------------------GAATTAGCAATC----GATAT----------GG---CTCGC-ATCGAGTCGAGGGCGT---GTGG----------AGTGGTTCACTTGCTTGCT----------GGACACGGTGGCTCT----GA---ACT----------A-CGA---TTAAGT---------TGGC
droEre2	scaffold_4784:16296342-16296461 -		ACG----------AGCAAGAAAAA-------G---------------------GCTATTAGCAATC----GATAT----------GG---CTCGA-ATCGAGTCGAGGGCGT---GTGG----------AGTGGTTCACTTGCTTGCT----------GGACACGGTGGCTGA----CT---ACTTCGATGCACTCGAAAAA-A------CG----------AAT
dp5	XR_group6:2222224-2222359 +		ACG----------A-GAACG---A-A-------AGTGAAAGTCGAAGGCAAAGAAAAAGGAAAAGGAAAAGAAGTAGAAGAGTAAGGCAATTAGCAATC----GATAT----------GG---GTTGCGATCGAGTCGAGGGCGT---GTGG----------AGTGGTTCACTTGCGGC----------GGACACGGTGGCTCT----GA---ACT----------A-CGA---TTAAGT---------TGGC
droPer2	scaffold_9:512934-513069 +		ACG----------A-GGACG---A-A-------AGTGAAAGTCGAAGGCAAAGAAAAAGGAAAAGGAAAAGAAGTAGAAGAGTAAGGCAATTAGCAATC----GATAT----------GG---GTTGCGATCGAGTCGAGGGCGT---GTGG----------AGTGGTTCACTTGCGGC----------GGACACGGTGGCTCT----GA---ACT----------A-CGA---TTAAGT---------TGGC
droWil2	scf2_1100000004762:1355293-1355409 +		AG----------AAAAAAAAAAAGAGAACGAG----------ACAATTAGCATT---------TTGAATTTTGATAT-------TG---TTCT----GTCGAGGGCGTGGTGTGACGTGCTG---GTTT-GGTGGTTCACCTTGTTGTT----GGACACGCTTGCCT----A---ACT----------A-CGA---TTAAGT---------TGGC
droVir3	scaffold_12928:5353270-5353363 -		TGT----------TGCAGT-----A-------CG----------T---GTT--------GTTGTTG-----A-------T---AGT----------GTTGTTGTTGCTGTTGT----------TTTTACTTT-----TT---A--CACACACACACACA-CA----GATGCACA----TGTT
droMoj3	scaffold_6540:26143691-26143816 +		CTT----------CTGCGG---A-A-------TGCTACAGCTGC----------AC---TGGCACGGGT---ATTTGCGATTCGCTGGCGATTTTG-----A-------GGGG----------GTTGTTGCTGCTGCTGC----------GCGGCTGCTTTCCTCTTTGTGTTCAGCTGTCAG-GATTGTGCAGT----A-------CG----------AAC
droGri2	scaffold_15245:11424130-11424282 +		ATT----------TAACA---T---A-------GAGCAAAT----------CTA--AATACATC----GATGT----------G---TTCGAGATTGAATAA---AGT---GTCA----------ATGGAAGGTTTAATAAACCGATCTTTGGCTGGGATAATCTGGCTTC---CT---AGTTTGTGG---ACACATTTC-AT---T-TTGTGT----TT----------CAAC

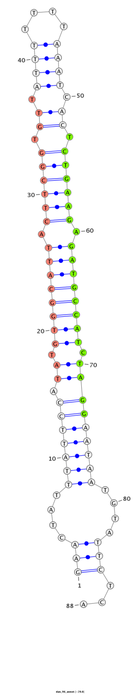
Generated: 09/08/2015 at 07:47 PM

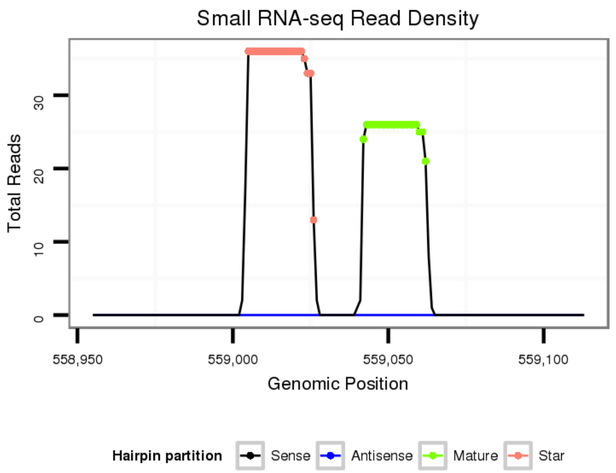
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

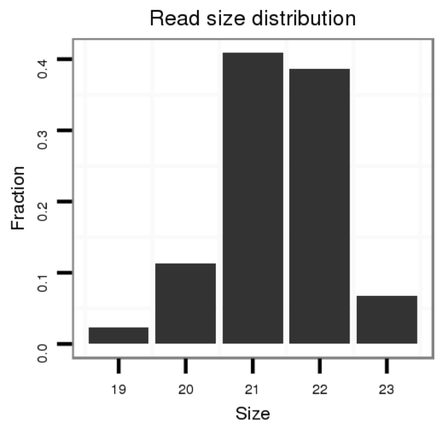
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_96	**scaffold_12903:559005-559063 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

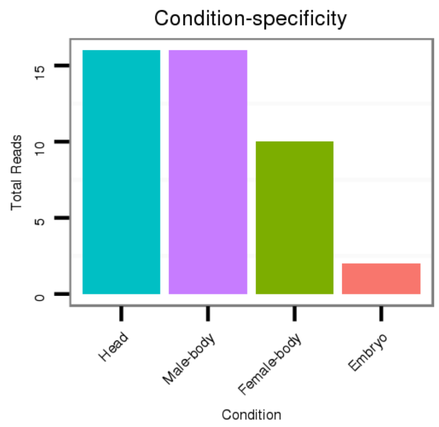
Legend: mature star mismatch in alignment mismatch in read

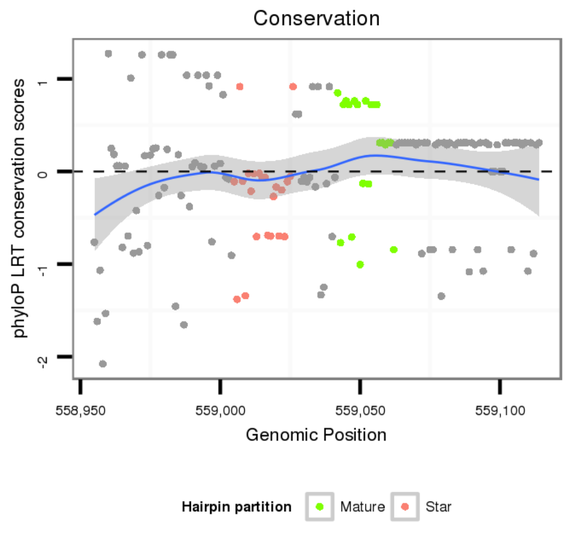
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CCTCATTAAGTGAGATTTAATATTTAAAATTAATAGAACTATTTATTCCATATGTGGCATTACTTCGGTGTTATTTTTTTAAATCACTCTGAAGAGATGCCATCTAGGAATAATGTATTCTCACTCTCCAATTTTGCTCAGTGCAGTTTTAAGACTAGA **********(((....(((((((.((.(((((((((.(((((((.((.((((....)))).)).)))))))).)))))))).)))))))))....)))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	female body	V105 male body	V055 head	M058 embryo
.....ATATGTGGCATTACTTCGGTGT.....	22	0	1	12.00	12	6	3	0	3	0
.....TCTGAAGAGATGCCATCTAGG.....	21	0	1	11.00	11	2	0	7	1	1
.....TATGTGGCATTACTTCGGTGTT.....	22	0	1	10.00	10	3	3	3	1	0
.....TATGTGGCATTACTTCGGTGT.....	21	0	1	7.00	7	4	2	1	0	0
.....TCTGAAGAGATGCCATCTAGGA.....	22	0	1	7.00	7	1	2	3	0	1
.....TCTGAAGAGATGCCATCTAGGT.....	22	1	1	6.00	6	0	5	1	0	0
.....TCTGAAGAGATGCCATCTAG.....	20	0	1	4.00	4	2	1	1	0	0
.....TATGTGGCATTACTTCGGTGTTT.....	23	1	1	3.00	3	1	1	1	0	0
.....TATGTGGCATTACTTCGGTGTTA.....	23	0	1	2.00	2	1	0	1	0	0
.....ATATGTGGCATTACTTCGGT.....	20	0	1	2.00	2	0	1	1	0	0
.....CATATGTGGCATTACTTCGGTGT.....	23	0	1	1.00	1	1	0	0	0	0
.....CATATGTGGCATTACTTCGG.....	20	0	1	1.00	1	0	1	0	0	0
.....CTGAAGAGATGCCATCTAGG.....	20	0	1	1.00	1	0	1	0	0	0
.....TGTGGCATTACTTCGGTGTTT.....	21	1	1	1.00	1	0	1	0	0	0
.....TATGTGGCATTACTTCGGTGTTG.....	23	1	1	1.00	1	1	0	0	0	0
.....CTGAAGAGATGCCATCTAGGAA.....	22	0	1	1.00	1	0	1	0	0	0
.....ACTCTGAAGAGATGCCATCTAGG.....	23	0	1	1.00	1	1	0	0	0	0
.....ATATGTGGCATTACTTCGGTT.....	21	1	1	1.00	1	0	1	0	0	0
.....ATATGTGGCATTACTTCGGTGTT.....	23	0	1	1.00	1	0	0	1	0	0
.....CTCTGAAGAGATGCCATCT.....	19	0	1	1.00	1	0	1	0	0	0
.....TCTGAAGAGATGCCATCTAGAT.....	22	2	1	1.00	1	0	0	1	0	0

Anti-sense strand reads

GGAGTAATTCACTCTAAATTATAAATTTTAATTATCTTGATAAATAAGGTATACACCGTAATGAAGCCACAATAAAAAAATTTAGTGAGACTTCTCTACGGTAGATCCTTTATTACATAAGAGTGAGAGGTTAAAACGAGTCACGTCAAAATTCTGATCT **********(((....(((((((.((.(((((((((.(((((((.((.((((....)))).)).)))))))).)))))))).)))))))))....)))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body

Show Alignment With Reads

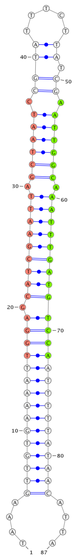
Re-alignment of all predicted orthologs

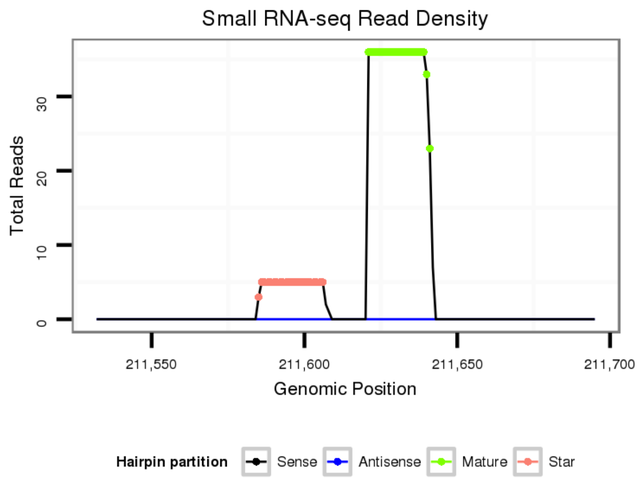
Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:558954-559113 +	dan_96	GCCTCATTAAGT-------GAGATTTAAT--ATTTAAAATT-----------AATAGAACTATTTATTCCA----TATG----------TGGCATTACTTCGGTGTTATTTTTTTAAATCACTCTGAAGAGATGCCATCTAGGAATAATGTATTCTCACTCTCCAAT---TTTGCTCAGTGCAGTTTTAAGACTAGA
droBip1	scf7180000395912:27836-28005 +		AC-GAATCAAATTTCCGTGAAAATGTGT--ACTTAAACAT-----------TTTG----GAAAACGAAAAAATATTTTTCATTGGTGGCATTGTTTTGGCGT--ATATTTTTGATCACACTGGAGCGATGCCATCTAAGAATAATGTTTTTCCAGTCTTCAATAATTGTGTTAAG--G--TTCTAAGAATTGA
droRho1	scf7180000780108:361719-361814 -		GCGAAAAT----------------TTAATCGAATAGAAATTAATAGAAAAATAGACGAAGCT-TATATTCTAAATATATA----------CGATTTTATGATTATTGTTATTATTCTATATTAC----------
droBia1	scf7180000302291:3460791-3460836 -		GGCTAATTAAATTTTTTT

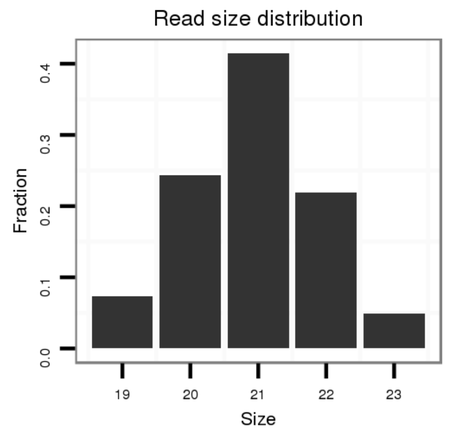
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_226	**scaffold_13335:211582-211645 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

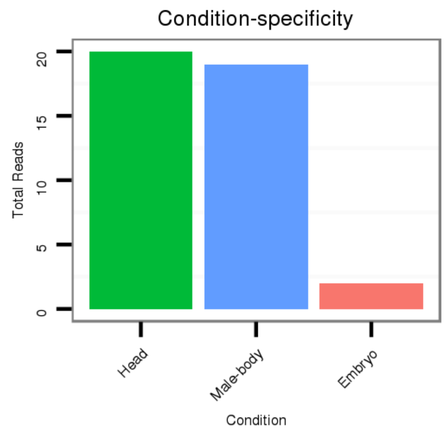
Legend: mature star mismatch in alignment mismatch in read

