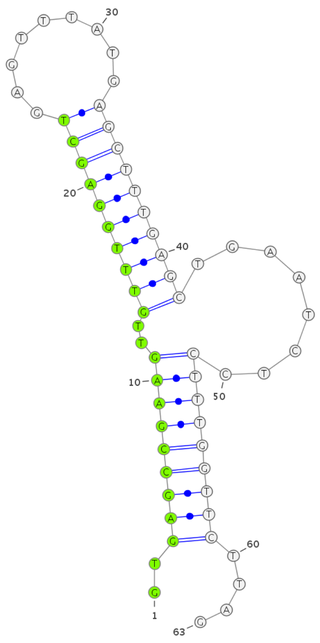
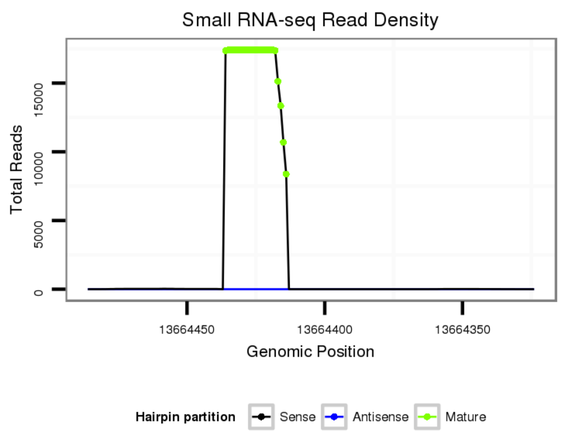
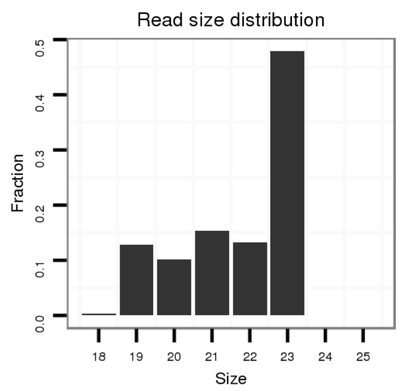
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_232	**scaffold_13337:13664374-13664436 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

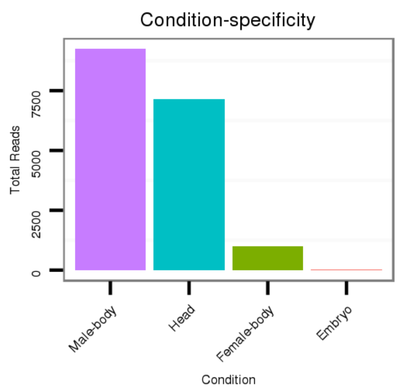
Legend: mature star mismatch in alignment mismatch in read

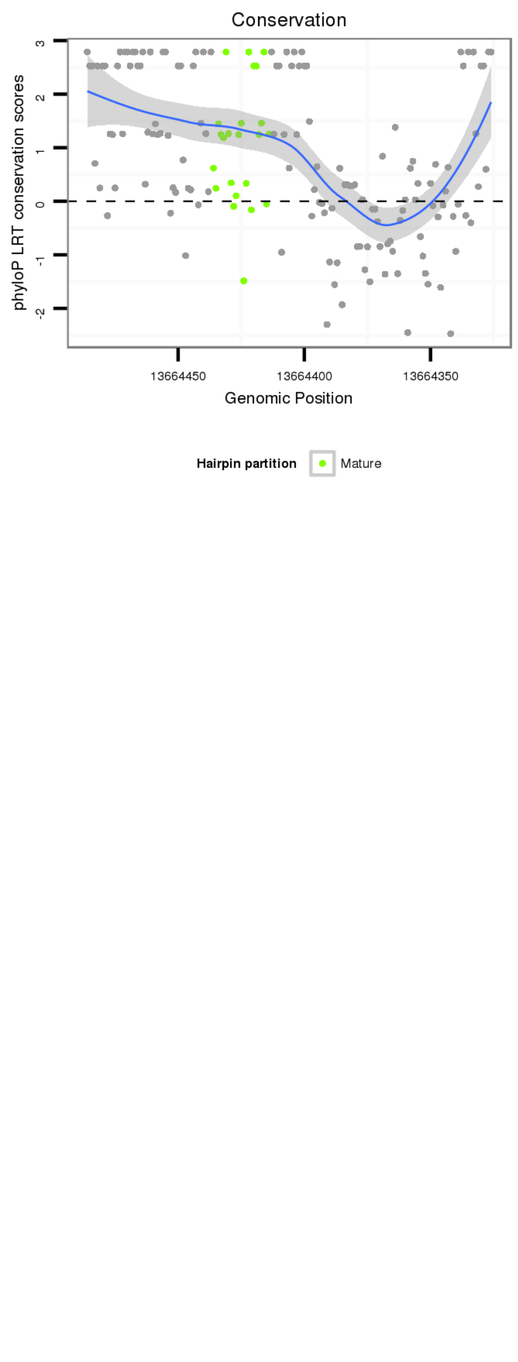
Predicted structure











dan_232_annot [-18.9]

Show Alternate Folds

Flybase annnotation

intron [Dana\GF23946-in]; CDS [Dana\GF23946-cds]; CDS [Dana\GF23946-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTACCGAGAAGCAGCTGGAGAGCGACATCGCCATTGTGCGCGTGGAGCAGGTGAGCCGAAGTTGTTTGGAGCT **********..(((((((((..(((((((((.....)))))))))).....)))))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V106 head	M044 female body	V055 head	M058 embryo	V039 embryo
.....GTGAGCCGAAGTTGTTTGGAGCT.....	23	0	1	8347.00	8347	4846	3007	356	125	7	6
.....GTGAGCCGAAGTTGTTTGGAG.....	21	0	1	2658.00	2658	1309	1078	115	152	1	3
.....GTGAGCCGAAGTTGTTTGGAGC.....	22	0	1	2295.00	2295	1216	769	207	93	8	2
.....GTGAGCCGAAGTTGTTTGG.....	19	0	1	2230.00	2230	864	1107	156	103	0	0
.....GTGAGCCGAAGTTGTTTGGA.....	20	0	1	1771.00	1771	993	609	103	65	1	0
.....GTGAGCCGAAGTTGTTTGGAGCTT.....	24	1	1	308.00	308	191	93	17	6	1	0
.....GTGAGCCGAAGTTGTTTGGAGT.....	22	1	1	124.00	124	61	44	12	7	0	0
.....GTGAGCCGAAGTTGTTTGGAGCTTT.....	25	2	1	54.00	54	27	21	2	4	0	0
.....GTGAGCCGAAGTTGTTTG.....	18	0	1	50.00	50	7	21	15	7	0	0
.....GTGAGCCGAAGTTGTTTGGAGA.....	22	1	1	46.00	46	19	22	0	4	1	0
.....GTGAGCCGAAGTTGTTTGGAT.....	21	1	1	36.00	36	16	19	0	1	0	0
.....GTGAGCCGAAGTTGTTTGGAA.....	21	1	1	33.00	33	17	11	1	2	0	2
.....GTGAGCCGAAGTTGTTTGT.....	19	1	1	28.00	28	5	22	1	0	0	0
.....TGAGCCGAAGTTGTTTGGAGCT.....	22	0	1	20.00	20	0	1	18	0	1	0
.....TGAGCCGAAGTTGTTTGGAGC.....	21	0	1	15.00	15	0	0	15	0	0	0
.....GTGAGCCGAAGTTGTTTGGAGCG.....	23	1	1	15.00	15	8	7	0	0	0	0
.....GTGAGCCGAAGTTGTTTGGAGCTA.....	24	1	1	13.00	13	3	8	0	2	0	0
.....TGAGCCGAAGTTGTTTGG.....	18	0	1	13.00	13	0	0	13	0	0	0
.....GTGAGCCGAAGTTGTTTGGAGCG.....	23	1	1	13.00	13	10	2	0	0	1	0
.....GTGAGCCGAAGTTGTTTGGAGCA.....	23	1	1	12.00	12	2	10	0	0	0	0
.....GTGAGCCGAAGTTGTTTGGTT.....	21	2	1	9.00	9	5	4	0	0	0	0
.....GTGAGCCGAAGTTGTTTGGT.....	20	1	1	9.00	9	3	5	0	1	0	0
.....GTGAGCCGAAGTTGTTTGGAGCTG.....	24	0	1	8.00	8	5	3	0	0	0	0
.....GTGAGCCGAAGTTGTTTGGAG.....	21	1	1	8.00	8	3	4	0	1	0	0
.....GCAGCTGGAGAGCGACATC.....	19	0	1	7.00	7	0	0	5	0	2	0
.....TCGCCATTGTGCGCGTGGAGCA.....	22	0	1	7.00	7	0	1	6	0	0	0
.....TGAGCCGAAGTTGTTTGGAG.....	20	0	1	6.00	6	0	0	6	0	0	0
.....GTGAGCCGAAGTTGTTTGGAAA.....	22	2	1	5.00	5	3	2	0	0	0	0
.....GTGAGCCGAAGTTGTTTT.....	18	1	2	4.50	9	0	9	0	0	0	0
.....TGAGCCGAAGTTGTTTGGA.....	19	0	1	4.00	4	0	0	4	0	0	0
.....ATCGCCATTGTGCGCGTGGAGC.....	22	0	1	4.00	4	0	0	1	0	2	1
.....CTTCGACCTGGTCAAGGAGC.....	20	0	1	4.00	4	1	1	2	0	0	0
.....TCGCCATTGTGCGCGTGGAGC.....	21	0	1	3.00	3	0	0	3	0	0	0
.....GAGAAGCAGCTGGAGAGCGACA.....	22	0	1	3.00	3	0	0	3	0	0	0
.....GAAGCAGCTGGAGAGCGACATC.....	22	0	1	3.00	3	0	0	2	0	1	0
.....AAGCAGCTGGAGAGCGACATCGCC.....	24	0	1	3.00	3	1	0	1	0	1	0
.....GTGAGCCGAAGTTGTTTGGAGTA.....	23	2	1	3.00	3	1	1	1	0	0	0
.....GCCATTGTGCGCGTGGAGCA.....	20	0	1	3.00	3	0	0	3	0	0	0
.....GTGAGCCGAAGTTGTTTGGAGCTTG.....	25	2	1	3.00	3	2	1	0	0	0	0
.....GTGAGCCGAAGTTGTTTGGACT.....	22	2	1	3.00	3	1	1	0	1	0	0
.....TCGCCATTGTGCGCGTGGAGCAGGTATC.....	28	3	1	3.00	3	1	0	2	0	0	0
.....AAGCAGCTGGAGAGCGACATCGCCA.....	25	0	1	2.00	2	0	2	0	0	0	0
.....GAGCCGAAGTTGTTTGGAGCT.....	21	0	1	2.00	2	1	1	0	0	0	0
.....GTGAGCCGAAGTTGTTTGGAAT.....	22	2	1	2.00	2	2	0	0	0	0	0
.....GTGAGCCGAAGTTGTTTGGCT.....	21	2	1	2.00	2	0	0	0	2	0	0
.....CGCCATTGTGCGCGTGGAGCAGGTA.....	25	1	1	2.00	2	0	0	2	0	0	0
.....GTGAGCCGAAGTTGTTTGA.....	19	1	1	2.00	2	1	1	0	0	0	0
.....TGGTCAAGGAGCAGGCCAAC.....	20	0	1	2.00	2	0	0	2	0	0	0
.....TGGAGAGCGACATCGCCATTGTGCGCG.....	27	0	1	2.00	2	0	0	2	0	0	0
.....GTGAGCCGAAGTTGTTTGGAGCTAT.....	25	2	1	2.00	2	1	1	0	0	0	0
.....TTCGACCTGGTCAAGGAGCAGGC.....	23	0	1	2.00	2	0	0	2	0	0	0
.....GCCATTGTGCGCGTGGAGCAGGTA.....	24	1	1	2.00	2	0	0	2	0	0	0
.....CTTCGACCTGGTCAAGGAGCA.....	21	0	1	2.00	2	0	0	2	0	0	0
.....GAAGCAGCTGGAGAGCGACA.....	20	0	1	2.00	2	1	0	1	0	0	0
.....GTGAGCCGAAGTTGTTTGGAGAA.....	23	2	1	2.00	2	1	1	0	0	0	0
GTACCGAGAAGCAGCTGGA.....	19	0	1	2.00	2	1	0	0	0	0	1
.....GCCCTTCCCCTTCGACCTGGT.....	21	0	1	2.00	2	0	0	2	0	0	0
.....GCAGCTGGAGAGCGACATCGCCATTG.....	26	0	1	2.00	2	0	2	0	0	0	0
.....GTGAGCCGAAGTTGTTTGGAGCTGA.....	25	0	1	2.00	2	2	0	0	0	0	0
.....CGCCATTGTGCGCGTGGAGCAGGT.....	24	0	1	2.00	2	0	0	2	0	0	0
.....GTGAGCCGAAGTTGTTTGTG.....	20	2	1	2.00	2	0	2	0	0	0	0
.....CCCCTTCGACCTGGTCAAG.....	19	0	1	2.00	2	0	0	2	0	0	0
.....TCGACCTGGTCAAGGAGCAGGCCAACC.....	27	0	1	2.00	2	0	0	1	1	0	0
.....GCTGGAGAGCGACATCGCC.....	19	0	1	2.00	2	0	0	2	0	0	0
.....TTCGACCTGGTCAAGGAGCAGGCCAACC.....	28	0	1	2.00	2	0	0	2	0	0	0