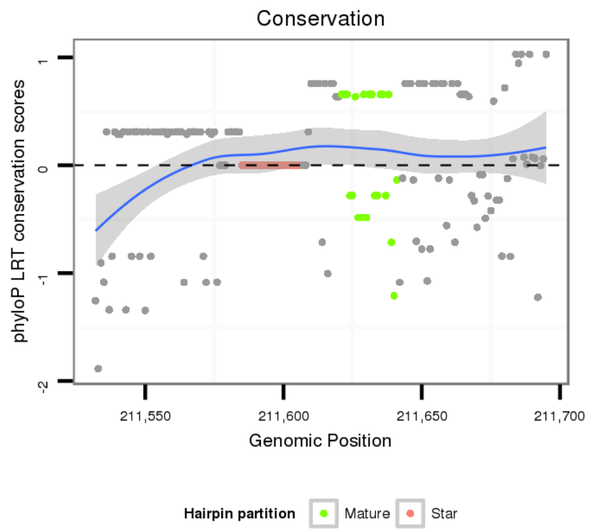
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATTTTCGTCCTCAGATATGTAAAATTGTAAATCCTTTTTAAAGTTGTGAAAATTGGAGCATCGAATTAGCTAATCCGTATTTCTTATCGAATTGGCAAATTTGATGTCCAATTTTTATAACATTATTCATCTTAAGATTCGTGAGTGCTCTTATTTTAAACCTT **********....((((((((((((((((.(((((((((.((((((.((((.....)).)).)))))).))))))))))))))))))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V055 head	V106 head	M058 embryo
..........AATTGGCAAATTTGATGTCCA..........	21	0	1	16.00	16	5	7	4	0
..........AATTGGCAAATTTGATGTCC..........	20	0	1	10.00	10	6	1	1	2
..........AATTGGCAAATTTGATGTCCAA..........	22	0	1	7.00	7	2	3	2	0
..........AATTGGCAAATTTGATGTC..........	19	0	1	3.00	3	2	0	1	0
..........TGGAGCATCGAATTAGCTAATC..........	22	0	1	2.00	2	1	0	1	0
..........GGAGCATCGAATTAGCTAATCCG..........	23	0	1	1.00	1	1	0	0	0
..........GGAGCATCGAATTAGCTAATC..........	21	0	1	1.00	1	1	0	0	0
..........TGGAGCATCGAATTAGCTAATCC..........	23	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

TAAAAGCAGGAGTCTATACATTTTAACATTTAGGAAAAATTTCAACACTTTTAACCTCGTAGCTTAATCGATTAGGCATAAAGAATAGCTTAACCGTTTAAACTACAGGTTAAAAATATTGTAATAAGTAGAATTCTAAGCACTCACGAGAATAAAATTTGGAA **********....((((((((((((((((.(((((((((.((((((.((((.....)).)).)))))).))))))))))))))))))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V039 embryo	V055 head

Show Alignment With Reads

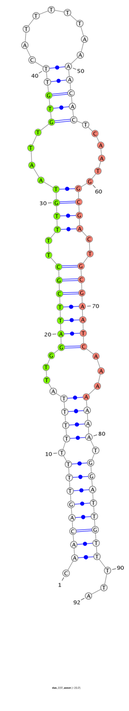
Re-alignment of all predicted orthologs

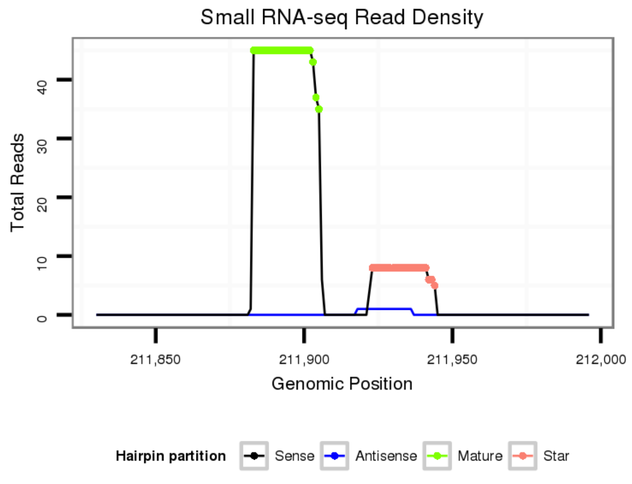
Species	Coordinate	ID	Alignment
droAna3	scaffold_13335:211532-211695 +	dan_226	ATTT------TCGTCCTCAGATATGTAAAATTGTAAATC--------------------CTTTTTAAAGTTGTGAAA---ATTGGAGCATCGAATTAGCTAATCGTATTTCTTATCGAATTGGCAAATTTGATGTCCAATTTTTATAACATTATTCATCTTAAGATTCGTGAGTGCTCTTATTTTAAACCTT
droBip1	scf7180000396778:4740-4871 -		TCCGTTGGGACTGATCCTGAAATGTCTGAAATTGTAAATATTGGTTTCCGACCATTTGTACCTTTTTGCAGTG---AAAACAAT----------TATTTTTTGATTTTTT

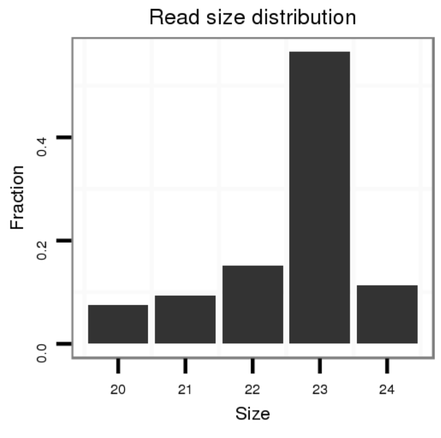
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_227	**scaffold_13335:211880-211946 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

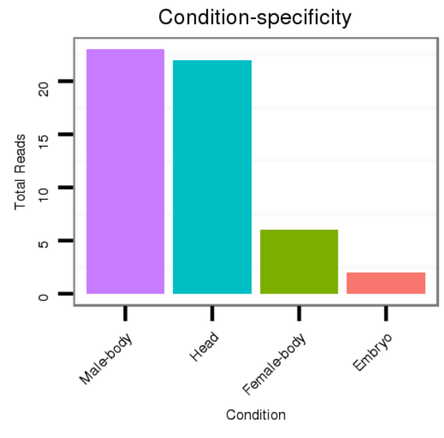
Legend: mature star mismatch in alignment mismatch in read

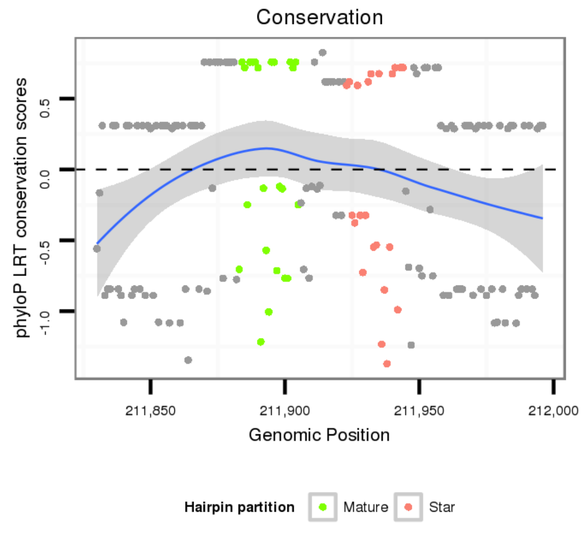
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAAACAAAGTGATAGTGTATCTAGTTTCGAACTCCAAACAACAGTTTTTTTTATTGGATTCGCTTTTGTAATTGTGTTCATTTTTAAAACACTCAATGGCGACTGCGAATCAAAAAAATGGATTGTTTTACATCGAATTTAGTGAAAGTGTCCCAAAAAAGTGTGAA **********.(((((((((.((((....(((((((..((((....(((((.........)))))).....)))))..)))))))...)))).)))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V106 head	M044 female body	V055 head	M058 embryo	V039 embryo
..........TTGGATTCGCTTTTGTAATTGTG..........	23	0	1	29.00	29	16	10	1	2	0	0
..........TTGGATTCGCTTTTGTAATTGTGT..........	24	0	1	6.00	6	3	1	1	0	1	0
..........TTGGATTCGCTTTTGTAATTG..........	21	0	1	5.00	5	0	3	1	1	0	0
..........CAATGGCGACTGCGAATCAAAA..........	22	0	1	4.00	4	1	1	0	1	1	0
..........TCAATGGCGACTGCGAATCA..........	20	0	1	2.00	2	1	0	1	0	0	0
..........TTGGATTCGCTTTTGTAATTGT..........	22	0	1	2.00	2	1	0	1	0	0	0
..........TTGGATTCGCTTTTGTAATT..........	20	0	1	2.00	2	0	2	0	0	0	0
..........TCAATGGCGACTGCGAATCAAA..........	22	0	1	1.00	1	0	0	1	0	0	0
..........ATTGGATTCGCTTTTGTAATTG..........	22	0	1	1.00	1	0	1	0	0	0	0
..........TCAATGGCGACTGCGAATCAAAA..........	23	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

TTTTGTTTCACTATCACATAGATCAAAGCTTGAGGTTTGTTGTCAAAAAAAATAACCTAAGCGAAAACATTAACACAAGTAAAAATTTTGTGAGTTACCGCTGACGCTTAGTTTTTTTACCTAACAAAATGTAGCTTAAATCACTTTCACAGGGTTTTTTCACACTT **********.(((((((((.((((....(((((((..((((....(((((.........)))))).....)))))..)))))))...)))).)))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	M058 embryo	V039 embryo
..........TGTGAGTTACCGCTGACGC..........	19	0	1	1.00	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13335:211830-211996 +	dan_227	AAAACAAAGTGA--TAGTGTATCTAGTTTCG------AACTCCAAACAACAGTTTTTT---TTATTGGATTCGCTTTTG--------TAATTGTGTTCATTTTTAAAACACTCAATGGCGACTGCGAATCAAAAA----------AATGGATTGT-TTTACATC-GAATTTAGTGAAAGTGTCCCAAAAAAGTGTGAA
droBip1	scf7180000396535:497545-497737 -		AAATTGAAAATAAGTTATATTTCAATTTTAGCAATAGAAATTGAAATAAAAGTTTATTGTGTTTCTGGATTCACGTTAAAAAATGGTATATGTGTCGTTTTC----------CCACTCCCCACAAAGGCTTTTATACTTAAATAAAAATGCTGATTTGATTTTTCTTCTAGGTTTTGTAATAAGTTTACAACTGAATAAGAA
droRho1	scf7180000777683:1515-1562 +		TT--TTTAAAATTATTCAGAGAGAACCGCACGCCAAAAG----------ATTGAATTTT-TT------------------------------
droEre2	scaffold_4690:7686446-7686492 +		CA----------------------------ACAATTTTTT---TTTTTGTATTCCTCTTTA--------CTATTGTTGTTACTGTT----------

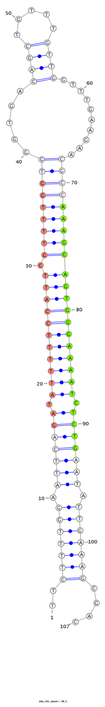
Generated: 09/08/2015 at 08:02 PM

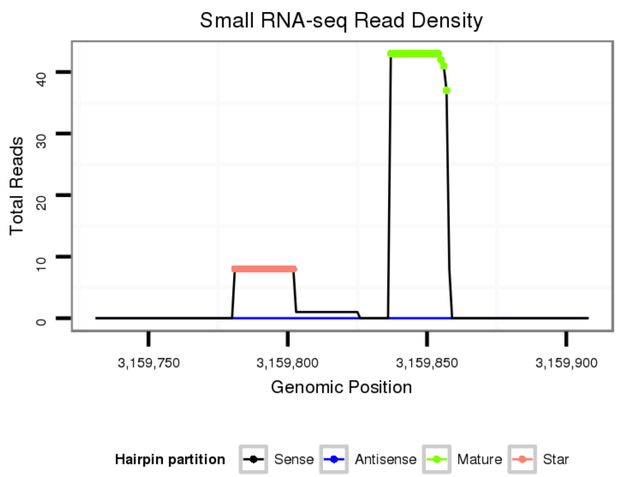
PASS/FAIL	
crit.size	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

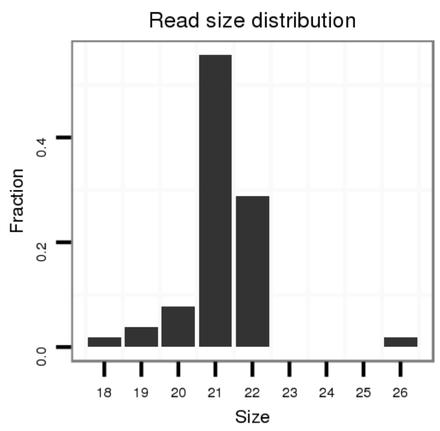
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_101	**scaffold_12929:3159781-3159858 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

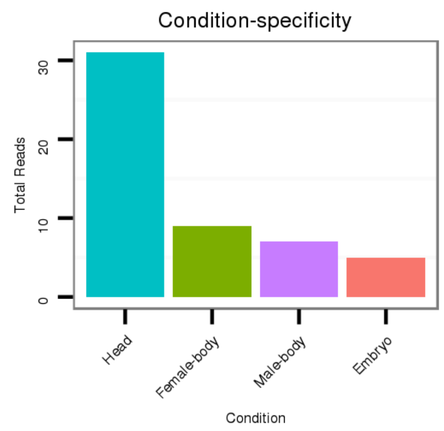
Legend: mature star mismatch in alignment mismatch in read

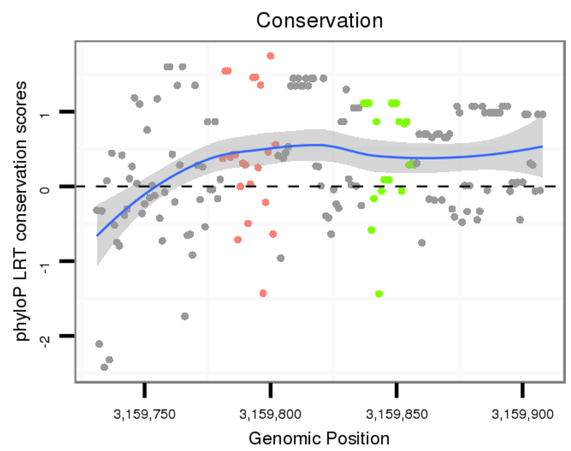
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TATTTGTTATTTGCATTTTTTTTCGGTTTTTTTTTTTCTTTTGGAATTCAGATATTTTTCCATTCGTTTTGGTGGGTGACAGCTGTTTGTTGGTTTGAAGAACGCCAAAGCAGTGGGAAAATCTCTGAATATTGAAAGCGACAAGCGGCAAGCTCCCGCGCAATCGGCCGAATCATCA	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	V105 male body	V055 head	M058 embryo	V039 embryo
**********..(((((((.(((((((.((((((((((.(((((((((.....((((.....)))).........)))))))))))))))))))).)))))))....**********											
.....AAAGCAGTGGGAAAATCTCTG.....	21	0	1	29.00	29	21	2	2	2	0	2
.....AAAGCAGTGGGAAAATCTCTGA.....	22	0	1	8.00	8	2	2	3	1	0	0
.....GATATTTTTCCATTCGTTTTGG.....	22	0	1	7.00	7	1	4	0	0	2	0
.....AAAGCAGTGGGAAAATCTCT.....	20	0	1	4.00	4	3	0	1	0	0	0
.....TGGTGGGTGACAGCTGTTTGTTGGTT.....	26	0	1	1.00	1	0	0	1	0	0	0
.....AAAGCAGTGGGAAAATCT.....	18	0	1	1.00	1	0	1	0	0	0	0
.....GATATTTTCCATTCGTTT.....	19	0	1	1.00	1	0	0	0	0	1	0
.....GCTCCCGCGCAATCGGCCGAATCATCG	27	1	1	1.00	1	0	1	0	0	0	0
.....AAAGCAGTGGGAAAATCTC.....	19	0	1	1.00	1	0	0	0	1	0	0
.....AAAGCAGTGGGAAAATCTCTT.....	21	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