Anti-sense strand reads

CATGGCTCTTCGTCGACCTCTCGCTGTAGCGGTAACACGCGCACCTCGTCCACTCGGCTTCAACAAACCTCGACTCAAATACTCGAAACTCGACTTAGAGGAAACCAAGAATCCATAGCGGGAAGGGGAAGCTGGACCAGTTCCTCGTCCGGTTGGAGATGTT **********..(((((((((..(((((((((.....)))))))))).....)))))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V106 head	V105 male body	V055 head	M058 embryo	V039 embryo
.....CTGAAGCTGGACCAGTTC.....	18	2	15	0.07	1	0	0	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13337:13664363-13664523 -	dan_232	TGCACGGGCCGTGTCTACTACGATCTGACCAAGACTCGTACCGAGAAGCAGCTGGAGAGCGACATCGCCATTGTGCGCGTGGAGCAGGTGAGCCGAAGTTGTTTGGAGC----------TGAGTT--T-------ATGAGCT----------TTGAG----------CTGAATCT--CC-TTTGG-TTCTTAGGTATCGCCCTT
droBip1	scf7180000395832:605797-605957 -		TGCACGGGCCGTGTCTACTACGATCTGACCAAGACTCGTACCGAGAAGCAACTGGAGAGCGACATCGCCATTGTGCGAGTGGAGCAGGTAAGCCGATGCTGTTTGGAAT----------TATCTT--T-------TTTTAT----------GCTCA----------CTGAATCA--TC-TTTGT-TTCTTAGGTCTCGCCCTT
droKik1	scf7180000302486:795598-795758 +		TGCACGGGTCGCGTCTACTACGACCTGACCAAGACCGTGCCGACAAGAAGCTGGAGAAGCGAGGTGGCCATTGTGCGTGTGGAGCAGGTAGCGATT-----C-------AACTTTTCCTTGAG------------------AATGAA--------GTATGCTTTA----------CTAATTAT--TC-ATTTT-CCCTTAGATTTCGCCCTT
droFic1	scf7180000454113:3650712-3650870 -		TGCTCGGGCCGCGTCTACTACGATCTGACCAAGACCGTGCGGAAAAGAAGCTGGAGAAGCGACGATCGCCATTGTGCCGTGGAGCAGGTGAGTGCTT--ATG-------GCTTTTAA-ACTCTT------------TA----------AAAATAT----------TTA----------CTAATCAATGCT-TGG--TATGCAGATCTCTGCCCTT
droEle1	scf7180000491255:3393350-3393508 +		TGCTCGGGCCGCGTCTACTACGATCTGACCAAGACCGCGGCGGAAAAGAAGCTGGAGAAGCGACATCGCCATTGTGCGCGTGGAGCAGGTGAGTGTTT--CTG-------GCTTTATT-TCTCTA------------------------CTGGACAT----------CTA----------CTAACTTATATT-TTGGTA-GCCCAGATCTCTGCCCTT
droRho1	scf7180000779902:113473-113630 -		TGCTCGGGCCGCGTCTACTACGATCTGACCAAGACCGTACGGAAAAGAAGTGGAGAAGCGACATCGCCATTGTGCCGTGGAGCAGGTGAGTGTAG--TTT-------ACTGTTTT-TGCTTA------------------------GGAACAT----------CTG----------CTAACTAACATG-TTGGTA-TCCCAGGTGTCTGCCCTT
droBia1	scf7180000302428:3154451-3154607 -		TGCTCGAGGACGCGTCTACTACGATCTGACCAAGCGCGTGCGGAAAAGAAGCTGGAGAACGACATCGCCATCGTGCGCGTGGAGCAGGTGAGTGCTCT--ATT-------GAATCATT-ACTGTG------------------------GGTGAAC----------CTT----------CTAACTAA--CT-TTT-TGTATTCAGATCTCTGCCTT
droTak1	scf7180000415352:403940-404096 -		TGCTCGGGCCGCGTCTACTACGATCTGACCAAGACCGTACGGAAAAGAAGCTGGAGAGCGACGCTCGCCATCGTGCGCGTGGAGCAGGTGAATGTAC--ATT-------AAATAATT-CTTTTG------------------------GGAGCAT----------CTT----------CTAACGCA--TG-TTT-TATGTGCAGATCTCTGCCTT
droEug1	scf7180000409711:380879-381036 -		TGCTCGGGCCGCGTCTACTACGATCTGACCAAGACCGTACGGAAAAGAAGCTGGAGAGCGACATCGCCATTGTGCGTGTGGAGCAGGTTAGTGAAC--TTA-------TAATTTTT-TCTCTA------------------------GAATCAT----------CTG----------CTAACTTGTATT-TTC-CCTTTTTAGATCTCTGCTTT
dm3	chr3L:16957778-16957934 +		TGCTCGGGCCGCGTCTACTACGATTGACCAAGACACGTAGCGAAAAGCAGCTGGAGCGCGAAATCGCCATTGTGCGCGTGGAGCAGGTGAGTGCCCC--ATA-------AAAATATT-TATATT------------------------GGTCGAT----------CTG----------CTAAAGTA--TT-TTG-TATGTTCAGATCTCTGCCTT
droSim2	3L:16540373-16540529 +		TGCTCGGGCCGCGTCTACTACGATTTGACCAAGACACGTAGCGAAAAGCAGCTGGAGCGCGAAATCGCCATTGTGCGCGTGGAGCAGGTGAGTGCCCC--ATA-------TGAATATT-TAAATT------------------------GGACCAT----------CTG----------CTAACGTA--TT-TTG-TATGTTCAGATCTCTGCCTT
droSec2	scaffold_0:9019211-9019367 +		TGCTCGGGCCGCGTCTACTACGATTTGACCAAGACACGTAGCGAAAAGCAGCTGGAGCGCGAAATCGCCATTGTGCGCGTGGAGCAGGTGAGTGCCCC--ATA-------TACATATT-TATGTT------------------------GATTCAT----------CTG----------CTAACGTA--TT-TTG-TATGTTCAGATCTCTGCCTT
droYak3	3L:17117441-17117597 -		TGCTCGGGCCGCGTCTACTACGATTTGACCAAGACCGTAAGGAAAAGCAGCTGGAGAGCGACATCGCCATCGTGCGCGTGGAGCAGGTGAGTGCCAC--ATG-------GAAATATT-TATGTT------------------------GTTCCAT----------CTG----------CTAACGTG--TT-TTG-TATGTTCAGATCTCTGCCTT
droEre2	scaffold_4784:16884944-16885100 -		TGCTCGGGTCGCGTCTACTACGATTTGACCAAGACGCGTAAGGAAAAGCAGCTGGAGCGCGAAATCGCCATCGTGCGCGTCGAGCAGGCGAGTTCAC--ATG-------AAAATATT-TATGTT------------------------GTTCCAT----------CTC----------CTAACGTA--TT-TTG-TATGTTCAGGTCTCTGCCTT
dp5	XR_group8:4780350-4780515 +		TGCTCGGGTCGCGTCTACTACGATCTGACCAAATGCGTACCGAGAAGCAGCTGGAGAGCGACGTTGCCATTCTGCGTGTGGAGCAGGTGAGTCGTT--GTC-------CCAGCTTG-TCTCTG------------------------TGAGCAGTGCTAAAGC----TCG----------TTCTCCAC--TC-CTC-TCCGTATAGGTCTCGCCCTT
droPer2	scaffold_29:400156-400325 +		TGCAGTGGCAAGGTCTACTACGACCTTTTCAAGGAGCGCGAGGAGCCACGAGCAAAACGAAACGGTGGGTCTCGTTCGAATCGAACAGGTACCGTTGA--TCT-------AAATCATC-TCTA----------------------GTGCAT----------TTCCTCGGATACAGTGGTGTCTCCGTC--TC-CCC-TTTACTTAGATCTGCCCTT
droWil2	scf2_1100000004511:1297444-1297612 +		TGCACGGGTCGCGTCTACTACGATCTGACCAAGTTCCGTACTGAGAAGCAGTTGGAGAGTTGATTATTGGCCATTGTGCGTGTGGAGCAGGTAAGTGTTG-GATG-------AAGTCAC--------ATTGCCATCCGATTCGA----TTGG-GGCT----------GTT----------CTACACG--TT-TAT-TGTATGCAGATCTCGCCCTT
droVir3	scaffold_13049:10205984-10206141 -		TGCACGGGTCGCGTTACTACGATCTGACCAAGCGCGTACCGAGAAGCAGTTGGAGAAGCGATATTGGCCATTGTGCGCGTGGAGCAGGTGCGCGTAT-CATT-------AAGTTATT-CATCAA----------------------TTTGCAT----------TTA----------AATGCATT--TT-TAA-CATTTGGCAGGTGTCGCCGTT
droMoj3	scaffold_6680:10591268-10591431 +		TGCACAGGTCGTGTCTACTACGACCTGACTAAGACGCGTGCCGAGAAGCAGCTGGAGAAGCGACATCGCCATCGTGCGTGTGGAGCAGGTGCGTGTTTGGGTT-------AAT--------GACTT--TATATGCAT-T----TGAA-TT----------TCA----------CTAAATTGAGTT-TTCGC-TTCATAGGTCTCACCCTT
droGri2	scaffold_15110:9036460-9036623 +		TGCACGGGTCGCGTCTACTACGATCTGACCAAGCGCGTGCCGACAAGCAACTGCAGAGCGATATTGGCCATTGTGCGCGTGGAGCAGGTGCGTGCTATTCATT-------AAGAAAT--------TTTCGC--A------ATCAAT----------TTGTA----------CTAAATTAAGTTGTGG-CATTTGTAGGTATCGCCCTT

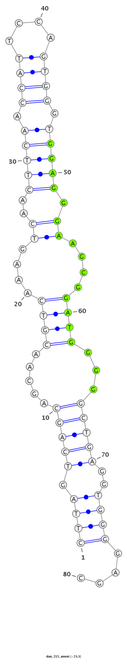
Generated: 09/08/2015 at 10:31 PM

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

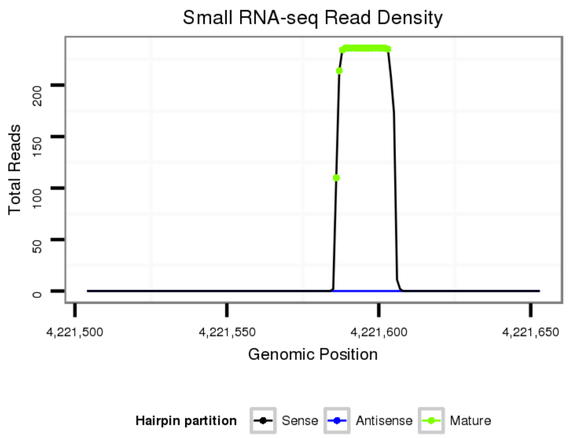
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_215	**scaffold_13337:4221554-4221603 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

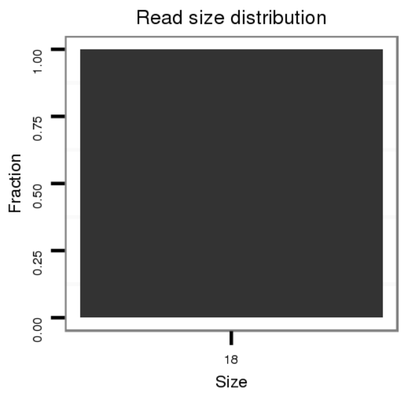
Legend: mature star mismatch in alignment mismatch in read

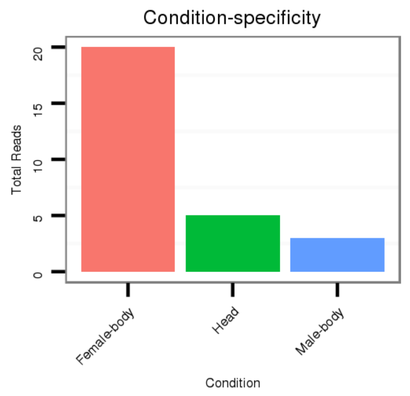
Predicted structure

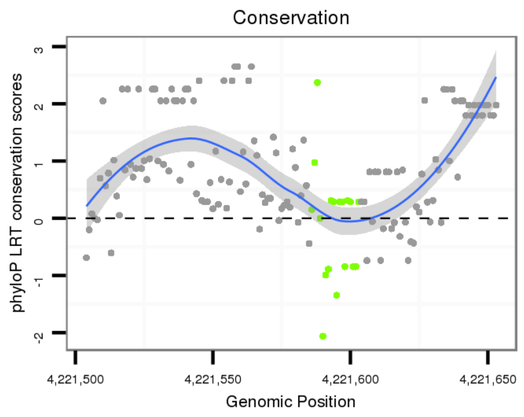


Show Alternate Folds









Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GCTGTTGGCCTTATGTTCGTGTGTTTTGTCCTCGCCTTAGTCAGCAGCAACGTCAAAGTCAACTTCAACCATTCCAGTGGGTGGAGGGAAGCGGATGGGGGCTGAGGTGGGGAGCAGAGGGCGGGACTGCTTATGCGCCACTCACATGCA	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	V105 male body	V055 head
********************************(((((.(((((.....((((....((..(((((.(((((....)))))..)))))..))....)))))...))))))..))))....********************************									
....GAGGGAAGCGGATGGGGGCG..........	20	1	1	455.00	455	190	232	30	3
....GGAGGGAAGCGGATGGGGGCG..........	21	1	1	209.00	209	48	136	21	4
....GAGGGAAGCGGATGGGGGC..........	19	0	1	84.00	84	39	37	8	0
....AGGGAAGCGGATGGGGGCG..........	19	1	2	66.00	132	17	113	2	0
....GGAGGGAAGCGGATGGGGC..........	20	0	1	59.00	59	15	38	6	0
....GGAGGGAAGCGGATGGGG..........	18	0	1	27.00	27	5	20	2	0
....GGAGGGAAGCGGATGGGGG..........	19	0	1	19.00	19	1	16	2	0
....AGGGAAGCGGATGGGGGC..........	18	0	2	18.00	36	1	34	1	0
....GAGGGAAGCGGATGGGGG..........	18	0	1	16.00	16	5	10	0	1
....GGGAAGCGGATGGGGGCG..........	18	1	3	13.33	40	3	37	0	0
....GAGGGAAGCGGATGGGGGTC..........	20	2	1	4.00	4	1	0	2	1
....GAGGGAAGCGGATGGGGGCT..........	20	0	1	4.00	4	1	3	0	0
....GGAGGGAAGCGGATGGGGGCT..........	21	0	1	3.00	3	2	1	0	0
....GAGGGAAGCGGATGGGGGAC..........	20	2	1	2.00	2	2	0	0	0
....GGAGGGAAGCGGATGGGGGTC..........	21	2	1	2.00	2	1	0	1	0
....GGAGGGAAGCGGATGGGGC..........	19	1	1	2.00	2	2	0	0	0
....GAGGGAAGCGGATGGGGGCTGGC..........	23	2	1	2.00	2	2	0	0	0
....GGAGGGAAGCGGATGGGGGG..........	20	1	1	1.00	1	0	1	0	0
....GAGGGAAGCGGATGGGGGT..........	19	1	1	1.00	1	1	0	0	0
....AGGGAAGCGGATGGGGGCTG..........	20	0	1	1.00	1	0	1	0	0
....GGAGGGAAGCGGATGGGGGCTGGC..........	24	2	1	1.00	1	0	1	0	0
....AGGGAAGCGGATGGGGGCT..........	19	0	1	1.00	1	0	1	0	0
....GGGAAGCGGATGGGGGCTG..........	19	0	1	1.00	1	0	1	0	0
....GGGAAGCGGATGGGGGCT..........	18	0	1	1.00	1	0	1	0	0
....TGGAGGGAAGCGGATGGGGGC..........	21	0	1	1.00	1	1	0	0	0
....GAGGGAAGCGGATGGGGGCA..........	20	1	1	1.00	1	1	0	0	0
....AGGGAAGCGGATGGGGGCTGG..........	21	1	1	1.00	1	0	1	0	0
....TGGAGGGAAGCGGATGGG..........	18	0	1	1.00	1	0	0	1	0
....GAGGGAAGCGGATGGGGC..........	18	1	1	1.00	1	0	0	1	0
....AGGGAAGCGGATGGGGGTC..........	19	2	2	0.50	1	0	1	0	0
....AGGGAAGCGGATGGGGG..........	17	0	2	0.50	1	0	0	0	1

Anti-sense strand reads

CGACAACCGGAATACAAGCACACAAAACAGGAGCGGAATCAGTCGTCGTTGCAGTTTCAGTTGAAGTTGGTAAGGTCACCCACCTCCCTTCGCCTACCCCCGACTCCACCCCTCGTCTCCCGCCCTGACGAATACGCGGTGAGTGTACGT	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V106 head	V039 embryo	V105 male body
********************************(((((.(((((.....((((....((..(((((.(((((....)))))..)))))..))....)))))...))))))..))))....********************************									
....TGGAGGGAAGCGGATGGGGGCA..........	20	1	1	1.00	1	1	0	0	0
....AGGGAAGCGGATGGGGGCTGG..........	21	1	1	1.00	1	0	1	0	0
....TGGAGGGAAGCGGATGGG..........	18	0	1	1.00	1	0	0	1	0
....GAGGGAAGCGGATGGGGC..........	18	1	1	1.00	1	0	0	1	0
....AGGGAAGCGGATGGGGGTC..........	19	2	2	0.50	1	0	1	0	0
....AGGGAAGCGGATGGGGG..........	17	0	2	0.50	1	0	0	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13337:4221504-4221653 +	dan_215	GCTGT----------TGGCCTTATGTTCGTGTGTTTTGTCC---TCGCC-----TTAGTCAGCAGCAACGTCAAAGTCAA------CTTCAACC------ATTCC-AGTGG----------GTG----------GAGG-------GAAGCGGATGGGGGCTGAGGTGGGGAGCAGA-GGGCGGGACTGCTTATGCGCCACTCACATGCA
droBip1	scf7180000395450:353047-353203 +		GCTGT----------TGGCCTTATGTTCGTGTGTTTTGTCG---TCGCC-----TTAGTCAGCAGCAACGTCAAAGTCAA------CTTCAACC------ATTCC-AGTGG----------GCG----------GAGAGGGGTTGGTAGCGGCTGAAGGCCGAGGCGGGGAGCAGCG-GGGCGGTACTGCTTATGCGCCACTCACATGCA
droKik1	scf7180000302383:1049030-1049171 -		GGCCAGCGATTGTGTACTTGGGTTTATGTTCGTGTGTTTTGTCG---TCGCC-----TTAGTC---GTTGGCAGCAACGTCAG------C------CTATA-GA-AG-AGG--------AGGT------CCT----GGCA----------TAGAGGC--GTCCA----------CCGGGGGTGATGGTTATGCGCCACTCACATGCA
droFic1	scf7180000453807:348927-349081 -		---------------GGGTTTATGTTCGTGTGTTTTGTCG---TCGCC-----TTAGTC---AGCACGTCAAGTCAA------C------CTCACG-AT-CC-GG---------GCAGCA----CCT----TGTGGC-AAGGAGCCAT----------CGAAGTGGGAGCCGG--GGAGTCCA-GAGAGAG--GG----------GGAAGGGCCTGCTTATGCGCCACTCACATGCA
droEle1	scf7180000491000:156672-156819 -		CCTG-----------GGGCTTGTGTTCGTGTGTTTTGTCG---TCGCC-----TTAGTC---AGCAACGTCAAGTCAA------C------CTCACG-AT-CC-AGC---------AGCA----CCT----TATGGAGAAGGTGCTAG----------CGAAGTGG----------GGCGAAAG--GGT-G----------GCAAGGGGCCTCCTTATGCGCCACTCACATGCA
droRho1	scf7180000777793:1821-1967 -		CCTG-----------GGGCGTATGTTCGTGTGTTTTGTCG---TCGCC-----TTAGTC---AGCAACGTCAAGTCAA------C------CTCACG-AT-CC-AGC---------AGCA----CCT----TATAGAGACGGTGCTAT----------CGAAGTGG----------TGAGAAG--GGA-G----------TCAAGGGCCTGCTTATGCGCCACTCACATGCA
droBia1	scf7180000302428:4987905-4988038 +		-----------GGGCTTATGTTCGTGTGTTTTGTCG---TCGCC-----TTAGTC---AGCACGTCAAGTCAA------C------CTCACG-AT-CC-AGG---------AGCA----CCT----TATAGAGAAGGTGCCAT----------CGAAACGG----------GGGA-------------------AAGGGGCGCTTATGCGCCACTCACATGCA
droTak1	scf7180000415149:126557-126698 +		-----------GGGGTTATGTTCGTGTGTTTTGTCG---TCGCC-----TTAGTC---AGCAACGTCAAGTCAA------C------CTCACG-AT-CC-AGC---------AGCA----CCT----TATAGAGACGGTCTTAT----------CGAAGTGGGA----------ACAG--GGTGC----------TCC-GGGCCTGCTTATGCGCCACTCACATGCA
droEug1	scf7180000409456:1151613-1151774 -		CTTG-----------GGGGTTATGTTCGTGTGTTTTGTCG---TCGCC-----TTAGTC---AGCAACGTCAAGTCAA------C------CTCACGGAT-CCCA----------GCAGCA----CCT----TATGGTGACGGTGTTAT----------CGAATTGGGGAAAGGACGGAAT----TAGAGG---GGA-G----------GCAAGGGGCCTGCTTATGCGCCACTCACATGCA
dm3	Chr3L:14893743-14893894 -		-----------GGGGTTATGTTCGTGTGTTTTGTCG---TCGCC-----TTAGTC---AGCAACGTCAAGTCAA------C------CTCACGGAT-CC-AGCA-----------GCAGCA----CCTTTCTCATAGAGAAGGTGCCATAC---------CCCTCG----------ATAGAGG---GGTCC----------TCGAGGGGCCTGCTTATGCGCCACTCACATGCA
droSim2	3L:14535286-14535438 -		-----------GGGGTTATGTTCGTGTGTTTTGTCG---TCGCC-----TTAGTC---AGCAACGTCAAGTCAA------C------CTCACGGGT-CC-AGCA-----------GCAGCA----CCTTCCTCATAGAGAAGGTGCTATAC---------CCCTCG----------ATAGAGG---GGTCC----------TCGAGGGGCCTGCTTATGCGCCACTCACATGCA
droSec2	scaffold_0:7012176-7012317 -		-----------GGGGTTATGTTCGTGTGTTTTGTCG---TCGCC-----TTAGTC---AGCAACGTCAAGTCAA------C------CTCACGGGT-CC-AGCA-----------GCAGCA----CCTTCCTTATAGGGGGGGT-CTA----------------------------TAGAGGG--GGTCC----------TCGAGGGGCCTGCTTATGCGCCACTCACATGCA
droYak3	3L:14979062-14979229 -		-----------GGGGTTATGTTCGTGTGTTTTGTCG---TCGCC-----TTAGTC---AGCAACGTCAAGTCAA------C------CTCACGGAT-CC-AGCAGCAGCAGCAGCA----CCT----CGTATAGAAGGTGCTATACCCCGTATACCCCTCGAA----------TAGAGAG--GGTAC----------TCGAGGGGACTGCTTATGCGCCACTCACATGCA
droEre2	scaffold_4784:14853601-14853738 -		-----------GGGGTTCGTTCGTGTGCTTTGTCG---TCGCC-----TTAGTC---AGCAACGTCAAGTCAA------C------CTCACGGAT-CC-AGCA-----------GCAGCA----CCT----CGTGGAGTAGGTGTGGTAC---------CCCTGG----------ATGGAGA---------------------------C----GGGCCTGCTTATGCGCCACTCACATGCA
dp5	XR_group6:846645-846778 +		ACTGTACG--TGTGTAC-GGGCTTATTTCGTGTATTTTGTCG---TCGAC-----TTAGTC---AAGGACGTCAAGTCAACGTCAACGATCGACC------ATC--------GT-----GCAGCACCTTGG----------CAGAGCA--ACT----------C-------CTGCTTATGCGCCACTCACATGCA
droPer2	scaffold_12:1526815-1526948 +		ACTGTACG--TGTGTAC-GGGCTTATATTCGTGTATTTTGTCG---TCGAC-----TTAGTC---AAGGACGTCAAGTCAACGTCAACGATCGACC------ATC--------GT-----GCAGCACCTTGG----------CAGAGCA--ACT----------C-------CTGCTTATGCGCCACTCACATGCA
droWil2	scf2_1100000004933:290309-290350 +		C-----------A---------------------------C---AACAACATCAACAACAA------CAACAACC------ATCC-AGTGG----------ATG---
droVir3	scaffold_12963:10399958-10400033 -		GT----------------TGCTGTGGATACATTTAGGCGCCCTCGAGTTTGATTCGGG---GGCAACGTCAAAGTCAA------AGTCAGCC------CG---AGT--------GGAG---
droMoj3	scaffold_6473:4254267-4254328 -		C-----------A---------------------------C---AGCAACAACAAAGCAA------CATGAAGT------GTTAG-ATTGG----------ATGTAGA----------GGAGAGCG--GG----------GCTCGGG-----------
droGri2	scaffold_14906:9824044-9824102 +		GGAA----------GGG---------------------------C---AA-----------GGAA----------TCGAAAG--GGGGC----------TGGGGTTGGTTGCAAA-TGGCTGGGTTGATTGTGGGC-----------

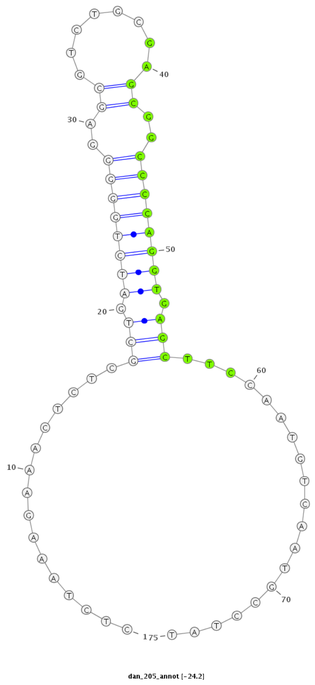
Generated: 09/08/2015 at 07:48 PM

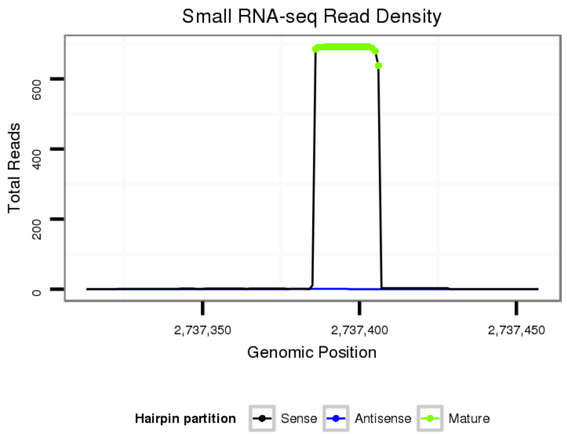
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	0
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

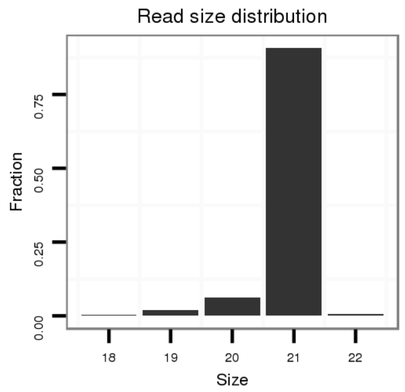
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_205	**scaffold_12943:2737363-2737407 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

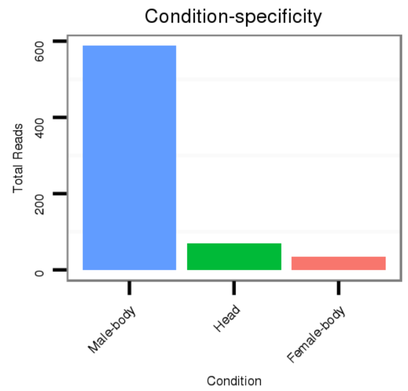
Legend: mature star mismatch in alignment mismatch in read

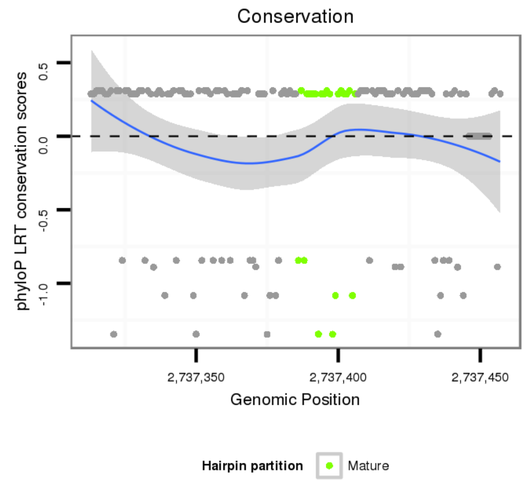
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GGTAAGGAGTTCTTCGCTTTAGAGTCGGCTCATGGCTCTAAAGAAACTCTCGCTGATCTGGGGGAGCGTCTGCGAGCGGCCCCAGGTGAGCTTCCAATGTCAATGCCTATGATGCGAATAGACTGGCCAACGGAGTTCCATGATG	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V055 head	V106 head	M044 female body	M058 embryo
**********.....(((.(((((((..((.....)).)))))))).)))..... **********										
.....GAGCGGCCCCAGGTGAGCTTC.....	21	0	1	627.00	627	536	34	29	28	0
.....GAGCGGCCCCAGGTGAGCTT.....	20	0	1	38.00	38	36	0	1	1	0
.....GAGCGGCCCCAGGTGAGCTTCT.....	22	1	1	24.00	24	23	0	1	0	0
.....GAGCGGCCCCAGGTGAGCT.....	19	0	1	8.00	8	5	0	3	0	0
.....GAGCGGCCCCAGGTGAGCTTG.....	21	1	1	6.00	6	5	0	0	1	0
.....AGCGGCCCCAGGTGAGCTTC.....	20	0	1	5.00	5	2	0	0	3	0
.....GAGCGGCCCCAGGTGAGCTTT.....	21	1	1	5.00	5	3	1	0	1	0
.....CGAGCGGCCCCAGGTGAGCTTC.....	22	0	1	5.00	5	3	1	0	1	0
.....GAGCGGCCCCAGGTGAGCTTA.....	21	1	1	4.00	4	4	0	0	0	0
.....CGAGCGGCCCCAGGTGAGC.....	19	0	1	3.00	3	1	1	1	0	0
.....CAATGTCAATGCCTATGATGCG.....	22	0	1	3.00	3	1	1	1	0	0
.....CGAGCGGCCCCAGGTGAGCTT.....	21	0	1	2.00	2	2	0	0	0	0
.....CGAGCGGCCCCAGGTGAGTT.....	19	1	1	2.00	2	0	0	2	0	0
.....TAAAGAAACTCTCGCTGATCTGGGGG.....	26	0	1	1.00	1	1	0	0	0	0
.....TCTTCGCTTTAGAGTCGGCTCATGG.....	25	0	1	1.00	1	1	0	0	0	0
.....GAGCGGCCCCAGGTGAGC.....	18	0	1	1.00	1	1	0	0	0	0
.....CATGGCTCTAAAGAAACTCTC.....	21	0	1	1.00	1	0	0	0	0	1
.....CTGATCTGGGGGAGCGTCT.....	19	0	1	1.00	1	0	0	0	1	0
.....CGAGCGGCCCCAGGTGAGCTTT.....	22	1	1	1.00	1	1	0	0	0	0
.....CAATGTCAATGCCTATGATGCT.....	22	1	1	1.00	1	1	0	0	0	0
.....GAGCGGCCCCAGGTGAGCTTCTG.....	23	2	1	1.00	1	0	1	0	0	0
.....AGCGGCCCCAGGTGAGCTT.....	19	0	1	1.00	1	0	0	0	1	0
.....CGAGCGGCCCCAGGTGAGCT.....	20	0	1	1.00	1	1	0	0	0	0
.....GAGCGGCCCCAGGTGAGCC.....	19	1	1	1.00	1	1	0	0	0	0
.....GAGCGGCCCCAGGTGAGCTTCA.....	22	1	1	1.00	1	1	0	0	0	0
.....CGAGCGGCCCCAGGTGATTT.....	19	2	1	1.00	1	1	0	0	0	0
.....CGAGCGGCCCCAGGTGAGCTTCT.....	23	1	1	1.00	1	1	0	0	0	0
.....CAATGTCAATGCCTATGATGCGTT.....	24	2	1	1.00	1	1	0	0	0	0
.....CGGCCCCAGGTGAGCTTC.....	18	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

CCATTCCTCAAGAAGCGAAATCTCAGCCGAGTACCGAGATTTCTTTGAGAGCGACTAGACCCCCTCGCAGACGCTCGCCGGGGTCCACTCGAAGGTTACAGTTACGGATACTACGCTTATCTGACCGGTTGCCTCAAGGTACTAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	M044 female body
**********.....(((.(((((((..((.....))..)))))))).)))..... **********|							
.....CGCAGACGCTCGCCGGGGT.....	19	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12943:2737313-2737457 +	dan_205	GGTAAGGAGTTCTTCGCTTTAGAGTCGGCTCATGGCTCTAAAGAAACT------CTCGCTGATCTGGGGGAGCGTCTGCGAGCGGCCCCAGGTGAGCTTCCAATGTCAATGCCTATGATGCGAATAGACTGGCCAACGGAGTTCCATGATG
droBip1	scf7180000396535:2134218-2134360 +		GGTAAGGAGTTTTCGCTTCAGTGTCTGCTTATGGCGGTGAAGGAATTCCCATTCCCGCTTACTAGGCCTATTGTCTGCAAACGGCGCCAGCGGAGCTGGCAATATCAATGCCAAAGATGCGAATAGGGGAGTCATCTG--------GAAG

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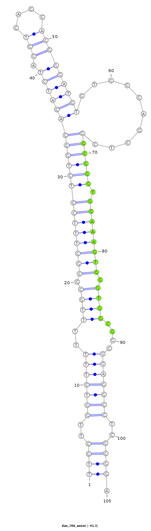
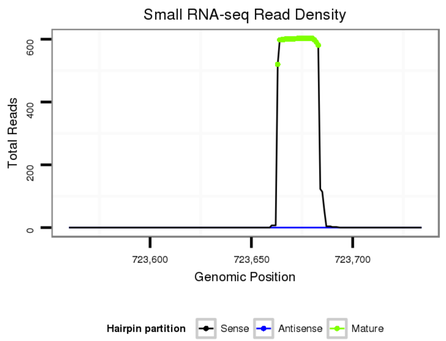
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

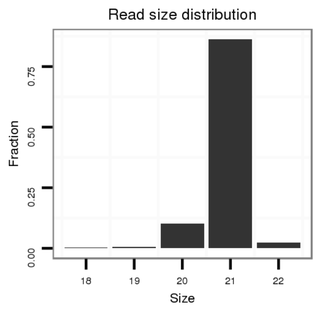
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_206	**scaffold_13047:723610-723684 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

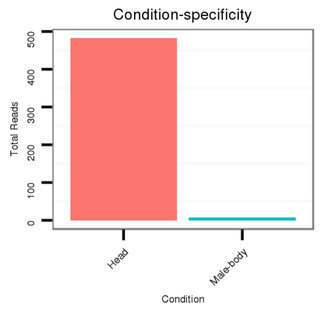
Legend: mature star mismatch in alignment mismatch in read

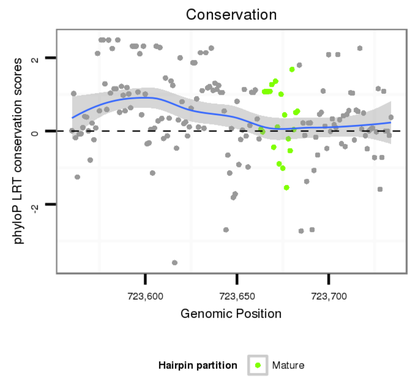
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF19186-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGGGGCCTCAGCCACAATTAAGTTTTATGAAATATTTGCTTGGTCTTTTTTTGCGCGCTTTCCTCTGCCACATCTACGTCAGCACGGGATGTGTGGCAGCTCGGCGGGTGGAAAGTGGGTGGCG	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	V055 head	M044 female body	M058 embryo
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGGCG	21	0	1	419.00	419	407	7	5	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGGCGGCG	24	0	1	47.00	47	45	2	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********CGGGTGGAAAGTGGGTGGCG	20	0	1	39.00	39	38	0	1	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********CGGGTGGAAAGTGGGTGGCGGC	22	0	1	34.00	34	34	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGGCGGC	23	0	1	24.00	24	22	2	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGGC	20	0	2	10.50	21	21	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGGCGG	22	0	1	9.00	9	9	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********CGGGTGGAAAGTGGGTGGCGGCG	23	0	1	4.00	4	4	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********TCGGCGGGTGGAAAGTGGGTG	21	0	1	4.00	4	4	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********TCGGCGGGTGGAAAGTGGGTGG	22	0	1	3.00	3	3	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGGCGT	21	1	2	3.00	6	6	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGG	19	0	2	3.00	6	6	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGGCGGCA	24	1	1	2.00	2	2	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GTGGAAAGTGGGTGGCGGCGGAG	23	0	1	2.00	2	1	0	0	1	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGGCGC	21	1	2	1.50	3	3	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********CGGGTGGAAAGTGGGTGG	18	0	3	1.33	4	3	1	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********AAGTGGGTGGCGGCGGAGGCCT	22	0	1	1.00	1	1	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGGCGGA	23	1	1	1.00	1	1	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GGGTGGAAAGTGGGTGGCGGC	21	0	1	1.00	1	1	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGGCGGT	23	1	1	1.00	1	1	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********AGTGGGTGGCGGCGGAGGCC	20	0	1	1.00	1	1	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********CGGGTGGAAAGTGGGTGGCGGC	23	1	1	1.00	1	1	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTG	18	0	2	1.00	2	2	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********CGGGTGGAAAGTGGGTGGC	19	0	2	0.50	1	1	0	0	0	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGGCGGAAA	25	3	2	0.50	1	1	0	0	0	0

Anti-sense strand reads

ACCCCGGAGTCGGTGTTAATTCAAAATACTTTATAAACGAACCAGAAAAAAACGCGCGAAAGGAGACGGTGTAGATGCAGTCGTGCCCTACACACCGTCGAGCCGCCCACCTTTCACCCACCGCCGCCTCCGGAGCGCCTCCACGCCTATCCGCGTACCTTGTCTCGTGCCGTGT	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	V055 head
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGGCG	21	0	1	419.00	419	407	12
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGGCGGC	24	0	1	47.00	47	45	2
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********CGGGTGGAAAGTGGGTGGCG	20	0	1	39.00	39	38	1
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********CGGGTGGAAAGTGGGTGGC	22	0	1	34.00	34	34	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGGCGGC	23	0	1	24.00	24	22	2
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGGC	20	0	2	10.50	21	21	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********GCGGGTGGAAAGTGGGTGGCGG	22	0	1	9.00	9	9	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********CGGGTGGAAAGTGGGTGGCGGCG	23	0	1	4.00	4	4	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********TCGGCGGGTGGAAAGTGGGTG	21	0	1	4.00	4	4	0
**********(((((..(((((((..(((((.((((((((((((((((((((.(((....)))))))))).....))))))).)))))))).))))....)))))))..)))))**********TCGGCGGGTGGAAAGTGGGTGG	22	0	1	3.00	3	3	0