ATAAACAATAAACGTAAAAAAAAGCCAAAAAAAAAAAGAAAACCTTAAGTCTATAAAAAGGTAAGCAAAACCACCCACTGTCGACAAACAACCAAACTTCTTGCGGTTTCGTCACCCTTTTAGAGACTTATAACTTTCGCTGTTCGCCGTTCGAGGGCGCGTTAGCCGGCTTAGTAGT	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	V055 head	V039 embryo
**********..(((((((.(((((((.((((((((((.(((((((((.....((((.....)))).........)))))))))))))))))))).)))))))....**********								
.....CCAAAAAAAAAAGAAAA.....	18	0	5	0.40	2	2	0	0
.....AAAAAAGCCAAAAAAAAAA.....	20	0	10	0.10	1	1	0	0
.....AAAAAGCCAAAAAAAAAA.....	19	0	14	0.07	1	1	0	0
.....AAAAAGCCAAAAAAAAAA.....	18	0	20	0.05	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12929:3159731-3159908 +	dan_101	TATTTGTTATTTGCATTTTTT-T------T--------------CGGTTTT-TT--TTTTTCTTTTGGAATTCAGAT----ATTTTTCCATTCGTTTT-GGTGGGTGACAGCTGTTT--GTTGGTTTGA--AGAACGCCAAAGCAGTGGGAAAATCTCTGAATATTGAAAGCGACAAG--CGGCAAGCTCCCGCGCAATCGGCCGAATCATCA
droBipl	scf7180000395987:12752-12922 +		T-TGC----------ATT----T------TCGGTTTTTT--TTTTGTGTGTT-TTTT--TG-----TGAAATTCAGAT----ATTT-TCCATTCGCTTTGGT--GTGACAGCTGTTGTTGTTGGCT-GAGTAGAACGCCAAAGCACTGGGAAAATCTCTGAAAATTGAAAGCGACAAG--CCGCAAGCTCCCGCGCAATCGGCCGAATCGTCA
droKik1	scf7180000302469:92421-92564 +		TTTTTTTCGCTC---------T-------T--------GTC--AT--ATTT-GCATTTTGAAGTTTG------AGAT----ATTT---TATTAGACAT--TTTGGTGACAGCTGTTGA-ACTCT------T-GAACACGAAAC----GGGAAA--------AAATCGTAAACGAAAAGTGTGTAAACTTCCCGCGCAATGAACCGAA--ATTA
droEug1	scf7180000409548:358589-358615 +		TATATTTCATTAGAATAT---T-------T-------------------------T--T--------------------------------TATTTCGGT----------T----------T---T--------------------------
dm3	chr3L:23495935-23495962 -		TTTTTTTT-------------T-------A-------------TGGTTTT-TT--TTTTTTTTTTG----------T-------------T-------------T----------T---T--------------------------
droSim2	x:4273472-4273552 +		AATTTG-------------T-------T-------------------T--T--------------------GTATTC---CATTAGAATTTATTTGGTGACAGCTGTTGA-ACTAC------T---CAG--TGAAAAAATCGCGCGCAATCAGGAAAA--ATTA
droSec2	scaffold_4:2147228-2147257 -		AATTTG-------------T-------T-------------------T--T--------------------GTATTG---CATTAGAATTTATTTGGT----------T----------T---T--------------------------
droYak3	X:3857557-3857667 -		TTTGCTG--CCCACA------T-------AC-------------TGGATTT-TT--TTTAAAGTTCGA------AATTGGTATTG---CATTAGGATTTATTTGGTGACAGCTGTTGA-ACTAC------T--G-------------------------------------AAG--TGAAAAAATCGCGCGCAATCAGCAA--------
droEre2	scaffold_4690:1959917-1960017 +		CAACTG-------------T-------T-------------TTT-TT--TTTAAAGTTCGA------AATTGGTATTG---CATTAGAATTTATTTGGTGACAGCTGTTGA-ACTAC------T--G-------------------------------------GAG--GGAAAAAATCGCGCGCAATCAGCAA--------
droVir3	scaffold_12875:16364571-16364628 +		ATTTCATTATTT---------T-------T--------CTTGCTT--GTTT-TGTTTCTGTAATCCC------TGAT----ATTT---AG------TTTTTCCATT----------T----------T---T--------------------------
droMoj3	scaffold_6473:8728524-8728664 -		TACACGTACATTAGGTTTGATTGGCTAGGACAGATTTTT--TTGCGAAATT-TTTT--TT-----CGTAGCTAAGATTATTCAAA---GTTTAGCTTTAATTAGTCGACAGCTGTTGA-ATTAGCCACA--AGGCCGCCAAAAAAAAAAAAAAAACT----------T----------T--------------------------

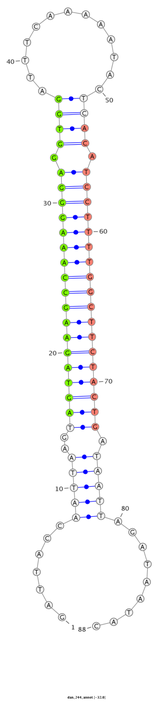
Generated: 09/08/2015 at 07:47 PM

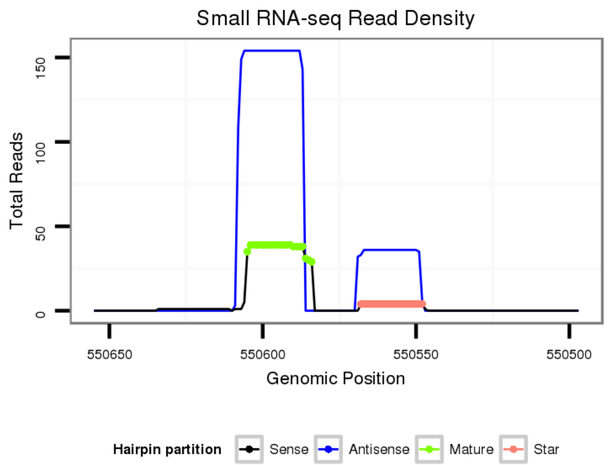
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

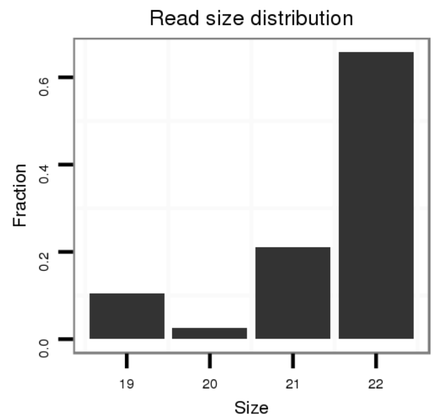
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_244	**scaffold_12903:550547-550605 -**	**confident**	**Testes-restricted**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

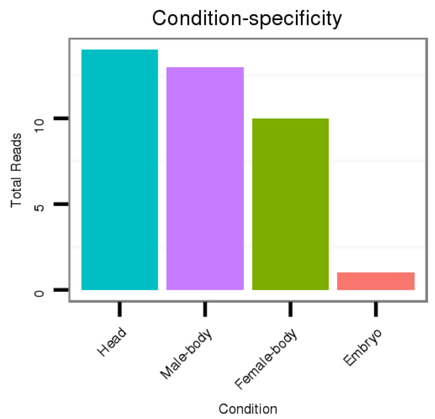
Legend: mature star mismatch in alignment mismatch in read

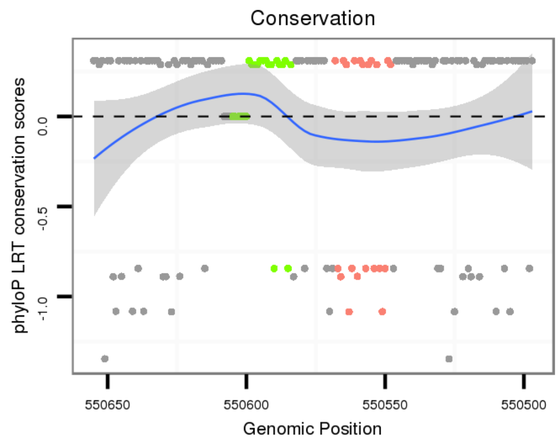
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF15947-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTCAGTTAGTTTTAGACTGTTTTTGAAGCAGTTTTGATTACCAATTAAGTAGTAGAAGCCAAAGGGAGGTGGATTTCAAAAATACTCACATCCTTTTGGCTTCTACTGATAATTAGATAATACTCCAAGAATTATTATCACTTTTTAAAAATTTTTTAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	M044 female body	M058 embryo	V055 head
**********.....(((((..(((((((((((((((((.((((.............)))).)))))))))))))))))).))))).....**********										
.....AGTAGAAGCCAAAGGGAGGTGG.....	22	0	1	24.00	24	11	9	4	0	0
.....GTAGAAGCCAAAGGGAGGTGG.....	21	0	1	4.00	4	1	1	2	0	0
.....AGTAGAAGCCAAAGGGAGG.....	19	0	1	4.00	4	2	2	0	0	0
.....AGTAGAAGCCAAAGGGAGT.....	19	1	1	4.00	4	3	1	0	0	0
.....ACATCCTTTTGGCTTCTACTG.....	21	0	1	3.00	3	0	0	2	1	0
.....TAGTAGAAGCCAAAGGGAGG.....	20	0	1	3.00	3	0	3	0	0	0
.....AGTAGAAGCCAAAGGGAGGTGT.....	22	1	1	2.00	2	1	0	0	0	1
.....AGTAGAAGCCAAAGGGAGGTG.....	21	0	1	1.00	1	0	1	0	0	0
.....AAGTAGTAGAAGCCAAAGG.....	19	0	1	1.00	1	0	0	0	1	0
.....AGTAGAAGCCAAAGGGAGGT.....	20	0	1	1.00	1	0	0	1	0	0
.....ACATCCTTTTGGCTTCTACTGA.....	22	0	1	1.00	1	0	0	1	0	0
.....TAGTAGAAGCCAAAGGGAGGTGG.....	23	0	1	1.00	1	1	0	0	0	0
.....TTTGAAGCAGTTTTGATTACCAAT.....	24	0	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

AAGTCAATCAAAATCTGACAAAAACTTCGTCAAAACTAATGGTTAATTCATCATCTTCGGTTTCCCTCCACCTAAAGTTTTTATGAGTGTAGGAAAACCGAAGATGACTATTAATCTATTATGAGGTTCTTAATAATAGTGAAAAATTTTTAAAAAATA	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V105 male body	V106 head	V055 head	M058 embryo
**********.....(((((..(((((((((((((((((.((((.............)))).)))))))))))))))))).))))).....**********										
.....TCATCATCTTCGGTTTCCCTCC.....	22	0	1	99.00	99	96	1	0	0	2
.....CATCATCTTCGGTTTCCCTCC.....	21	0	1	36.00	36	32	1	2	1	0
.....GTGTAGGAAAACCGAAGATGA.....	21	0	1	26.00	26	4	11	9	1	1
.....TCATCATCTTCGGTTTCCCTC.....	21	0	1	6.00	6	6	0	0	0	0
.....CATCATCTTCGGTTTCCCTC.....	20	0	1	5.00	5	5	0	0	0	0
.....ATCATCTTCGGTTTCCCTCC.....	20	0	1	5.00	5	4	0	1	0	0
.....GTGTAGGAAAACCGAAGATGAC.....	22	0	1	5.00	5	0	4	1	0	0
.....TTCATCATCTTCGGTTTCCCTCC.....	23	0	1	3.00	3	3	0	0	0	0
.....GTAGGAAAACCGAAGATGA.....	19	0	1	2.00	2	0	1	1	0	0
.....ATCATCATCTTCGGTTTCCCTCC.....	23	1	1	2.00	2	2	0	0	0	0
.....TTGTGTAGGAAAACCGAAGATGA.....	23	2	1	2.00	2	0	1	1	0	0
.....CTGTAGGAAAACCGAAGATGA.....	21	1	1	2.00	2	0	0	1	1	0
.....GTGTAGGAAAACCGAAGATG.....	20	0	1	1.00	1	1	0	0	0	0
.....CCATCATCTTCGGTTTCCCTCC.....	22	1	1	1.00	1	0	0	0	0	1
.....ATGTAGGAAAACCGAAGATGA.....	21	1	1	1.00	1	0	1	0	0	0
.....GTAGGAAAACCGAAGATGAC.....	20	0	1	1.00	1	0	0	1	0	0
.....TGTAGGAAAACCGAAGATGA.....	20	0	1	1.00	1	0	0	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:550497-550655 -	dan_244	TTCAGTTAGTTTTA----------GACTGTTTTTGAAGCAGTTTTGATTACCAATTAAGTAGTAGAAGCCAAAGGGAGGT----------GGATTTCAAAAATACTCACATCCTTTTGGCTTCTACTG--ATAATTAGATAATACTC----------CAAGAATTATTATCACTT----------TTTAAAAATTTTTTAT
droBip1	scf7180000395912:19101-19302 -		TTCAGTTATTATTAATTATTATTATTATTATTATTTTTTGTTGAAGATTTGATTATCAATTA--------AGCCAAAGGAAGGTATAATGTAATAGTTTTTAAAAATATGTATTTCACTATGACGCCCTTGTAGTAATTAGATAATACTTTTTTTTTGTATTTTAACACTTTTCTTGTCTTGAACTTTAATTTGAACACTTTTTTGT