Show Alignment With Reads

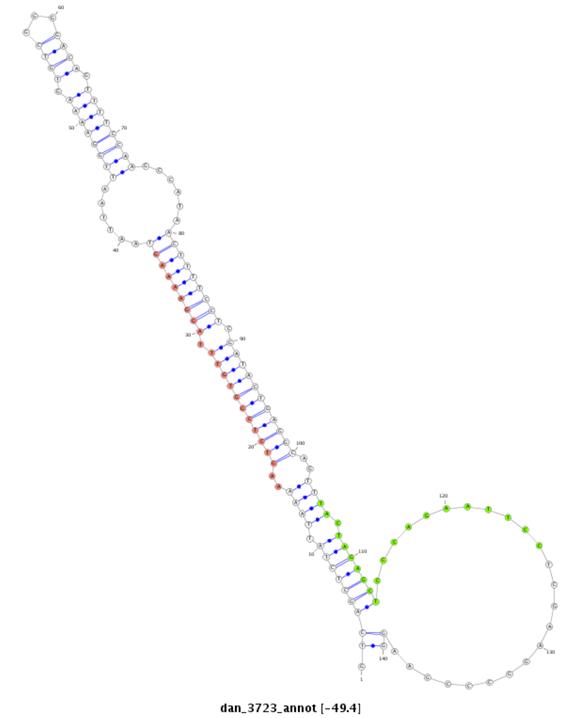
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13047:723560-723734 +	dan_206	TGGGGCCTCAGCCACAATTAAGTT-TTATGAAA-TATTTGCTTGGTCTTTTTT--------TG----------C-------GCGCT----------TT-C-------CTCTGCCACATCTACGTCAGCACGGGAT-GTG----TG-GCAGCT----------CGGCGG-T----------GGAAAGT-G----------GGT--GGCGGC---GGAGGC--------CTC----------GCGGAGGTG-CGGAT---AGGCGCATG-----GAACAGAGCAC---GGCACA
droBipl	scaf7180000396431:508894-509056 +		TGGTGCCTCAGCCACAATTAAGTTTTTGAAA-TATTTGCTTGGTTTTTTT--------TG----------C-------GCGTT----------TT-C-------CTCTGCCACATCTACGTCAGCAGGGAT-GTG----TG-GCGCT----------[redacted]-GGTGGAGTGTGGAGCG----GGGG------GGT-----GGTGGGCGCTGCC---------GGGGCATG-----GAACAGAACAG---AG---CA
droKik1	scaf7180000302698:186124-186254 -		TGAAAACTCAGCCGCAATTAAGTT-TTATGAAA-CATTCGTTTCAGATTCTT-------------C-------T----TCTTT--TTTGC--TATT----TT-T-------C----------TCGTCAATGAC----------G-G-TG---TG----------[redacted]-GCA-----GGTGTGTGT-CTA----------TTTGTGGCGC-AGGTT---GGGCGTATG-----GAG----------
droFic1	scaf7180000453829:869495-869659 +		------CTCAGTGTACAATTAAGTT-TTATGAAA-CATTTGTTGGTTTTTTT--------TG----------T-------T----GCGTTTT--CTCGC--GTTT----TT-C-------TGTTGCCACAACTACGTCAGCACTCTGGA-GT----GG-TG---TTTGTGTGTGTGTGT----------GCG-----[redacted]-A----------ATG---------TGTAT--GTGTGGGTG---GGC---------GA---------A-----AAGGGGGTGGACAAGGGCGTAA----------[redacted]----------
droEle1	scaf7180000491006:2405572-2405739 +		---------------AATTAAGTT-TTATGAAA-CATTTGTTTTGCTTTTTT--------TG----------T-------C----GCATTTT----------TT-T-------C------TTTCTACGTCAGCAGTGAATGTG----T-G-TG---TG----TGTGTGTGTGTGTGCGTGGGGGGTAATGGGCGGAAAAAGGGGC----------[redacted]-CGAAA----------[redacted]----------AAGGGGGTGGGCAAGGCGCTAGGTG-AGGAT---GGGCGCATG-----GAG----------
droRho1	scaf7180000779841:416950-417121 +		---------------AATTAAGTT-TTATGAAA-CATTTGTTTTGTTTTTTT-C---T----------T-------C----GCCTCTTT--CTCGC--CTTC----TT-T-------C----TTGTGCCACAACTACGTCAGCATTCTGGA----T----------GTATGTGCGTGGGGGGCGGTGGGCG-GGAAAAGGGGC----------[redacted]-CTAA----------[redacted]----------AAGGGGGTGGGCAAGGCGCTAGGTG-AGGAT---AGGCGCATG-----GAG----------
droBia1	scaf7180000301760:2628154-2628289 +		------CTCAGCTACAATTAAGTT-TTATGAAA-CATTTGTTGGTTTTTTC--------TG----------T-------T--TGGTTT--CTCGC--GATT----TT-C-------CTTCGCCGCAACTACGTCAGCAGTATGTT----G-GCGCT----------[redacted]-GGGGTGGGCAGGGCGCTGGTG-G-TTT-GGAGGCGCA----------[redacted]----------
droTak1	scaf7180000415169:1020967-1021136 -		------CTCAGTGTACAATTAAGTT-TTATGAAA-CATTTGTTGGTTTTTTG--------TG----------GCAT----C-------GCTTTTT--CTCGC--GTTT----TT-C-------CTTCGCCACAACTACGTCAGCATTCGCATGG----TG-GCGG---GG----------[redacted]-GGAAAAGGGGC----------[redacted]----------A----AAGGGGGCGGGCAAGGCGCTAGGTG-AGGATGGGAGGCGCATG-----GAG----------
droEug1	scaf7180000408176:338050-338228 +		------CTCAGTGTACAATTAAGTT-TTATGAAA-CATTTGTTGGTTTTCTTA----TTTTGC---TTTACTCGTTTTCCCCCTTCG--TTTT----CTCGCGCTTTT----TTCC-------TTTTGCCACAACTACGTCAGCATTTTGGT---AG---GCGG---GG----------[redacted]-GC----------[redacted]-GCGGTGGGGGGG----------[redacted]----------TGCAAGGGCGTAGGTG-AGCGT---GGGCGCATG-----GAG----------
dm3	chrX:8900774-8900942 +		------CTTATACAACATTAAGTT-TTATGAAA-CATTTGTTGGCAGTTTTTGC---TTTTGCGTTCCGTTAT----------C-------GCGTT----------TT-C-------CTTGCCACAACTACGTCAGCACTTAAAG---GGGG--G-----------[redacted]-CGTTGGGCGGTTGCTGCG-GGGCGT-----[redacted]---GGCGGC---GGC---------GGCAAGGCGTAGGTG-AGCGT---GGGCGCAG-----GAG----------
droSim2	x:8449580-8449770 +		------CTCGTTACAACATTAAGTT-TTATGAAA-CATTTGTTGGCAGTTTTTGC---TTTTGCGTTCCTGTTAT----------C-------GCGTT----------TT-C-------CTTGCCACAACTACGTCAGCAGTTAAAG---GGGG--G-----------[redacted]-GCGTTGTGCCGGTTGCAAGCGGGCGT-----[redacted]---GGCGGCGGGCC---GGC---------GGCAAGGCGTAGGTG-AGCGT---GGGCGCATG-----GAG----------
droSec2	scaffold_34:263305-263494 +		------CTCGTTACAATTAAGTT-TTATGAAA-CATTTGTTGGCAGTTTTTT--------TTTGTGTTCTGTTAT----------C-------GCGTT----------TT-C-------CTTGCCACAACTACGTCAGCAGTTAAAG----T----------[redacted]-GGG-----------[redacted]-GCGTTGGGCGGTTGCAAGCGGGCGT-----[redacted]---GGCGGCGGGCC---GGC---------GGCAAGGCGTAGGTG-AGCGT---GGGCGCATG-----GAG----------
droYak3	X:12412335-12412485 -		------CTGCGGCTACAATTAAGTT-TTATGAAA-CATTTGTTGGCAGTTTTTT--------TTTGCGGGCTGTTAT----------C-------GCGTT----------TT-C-------CGCTGCCACAACTACGTCAGCAGTTAAGG---GG----T----------[redacted]-GC----------[redacted]-GCGGCGGGCC---GGC---------GGGGCAAGGCGTAGGTG-AGCGT---GGGCGCATG-----GAG----------
droEre2	scaffold_4690:6212406-6212580 -		---------------AATTAAGTT-TTATGAAA-CATTTGCGTT----TT----------TTTACGTTCTCTTAT----------C-------GCAGTTTTTCGTCGC----TTTT----TT-C-------CTTGCCACAACTACGTCAGCATCCTA-G----GGGG--GCGG---TG----------[redacted]-AAGA-GGGCGGGGGC-GACGGCGGCGG---GACGC---------[redacted]----------GGCAAGGCGTAGGTG-AGCGT---GGGCGCATGGGGC---GAA----------
dp5	XL_group:8174824-8174907 +		------ARG---TG-GATGGAATG-TGTGTG---[redacted]-GTGTGT----------GGCGGGGAG---GGG----------AG-----GGAA-----GGCAGGGT-----GCAGGAGAGTGGGGAT---AGACGCATG-----GAG----------
droPer2	scaffold_13:392237-392354 +		--GCCACACTACGTCAGCAGCAGAGG-CA----T-CAG---CG----------TCAGAGTGTGGGGCGG-----[redacted]-ATCTGCGATGGAATGTG-------TGTGT--GGCGGGAG---GGC---------GG-----GGAGGGCTGGGAT---GGT-----GCAGGAGAGTGGGG-----[redacted]-G-----A----------[redacted]---TA
droWil2	scf2_1100000004963:775544-775696 -		GG--ACCTCAA-AACAATTAAGTT-TTATGAAAGTATTTGTTTTTTT

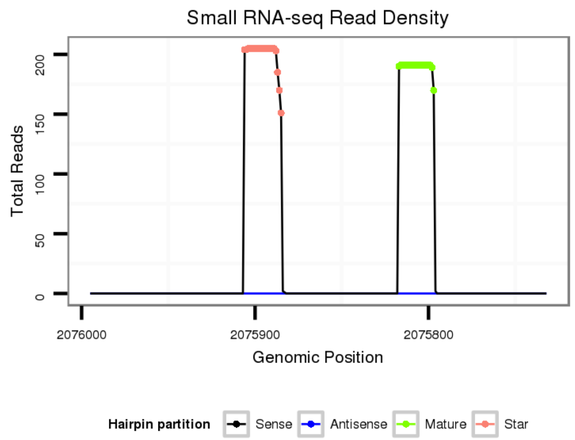
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_3723	**scaffold_13417:2075782-2075945 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

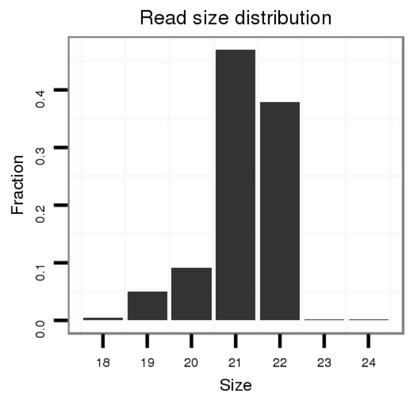
Legend: mature star mismatch in alignment mismatch in read

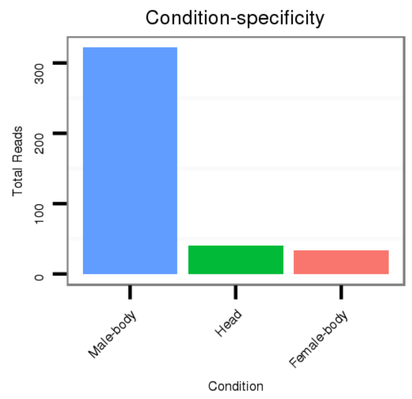
Predicted structure



dan_3723_annot [-49.4]







No conservation details.

Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTTCCTCTAGTGCCACAGGAAGTGTCTGGGTATCAGGGACAGTCTCCGAGTCCCTCGGGACTTTGAGTACTTCTGTCAGCTCTATTAAAAAGTCTCGGTGTTTAGGAAAAGTAATTAATTGGAAAAGTGTCGGGGACAGTTTTCCAAGCCATAACTTTTCCTCGATACTGAGGCAGTTTACTAGAGCTCCCAGAATTCCTCGAAGGCCCGAAGGAGACGTCCAGTGATTGGTTTCCGGCTTAGTCAGATCCGTATCGTGGGGCG						V105	M044		V106	V055
.(((((((((.((((..(((((((((((.(((((((((.....(((((((((.((((...)))).)))))))).....)))))))))).)))))))))))..)))).))))))).....))	Read size	# Mismatch	Hit Count	Total Norm	Total	male body	female body	head	head
..TACTAGAGCTCCCAGAATTCC..	21	0	1	167.00	167	142	15	1	9
..AAGTCTCGGTGTTTAGGAAAAG..	22	0	1	148.00	148	119	12	11	6
..AAGTCTCGGTGTTTAGGAAAA..	21	0	1	19.00	19	12	1	4	2
..TACTAGAGCTCCCAGAATTC..	20	0	1	19.00	19	18	1	0	0
..AAGTCTCGGTGTTTAGGAA..	19	0	1	18.00	18	15	1	2	0
..AAGTCTCGGTGTTTAGGAAA..	20	0	1	15.00	15	12	1	2	0
..AAGTCTCGGTGTTTAGGAAAAA..	22	1	1	5.00	5	4	0	1	0
..TACTAGAGCTCCCAGAATTCA..	21	1	1	3.00	3	3	0	0	0
..AAGTCTCGGTGTTTAGGAAAAGA..	23	1	1	3.00	3	3	0	0	0
..AAGTCTCGGTGTTTAGGATT..	20	2	1	3.00	3	3	0	0	0
..AAGTCTCGGTGTTTAGGA..	18	0	1	2.00	2	0	0	0	2
..TACTAGAGCTCCCAGAATTCCT..	22	0	1	2.00	2	1	1	0	0
..TACTAGAGCTCCCAGAATT..	19	0	1	2.00	2	1	0	1	0
..GTCTCGGTGTTTAGGAAAAG..	20	0	1	1.00	1	0	1	0	0
..ACTAGAGCTCCCAGAATTCC..	20	0	1	1.00	1	0	1	0	0
..TACTAGAGCTCCCAGAATTCG..	21	1	1	1.00	1	1	0	0	0
..AAGTCTCGGTGTTTAGGAGT..	20	2	1	1.00	1	0	0	1	0
..AAGTCTCGGTGTTTAGGAAT..	20	1	1	1.00	1	1	0	0	0
..AAGTCTCGGTGTTTAGGAAAATA..	23	2	1	1.00	1	1	0	0	0
..AAGTCTCGGTGTTTAGGAAAAGT..	23	0	1	1.00	1	1	0	0	0
..AAGTCTCGGTGTTTAGGAAAAAA..	23	2	1	1.00	1	1	0	0	0
..AAGTCTCGGTGTTTAGGAATTA..	22	3	1	1.00	1	0	0	0	1
..AAGTCTCGGTGTTTAGGAAAAGTA..	24	0	1	1.00	1	1	0	0	0
..AAGTCTCGGTGTTTAGGAAAG..	21	1	1	1.00	1	1	0	0	0
..TACTAGAGCTCCCAGAATTCT..	21	1	1	1.00	1	1	0	0	0
..AAGTCTCGGTGTTTAGGGT..	19	2	2	0.50	1	1	0	0	0
..AAGTCTCGGTGTTTAGGTTT..	20	3	9	0.11	1	1	0	0	0

Anti-sense strand reads

GAAGGAGATCACGGTGTCCTTCACAGACCCATAGTCCCTGTCAGAGGCTCAGGGAGCCCTGAAACTCATGAAGACAGTCGAGATAATTTTTCAGAGCCACAAATCCTTTTCATTAATTAACCTTTTCACAGCCCCTGTCAAAAGGTTCGGTATTGAAAAGGAGCTATGACTCCGTCAAATGATCTCGAGGGTCTTAAGGAGCTTCCGGGCTTCCTCTGCAGGTCACTAACCAAAGGCCGAATCAGTCTAGGCATAGCACCCCGC						M044	V055
.(((((((((.((((..(((((((((((.(((((((((.....(((((((((.(((((...)))).)))))))))).....)))))))))).)))))))))))..)))).))))))).....))	Read size	# Mismatch	Hit Count	Total Norm	Total	female body	head
..TACTAGAGCTCCCAGAATTCC..	21	0	1	167.00	167	142	15	1	9
..AAGTCTCGGTGTTTAGGAAAAG..	22	0	1	148.00	148	119	12	11	6
..AAGTCTCGGTGTTTAGGAAAA..	21	0	1	19.00	19	12	1	4	2
..TACTAGAGCTCCCAGAATTC..	20	0	1	19.00	19	18	1	0	0
..AAGTCTCGGTGTTTAGGAA..	19	0	1	18.00	18	15	1	2	0
..AAGTCTCGGTGTTTAGGAAA..	20	0	1	15.00	15	12	1	2	0
..AAGTCTCGGTGTTTAGGAAAAA..	22	1	1	5.00	5	4	0	1	0
..TACTAGAGCTCCCAGAATTCA..	21	1	1	3.00	3	3	0	0	0
..AAGTCTCGGTGTTTAGGAAAAGA..	23	1	1	3.00	3	3	0	0	0
..AAGTCTCGGTGTTTAGGATT..	20	2	1	3.00	3	3	0	0	0
..AAGTCTCGGTGTTTAGGA..	18	0	1	2.00	2	0	0	0	2
..TACTAGAGCTCCCAGAATTCCT..	22	0	1	2.00	2	1	1	0	0
..TACTAGAGCTCCCAGAATT..	19	0	1	2.00	2	1	0	1	0
..GTCTCGGTGTTTAGGAAAAG..	20	0	1	1.00	1	0	1	0	0
..ACTAGAGCTCCCAGAATTCC..	20	0	1	1.00	1	0	1	0	0
..TACTAGAGCTCCCAGAATTCG..	21	1	1	1.00	1	1	0	0	0
..AAGTCTCGGTGTTTAGGAGT..	20	2	1	1.00	1	0	0	1	0
..AAGTCTCGGTGTTTAGGAAT..	20	1	1	1.00	1	1	0	0	0
..AAGTCTCGGTGTTTAGGAAAATA..	23	2	1	1.00	1	1	0	0	0
..AAGTCTCGGTGTTTAGGAAAAGT..	23	0	1	1.00	1	1	0	0	0
..AAGTCTCGGTGTTTAGGAAAAAA..	23	2	1	1.00	1	1	0	0	0
..AAGTCTCGGTGTTTAGGAATTA..	22	3	1	1.00	1	0	0	0	1
..AAGTCTCGGTGTTTAGGAAAAGTA..	24	0	1	1.00	1	1	0	0	0
..AAGTCTCGGTGTTTAGGAAAG..	21	1	1	1.00	1	1	0	0	0
..TACTAGAGCTCCCAGAATTCT..	21	1	1	1.00	1	1	0	0	0
..AAGTCTCGGTGTTTAGGGT..	19	2	2	0.50	1	1	0	0	0
..AAGTCTCGGTGTTTAGGTTT..	20	3	9	0.11	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13417:2075732-2075995 -	dan_3723	CTTCCTCTAGTGCCACAGGAAGTGTCTGGGTATCAGGGACAGTCTCCGAGTCCCTCGGGACTTTGAGTACTTCTGTCAGCTCTATTAAAAAGTCTCGGTGTTTAGGAAAAGTAATTAATTGGAAAAGTGTCGGGGACAGTTTTCCAAGCCATAACTTTTCCTCGATACTGAGGCAGTTTACTAGAGCTCCCAGAATTCCTCGAAGGCCCGAAGGAGACGTCCAGTGATTGGTTTCCGGCTTAGTCAGATCCGTATCGTGGGGCG

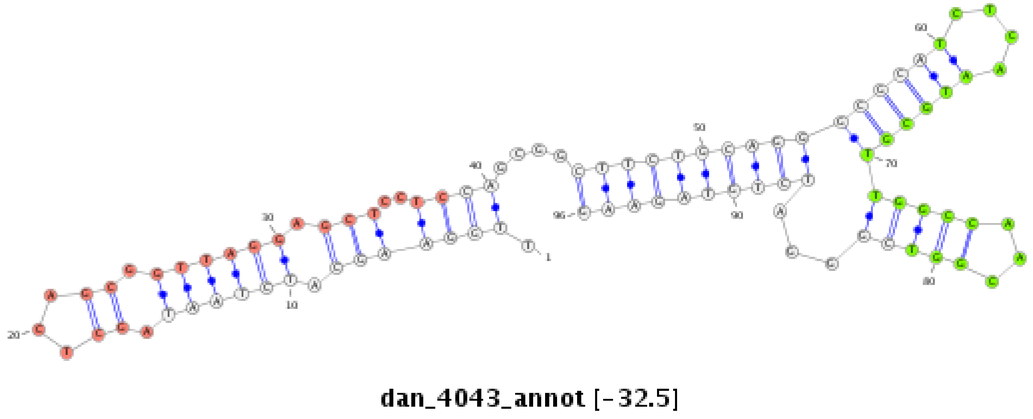
Generated: 09/08/2015 at 07:48 PM

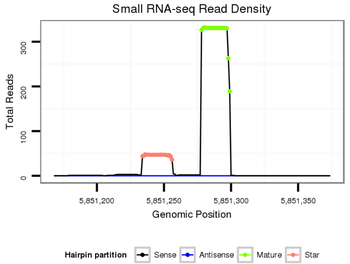
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	0
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

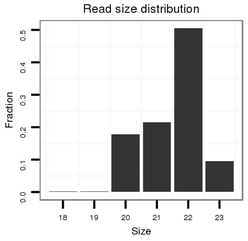
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_4043	**scaffold_13340:5851218-5851324 +**	**confident-exception**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

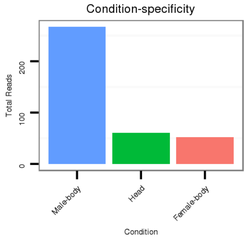
Legend: mature star mismatch in alignment mismatch in read

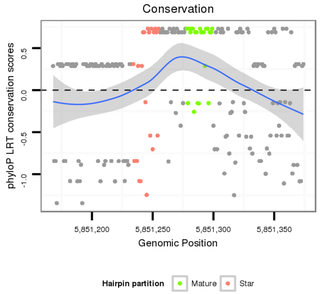
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTCCTTCAGGCTAAACTCCAGACACTTTGCGATCGTGCGGACTGGAGCCAGTTGGAAGCATCTAATAGCTCAGCGGTTAGGAGCTCCTCCAGCGGCTTCTGCAGGGCGCATCTCAATGCGTTGGCCAACGGTCGGGATCTGTAGAAGTAGAGGCAGCCTATGATAGAACTAATCCAAGTGGGTCCCCAGAATTCCGCTTCATTTCGT					V10S	M044		V10G	V05S	M058
.((((((((.(((((((.((...)).)))))).)))..))))....(((((((((((((((((....))))))))(((((...)))))...)))))))))))	Read size	# Mismatch	Hit Count	Total Norm	Total	male body	female body	head	head	embryo
..TCTCAATGCGTTGGCCAACGGT..	22	0	1	183.00	183	146	16	9	12	0
..TCTCAATGCGTTGGCCAACGG..	21	0	1	74.00	74	54	16	3	1	0
..TCTCAATGCGTTGGCCAACG..	20	0	1	67.00	67	38	1	21	7	0
..AGCTCAGCGGTTAGGAGCTCCTC..	23	0	1	32.00	32	17	10	1	4	0
..TCTCAATGCGTTGGCCAACGGTA..	23	1	1	7.00	7	5	2	0	0	0
..AGCTCAGCGGTTAGGAGCTCCT..	22	0	1	7.00	7	4	2	1	0	0
..CTCAATGCGTTGGCCAACGGT..	21	0	1	4.00	4	1	3	0	0	0
..CTCAGCGGTTAGGAGCTCCTCCA..	23	0	1	3.00	3	3	0	0	0	0
..AGCTCAGCGGTTAGGAGA..	18	1	1	2.00	2	1	0	0	1	0
..TCTCAATGCGTTGGCCAACGGTA..	23	1	1	2.00	2	1	0	0	1	0
..AGCTCAGCGGTTAGGAGCTCC..	21	0	1	2.00	2	0	2	0	0	0
..AGCTCAGCGGTTAGGAGTA..	19	2	2	1.50	3	1	0	1	1	0
..TCAATGCGTTGGCCAACGGTCGG..	23	0	1	1.00	1	1	0	0	0	0
..AGCTCAGCGGTTAGGAGCTCCTC..	24	1	1	1.00	1	0	0	1	0	0
..CCAGTTGGAAGCATCTAATAGC..	22	0	1	1.00	1	0	0	0	1	0
..AGCTCAGCGGTTAGGAGCTCCT..	23	1	1	1.00	1	1	0	0	0	0
..GGCTTCTGCAGGGCGCATCTC..	21	0	1	1.00	1	0	0	1	0	0
..TAGCTCAGCGGTTAGGAGCTCC..	22	0	1	1.00	1	1	0	0	0	0
..TCAATGCGTTGGCCAACGGT..	20	0	1	1.00	1	1	0	0	0	0
..TCTCAATGCGTTGGCCAACGT..	22	1	1	1.00	1	1	0	0	0	0
..AGCCAGTTGGAAGCATCTAA..	20	0	1	1.00	1	1	0	0	0	0
..TAAACTCCAGACACTTTGCGATCGTG..	26	0	1	1.00	1	1	0	0	0	0
..AGCTCAGCGGTTAGGAGC..	18	0	1	1.00	1	0	0	0	1	0
..TCTCAATGCGTTGGCCAACGA..	21	1	1	1.00	1	1	0	0	0	0
..CAGCGGCTTCTGCAGGGCGCA..	21	0	1	1.00	1	0	1	0	0	0
..ACTGGAGCCAGTTGGAAGCATCT..	23	0	1	1.00	1	1	0	0	0	0
..GCTCAGCGGTTAGGAGCTCCTC..	22	0	1	1.00	1	1	0	0	0	0
..TCTCAATGCGTTGGCCAAC..	19	0	1	1.00	1	0	1	0	0	0
..AGCTCAGCGGTTAGGAGA..	18	1	2	0.50	1	1	0	0	0	0
..TCTCAATGCGTTGGCCAAAG..	20	2	3	0.33	1	1	0	0	0	0
..AGCTCAGCGGTTAGGAGA..	18	2	5	0.20	1	0	0	0	1	0

Anti-sense strand reads

GAGGAAGTCCGATTTGAGGTCTGTGAAACGCTAGCACGCCTGACCTCGGTCAACCTTCGTAGATTACGAGTCGGCCAATCCTCGAGGAGGTCGCCGCGAAGACGTCCCGCGTAGAGTTACGCAACCGGTTGCCAGCCCTAGACATCTTCATCTCCGTCGGATACTATCTTGATTAGGTTCACCCAGGGGTCTTAAGGCGAAGTAAAGCA					M058	M044		V05S	V039
.((((((((.(((((((.((...)).)))))).)))..))))....(((((((((((((((((....))))))))(((((...)))))...)))))))))))	Read size	# Mismatch	Hit Count	Total Norm	Total	embryo	female body	head	head	embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13340:5851168-5851374 +	dan_4043	CTCCTTCAGGCTAAACTCCAGACACTTTGCGATCGTGCGGACTGGAGCCAGTTGGAAGCATCTAATAGCTCAGCGGTTAGGAGCTCCTCCAGCGGCTTCTGCAGGGCGCATCTCAATGCGTTGGCCAACGGTCGGGATCTGTAGAAGTAGAGGCAGCCTATGATA---------GAACT---------AATCCAAGTGGGT--CCCCAGAATTCCGCTTCA--TTTCGT
droBip1	scf7180000396708:2962188-2962461 -		-CTGTTCAGATAACTCCAGATGTTTGCGATCGTGCGGACAAGAGCCAGTGGAAGCCTAAATAGCTCAGCGGTTAGGAGCTCCTCAGCGGCTTCTGCAGGGCGCATCTCAATGCGTTGGCCAACGGTCGGGATCTGCGCTCGGTTGTGAACTTTCCACATACGGTCCGCGAAGGT--CTCCAATGTTTTGCGAAGCCAAAGGACAGCCAAGATCACCAAAACATCCTTCCAAGATGAAGAAAGAAGT
droTak1	scf7180000412807:183802-183917 +		--GCCAGGAATCTCCTCAGCGGCTTCTGAAGCGTCAATCTCAGCGAAGGCGGTGGTCGAGATAATCTGTGAAAGGCCGCAGCTCGTGATCT--

Generated: 09/08/2015 07:51:17 PM

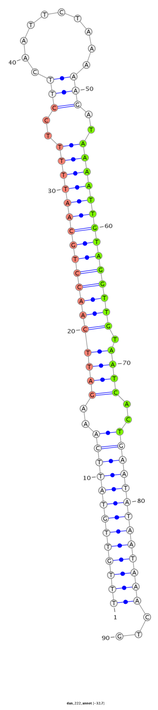
PASSIGN

crit.star	1
crit.loop	1
crit.mor	1
crit.half	0
crit.total	1
crit.pairing	0
crit.stop5	1
crit.stop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.subdominant	0
rescue.confident	0
rescue.candidate	1

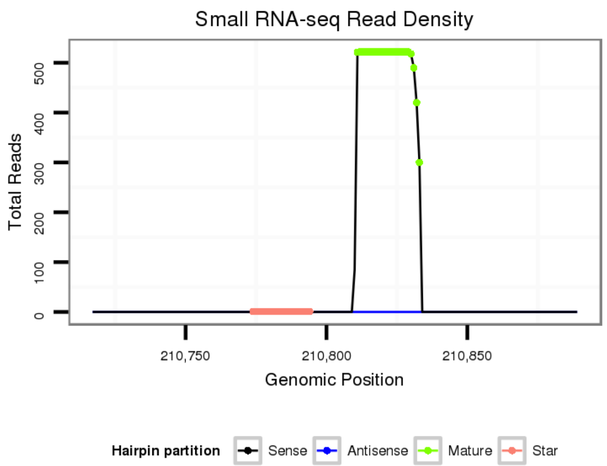
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_222	**scaffold_13335:210767-210839 +**	**confident-exception**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

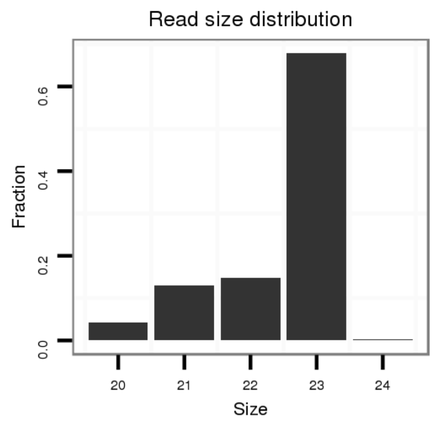
Legend: mature star mismatch in alignment mismatch in read

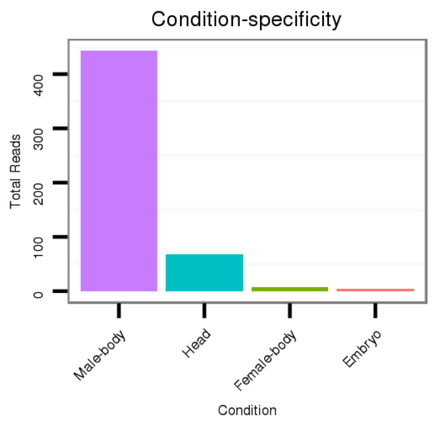
Predicted structure

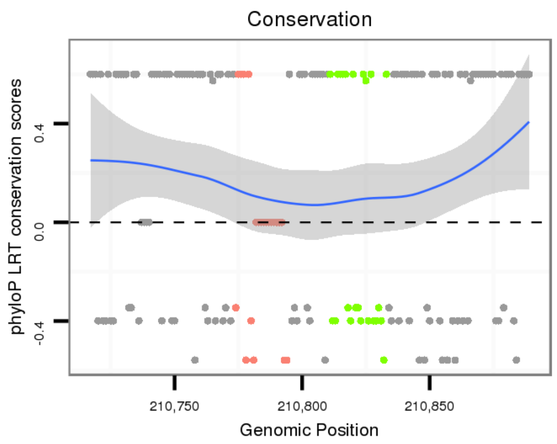


Show Alternate Folds









Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATTTATTTTAAATATCCAAATAATAAATTAATTTATAAAATCTTTGTTGTATTCAAAGATTCAACCTGCAATTTTTCCTTCAATTCTAAAAAGATAAAATTGTAGGTTGTAATCACTGAATATAATAAACTGCTTTTTCAGAACAAAAACTTTTTAATAAATTAAATGAAAAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V106 head	V055 head	M044 female body	M058 embryo	V039 embryo
(((((((((((((..(((((((((((((((((((..(((..........)))..))))))))))))))).))))..))))))))))))...											
.....TAAAATTGTAGGTTGTAATCACT.....	23	0	1	298.00	298	259	19	13	4	2	1
.....TAAAATTGTAGGTTGTAATCAC.....	22	0	1	63.00	63	51	10	2	0	0	0
.....TAAAATTGTAGGTTGTAATCA.....	21	0	1	57.00	57	55	0	2	0	0	0
.....ATAAAATTGTAGGTTGTAATCAC.....	23	0	1	57.00	57	40	12	4	0	0	1
.....TAAAATTGTAGGTTGTAATC.....	20	0	1	18.00	18	14	2	0	2	0	0
.....ATAAAATTGTAGGTTGTAATCA.....	22	0	1	13.00	13	12	1	0	0	0	0
.....ATAAAATTGTAGGTTGTAATC.....	21	0	1	10.00	10	8	2	0	0	0	0
.....TAAAATTGTAGGTTGTAATCACA.....	23	1	1	7.00	7	7	0	0	0	0	0
.....ATAAAATTGTAGGTTGTAAT.....	20	0	1	4.00	4	3	0	1	0	0	0
.....TAAAATTGTAGGTTGTAATCAT.....	22	1	1	3.00	3	3	0	0	0	0	0
.....TAAAATTGTAGGTTGTAATCACTT.....	24	1	1	3.00	3	3	0	0	0	0	0
.....TAAAATTGTAGGTTGTAATCAA.....	22	1	1	3.00	3	2	0	0	0	1	0
.....ATAAAATTGTAGGTTGTAATCACA.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TAAAATTGTAGGTTGTAATCT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....ATAAAATTGTAGGTTGTAATT.....	21	1	1	1.00	1	0	0	1	0	0	0
.....TAAAATTGTAGGTTGTAATCACTA.....	24	1	1	1.00	1	1	0	0	0	0	0
.....GATTCAACCTGCAATTTTTCC.....	21	0	1	1.00	1	0	0	0	1	0	0
.....AAAATTGTAGGTTGTAATCACT.....	22	0	1	1.00	1	0	0	0	1	0	0
.....ATAAAATTGTAGGTTGTAAA.....	20	1	1	1.00	1	1	0	0	0	0	0
.....TAAAATTGTAGGTTGTAATCACG.....	23	1	1	1.00	1	1	0	0	0	0	0
.....ATAAAATTGTAGGTTGTAATCACT.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TAAAATTGTAGGTTGTAATCG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....ATAAAATTGTAGGTTGTAATCAA.....	23	1	1	1.00	1	0	0	1	0	0	0
.....ATAAAATTGTAGGTTGTAATCAT.....	23	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

TAAATAAAATTTATAGGTTTATTATTTAATTAAATATTTTAGAAACAACATAAGTTTCTAAGTTGGACGTTAAAAAGGAAGTTAAGATTTTTCTATTTTAACATCCAACATTAGTGACTTATATTATTTGACGAAAAAGTCTTGTTTTTGAAAAATTATTTAATTTACTTTTA	Read size	# Mismatch	Hit Count	Total Norm	Total	V039 embryo	M044 female body
(((((((((((((..(((((((((((((((((((..(((..........)))..))))))))))))))).))))..))))))))))))...							
.....TGATTTTAACATCCAACATT.....	20	2	2	0.50	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13335:210717-210889 +	dan_222	ATTTATTTTAAATATCCAAATAATAAATTAATTTATAAAATCTTTGTTGTATTCAAAGATTCAACCTGCAATTTTTCCTTCAATTCTAAAAAGATAAAATTGTAGGTTGTAATCACTGAATATAATAAACTGCTT-----TTTCAGAACAAAAACTTTTTAATAAATTAAATGAAAAT
droKik1	scf7180000302610:1796883-1797045 +		ATTTAAAATATAATATTTAAT----AAATAAATAATAAAATATTTAATGAATATATAAATTAATA----------AATATTATTTAAAAATATTTAATTAAAAATGAATATTATTATATTTAAAAAATTTATCTATGTTAAATTATATAATCTTTTTAATATTTCAAAATAAAAT