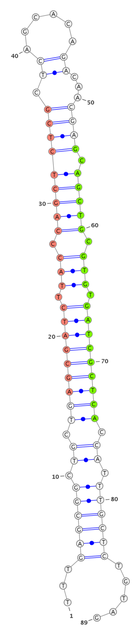
Generated: 09/08/2015 at 08:03 PM

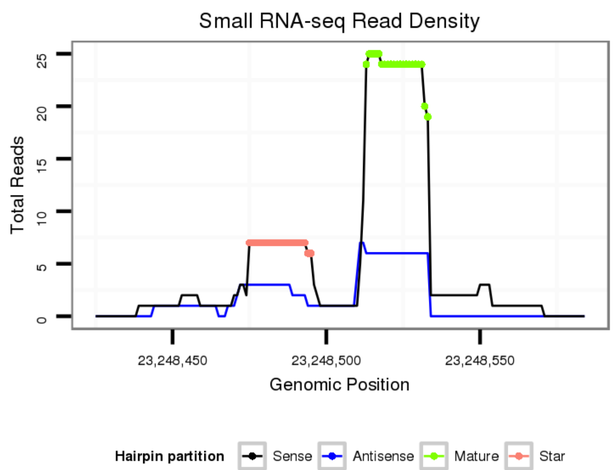
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

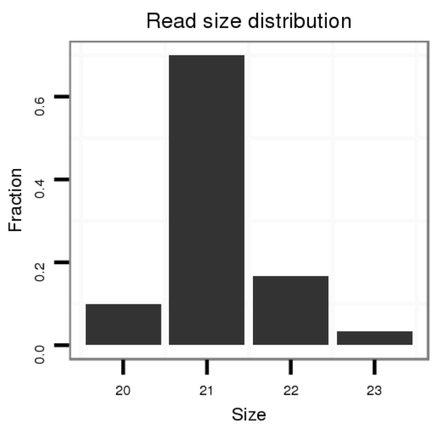
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_106	**scaffold_13340:23248475-23248534 +**	**confident**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

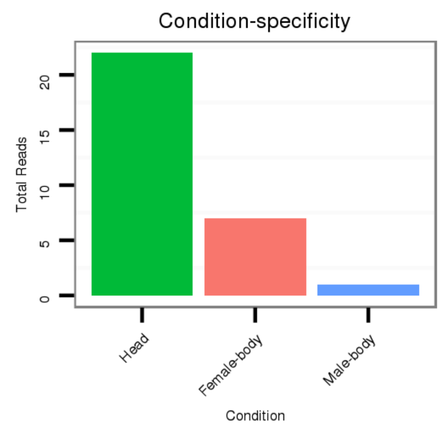
Legend: mature star mismatch in alignment mismatch in read

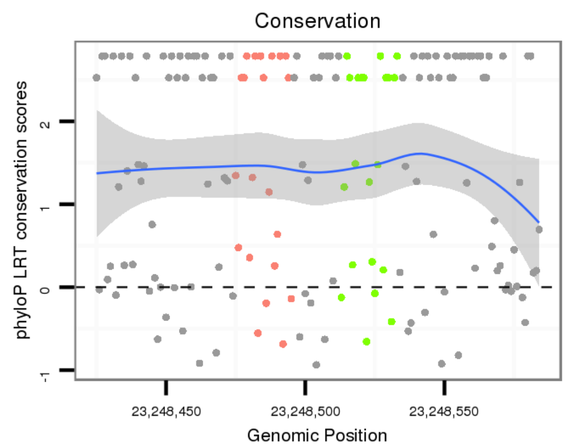
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dana\GF18929-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GCTACTTGCACAAGGACATCAGTCTGGACGACCACTTTGAGCGGCTGCTGAGCGATCTTACCCAGCTCTCGCTCAGCACAGACAACGAGCAGCTGCGTGTGATCGCTCACCATTTGCTCTGTAGTCTGGTTAACAAGATGGAAAGCAATCCGGAGAACCG	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	V055 head	M058 embryo	V105 male body	V039 embryo
********************************...(((((((.((.((((((((((.(((.((((((((((.((.....)).)...)))).)))))).)))).)))))))).)).))))))).....********************************											
.....GCAGCTGCGTGTGATCGCTCA.....	21	0	1	12.00	12	7	4	1	0	0	0
.....AGCGATCTTACCCAGCTCTCG.....	21	0	1	4.00	4	3	0	1	0	0	0
.....AGCAGCTGCGTGTGATCGCTCA.....	22	0	1	3.00	3	2	1	0	0	0	0
.....GAGCAGCTGCGTGTGATCGCT.....	21	0	1	3.00	3	3	0	0	0	0	0
.....ACCATTTGCTCTGTAGTCTGG.....	21	0	1	2.00	2	0	2	0	0	0	0
.....AGCAGCTGCGTGTGATCGCTC.....	21	0	1	2.00	2	2	0	0	0	0	0
.....AGCGATCTTACCCAGCTCTCGC.....	22	0	1	1.00	1	0	0	1	0	0	0
.....CGACCACTTTGAGCGGCTGCT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....AGCAGCTGCGTGTGATCGCT.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GAGCAGCTGCGTGTGATCGCTCA.....	23	0	1	1.00	1	0	1	0	0	0	0
.....GACATCAGTCTGGACGACCA.....	20	0	1	1.00	1	0	0	0	1	0	0
.....CTGAGCGATCTTACCCAGCTCT.....	22	0	1	1.00	1	0	1	0	0	0	0
.....CTCAGCACAGACAACGAGCAGC.....	22	0	1	1.00	1	0	0	0	0	1	0
.....CAGCTGCGTGTGATCGCTCA.....	20	0	1	1.00	1	0	1	0	0	0	0
.....CTGGTTAACAAGATGGAAAGC.....	21	0	1	1.00	1	0	0	0	1	0	0
.....GCAGCTGCGTGTGATCGCTC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TGCTGAGCGATCTTACCCAGCTCTCGCT.....	28	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

CGATGAACGTGTTCCTGTAGTCAGACCTGCTGGTGAAACTCGCCGACGACTCGCTAGAATGGGTCGAGAGCGAGTCGTGTCTGTTGCTCGTCGACGCACACTAGCGAGTGGTAAACGAGACATCAGACCAATTGTTCTACCTTTCGTTAGGCCTCTTGGC	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	V105 male body	V055 head	M058 embryo
********************************...(((((((.((.((((((((((.(((.((((((((((.((.....)).)...)))).)))))).)))).)))))))).)).))))))).....********************************										
.....GCTCGTCGACGCACACTAGCGAGT.....	24	0	1	3.00	3	3	0	0	0	0
.....CTCGTCGACGCACACTAGCGAGT.....	23	0	1	3.00	3	3	0	0	0	0
.....GACTCGCTAGAATGGGTCGAGA.....	22	0	1	1.00	1	1	0	0	0	0
.....CGACGACTCGCTAGAATGGGT.....	21	0	1	1.00	1	0	1	0	0	0
.....CGACTCGCTAGAATGGGTCGAGA.....	23	0	1	1.00	1	1	0	0	0	0
.....GCGAGTCGTGTCTGTTGCT.....	19	0	1	1.00	1	0	1	0	0	0
.....GTCAGACCTGCTGGTGAAACT.....	21	0	1	1.00	1	0	0	1	0	0
.....CCCATCAGACCAATTGTT.....	18	2	9	0.11	1	0	0	0	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13340:23248425-23248584 +	dan_106	GCTACTTGCACAAGGACATCAGTCTGGACGACCACTTTGAGCGGCTGCTGAGCGATCTTACCCAGCTCTCGCTCAGCACAGACAACGAGCAGCTGCGTGTGATCGCTCACCATTTGCTCTGTAGTCTGGTTAACAAGATGGAAAGCAATCCGGAGAACCG
droBip1	scf7180000396395:249163-249322 +		GCTACTTGCACAAGGACATCAGCTGGACGACCACTTTGAGCGGCTGCTGAGCGATCTCACCCAGCTCTCGCTCAGCACAGACAACGAGCAGCTGCGTGTGATCGCTCACCACCTGCTCTGCAGCCTGGTTAACAAGATGGAAAGCAGTCCGGAGAACCG
droKik1	scf7180000302707:160128-160287 +		GCTATCTTCACAAGGACATCAGCTGGACGATCACTTTGAGCGACTGCTGAGCGATCTCACCCAGCTCTCGCTCAGCACGACAACGAGCAGCTGCGCGTGATCGCTCACCAGTTGCTCTGCAGCGTTGGTCAACAAGATGGAGCAGCAATCCGGCCAATCG
droFic1	scf7180000453850:432670-432829 +		GCTACCTGGATAAAGCCATCACTTTGGACGACCACTTCGAGCGGCTGCTGAGCGATTTAACCCAGCTCTCTCTCAGCTCGGACAACGAACAGCTGCGTGTGATCGCTCACCACCTGCTCTGCAGTATGGTCAACAAGATGGAGCAGCAACCCAGCCAACTT
droEle1	scf7180000491104:2888104-2888263 +		GCTACCTGCACAAAGACATCGCCTCTGGACGATCACTTCGAGCGACTGCTCACCGACTTAACCCAGCTCTCTCTCAGCACGGACAATGAGCAGCTGCGTGTGATTGCTCATTCATCTGCTCTGCAGCATGGTAAACAAAATGGAGCAGCAATCCAGCGAACTT
droRho1	scf7180000776795:6412-6571 -		GTTACCTGCATAAAGACATGCCTCTGGATGACCACTTTGAGCGATTGCTGACCGATTTAACCCAGCTCTCTCTATCCACGGACAATGAACAGCTGCGTGTGATTGCCCACCAGTTGCTCTGCAGCATGGTCAACAAGATGGAGCAGCAATCCAGCCAACTT
droBia1	scf7180000302411:807812-807971 +		GCTACCTGCATAAGGACGTAACTCTAGATGATCACTTTGAGCGGCTTCTGACCGATTTAACCCAGCTCTCTCTCAACACGAGAACGAACAGTTGCGCGTGATCGCGCACCACCTGCTTTGCAGCATGGTCAACAAAATGGAGCAGCAATCCAGCCAACTT
droTak1	scf7180000415789:834157-834316 +		GCTACCTGCATAAAGACATCACGTTGGATGACCACTTTGAGCGGCTTCTGACCGACTTAACCCAGCTCTCTCTCAACACGGAAAACGAACAGTTGCGCGTGATCGCTCATCACCTACTTGCAGTATGGTGCAACAAGATGGAGCAGCAATCCGGCCAACCT
droEug1	scf7180000409759:1028205-1028364 +		GCTACTTGCATAAAGATATAACCCTGGATGATCATTTGGAGCGCCTTCTGACCGACTTAAGCAGCTGTCTCTCAACACGGAAAACGAACAGTTGCGCGTTCTCGCCACCACCTGCTTTGCAGTATGGTCAACAAGATGGAGCAGCAATCCAGCCAACTT
dm3	chr3R:1060662-1060821 +		GCTACCTTCATAAAGACATAACCCTGGATGACCACTTCGAGCGGCTTCTGACCGATTTGACGCAGCTTTCGCTTAATTCGGACAACGAACAGTTGCGTGTAATCGCTCACCACCTGCTCTGTAGCATGGTCAACAAGATGGAGTCGAACCCAGCTAAACT
droSim2	3r:967376-967535 +		GCTACCTTCATAAAGACATAACCCTGGATGACCACTTCGAGCGGCTTCTGACCGATTTGACGCAACTTTCGCTTAATTGGGACAACGAACAGTTGCGTGTAATCGCTCACCACCTGCTCTGTAGCATGGTCAACAAGATGGAGTCGAACCCAGCTAACCT
droSec2	scaffold_6:1184691-1184850 +		GCTACCTTCATAAAGACATAACCCTGGATGACCACTTTGAGCGGCTTCTGACCGATTTGACGCAGCTTTCGCTTAATTCGGACAACGAACAGTTGCGTGTAATCGCTCACCACCTGCTCTGTAGCATGGTCAACAAGATGGAGTCGAACCCAGCTAACCG
droYak3	3R:1421953-1422112 +		GCTACCTTCATAAAGACATAACCCTTGATGATCACTTTGAGCGGCTTTGACCGATTTGACACAGCTTTGTCTTAATACGGATAACGAACAGTCGCGTGTAATTGCTCACCATCTGCTTTGTAGCATGGTCAACAAGATGGACTATAACCCAGCTAACCT
droEre2	scaffold_4770:1337314-1337473 +		GCTACCTTCATAAAGACATAACCCTGGATGACCATTTGAGCGGCTTCTGACCGATTTGACACAGCTCTCTCTTAATACGGATAACGAACAGTTGCGTGTAGCATGGTCAACAAGATGGACGTAACCCAGCTAACCT
dp5	2:21727640-21727799 -		GCTACCTCCACAAGGACATAAGCCTGGACGATCACTTCGAGCGGCTGCTGAGCGATCTCACCCAGCTCTGCCTGACCACGACAACGAGCAGCTGCGCGTGATTGCCCACCATTTGCTTTGCAGTTTGGTGAACAAAATGGACAACCACAAGGGGAACCG
droPer2	scaffold_3:4511847-4512006 -		GCTACCTCCACAAGGACATAAGCCTGGACGATCACTTCGAGCGGCTGCTGAGCGATCTCACCCAGCTCTCCCTGACCACGACAACGAGCAGCTGCGCGTGATTGCCCACCATTTGCTCTGCAGTTTGGTGAACAAAATGGACAACCACAAGGGGAACCG
droWil2	scf2_1100000004943:12869958-12870117 -		GTTATCTTCATCAAGACATCAGTTTGGATGATCATTTTGAGCGTTTGCTAAACGATCTAACAAACTATGCCTGAGCTCTGATAATGAAAAGCTGCGAGTGATTGCCCATTCATCTGCTATGCAGTTTGGTTAACAAAATGGACAATACGCCAGAAAATCG
droVir3	scaffold_12855:7845104-7845263 -		GTTACTTGCACAAGGACATCAGTTTGGATGATCATTTCGAGCGGTTGCTCGACGATCTAACTAAGTTATCGGCTAAGCACGGATAACGAGCAGCTGCGTGAGATTGCCATCACCTGCTCTGCAGTCTGGTCAATAAAATGGACAACAATGAGGCAAATCG
droMoj3	scaffold_6540:23067685-23067844 -		GCTATCTGCACAAGGACATTTCTCTCGACGATCACTTCGAGCGTCTGCTGACGATCTCACCAAGCTGTCGCTCAGCTCTGACAATGAACAGTTGCGCACCATTGCCCATCATTTGCTCTGCAGCTTGGTGAACAAAATGGACAACACTAAGGAGAATCG
droGri2	scaffold_15074:4415193-4415352 -		GCTATCTGCACAAGGACATCACTCTCGACGATCACTTCGAGCGACTGCTCGACGATCTAACCAAATTGTCGCTCAACGCGCACAATGAACAGTTGCGTGCCATTGCCCATCGCTTGCTCTGCAGCCTGGTCAACAAAATGGACAACAATTCAACGAAATCG