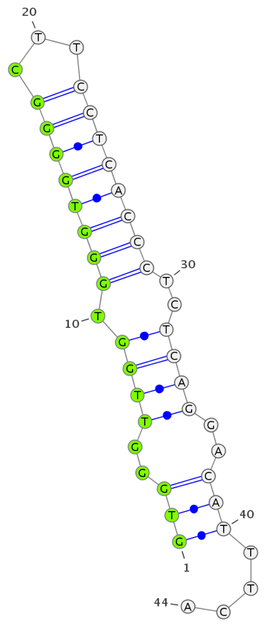
Generated: 09/08/2015 at 05:12 PM

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

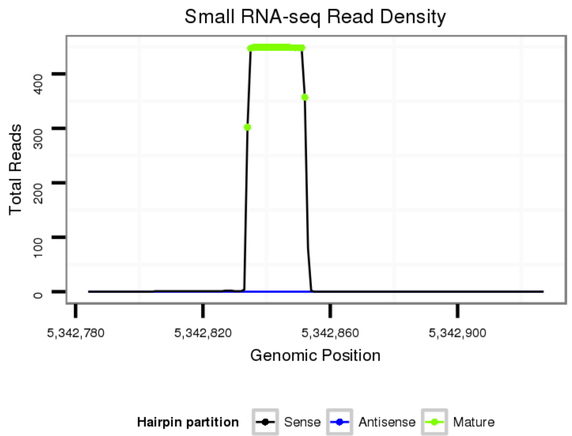
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_216	**scaffold_13337:5342834-5342877 +**	**candidate**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

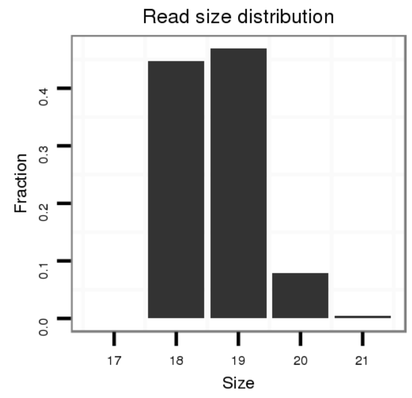
Legend: mature star mismatch in alignment mismatch in read

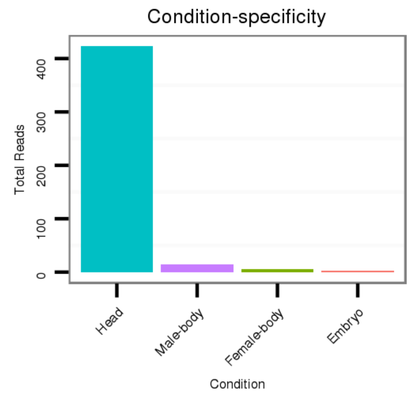
Predicted structure

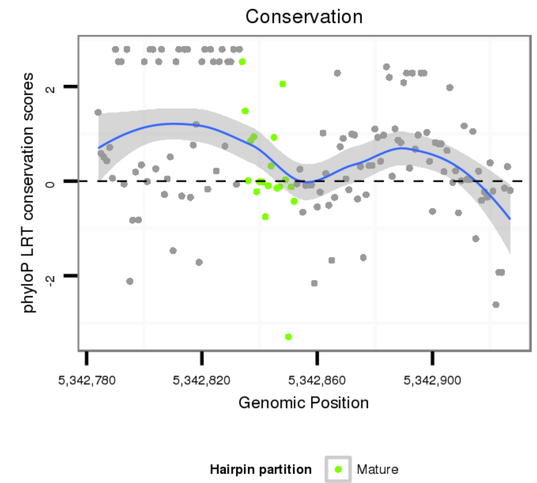


dan_216_annot [-17,6]









Show Alternate Folds

Flybase annnotation

intron [Dana\GF25232-in]; CDS [Dana\GF25232-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACCGAGTGGCTGGCCAGCTTCGATTCTGTTATCACGGACTGCGATGGTGAGTGGGTTGGTGGGTGGGGCTTCCTCACCCTCTCAGGACATTTCACCAGGAAGTGGGGTTACATAAAAATATGTACCCACTTGTATCTAAAACCA **********(((..((((.(((((((((...)))))))))..))))..)))....**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V106 head**	**M044 female body**	**V105 male body**	**V055 head**	**M058 embryo**	**V039 embryo**
..........GTGGGTTGGTGGGTGGGGC..........	19	0	1	170.00	170	166	0	3	1	0	0
..........TGGGTTGGTGGGTGGGGC..........	18	0	1	106.00	106	98	4	3	0	1	0
..........GTGGGTTGGTGGGTGGGG..........	18	0	2	91.00	182	172	1	8	1	0	0
..........TGGGTTGGTGGGTGGGGCT.........	19	0	1	39.00	39	37	1	0	0	1	0
..........GTGGGTTGGTGGGTGGGGCT.........	20	0	1	35.00	35	30	0	4	1	0	0
..........GTGGGTTGGTGGGTGGGGCA.........	20	1	1	10.00	10	10	0	0	0	0	0
..........TGGGTTGGTGGGTGGGGCA.........	19	1	1	7.00	7	5	0	1	1	0	0
..........TGGGTTGGTGGGTGGGGT..........	18	1	7	4.43	31	31	0	0	0	0	0
..........GTGGGTTGGTGGGTGGGGT.........	19	1	6	3.50	21	20	0	1	0	0	0
..........GTGGGTTGGTGGGTGGGGCTA.......	21	1	1	3.00	3	3	0	0	0	0	0
..........GTGGGTTGGTGGGTGGGGCTT.......	21	0	1	2.00	2	2	0	0	0	0	0
..........AGTGGGTTGGTGGGTGGGGCT.......	21	0	1	2.00	2	2	0	0	0	0	0
..........GGGTTGGTGGGTGGGGCT..........	18	0	1	2.00	2	1	0	1	0	0	0
..........TGGGTTGGTGGGTGGGGCTTA.......	21	1	1	1.00	1	0	0	0	1	0	0
..........GATTCTGTTATCACGGACTGCGATG....	25	0	1	1.00	1	0	0	1	0	0	0
..........TGGGTTGGTGGGTGGGGCTA.......	20	1	1	1.00	1	0	1	0	0	0	0
..........AGTGGGTTGGTGGGTGGGGC........	20	0	1	1.00	1	1	0	0	0	0	0
..........ATGGTGAGTGGGTTGGTGGGT.......	21	0	1	1.00	1	1	0	0	0	0	0
..........GTGGGTTGGTGGGTGGGGCTTAAA....	24	3	3	0.67	2	2	0	0	0	0	0
..........TGGGTTGGTGGGTGGGG...........	17	0	2	0.50	1	0	0	0	1	0	0
..........TGGGTTGGTGGGTGGGGCTTAAA.....	23	3	4	0.50	2	1	0	0	1	0	0
..........TGGGTTGGTGGGTGGGGG..........	18	1	5	0.20	1	1	0	0	0	0	0
..........GTGGGTTGGTGGGTGGGA..........	18	1	6	0.17	1	1	0	0	0	0	0
..........GTGGGTTGGTGGGTGGGC..........	18	1	12	0.08	1	1	0	0	0	0	0

Anti-sense strand reads

TGGCTCACCGACCGGTCGAAGCTAAGACAATAGTGCCTGACGCTACCACTCACCCAACCACCCACCCCGAAGGAGTGGGAGAGTCCTGTAAAGTGGTCCTTCACCCCAATGTATTTTTATACATGGGTGAACATAGATTTTGGT **********(((..((((.(((((((((...)))))))))..))))..)))....**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M058 embryo**	**V055 head**	**V106 head**	**M044 female body**	**V105 male body**
..........GTGGGTTGGTGGGTGGGGCTTAAA....	24	3	3	0.67	2	2	0	0	0	0
..........TGGGTTGGTGGGTGGGG...........	17	0	2	0.50	1	0	0	0	1	0
..........TGGGTTGGTGGGTGGGGCTTAAA.....	23	3	4	0.50	2	1	0	0	1	0
..........TGGGTTGGTGGGTGGGGG..........	18	1	5	0.20	1	1	0	0	0	0
..........GTGGGTTGGTGGGTGGGA..........	18	1	6	0.17	1	1	0	0	0	0
..........GTGGGTTGGTGGGTGGGC..........	18	1	12	0.08	1	1	0	0	0	0

Show Alignment With Reads

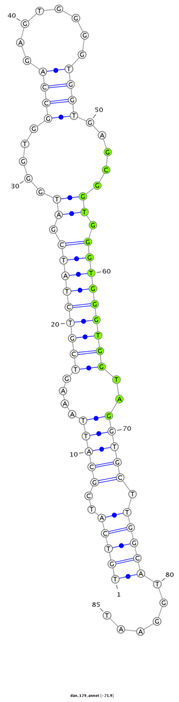
Re-alignment of all predicted orthologs

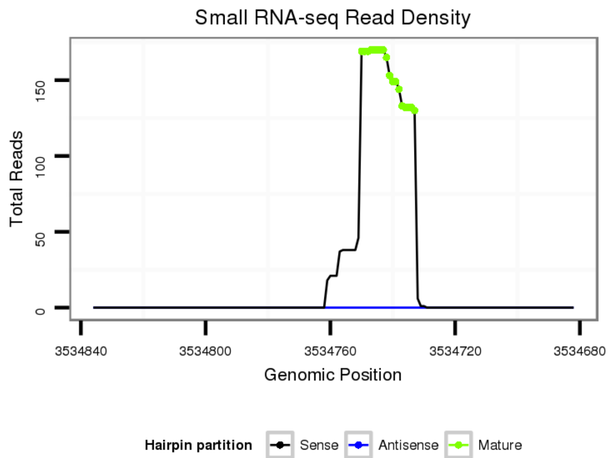
Species	Coordinate	ID	Alignment
droAna3	scaffold_13337:5342784-5342927 +	dan_216	ACCGAGTGGCTGGCCAGCTTCGATTCTGTTATCACGGACTGCGATGGTGAGTGGGTT--GG-----TGGG------TGGG---GCTTC----------CTC---------ACCCTCT-CAGGACA-TT-TCACC----AGGAAGTGGGGTTACATAAAAATATGT----AC--CCACTTG----------T--ATCTAA----AACCA
droBip1	scf7180000396371:669182-669321 +		ACCGAGTGGCTGGCCAGCTTCGATTCTGTTATCACGGATTGCGATGGTGAGTGGGTC--GGCC---TGGGAGA----GGGT---TACAT--ATCTAT----AACCA
droKik1	scf7180000302626:259285-259425 -		ACCGAGTGGATAGCAGGCTTTGATTCTGTTATAACAGACTGCGATGGTGAGTGGGGGGGT-----TGGG------TGGA---A----------AAGGGG-----------GC------GAAGGATA-TT-CACCC----AGGAAGTTGCGTTACATAAAGATATGT----CT--ACACC----------AATTTATGG----GGTCA
droFic1	scf7180000454107:1435238-1435368 -		ACCGAGTGGATATCGAGCTTCGATTCGGTGATAACGACTGCGATGGTGAGTGGGTC--G-----TGGG------TGGCTTACTTTGC------CGTATT----------------A--AAAGGG--TT-TCTCCC---AGGAAGTTGCGTTACATAAAGATATGT----GTATCCATAC-----------------------
droEle1	scf7180000490993:759390-759551 -		AACGAGTGGATGTCGAGTTCGACTCCGTTATAACGAATGCGATGGTAAGTGGGTC--GCTATGGGTGTGTG---TGT-----GTGTGTGTGGG----GT----GTTCCC-------GGTCATGGAAGAC--TTCCCCTGT---AGGAAGTTGCGTTACATAAATATACATATGCGT--ATACC----------------AA---AATCG
droRho1	scf7180000779490:158257-158396 -		AACGAGTGGATTTCGAGTTCGATTCTGTTATAACAGATTGCGATGGTAAGTGGGGGTCG-----TGGGAGGTGGGTGGG---GT----------------GTTCC-------GGTCACGGAAGGA--TTC-CCACC---AGGAAGTTGCGTTACATAAAGATACATATGTGT--ATA-----------------------
droBia1	scf7180000302193:1159805-1159942 -		ACCGAGTGGATTTCGAGCTTCGACTCCGTCATTACAGACTGTGATGGTGAGTGGGTC--G-----TGGGTGGTGGGCGGG---------------------TCTCCCTGC------C---CCGAAGGA--GTC-CCCC---AGGAAGTTGCGTCACATAAAGATATGTATACGT--ATGCC----------------------A
droTak1	scf7180000415794:87007-87159 -		ACCGAGTGGATTTCGAGCTTCGATTCGGTCATTACAGACTGTGATGGTGAGTGGGGTTG-GG---TGGG------TGG-----TTG-----GGAGTAGGGCGGGAACTTCCTGCTCGC----------CAAGGA--TTT-CCCCC---AGGAAGTTGCGTTACATAAAGATATGTTTGTGT--ATACC----------------------A
droEug1	scf7180000409471:1712198-1712348 +		ACCGAGTGGCTCCAGAGTTTGATTCAGTAATTACTGACTGCGATGGTAAGTGGGTC--G-----TGGATGGTGGGTGGT---A----------GAAGATGTACTCCCTACTCCCTTCT--CAA-AAGGA--TTC-CTCCC---AGGAAGTTGCGTTACATAAAGATATGT----GT--ATACC----------------------A
dm3	chr3L:17836284-17836420 -		ACCGAGTGGCTAGCAGGCTTCGACAGTGTAATAACGACTGCGATGGTAAGTCGGTCG--G-----TGGG--GA---TGAG---AT----------------ACTACTAACTCGCC---ACCCACG-CAGGA--TTC-CCCCC---AGGAAGTTGCGTTACATAAAGATATGT----GT--ATACC-----------------------
droSim2	3l:17415515-17415653 -		ACCGAGTGGCTAGCAAGCTTCGACAGTGTAATAACGACTGCGATGGTAAGTGGGTC--G-----TGGG--C----TGCC---AT----------------ACTCCAAACTCCCTCCCCCCCACG-CAGGA--TTC-CCCCC---AGGAAGCTGCGTTACATAAAAATATGT----GT--ATACC-----------------------
droSec2	scaffold_0:9882008-9882145 -		ACCGAGTGGCTAGCAAGCTTCGACAGTGTAATAACGACTGCGATGGTAAGTGGGTC--G-----TGGG------TGCC---AT----------------ACTCCAAACTCCCTCCCCCCCACG-CAGGA--TTC-CCCCC---AGGAAGCTGCGTTACATAAAAATATGT----GT--ATACC-----------------------
droYak3	3L:16217382-16217513 +		ACCGAGTGGATATCAAGCTTCGACAGTGTAATAACGACTGCGATGGTAAGGGGGTCG--G-----TGGG--GTG---GGC---AT----------------ACTCTCAACTCGCC---------CATAGGA--TTC-CGCCC---AGGAAGCTGCGTTACATAAAGATATGT----GT--ATACC-----------------------
droEre2	scaffold_4784:16027960-16028091 +		ACCGAGTGGATATCAAGCTTCGACAGTGTAATAACGACTGCGATGGTAAGTGGGTC--G-----TGGG--GTG---GGC---AC----------------ACTCCAACTCGCC---------CATAGGA--TTC-CGCCC---AGGAAGCTGCGTTACATAAAGATATGT----GT--GTACC-----------------------
dp5	XR_group6:10709524-10709670 -		ACGGAATGGCTCGAAGGCTTCGACAGTCATAACAGACTGTGACGGTAAGTATTTC--T-----CGGGGGC----AGGT---AAATTA-----TGAATG----------------ATT-CAGGT-A-CT-CCCACAGGAAGGCAGTTGCGTAATGTAATGCATGGTC---A--GCATCC----------------T--GGCTGG----CCCTG
droPer2	scaffold_20:621975-622119 -		ACGGAATGGCTCGAAGGCTTCGACACAGTCATAACAGACTGTGACGGTAAGTATTTC--T-----CGGGGGC----AGGT---AAATTA-----TGAATG----------------ATT-CAGGT-A-CT-CCCACGGGAAGGCAGTTGCGTAATGTAATACATGGTC---A--GCATCC----------------T--GGC--T----GCCC
droWil2	scf2_1100000004540:2489298-2489349 +		TGATCATGGCTATCTAGTTTGATAGCGTCATCTCGGATTGTGATGGTAAGT---

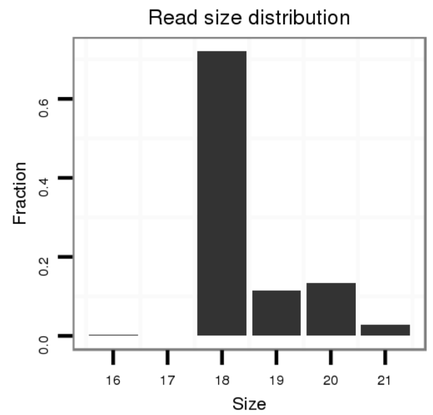
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_129	**scaffold_13117:3534732-3534786 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

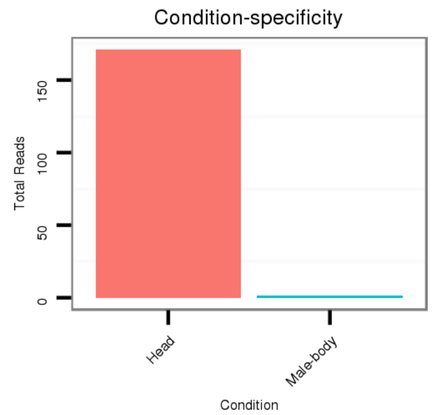
Legend: mature star **mismatch in alignment** mismatch in read

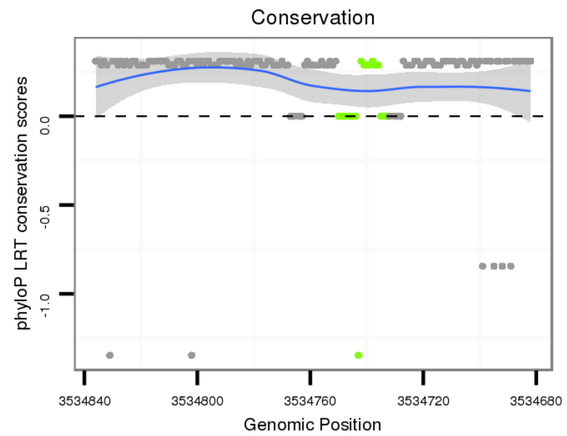
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF20893-in]

No Repeatable elements found

mature	star
1. dan_129 scaffold_13117:3534733-3534750 - 2. dan_127 scaffold_13266:1454835-1454852 - 3. scaffold_13337:15034009-15034026 -	

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTCTCGAACAGTCATCCCGTTATTTTCCCATGCAGTGTCATCGCATTAAAGTCGTCTATCGATGGGTGGCCAGAGTGGGGTGGTGAGCGGTGGGTGGGTGGTAGGTGCTTGGCATGGAATGCGAAAAAGTTGGTTGAGAAAAAATAAGAAAAAAA **********(((((..(((((....((((((((((.((.....((((........))))).....)).)))))))))..)))))..)))))......**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	V055 head	M044 female body	V039 embryo
.....GCGGTGGGTGGGTGGTAG.....	18	0	3	118.33	355	350	1	4	0	0
.....TGGGGTGGTGAGCGGTGGGT.....	20	0	1	12.00	12	12	0	0	0	0
.....GTGGTGAGCGGTGGGTGGGT.....	20	0	1	10.00	10	10	0	0	0	0
.....AGCGGTGGGTGGGTGGTAG.....	19	0	2	6.00	12	12	0	0	0	0
.....GCGGTGGGTGGGTGGTAGG.....	19	0	3	5.67	17	17	0	0	0	0
.....GTGGTGAGCGGTGGGTGGG.....	19	0	1	5.00	5	4	1	0	0	0
.....TGGGGTGGTGAGCGGTGGGTG.....	21	0	1	4.00	4	4	0	0	0	0
.....GGGGTGGTGAGCGGTGGG.....	18	0	1	3.00	3	3	0	0	0	0
.....AGCGGTGGGTGGGTGGTA.....	18	0	2	2.50	5	5	0	0	0	0
.....TGGGGTGGTGAGCGGTGGG.....	19	0	1	2.00	2	2	0	0	0	0
.....GTGGTGAGCGGTGGGTGGGTGGTAA.....	25	1	1	2.00	2	2	0	0	0	0
.....GTGGGTGGGTGGTAGGTGCA.....	20	1	2	2.00	4	4	0	0	0	0
.....GCGGTGGGTGGGTGGTAT.....	18	1	3	1.33	4	4	0	0	0	0
.....GTGGTGAGCGGTGGGTGGGTG.....	21	0	1	1.00	1	1	0	0	0	0
.....TGGGGTGGTGAGCGGTGGGTGT.....	22	1	1	1.00	1	1	0	0	0	0
.....GTGGTGAGCGGTGGGTGGGA.....	20	1	1	1.00	1	1	0	0	0	0
.....TGGTGAGCGGTGGGTGGGT.....	19	0	1	1.00	1	1	0	0	0	0
.....GTGGGTGGGTGGTAGGTG.....	18	0	2	1.00	2	2	0	0	0	0
.....AGCGGTGGGTGGGTGGTAGAA.....	21	2	3	0.67	2	2	0	0	0	0
.....GAGCGGTGGGTGGGTGGTAG.....	20	0	2	0.50	1	1	0	0	0	0
.....GTGGTGAGCGGTGGGTGGGTT.....	21	1	2	0.50	1	1	0	0	0	0
.....AGCGGTGGGTGGGTGGTAGG.....	20	0	2	0.50	1	1	0	0	0	0
.....GAGCGGTGGGTGGGTGGT.....	18	0	2	0.50	1	1	0	0	0	0
.....GTGGGTGGGTGGTAGG.....	16	0	8	0.50	4	0	0	4	0	0
.....GCGGTGGGTGGGTGGTAA.....	18	1	5	0.40	2	2	0	0	0	0
.....GCGGTGGGTGGGTGGTAGT.....	19	1	4	0.25	1	1	0	0	0	0
.....TGGAATGCGAAAAAGTCT.....	18	2	16	0.06	1	0	0	1	0	0

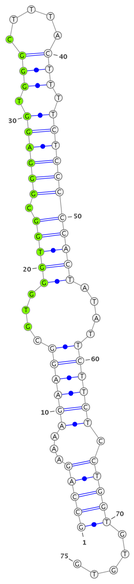
Anti-sense strand reads

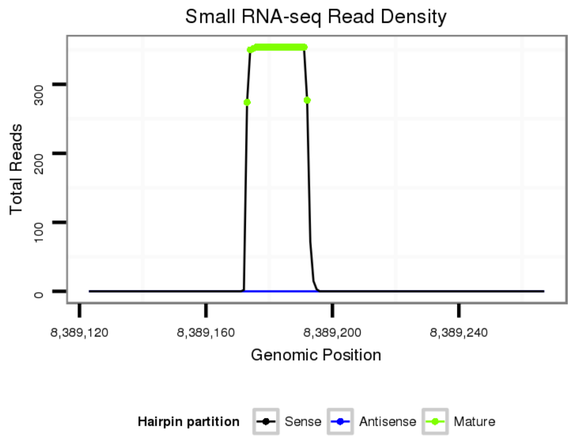
AAGAGCTTGTCAGTAGGGCAATAAAAGGGTACGTCACAGTAGCGTAATTTCAGCAGATAGCTACCCACCGGTCTCACCCCACCACTCGCCACCCACCCACCATCCACGAACCGTACCTTACGCTTTTTCAACCAACTCTTTTTTATTCTTTTTTT **********(((((..(((((....((((((((((.((.....((((........))))).....)).)))))))))..)))))..)))))......**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V039 embryo	M058 embryo	M044 female body	V105 male body
.....GCGGTGGGTGGGTGGTAGGTGCTTGGCATGGAATGCGAAAAAGTTGGTTGAGAAAAAATAAGAAAAAAA.....	18	0	3	118.33	355	350	1	4	0	0
.....GCGGTGGGTGGGTGGTAGGTGCTTGGCATGGAATGCGAAAAAGTTGGTTGAAAAAAATAAGAAAAAAA.....	19	1	3	39.33	118	116	1	1	0	0
.....GCGGTGGGTGGGTGGTAGGTGCTTGGCATGGAATGCGAAAAAGTTGGTTGAG

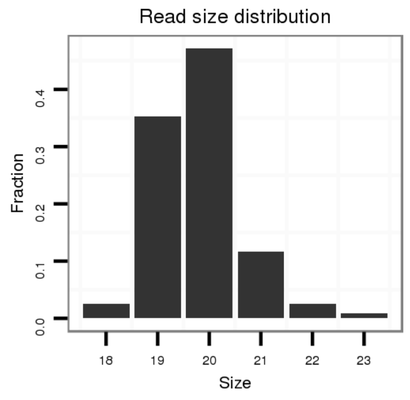
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_290	**scaffold_13337:8389173-8389217 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

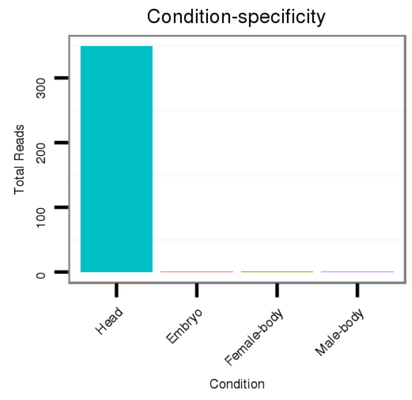
Legend: mature star mismatch in alignment mismatch in read

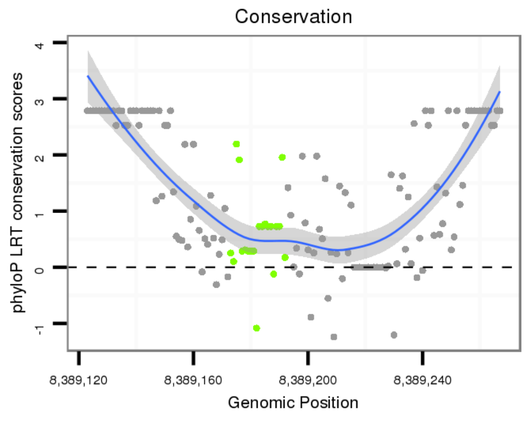
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAAATAATTTGATGGTTTCATAAACTCGCTTCGGGGCCAGAAAAGAAGGCGTGGGTGGCGGGAGGTGGGCTTTACTTTTCTCCCCCACTATATTCTTCTCCTGGTGTGTGTGTGTTTTTGTGTGTATTTTCAGATAAAATTGCAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	V105 male body	V055 head	M058 embryo
((((((...((((((....((((((.((((((.(((.....))).)))))))))))....))))))..))))).....											
.....GTGGGTGGCGGGAGGTGGGC.....	20	0	1	150.00	150	149	0	0	0	1
.....GTGGGTGGCGGGAGGTGGG.....	19	0	1	72.00	72	71	0	1	0	0
.....TGGGTGGCGGGAGGTGGGC.....	19	0	1	52.00	52	52	0	0	0	0
.....GTGGGTGGCGGGAGGTGGGCT.....	21	0	1	38.00	38	38	0	0	0	0
.....TGGGTGGCGGGAGGTGGGCT.....	20	0	1	16.00	16	15	1	0	0	0
.....GTGGGTGGCGGGAGGTGGGCTT.....	22	0	1	9.00	9	9	0	0	0	0
.....TGGGTGGCGGGAGGTGGG.....	18	0	1	5.00	5	4	0	0	1	0
.....GTGGGTGGCGGGAGGTGGGCA.....	21	1	1	4.00	4	4	0	0	0	0
.....TGGGTGGCGGGAGGTGGGCTT.....	21	0	1	3.00	3	3	0	0	0	0
.....GTGGGTGGCGGGAGGTGGGCTTT.....	23	0	1	3.00	3	3	0	0	0	0
.....GGTGGCGGGAGGTGGGCT.....	18	0	1	2.00	2	2	0	0	0	0
.....TGGGTGGCGGGAGGTGGGCA.....	20	1	1	2.00	2	2	0	0	0	0
.....GGGTGGCGGGAGGTGGGC.....	18	0	1	2.00	2	2	0	0	0	0
.....GTGGGTGGCGGGAGGTGGGA.....	20	1	2	1.50	3	3	0	0	0	0
.....GGTGGCGGGAGGTGGGCA.....	18	1	1	1.00	1	1	0	0	0	0
.....CGTGGGTGGCGGGAGGTGGGC.....	21	0	1	1.00	1	1	0	0	0	0
.....GTGGGTGGCGGGAGGTGGC.....	19	1	1	1.00	1	1	0	0	0	0
.....CGTGGGTGGCGGGAGGTGGGCG.....	22	1	1	1.00	1	1	0	0	0	0
.....CGTGGGTGGCGGGAGGTGGGCT.....	22	0	1	1.00	1	1	0	0	0	0
.....GTGGGTGGCGGGAGGTGGGCG.....	21	1	1	1.00	1	1	0	0	0	0
.....GTGGGTGGCGGGAGGTGGGT.....	19	1	6	0.50	3	3	0	0	0	0
.....GTGGGTGGCGGGAGGTGGGTT.....	20	1	6	0.17	1	1	0	0	0	0
.....TGGGTGGCGGGAGGTGGGT.....	19	1	6	0.17	1	1	0	0	0	0
.....GGCGGGAGGTGGGCTTA.....	17	1	8	0.13	1	0	0	0	1	0

Anti-sense strand reads

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

Show Alignment With Reads

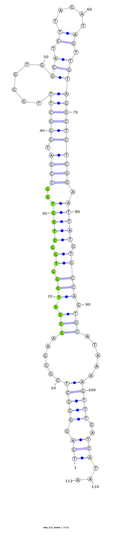
Re-alignment of all predicted orthologs

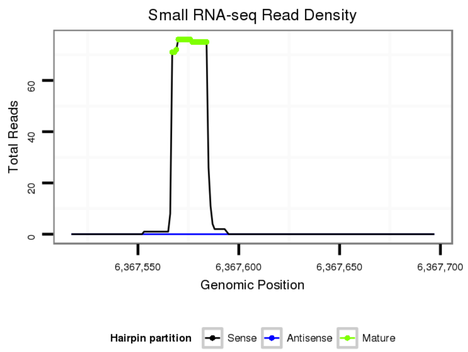
Species	Coordinate	ID	Alignment
droAna3	scaffold_13337:8389123-8389267 +	dan_290	AAAATAATTTGATGGTTTCATAAACTCGCTTCGGGG----CC-AGAA---AAGAAGGCG-TGGGTGGCGGGAGGTG--GGC---TTTACTTTTCTCCCCC-ACTA----TATTCTTCTCCTGGTGTGTG----------TGTGTTTTTGTGTGTATTTTCAGATAAAATTGCAA
droBip1	scf7180000396541:536022-536166 +		AAAATAATTTGATGGTTTCATAAACTCGCTTCGGGG----CC-AGAA---AAGAAGGCG-TGGGTGGCAGGAGGTGGGGC---ACTACTTTACTCCCCCAACTA----TATT---------CTTCTGTGGGTGGATG---TGTGTGTGTGTGTATTTTCAGATAAAATTGCAA
droKik1	scf7180000302474:776489-776595 +		AAAATAATTTGATGGTTTCATAAACTCGCTTCGGGGC---CCCAGGC---AGGGAGGCG-TGG----------GTGGT--GGTTT-TTCCCCTAA---------------------CTG---TAT--GTGTGTGTAT-TTCAGATAAAATTGCAA
droFic1	scf7180000454107:995080-995197 +		AAAATAATTTGATGGTTTCATAAACTCGCTTCGGGGC---CC-A-G---AAGGAGGCG-TGG----------GTGGT--GGTTT-TGCCCTGACTGTGAATA----------TATG----------TGTGTTTGTGTGTGTAT-TTCAGATAAAATTGCAA
droEle1	scf7180000490993:359007-359117 +		AAAATAATTTGATGGTTTCATAAACTCGCTTCGGGGC---CC-A-AA---AAAGGGGCG-TGG----------GTGG-----TT--TGTCCTGTCTG----------TTG----------TGTGTATGTGTGTGTAT-TTCAGATAAAATTGCAA
droRho1	scf7180000779956:107087-107197 +		AAAATAATTTGATGGTTTCATAAACTCGCTTCGGGGC---CC-A-AA---AAGAAGGCG-TGG----------GTGG-----TT--TTCCCCTGGCTC----------TTG----------TGTGTGGGTGTGTGATAT-TTCAGATAAAATTGCAA
droBia1	scf7180000302428:6806691-6806804 +		AAAATAATTTGATGGTTTCATAAACTCGCTTCGGGGC---CC-A-AA---AAGGAGGCG-TGG----------GTGGT--GGTTT-TTCCCTCGTCTC----------TGA-------CTG---TGTGTGTGTGTGTAT-TTCAGATAAAATTGCAA
droTak1	scf7180000416006:342598-342702 -		AAAATAATTTGATGGTTTCATAAACTCGCTTCGGGGC---CC-A-AA---AAGGAGGCG-TGG----------GTGG-----TT--TTCCCATGG---------------------CTG---TGTGTGTGTGTGTAT-TTCAGATAAAATTGCAA
droEug1	scf7180000409471:2131160-2131266 -		AAAATAATTTGATGGTTTCATAAACTCGCTTCGGGGC---CC-A-AA---AAAGAGGCG-TGG----------GTGGT--GGTTT-TTGCTTGG---------------------ATG---TGTGTGTGTGTGTATAT-TTCAGATAAAATTGCAA
dm3	chr3L:17435220-17435330 +		AAAATAATTTGATGGTTTCATAAACTCGCTTCGTGGC---CC-A-AA---AAGGAGGCGGCGG----------GTGGTTCGGTT--TTCCCCTGC---------------------CTG---TGTGGGTGTGTGTAT-TTCAGATAAAATTGCAA
droSim2	3L:17031624-17031734 +		AAAATAATTTGATGGTTTCATAAACTCGCTTCGTGGC---CC-A-AA---AAGGAGGCGGCGG----------GTGGTTCGCTT--GTCCCCTGC---------------------CTG---TGTGGGTGTGTGTAT-TTCAGATAAAATTGCAA
droSec2	scaffold_0:9487814-9487924 +		AAAATAATTTGATGGTTTCATAAACTCGCTTCGTGGC---CC-A-AA---AAGGCGGCGGCGG----------GTGGTTCGCTT--TTCCCCTGC---------------------CTG---TGTGGGTGTGTGTAT-TTCAGATAAAATTGCAA
droYak3	3L:16630805-16630915 -		AAAATAATTTGATGGTTTCATAAACTCGCTTCAGGG---CC-A-AA---AAGAAAGCGCCGG----------GTGGTTCGGTT--TTCCCTTTG---------------------CTG---TGTGGGTGTGTGTAT-TTCAGATAAAATTGCAA
droEre2	scaffold_4784:16412158-16412267 -		AAAATAATTTGATGGTTTCATAAACTCGCTTCGGGGC---CC-A-AA---AAGCAGGCG-CGG----------GTGGTTCGGTT--TTCCCCTGG---------------------CTG---TGTGGGTGTGTGTAT-TTCAGATAAAATTGCAA
dp5	XR_group6:9200696-9200825 -		AAAATAATTTGATGGTTTCATAAAGTCGCTTGGGGGTCGCC-A-AAGGAGAGAAGTT-TG--------GGAGGAG--GGCTAG-----TA--TTTC---------TATT----------TGTGTGTGTGTT----CGTGTGTGTATGTCGTGTGTTTCAGATAAAATTGCAAA
droPer2	scaffold_35:522172-522300 +		AAAATAATTTGATGGTTTCATAAAGTCGCTTGGGGGTCGCC-A-AAGGAGAGAAGTT-TG--------GGAGGAG--GGCTAG-----TA--TTTC---------TATT----------TGTGTGTGTGTT----CGTGTGTGTATGTCTGTGTTTCAGATAAAATTGCAA
droWil2	scf2_1100000004822:3486305-3486429 -		AAAATAATTTGATGGTTTCATAAAGTTGCTTTGGG---TTGTGTGTGTGTGTGTGATAAAATTGCAAACTTCCCCCTCAACAATGCCCGAGTATGTATAATATATATGTATATGTGTATGTGTATGTACAT
droVir3	scaffold_13049:5845559-5845679 -		AAAATAATTTGATGGTTTCATAAAGTCGCTGCATGC--CAGGTG-CGGGAGAGGCGGCGGCG----------TAAATGTAAGTGTG----------TGTGCGTGT----GTGTGTGCGTGTGTGTGTGCGT-TTGTGATAAAATTGCAA
droMoj3	scaffold_6680:4177662-4177746 -		AAAATAATTTGATGGTTTCATAAAGTCGCTGC-----------------AA---GAGGAGGTTGGGG----------GTG-----------TCTGTATATGTATCTGT-GTGTGATAAAATTGCAA
droGri2	scaffold_15110:13233377-13233541 +		AAAATAATTTGATGGTTTCATAAAGTCGCTGCATGT--CGGGAA-CA---CAGAATGGG----------G---TGTGTGTGTGTGTGT