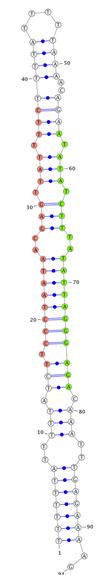
Generated: 09/08/2015 at 07:47 PM

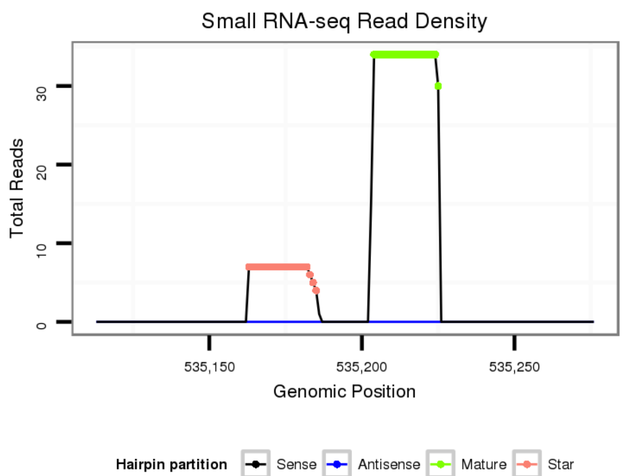
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

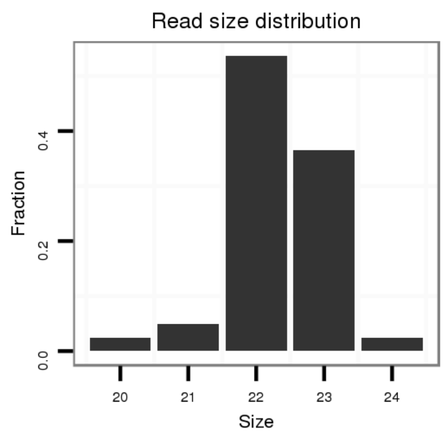
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_103	**scaffold_12903:535163-535226 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

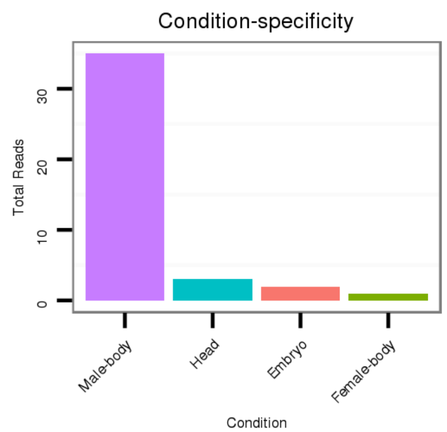
Legend: mature star mismatch in alignment mismatch in read

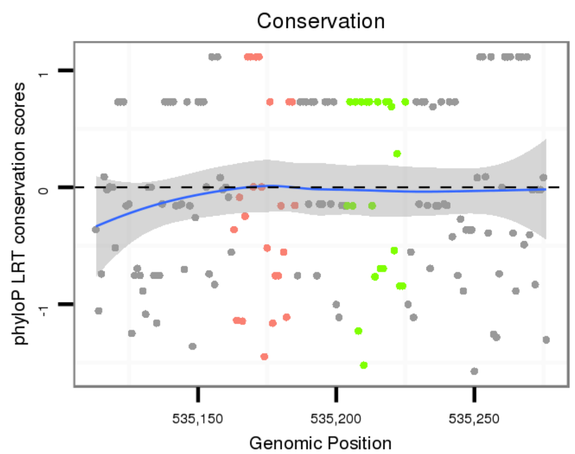
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTAAATTTTTTAACAAAAGTGACATTTTTTCAGTTTTTTTTATTTTTATCTTCCCTAATAACGAGTTATTTTCTTTTATTTTTAAAACAGAATATATCTTTATATTAGGGAGACAAATTTGAGAAAAGTCTACAATTCAAAAATTGTTATTAAATATGTTTTTT	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	M058 embryo	V055 head	V106 head	M044 female body	V039 embryo
**********(((((((..(((.(((.(((((((((..(((.(((.(((((((((....)))))..))))).))).))).))))))))))).)))..)))))))..**********											
.....ATATATCTTTATATTAGGGAGA.....	22	0	1	18.00	18	17	0	0	1	0	0
.....AATATATCTTTATATTAGGGAGA.....	23	0	1	12.00	12	12	0	0	0	0	0
.....TTCCCTAATAACGAGTTATTTTC.....	23	0	1	3.00	3	1	1	0	0	1	0
.....AATATATCTTTATATTAGGGAG.....	22	0	1	3.00	3	3	0	0	0	0	0
.....TTCCCTAATAACGAGTTATT.....	20	0	1	1.00	1	1	0	0	0	0	0
.....ATATATCTTTATATTAGGGAGAA.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TTCCCTAATAACGAGTTATTTT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....ATATATCTTTATATTAGGGAG.....	21	0	1	1.00	1	0	0	0	1	0	0
.....TTCCCTAATAACGAGTTATTTTCT.....	24	0	1	1.00	1	0	1	0	0	0	0
.....TTCCCTAATAACGAGTTATTT.....	21	0	1	1.00	1	0	0	1	0	0	0
.....ATATATCTTTATATTAGGGAGAT.....	23	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

AATTTAAAAAATTGTTTTCACTGTAAAAAAGTCAAAAAAAATAAAAATAGAAGGGATTATTGCTCAATAAAAGAAAATAAAAATTTTGTCTTATATAGAAATATAATCCCTCTGTTTAAACTCTTTTCAGATGTTAAGTTTTTAACAATAATTTATACAAAAAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body
**********(((((((..(((.(((.(((((((((..(((.(((.(((((((((....)))))..))))).))).))).))))))))))).)))..)))))))..**********						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:535113-535276 +	dan_103	TTAAATTTTTTAACAAAAGTGACATTTTTTCAGTTTTTTTTATTTTTA----------TCTTCCCTAA--TAACG-----AGTTATTTTCTTTTATTTTTAAAACAGAATATATCTTTATATTAGGGAGACAAATTTGAGAA--AAGTCTACAATTCAAAAATTGTTATTAAA------TATGTTT-----TTT
droBip1	scf7180000395952:1135-1307 -		TACATTT-TTTAATTGTTT--TGTTTTTTTCATTGTTTTTCTATTAATTCCTGATCCTCTGCTCTAA--TAAG-----ACAACATTCATTTATTATTAAAAATGAATATCTGTTTTTGCTAGAGGAAGTATTTGCGAA--AAGTCTTCG---GAAAAGTGCGTATTGGA------TTTAAAAAACATATG
droTak1	scf7180000415843:978126-978297 -		CCAAACAGTTTTGGAAA----ACACTTTTATGATACGTTTCATTTTTT----------AACATGATAGAATAGAAACTGTAGTTTCCTTTTTTTGTTTCCAACGAACATTTTTTTTTTTATTATTAGG---AAGCACTTAAGTTTTAGATGTAAATAAAAAAAATAGTAATTAAAGGTTGCTTTATTT-----TTC
droGri2	scaffold_14822:226626-226689 -		ATACATT----------TATATATA----------AGAATGATAAACTAAGCCCTG----------T---CTAACATTATTATTATA------TTTATAT-----TAT

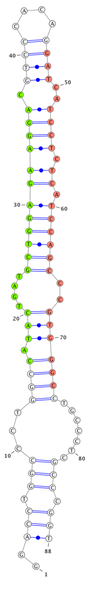
Generated: 09/08/2015 at 08:05 PM

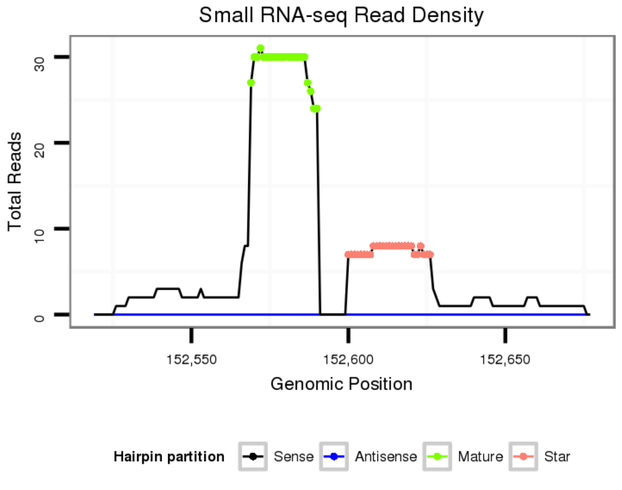
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

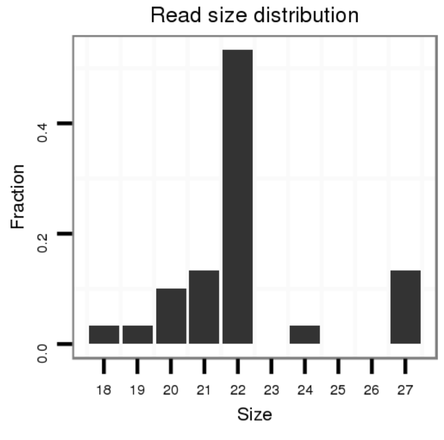
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_169	**scaffold_12929:152569-152627 +**	**confident**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

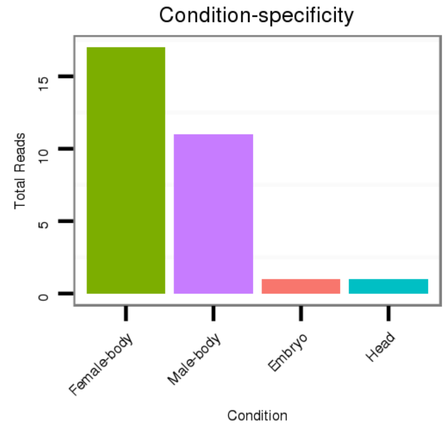
Legend: mature star mismatch in alignment mismatch in read

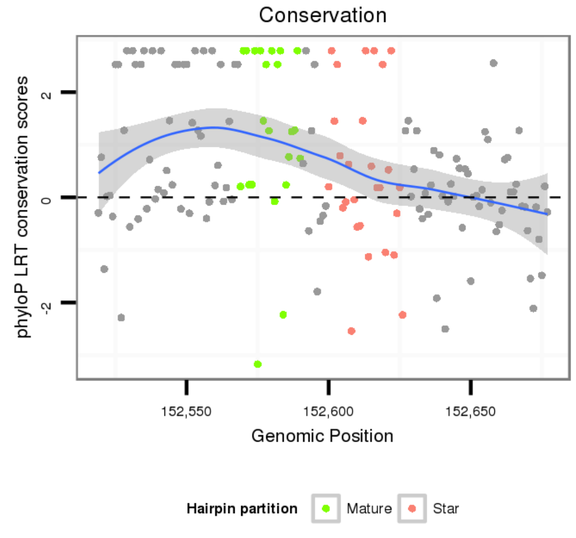
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dana\GF22086-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTTGTGGGAGTTACTCACATTTACCAGCCGCCCCAGGACCTGGCCCTGGCCATACTGATGCTGGAGAAGGACGTCCCACAGGATCATCCTCTCATCCAGCCCGTGGGCCTGCCCTCGCCCGGTGAGACTTCTGTCCTGGATTCCTCCGATGCTTCGCAG **********..(((.(((...((((.(((....(((((((((((.((((....)))))..))))).)).)))))).))))))).....)))********** **Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M044 female body**	**V105 male body**	**M058 embryo**	**V055 head**	**V106 head**	**V039 embryo**
.....CATACTGATGCTGGAGAAGGAC..... 22	0	1	16.00	16	6	8	1	0	1	0
.....GATCATCCTCTCATCCAGCCCGTGGGC..... 27	0	1	4.00	4	4	0	0	0	0	0
.....ATACTGATGCTGGAGAAGGAC..... 21	0	1	3.00	3	1	2	0	0	0	0
.....GGCCATACTGATGCTGGAGAAGGAC..... 25	0	1	3.00	3	1	0	2	0	0	0
.....GGCCATACTGATGCTGGAGAA..... 21	0	1	2.00	2	2	0	0	0	0	0
.....CATACTGATGCTGGAGAAGG..... 20	0	1	2.00	2	1	1	0	0	0	0
.....GATCATCCTCTCATCCAGCCC..... 21	0	1	1.00	1	1	0	0	0	0	0
.....GATTCCTCCGATGCTTCGC.. 19	0	1	1.00	1	1	0	0	0	0	0
.....GATCATCCTCTCATCCAGCCCGTGGGCCT..... 29	0	1	1.00	1	1	0	0	0	0	0
.....GATCATCCTCTCATCCAGCCCGTG..... 24	0	1	1.00	1	1	0	0	0	0	0
.....GCCATACTGATGCTGGAGAAGGAC..... 24	0	1	1.00	1	1	0	0	0	0	0
.....CATACTGATGCTGGAGAA..... 18	0	1	1.00	1	1	0	0	0	0	0
.....GCCATACTGATGCTGGAGAAG..... 21	0	1	1.00	1	0	1	0	0	0	0
.....ACTGATGCTGGAGAAGGAC..... 19	0	1	1.00	1	1	0	0	0	0	0
.....TTACCAGCCGCCCCAGGACCTGGCCCT..... 27	0	1	1.00	1	1	0	0	0	0	0
.....GTGAGACTTCTGTCCTGGATT..... 21	0	1	1.00	1	1	0	0	0	0	0
..........TACTCACATTTACCAGCCGCCCCA..... 24	0	1	1.00	1	1	0	0	0	0	0
.....TCTCATCCAGCCCGTGGGCC..... 20	0	1	1.00	1	1	0	0	0	0	0
..............................AGGACCTGGCCCTGGCCATA..... 20	0	1	1.00	1	1	0	0	0	0	0
.....GGGCCTGCCCTCGCCCGGTGAGA..... 23	0	1	1.00	1	1	0	0	0	0	0
.......GAGTTACTCACATTTACCAGC..... 21	0	1	1.00	1	0	0	1	0	0	0

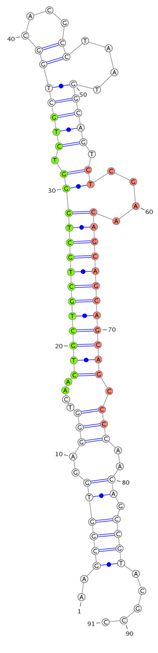
Anti-sense strand reads

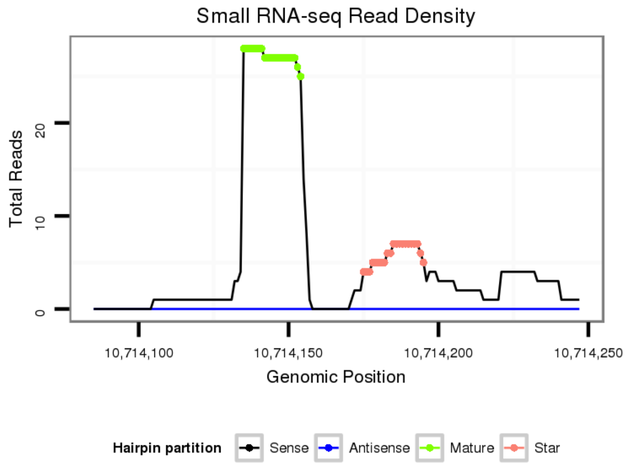
CAACACCCTCAATGAGTGTAAATGGTCGGCGGGGTCCTGGACCGGGACCGGTATGACTACGACCTCTTCCTGCAGGGTGTCCTAGTAGGAGAGTAGGTCGGGCACCCGGACGGGAGCGGGCCACTCTGAAGACAGGACCTAAGGAGGCTACGAAGCGTC **********..(((.(((...((((.(((....(((((((((((.((((....)))))..))))).)).)))))).))))))).....)))********** **Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V055 head**	**V105 male body**	**M044 female body**	**V106 head**	**M058 embryo**
..TTACCAGCCGCCCCAGGACCTGGCCCT..... 27	0	1	1.00	1	1	0	0	0	0
..........TACTCACATTTACCAGCCGCCCCA..... 24	0	1	1.00	1	1	0	0	0	0
.....GTGAGACTTCTGTCCTGGATT..... 21	0	1	1.00	1	1	0	0	0	0
.....ACTGATGCTGGAGAAGGAC..... 19	0	1	1.00	1	1	0	0	0	0
.....GCCATACTGATGCTGGAGAAG..... 21	0	1	1.00	1	0	1	0	0	0
.....GCCATACTGATGCTGGAGAA..... 18	0	1	1.00	1	1	0	0	0	0
.....GCCATACTGATGCTGGAGAAGGAC..... 24	0	1	1.00	1	1	0	0	0	0
.....GATCATCCTCTCATCCAGCCCGTG..... 24	0	1	1.00	1	1	0	0	0	0
.....GATCATCCTCTCATCCAGCCCGTGGGCCT..... 29	0	1	1.00	1	1	0	0	0	0
.....GATTCCTCCGATGCTTCGC.. 19	0	1	1.00	1	1	0	0	0	0
.....CCCTCTCCGGACGCCACTTCGATCCTGGACGATCGGA---GGCAGGATAA-									
.....CCCTCTCCGGACGCCACTTCCATCCTGGACGCT

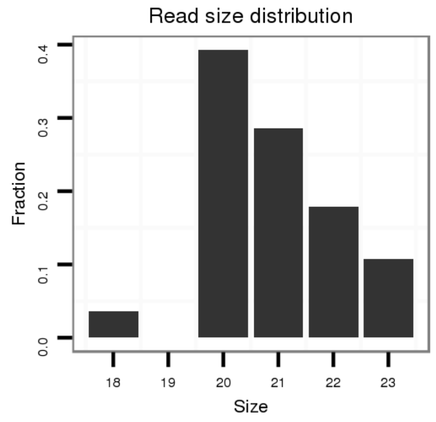
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_185	**scaffold_13266:10714135-10714197 +**	**confident**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

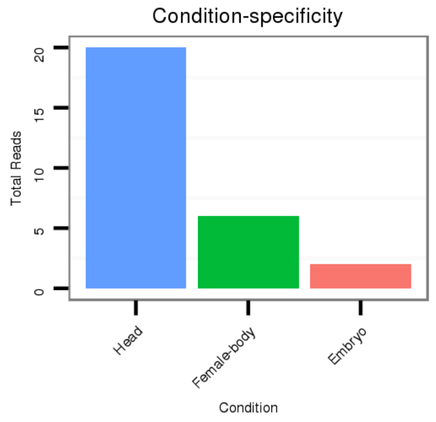
Legend: mature star mismatch in alignment mismatch in read

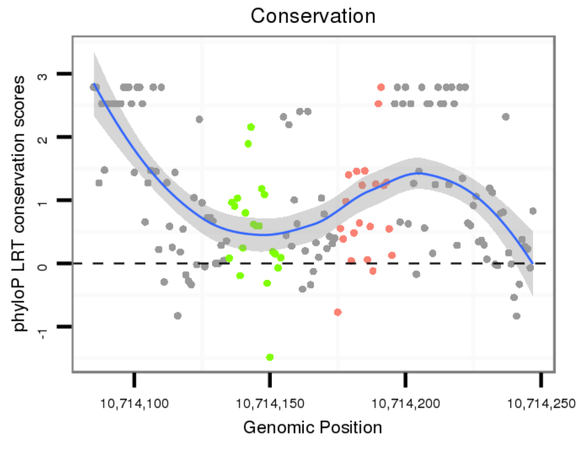
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dana\GF13242-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATCCAGCCGGGTATGATACGTATTATCCCCAATGCAAGCGGTGGAGGGTCAACTGCTGCTGCTGGGTCTGCTGGCACGCCTAATGGCAGTCTCGAACAGCAGCAGCAGCCCCAACAGCCGTACGCCCTGCATACGTAACCCCAAGCTCGTGCTGCTTTAACTG	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	M058 embryo	V055 head	V105 male body	V039 embryo
**********..(((((((..(((....(((((((((((((((.(((((((....))....))))))..))....))))))))))))).)))..))..))))).....**********											
.....AACTGCTGCTGCTGGGTCTG.....	20	0	1	11.00	11	9	2	0	0	0	0
.....AACTGCTGCTGCTGGGTCTGC.....	21	0	1	6.00	6	4	2	0	0	0	0
.....AACTGCTGCTGCTGGGTCTGCT.....	22	0	1	5.00	5	5	0	0	0	0	0
.....AACCCCAAGCTCGTGCTGCT.....	20	0	1	2.00	2	0	1	1	0	0	0
.....GTCAACTGCTGCTGCTGGGTCTGCT.....	25	0	1	2.00	2	0	2	0	0	0	0
.....CTCGAACAGCAGCAGCAGCCC.....	21	0	1	2.00	2	0	0	2	0	0	0
.....AACAGCCGTACGCCCTGC.....	18	0	1	1.00	1	0	1	0	0	0	0
.....GAACAGCAGCAGCAGCCCCAAC.....	22	0	1	1.00	1	0	0	1	0	0	0
.....AGCAGCAGCCCCAACAGCCGT.....	21	0	1	1.00	1	0	0	0	0	0	1
.....CAGTCTCGAACAGCAGCAGCAGC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....AGTCTCGAACAGCAGCAGCAGCC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....AACTGCTGCTGCTGGGTCTGCTG.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GGTGGAGGGTCAACTGCT.....	18	0	1	1.00	1	0	0	0	0	1	0
.....AACTGCTGCTGCTGGGTC.....	18	0	1	1.00	1	0	0	0	1	0	0
.....AACCCCAAGCTCGTGCTGCTTTAACTG	27	0	1	1.00	1	0	1	0	0	0	0
.....CAACTGCTGCTGCTGGGTCT.....	20	0	1	1.00	1	0	0	0	0	1	0
.....AACTGCTGCTGCTGGGTCTGT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TATTATCCCCAATGCAAGC.....	19	0	1	1.00	1	0	0	1	0	0	0
.....AACTGCTGCTGCTGGGTCTT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....GTACGCCCTGCATACGTAACCCCAAGCTC.....	29	0	1	1.00	1	0	0	1	0	0	0
.....GCAGCAGCAGCCCCAACAGCC.....	21	0	1	1.00	1	0	0	1	0	0	0
.....GCTGCTGGGTCTGCTGGCACGCCG.....	24	1	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

TAGGTCGGCCCATACTATGCATAATAGGGGTTACGTTCGCCACCTCCCAGTTGACGACGACGACCCAGACGACCGTGCGGATTACCGTCAGAGCTTGTCGTCGTCGTCGGGGTTGTCGGCATGCGGGACGTATGCATTGGGGTTCGAGCACGACGAAATTGAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	V055 head	V105 male body	V039 embryo
**********..((((((..(((....(((((((((((((((.(((((((....))....))))))..))....))))))))))))).)))..))..))))).....**********									
.....AACTGCTGCTGCTGGGTCTG.....	20	0	1	11.00	11	9	2	0	0	0	0
.....AACTGCTGCTGCTGGGTCTGC.....	21	0	1	6.00	6	4	2	0	0	0	0
.....AACTGCTGCTGCTGGGTCTGCT.....	22	0	1	5.00	5	5	0	0	0	0	0
.....AACCCCAAGCTCGTGCTGCT.....	20	0	1	2.00	2	0	1	1	0	0	0
.....GTCAACTGCTGCTGCTGGGTCTGCT.....	25	0	1	2.00	2	0	2	0	0	0	0
.....CTCGAACAGCAGCAGCAGCCC.....	21	0	1	2.00	2	0	0	2	0	0	0
.....AACAGCCGTACGCCCTGC.....	18	0	1	1.00	1	0	1	0	0	0	0
.....GAACAGCAGCAGCAGCCCCAAC.....	22	0	1	1.00	1	0	0	1	0	0	0
.....AGCAGCAGCCCCAACAGCCGT.....	21	0	1	1.00	1	0	0	0	0	0	1
.....CAGTCTCGAACAGCAGCAGCAGC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....AGTCTCGAACAGCAGCAGCAGCC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....AACTGCTGCTGCTGGGTCTGCTG.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GGTGGAGGGTCAACTGCT.....	18	0	1	1.00	1	0	0	0	0	1	0
.....AACTGCTGCTGCTGGGTC.....	18	0	1	1.00	1	0	0	0	1	0	0
.....AACCCCAAGCTCGTGCTGCTTTAACTG	27	0	1	1.00	1	0	1	0	0	0	0
.....CAACTGCTGCTGCTGGGTCT.....	20	0	1	1.00	1	0	0	0	0	1	0
.....AACTGCTGCTGCTGGGTCTGT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TATTATCCCCAATGCAAGC.....	19	0	1	1.00	1	0	0	1	0	0	0
.....AACTGCTGCTGCTGGGTCTT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....GTACGCCCTGCATACGTAACCCCAAGCTC.....	29	0	1	1.00	1	0	0	1	0	0	0
.....GCAGCAGCAGCCCCAACAGCC.....	21	0	1	1.00	1	0	0	1	0	0	0
.....GCTGCTGGGTCTGCTGGCACGCCG.....	24	1	1	1.00	1	0	0	1	0	0	0

Show Alignment With Reads

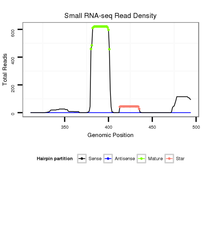
Re-alignment of all predicted orthologs

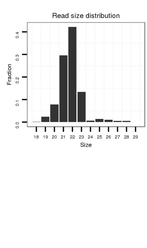
Species	Coordinate	ID	Alignment
droAna3	scaffold_13266:10714085-10714247 +	dan_185	ATCCAGCCGGGTATGATACGTATTATCCCCAATGCAAGCGGT---GGAGGGTCAACTGCTGCTGCTGGGTCTGCTGGCACGCCTAATGGCAGTCTCG-AA----CA----------GCAGCAGCA----------G----------CCCCAACAGCCGTACGCCCTGCATACGTAACCCCA-----AGC------TCG----------TGCTGCTTTAACTG
droBip1	scf7180000396428:1143035-1143209 +		ATCCAGCCGGGTATGATACGTATTATCCCCAAGCAAGCGGTGCCGG---GGCAGCTGCTGC---TGCCTCGCTGGCACGCCCAACGGCAGTCTCG-AA----CA----------GCAGCAGCAGCC----------G----------CCCCAACAACCGTACGCCCTGCATACGTAACCCCAGCTCCAGGTCGTGCTCG----------TGCTGCT--T-AAAACTG
droKik1	scf7180000302682:1016918-1017040 +		ATTCAGCCGGGTATGCTACACTTTGTACCCC----------CGTTCTGC---TGCGGCTGCT---------GGCGGCGGACTGGA----GA----------TCAGCAGCAGCAGCAGCC----------G----------CCCCAGCAGCCCTACGCACTGCATACGTAACCC----------CCCCC

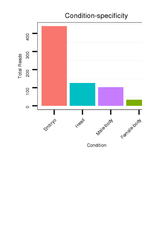
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_4035	scaffold_2263:361-444 +	confident	Canonical miRNA	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

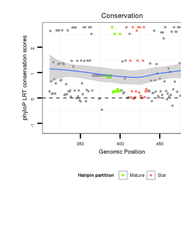
Legend: mature star mismatch in arm/star mismatch in loop

Predicted structure









Show Alternate Folds

FlyBase annotation

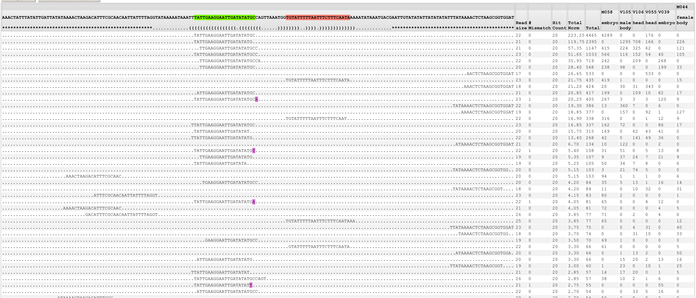
dsRNA:[Dsur2.0]dsRNA(CJT3600-RA)

No flyanatble elements found

mature	star
1. scaffold_2826:992-1013 - 2. scaffold_3108:1361-1382 - 3. scaffold_3159:666-687 - 4. scaffold_3159:1000-1021 - 5. scaffold_3164:897-918 - 6. scaffold_3368:964-985 - 7. scaffold_3434:1000-1021 - 8. scaffold_3434:824-846 - 9. scaffold_3450:1062-1083 - 10. scaffold_3453:980-1001 - 11. scaffold_3474:633-674 - 12. scaffold_3474:1000-1021 - 13. scaffold_4336:700-721 - 14. scaffold_4845:777-798 - 15. scaffold_4894:1000-1021 - 16. scaffold_4904:1061-1082 - 17. scaffold_5016:639-680 - 18. scaffold_5185:989-1010 - 19. scaffold_5352:8525-8545 - 20. scaffold_5352:8525-8545_MM4 21. dan_4035 scaffold_2263:286-405 + 22. scaffold_2264:233-254 - 23. scaffold_2847:58-81 + 24. scaffold_2847:58-81 + 25. scaffold_2624:589-610 - 26. scaffold_2837:586-607 + 27. scaffold_3261:240-261 + 28. scaffold_3261:240-261 + 29. scaffold_3402:341-362 + 30. scaffold_3404:584-605 + 31. scaffold_3432:586-607 + 32. scaffold_3496:2-23 + 33. scaffold_3496:2-23 + 34. scaffold_4374:586-607 + 35. scaffold_4374:616-638 + 36. scaffold_4374:616-638 + 37. scaffold_4569:91-112 + 38. scaffold_5100:369-390 + 39. scaffold_5124:577-598 + 40. scaffold_5183:6424-6445 + 41. scaffold_5183:6424-6445 + 42. scaffold_5094:1502-1523 + 43. scaffold_3402:385-406 +	1. dan_4035 scaffold_2263:410-431 + 2. scaffold_2264:306-368 + 3. scaffold_2387:385-425 + 4. scaffold_2624:632-653 + 5. scaffold_2624:632-644 + 6. scaffold_2837:639-661 + 7. scaffold_3402:384-405 + 8. scaffold_3405:609-631 + 9. scaffold_3403:276-306 + 10. scaffold_3403:248-269 + 11. scaffold_3450:613-639 + 12. scaffold_3474:613-639 + 13. scaffold_3496:25-51 + 14. scaffold_4045:677-679 + 15. scaffold_4045:677-679 + 16. scaffold_5035:631-651 + 17. scaffold_4879:274-306 + 18. scaffold_4569:961-1004 + 19. scaffold_5100:402-424 + 20. scaffold_5352:8525-8579 + 21. scaffold_5124:618-632 +

Sense Strand Reads

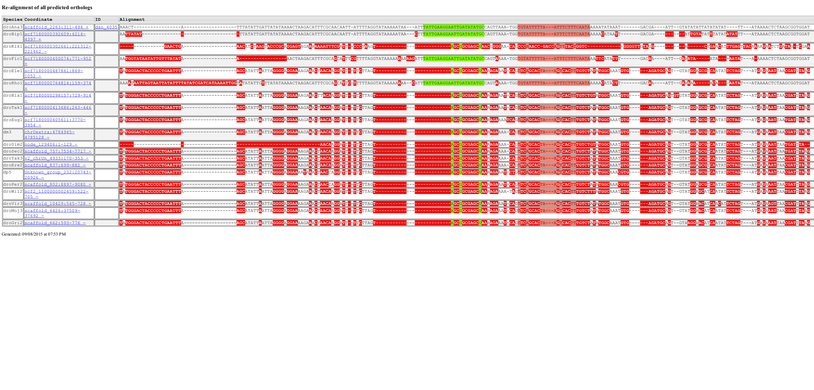
hide 3p reads | show mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

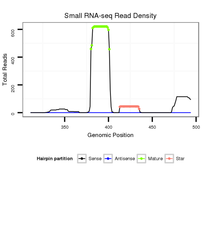


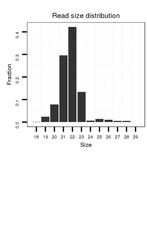
Generated 09/08/2015 at 07:53 PM

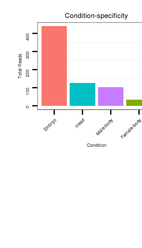
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_4035	scaffold_2263:361-444 +	confident	Canonical miRNA	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

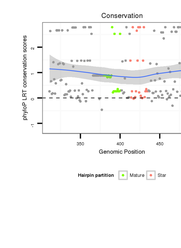
Legend: mature star mismatch in arm/star mismatch in loop

Predicted structure









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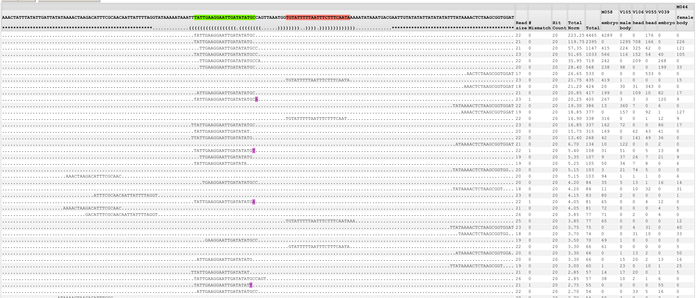
Sense Strand Reads

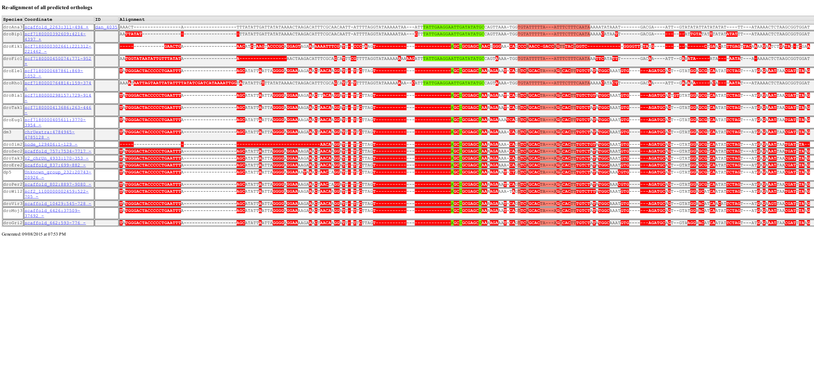
hide 3p reads | show mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

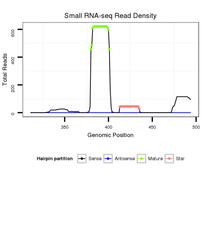


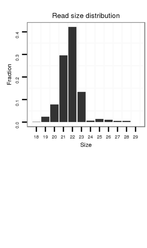
Generated 09/08/2015 at 07:53 PM

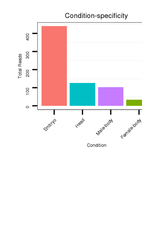
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_4035	scaffold_2263:361-444 +	confident	Canonical miRNA	intergenic	[View on UCSC Genome Browser (Cornell Mirror)]

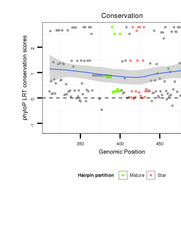
Legend: mature star mismatch in arm/star mismatch in loop

Predicted structure









Show Alternate Folds

FlyBase annotation

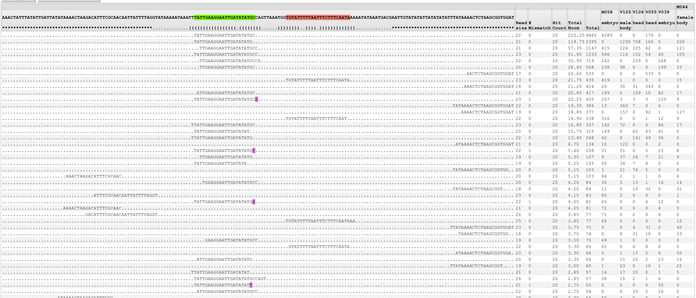
dsRNA:[Dsur2.0]dsRNA(CJT3600-RA)

No flyanatble elements found

mature	star
1. scaffold_2826:992-1013 - 2. scaffold_3108:1361-1382 - 3. scaffold_3159:666-687 - 4. scaffold_3159:1000-1021 - 5. scaffold_3164:897-918 - 6. scaffold_3368:964-985 - 7. scaffold_3434:1000-1021 - 8. scaffold_3434:824-846 - 9. scaffold_3450:1062-1083 - 10. scaffold_3453:980-1001 - 11. scaffold_3474:633-674 - 12. scaffold_3474:1000-1021 - 13. scaffold_4336:700-721 - 14. scaffold_4845:777-798 - 15. scaffold_4894:1000-1021 - 16. scaffold_4904:1061-1082 - 17. scaffold_5016:639-680 - 18. scaffold_5185:989-1010 - 19. scaffold_5352:8525-8545 - 20. scaffold_5352:8525-8545_MM4 21. dan_4035 scaffold_2263:286-405 + 22. scaffold_2264:233-254 - 23. scaffold_2847:58-81 + 24. scaffold_2847:58-81 + 25. scaffold_2624:589-610 - 26. scaffold_2837:586-607 + 27. scaffold_3261:240-261 + 28. scaffold_3261:240-261 + 29. scaffold_3402:341-362 + 30. scaffold_3404:584-605 + 31. scaffold_3432:586-607 + 32. scaffold_3496:2-23 + 33. scaffold_3496:2-23 + 34. scaffold_4374:586-607 + 35. scaffold_4374:616-638 + 36. scaffold_4374:616-638 + 37. scaffold_4569:91-112 + 38. scaffold_5100:369-390 + 39. scaffold_5124:577-598 + 40. scaffold_5183:6424-6445 + 41. scaffold_5183:6424-6445 + 42. scaffold_5094:1502-1523 + 43. scaffold_3402:385-406 +	1. dan_4035 scaffold_2263:410-431 + 2. scaffold_2264:306-368 + 3. scaffold_2387:385-425 + 4. scaffold_2624:632-653 + 5. scaffold_2624:632-644 + 6. scaffold_2837:639-661 + 7. scaffold_3402:384-405 + 8. scaffold_3405:609-631 + 9. scaffold_3403:276-306 + 10. scaffold_3403:248-269 + 11. scaffold_3450:613-639 + 12. scaffold_3474:613-639 + 13. scaffold_3496:25-51 + 14. scaffold_4045:677-679 + 15. scaffold_4045:677-679 + 16. scaffold_5035:631-651 + 17. scaffold_4879:274-306 + 18. scaffold_4569:961-1004 + 19. scaffold_5100:402-424 + 20. scaffold_5352:8525-8579 + 21. scaffold_5124:618-632 +

Sense Strand Reads

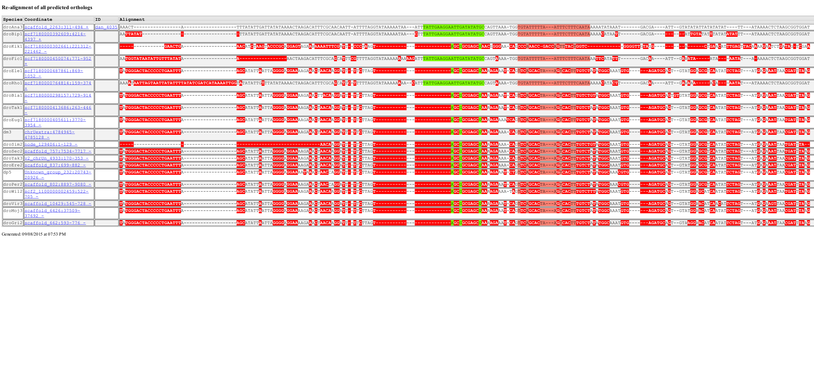
hide 3p reads | show mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

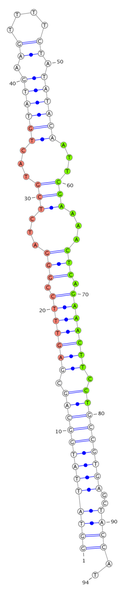


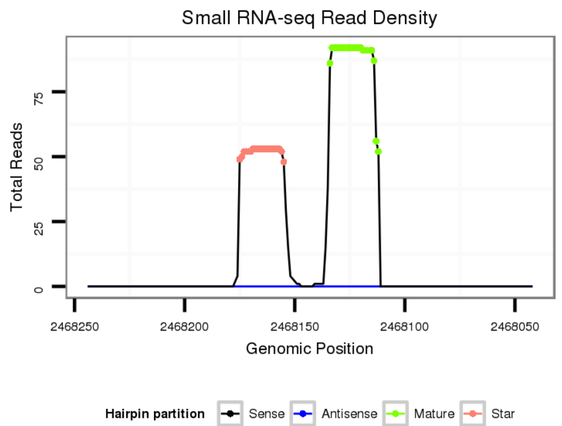
Generated 09/08/2015 at 07:53 PM

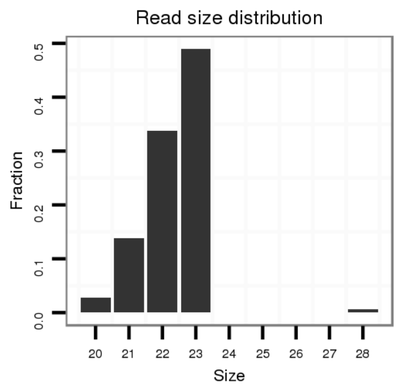
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_229	**scaffold_13417:2468092-2468194 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

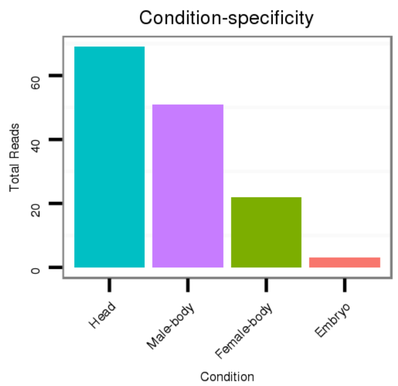
Legend: mature star mismatch in alignment mismatch in read

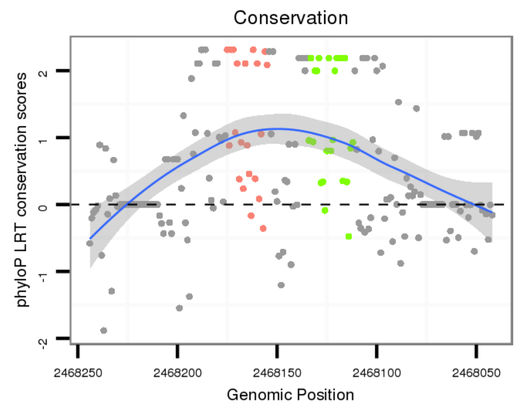
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTCCCCGCACTGAGACAGCTCCTGTGCGACAACCACGGGGTGCGGGGAGTACCTGGTATTATGGCAGCGAGTTTCCGGGATCTCGTACTGTATGAAGTTTTCTATATACAATTCGAAAACTCAGAAACTTCCTGCCGTGAGCTACCATTGATCAACGGCTGAGTATGCGACCGGAAAGGGGACGCGAATGCGAGGACTAAAGG	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	V055 head	M044 female body	M058 embryo
**********(((((((((((((.(((((((.(((...(((...(((((((.((....)).)))))))...)))...)))).)))))))..)))))..)))))..**********										
..ATTCGAAAACTCAGAAACTTCCT..	23	0	1	46.00	46	29	8	5	3	1
..AATTCGAAAACTCAGAAACTTC..	22	0	1	20.00	20	7	4	4	4	1
..AGTTTCCGGGATCTCGTACTG..	21	0	1	17.00	17	1	13	0	3	0
..AGTTTCCGGGATCTCGTACTGT..	22	0	1	14.00	14	0	8	1	5	0
..AGTTTCCGGGATCTCGTACTGTA..	23	0	1	11.00	11	1	4	2	4	0
..CAATTCGAAAACTCAGAAACTTC..	23	0	1	10.00	10	3	2	4	0	1
..TTCGAAAACTCAGAAACTTCCT..	22	0	1	6.00	6	4	1	1	0	0
..CAATTCGAAAACTCAGAAACTT..	22	0	1	4.00	4	2	2	0	0	0
..AGTTTCCGGGATCTCGTACT..	20	0	1	3.00	3	2	1	0	0	0
..AATTCGAAAACTCAGAAACTTCC..	23	0	1	3.00	3	1	1	0	1	0
..ATTCGAAAACTCAGAAACTTCCTT..	24	1	1	2.00	2	1	0	0	1	0
..ATTCGAAAACTCAGAAACTTC..	21	0	1	1.00	1	0	1	0	0	0
..CGAGTTTCCGGGATCTCGTACTGTATGA..	28	0	1	1.00	1	0	0	0	1	0
..TTTCCGGGATCTCGTACTGTAT..	22	0	1	1.00	1	0	1	0	0	0
..ATTCGAAAACTCAGAAACTTCCC..	23	1	1	1.00	1	1	0	0	0	0
..AGTTTCCGGGATCTCGTACTT..	21	1	1	1.00	1	0	1	0	0	0
..AATTCGAAAACTCAGAAACTTT..	22	1	1	1.00	1	0	0	0	1	0
..AGTTTCCGGGATCTCGTACTGTAAA..	25	2	1	1.00	1	0	0	1	0	0
..AATTCGAAAACTCAGAAACTTCA..	23	1	1	1.00	1	0	0	0	1	0
..ATTCGAAAACTCAGAAACTTCC..	22	0	1	1.00	1	1	0	0	0	0
..GAGTTTCCGGGATCTCGTACT..	21	0	1	1.00	1	0	1	0	0	0
..AGTTTCCGGGATCTCGTACTA..	21	1	1	1.00	1	0	1	0	0	0
..GTTTCCGGGATCTCGTACTG..	20	0	1	1.00	1	0	0	1	0	0
..GAGTTTCCGGGATCTCGTACTG..	22	0	1	1.00	1	0	1	0	0	0
..AGTTTCCGGGATCTCGTACTGTAA..	24	1	1	1.00	1	0	1	0	0	0
..TTTCCGGGATCTCGTACTGTATG..	23	0	1	1.00	1	0	0	0	1	0
..CGGGATCTCGTACTGTATGAAG..	22	0	1	1.00	1	0	1	0	0	0
..ATATACAATTCGAAAACTCAGA..	22	0	1	1.00	1	0	1	0	0	0
..GTTTCCGGGATCTCGTACTGTT..	22	1	1	1.00	1	0	0	0	1	0
..CGAGTTTCCGGGATCTCGTAC..	21	0	1	1.00	1	0	1	0	0	0
..GAGTTTCCGGGATCTCGTACTGA..	23	1	1	1.00	1	0	1	0	0	0

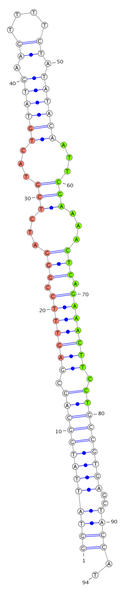
Anti-sense strand reads

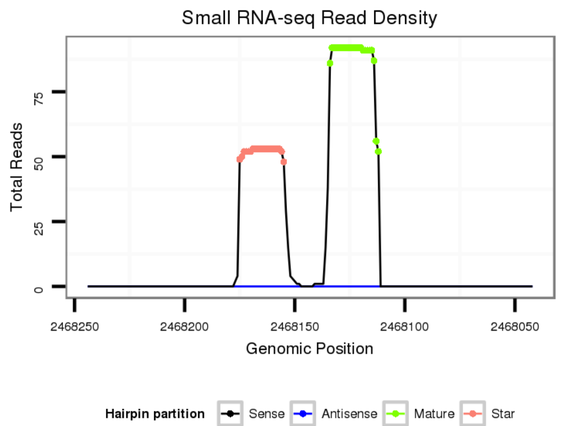
AAGGGGCGTGACTCTGTCGAGGACACGCTGTTGGTGCCCCACGCCCCTCATGGACCATAATACCGTCGCTCAAAGGCCCTAGAGCATGACATACTTCAAAAGATATATGTTAAGCTTTTGAGTCTTTGAAGGACGGCACTCGATGGTAACTAGTTGCCGACTCATACGCTGGCCTTTCCCCTGCGCTTACGCTCCTGATTTCC	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V105 male body	M058 embryo	V039 embryo	V106 head
**********(((((((((((((.(((((((.(((...(((...(((((((.((....)).)))))))...)))...)))).)))))))..)))))..)))))..**********										
..CCTGGTATAGCCGCAGAAAGTTTCCGAGTTTCGTAATGTATGGTTA...TATTTGAAAT..	22	0	1	14.00	14	0	8	1	5	0
..CCTGGTATTATCGCAGCAAGTTTCCGGGACTTCGTACTGTATGAA-G...AATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..AG...TC..CTCGAAGAC-AA..CAAGTCGTTGGTATTATCGCAGCAAGTTTCCGGGATTTCGTACTGTATGAC-A...AATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..CCTGGTATTATCGCAGCAAGTTTCCGGGATTTCGTACTGTATGAC-A...AATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..CCTGGTATTATCGCAGCAAGTTTCCGGGATTTCGTACTGTATGACTA...GATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..CCTGGTATTATCGCAGCAAGTTTCCGGGATTTCGTACTGTATGCT-G...AATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..TA..CCCTGATAGAGG..CGACATCGTGGTATTATCGCAATAAGTTCCTGGGATTTCCCACTGTATTAC-G...ATTTTTACAT..	23	0	1	10.00	10	3	2	4	0	1
..GGCTTTCCGGGATCTCGTACTT..	21	0	1	1.00	1	0	1	0	0	0
..GTTTCCGGGATCTCGTACTGTAT..	22

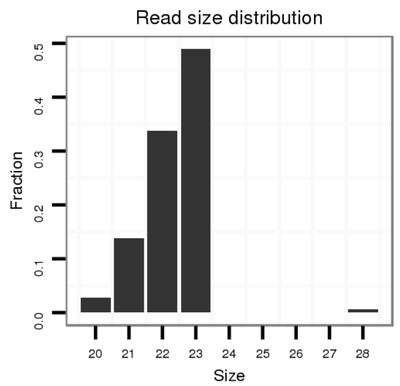
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_229	**scaffold_13417:2468092-2468194 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

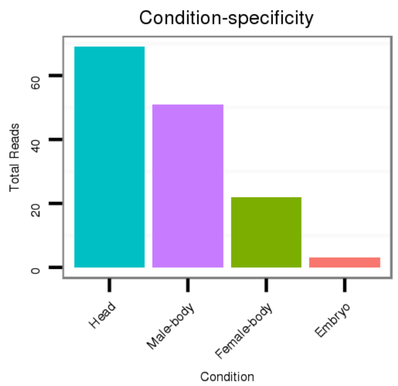
Legend: mature star mismatch in alignment mismatch in read

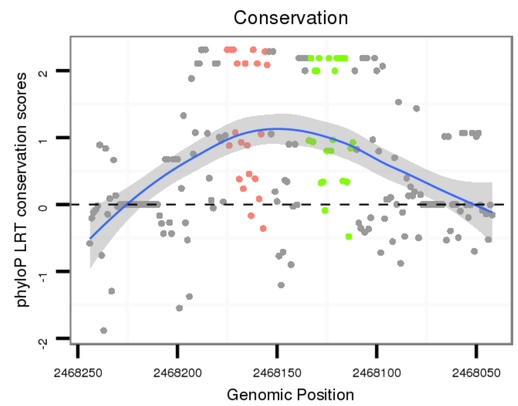
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTCCCCGCACTGAGACAGCTCCTGTGCGACAACCACGGGGTGCGGGGAGTACCTGGTATTATGGCAGCGAGTTTCCGGGATCTCGTACTGTATGAAGTTTTCTATATACAATTCGAAAACTCAGAAACTTCCTGCCGTGAGCTACCATTGATCAACGGCTGAGTATGCGACCGGAAAGGGGACGCGAATGCGAGGACTAAAGG	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	V055 head	M044 female body	M058 embryo
**********(((((((((((((.(((((((.(((...(((...(((((((.((....)).)))))))...)))...)))).)))))))..)))))..)))))..**********										
..ATTCGAAAACTCAGAAACTTCCT..	23	0	1	46.00	46	29	8	5	3	1
..AATTCGAAAACTCAGAAACTTC..	22	0	1	20.00	20	7	4	4	4	1
..AGTTTCCGGGATCTCGTACTG..	21	0	1	17.00	17	1	13	0	3	0
..AGTTTCCGGGATCTCGTACTGT..	22	0	1	14.00	14	0	8	1	5	0
..AGTTTCCGGGATCTCGTACTGTA..	23	0	1	11.00	11	1	4	2	4	0
..CAATTCGAAAACTCAGAAACTTC..	23	0	1	10.00	10	3	2	4	0	1
..TTCGAAAACTCAGAAACTTCCT..	22	0	1	6.00	6	4	1	1	0	0
..CAATTCGAAAACTCAGAAACTT..	22	0	1	4.00	4	2	2	0	0	0
..AGTTTCCGGGATCTCGTACT..	20	0	1	3.00	3	2	1	0	0	0
..AATTCGAAAACTCAGAAACTTCC..	23	0	1	3.00	3	1	1	0	1	0
..ATTCGAAAACTCAGAAACTTCCTT..	24	1	1	2.00	2	1	0	0	1	0
..ATTCGAAAACTCAGAAACTTC..	21	0	1	1.00	1	0	1	0	0	0
..CGAGTTTCCGGGATCTCGTACTGTATGA..	28	0	1	1.00	1	0	0	0	1	0
..TTTCCGGGATCTCGTACTGTAT..	22	0	1	1.00	1	0	1	0	0	0
..ATTCGAAAACTCAGAAACTTCCC..	23	1	1	1.00	1	1	0	0	0	0
..AGTTTCCGGGATCTCGTACTT..	21	1	1	1.00	1	0	1	0	0	0
..AATTCGAAAACTCAGAAACTTT..	22	1	1	1.00	1	0	0	0	1	0
..AGTTTCCGGGATCTCGTACTGTAAA..	25	2	1	1.00	1	0	0	1	0	0
..AATTCGAAAACTCAGAAACTTCA..	23	1	1	1.00	1	0	0	0	1	0
..ATTCGAAAACTCAGAAACTTCC..	22	0	1	1.00	1	1	0	0	0	0
..GAGTTTCCGGGATCTCGTACT..	21	0	1	1.00	1	0	1	0	0	0
..AGTTTCCGGGATCTCGTACTA..	21	1	1	1.00	1	0	1	0	0	0
..GTTTCCGGGATCTCGTACTG..	20	0	1	1.00	1	0	0	1	0	0
..GAGTTTCCGGGATCTCGTACTG..	22	0	1	1.00	1	0	1	0	0	0
..AGTTTCCGGGATCTCGTACTGTAA..	24	1	1	1.00	1	0	1	0	0	0
..TTTCCGGGATCTCGTACTGTATG..	23	0	1	1.00	1	0	0	0	1	0
..CGGGATCTCGTACTGTATGAAG..	22	0	1	1.00	1	0	1	0	0	0
..ATATACAATTCGAAAACTCAGA..	22	0	1	1.00	1	0	1	0	0	0
..GTTTCCGGGATCTCGTACTGTT..	22	1	1	1.00	1	0	0	0	1	0
..CGAGTTTCCGGGATCTCGTAC..	21	0	1	1.00	1	0	1	0	0	0
..GAGTTTCCGGGATCTCGTACTGA..	23	1	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

AAGGGGCGTGACTCTGTCGAGGACACGCTGTTGGTGCCCCACGCCCCTCATGGACCATAATACCGTCGCTCAAAGGCCCTAGAGCATGACATACTTCAAAAGATATATGTTAAGCTTTTGAGTCTTTGAAGGACGGCACTCGATGGTAACTAGTTGCCGACTCATACGCTGGCCTTTCCCCTGCGCTTACGCTCCTGATTTCC	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V105 male body	M058 embryo	V039 embryo	V106 head
**********(((((((((((((.(((((((.(((...(((...(((((((.((....)).)))))))...)))...)))).)))))))..)))))..)))))..**********										
..CCTGGTATAGCCGCAGAAAGTTTCCGAGTTTCGTAATGTATGGTTA...TATTTGAAAT..	22	0	1	14.00	14	0	8	1	5	0
..CCTGGTATTATCGCAGCAAGTTTCCGGGACTTCGTACTGTATGAA-G...AATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..AG...TC..CTCGAAGAC-AA..CAAGTCGTTGGTATTATCGCAGCAAGTTTCCGGGATTTCGTACTGTATGAC-A...AATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..CCTGGTATTATCGCAGCAAGTTTCCGGGATTTCGTACTGTATGAC-A...AATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..CCTGGTATTATCGCAGCAAGTTTCCGGGATTTCGTACTGTATGACTA...GATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..CCTGGTATTATCGCAGCAAGTTTCCGGGATTTCGTACTGTATGCT-G...AATTCTATAT..	23	0	1	10.00	10	3	2	4	0	1
..TA..CCCTGATAGAGG..CGACATCGTGGTATTATCGCAATAAGTTCCTGGGATTTCCCACTGTATTAC-G...ATTTTTACAT..	23	0	1	10.00	10	3	2	4	0	1
..GGCTTTCCGGGATCTCGTACTT..	21	0	1	1.00	1	0	1	0	0	0
..GTTTCCGGGATCTCGTACTGTAT..	22