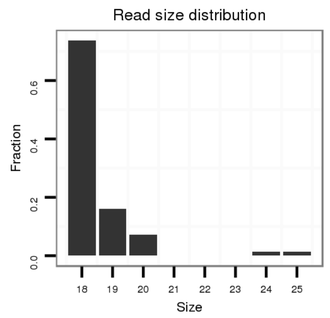
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_132	**scaffold_12916:6367567-6367647 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

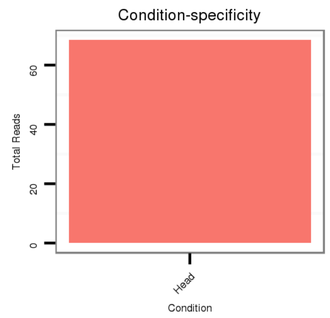
Legend: mature star mismatch in alignment mismatch in read

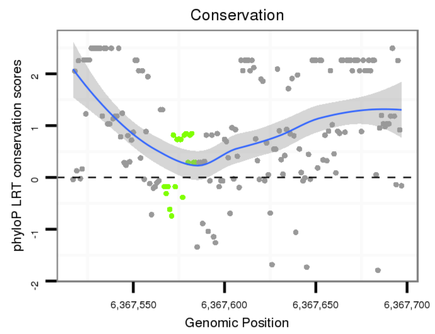
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dana\GF15308-in]

No Repeatable elements found

mature	star
1. dan_132 scaffold_12916:6367567-6367584 + 2. dan_138 scaffold_12916:6970798-6970815 +	

Sense Strand Reads

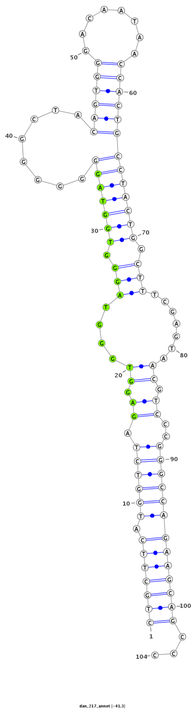
hide 3p reads | show mid mismatch reads

| | | |

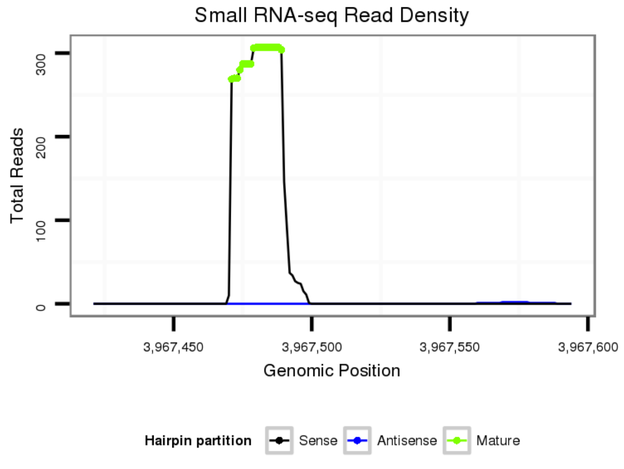
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_217	**scaffold_13117:3967471-3967544 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

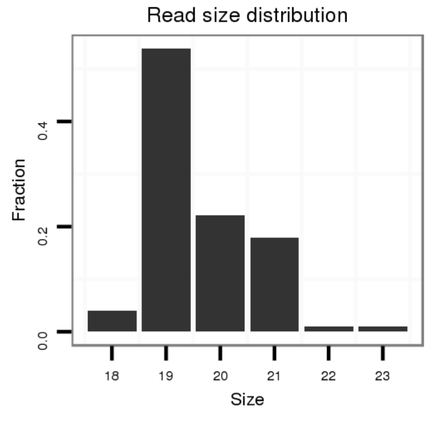
Legend: mature star **mismatch in alignment** mismatch in read

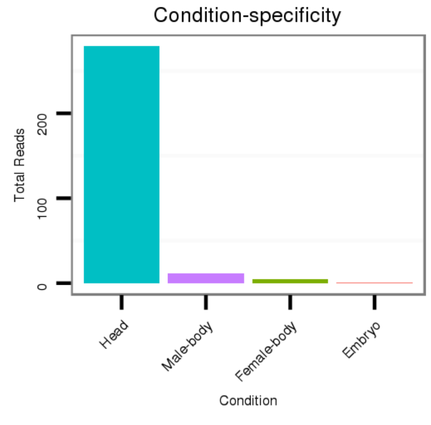
Predicted structure

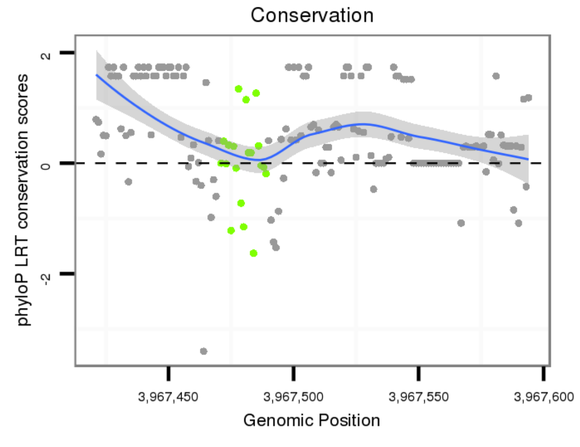


Show Alternate Folds









Flybase annnotation

intron [Dana\GF21406-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTGACACAGCTTGTCCCACTGTGCGTTTGTTGCTTCTGCTTCATGGTCTAGAGGTGGGTAGGGTGGTAGGGGGGGCTACAGTGGGACAATAACCACTGCCTACTGGCTTTCGAGTAACGTCCCGGGCCAGAAGCAGCCCCAGTCCCAGTCCCAGCTGGGTCAAAAAATAACAGC **********(((((((.(((((((.((.((....(((.(((((((((.....(((((.....)))))))))))))).)))....)).))..)))))))))))))...**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V106 head**	**V105 male body**	**V055 head**	**M044 female body**	**M058 embryo**	**V039 embryo**
.....GAGGTGGGTAGGGTGGTAG.....	19	0	1	154.00	154	147	5	2	0	0	0
.....GAGGTGGGTAGGGTGGTAGGG.....	21	0	1	51.00	51	47	2	1	1	0	0
.....GAGGTGGGTAGGGTGGTAGG.....	20	0	1	50.00	50	41	4	2	3	0	0
.....TAGGGTGGTAGGGGGGGCTA.....	20	0	1	10.00	10	10	0	0	0	0	0
.....TAGGGTGGTAGGGGGGGC.....	18	0	1	5.00	5	4	0	0	0	1	0
.....AGAGGTGGGTAGGGTGGTAGG.....	21	0	1	5.00	5	4	0	1	0	0	0
.....GTGGGTAGGGTGGTAGGGGG.....	20	0	1	4.00	4	4	0	0	0	0	0
.....AGAGGTGGGTAGGGTGGTAG.....	20	0	1	4.00	4	4	0	0	0	0	0
.....TAGGGTGGTAGGGGGGGCT.....	19	0	1	3.00	3	3	0	0	0	0	0
.....GAGGTGGGTAGGGTGGTA.....	18	0	1	3.00	3	3	0	0	0	0	0
.....TAGGGTGGTAGGGGGGGCTAA.....	21	1	1	2.00	2	2	0	0	0	0	0
.....TGGGTAGGGTGGTAGGGG.....	18	0	1	2.00	2	2	0	0	0	0	0
.....TGGGTAGGGTGGTAGGGGG.....	19	0	1	2.00	2	2	0	0	0	0	0
.....GAGGTGGGTAGGGTGGTAGGG.....	21	1	1	2.00	2	2	0	0	0	0	0
.....TGGGTAGGGTGGTAGGGGGGC.....	22	0	1	2.00	2	1	1	0	0	0	0
.....GTGGGTAGGGTGGTAGGGGGGC.....	23	0	1	2.00	2	2	0	0	0	0	0
.....GAGGTGGGTAGGGTGGTAGGA.....	21	1	1	1.00	1	1	0	0	0	0	0
.....GTGGGTAGGGTGGTAGGGGGAA.....	23	2	1	1.00	1	0	0	0	0	1	0
.....TAGGGTGGTAGGGGGGCTT.....	20	1	1	1.00	1	1	0	0	0	0	0
.....GTGGGTAGGGTGGTAGGGGG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GTGGGTAGGGTGGTAGGGG.....	19	0	1	1.00	1	1	0	0	0	0	0
.....GAGGTGGGTAGGGTGGTAT.....	19	1	1	1.00	1	1	0	0	0	0	0
.....AGGGTGGTAGGGGGGGCT.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TGGGTAGGGTGGTAGGGGT.....	19	1	1	1.00	1	1	0	0	0	0	0
.....GTGGGTAGGGTGGTAGGGGGGG.....	22	0	1	1.00	1	1	0	0	0	0	0
.....AGAGGTGGGTAGGGTGGTAGGG.....	22	0	1	1.00	1	1	0	0	0	0	0
.....GAGGTGGGTAGGGTGGTAGGGA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....GTGGGTAGGGTGGTAGGG.....	18	0	1	1.00	1	1	0	0	0	0	0
.....AGGTGGGTAGGGTGGTAGGG.....	20	0	1	1.00	1	0	0	0	1	0	0
.....GAGGTGGGTAGGGTGGTAGGGGG.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TAGGGTGGTAGGGGGGGC.....	19	1	1	1.00	1	1	0	0	0	0	0
.....TGGGTAGGGTGGTAGGGGGG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TAGGGTGGTAGGGGGGGCTAC.....	21	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

AACTGTGTCGAACAGGGTGACACGCAAACAACGAAGACGAAGTACCAGATCTCCACCCATCCCACCATCCCCCCGATGTCACCCTGTTATTGGTGACGGATGACCGAAAGCTCATTGCAGGGCCCGGTCTTCGTCGGGGTCAGGGTCAGGGTCGACCCAGTTTTTTATTGTCG **********(((((((.(((((((.((.((....(((.(((((((((.....(((((.....)))))))))))))).)))....)).))..)))))))))))))...**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M058 embryo**	**M044 female body**	**V105 male body**	**V039 embryo**	**V055 head**	**V106 head**
.....GTCAGGGTCAGGGTCGACC.....	19	0	1	1.00	1	0	1	0	0	0	0
.....AGGGTCGACCCAGTTTTTTA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GGTCGACCCAGTTTTTTA.....	18	0	3	0.33	1	0	1	0	0	0	0
.....CGTCGACCCAGTTTTTTA.....	18	1	4	0.25	1	1	0	0	0	0	0
.....CGGTCGACCCAGTTTTTT.....	18	1	4	0.25	1	1	0	0	0	0	0
.....GTCAGGGTCAGGGTCGA.....	18	1	11	0.18	2	0	0	2	0	0	0
.....GTCGGGGTCAGGGTCAGGGTC.....	21	0	10	0.10	1	0	0	0	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13117:3967421-3967594 +	dan_217	TTGACACAGCTTGTCC-CACTGTGCGTTTGTTGCTTCTGCTTCATGGTCT------AGAGGTGGGTAGGG----------TG-------GT----------AG--GGGGGGCTACAGTGGGACAATAACCACTGCCT--ACTGGCTTTCGAGTAACGTCCCGGGCCAGAAGCAGCCCCAGTCCCAGTCCCAGCTGGGTCAAAA-AATAACAGC
droBipl	scf7180000396383:410375-410526 -		TTGACACAGCTTGGAC-CACTGTGCGTTTGTTGCTCCTGTTTCGGGGGG------------------GTGGCGGCCGCGGCGGCGCG------TCGGGT--GCGGGGGTACAGTGGGACAA---CCACTGCCTACTAGCCTTG----GGGTCCT----------C-GTCCCAGCTGGGTCAAAATAACACAGC
droKik1	scf7180000302230:98446-98539 -		TTAGTACAGCTTGGAC-CACTGTGCGTTTGTTGCTCCTGTTTGGTGGTT--------------------------------------GTAGACTGGGACAGT----GCTGCCT--ACTAACTTTT-----TTGTCCCGGGC----------TGGCC-----------|
droFic1	scf7180000454050:1156114-1156246 -		TTTGCACAGCTTGAAC-CACTGTGCGTTTGTTGCTCCTCCTGGGTGGTTGC------AAAAATGGGGCGGT----------GGGTGTTTTTTT--TTGGGGGTGAGGTCGTGTACAGTGGGA----------TCT--ACTAACTTTT-----TTGTCCCGGGC----------AGACGGAG-----------|
droEle1	scf7180000491001:1854796-1854927 +		TTTGCACAGCTTGAAC-CACTGTGCGTTTGTTGCTCCTTTCGGGCGGTTA------AAAAGTTGTGTGGGTTTGGCGTG-------AGAGGCG--------CG----------GGGGTTGTACAGTGGGA----------TCT--ACCAACTTTT-----TTCTCCCGGTC----------TGGCCGAG-------AAC
droRho1	scf7180000779333:965971-966086 -		TTTGCACAGCTTTAAC-CACTGTGCGTTTGTTGCTCCTTTCGGGTGGTTA------AAAAGTGGTAGGTATGA----------GG--------GG----------GGGCCTATACAGTTGGA----------TCT--ACTAACTTTT-----TTGTCCCGGGC----------AGGCCGAG-----------|
droBia1	scf7180000302421:1718669-1718784 -		TTTGCACAGCCTGGAC-CACTGTGCGTTTGTTGCTCCTCTCGGGCGGTTG------ATACGGGCGGA---------------------GGG--------GT----------GGCGCCTGTACAGTGGGA----------TCT--ACTAACTTTT-----TTGTCCCGGGC----------AGGCCGAG-------AGC
droTak1	scf7180000414113:103057-103189 -		TTTGCACAGCTTGAAC-CACTGTGCGTTTGTTGCTCCTCTCGGCTGGGTT------GAAAAGGGGTGGGTTG----------GTTG-------GT-TGCTTGCTTC-----GATGGCTGTACAGTGGGA----------TCT--ACTAACTTTT-----TTGTCCCGGGC----------AGGCCGAG-------AGC
droEug1	scf7180000409110:1643412-1643533 -		TTTGCACAGCTTGAACCCACTGTGCGTTTGTTGCTCCTCTCGG----CGGAGGTGGAAAAAGTGGGTG----------GTG-------GT----------GTGGGGCTCTACACAGTGGGA----------TCT--ACTAACTTTTT----TTGTCCCGGGC----------AGGAGGA-----------C
dm3	chrX:13175260-13175389 -	dme_295	TTTGCACAGCTTGAAC-CACTGTGCGTTTGTTGCTCCTCTCATTGGGCGG------AAAAGTGGGGGGGTATAATGGG-------TGGGTTG-------GT----------GGGTCTCTGTACAGTGGGA----------TCT--ACTGACTTTT-------TGTCCCGGGC----------AGGCCGAG-------ACC
droSim2	x:12520140-12520267 -		TTTGCACAGCTTGAAC-CACTGTGCGTTTGTTGCTCCTCTCATTCGGCGCG------AAAAGTGGGGGGGTTTAATGGG---------GGGTG-------GT----------GGCTCTGTACAGTGGGA----------TCT--ACTAACTTTT-------TGTCCCGGGC----------AGGCCGAG-------ACC
droSec2	scaffold_21:930561-930688 -		TTTGCACAGCTTGAAC-CACTGTGCGTTTGTTGCTCCTCTCATTCGGCGCG------AAAAGTGGGGGGGTTTAATGGG---------AGGTG-------GT----------GGCTCTGTACAGTGGGA----------TCT--ACTAACTTTT-------TGTCCCGGGC----------AGGCCGAG-------ACC
droYak3	X:7452495-7452624 -		TTTGCACAGCTTGAAC-CACTGTGCGTTTGTTGCTCCTCTCGTTCGGCGG------AACAGAGGGG-GATTCACCGGGGGGCGT----GGTG-------GT----------GGGTCTCTGTACAGTGGGA----------TCT--ACTAACTTTT-----TTGTCCCGGGC----------AGGCCCGG-----------|
droEre2	scaffold_4690:13698620-13698735 +		TTTGCACAGCTTGAAC-CACTGTCGTTTGTTGCTCCTCTCATTGGGTG------------------GTCGGAGGAGGGGGGGTTGT----------GG--------TT----------CTTCTCTGTACAGTGGGA----------GCT--ACTAACTTTT-----TTGTCCCGGGC----------AAGCCCGAG-----------|
dp5	XL_group1a:907151-907153 -		AGG----------G--G------------------GG-------GG----------GG--G----------------------------G--G--G---------|
droPer2	scaffold_26:1020141-1020143 -		AGG----------G--G------------------GG-------GG----------GG--G----------------------------G--G--G---------|

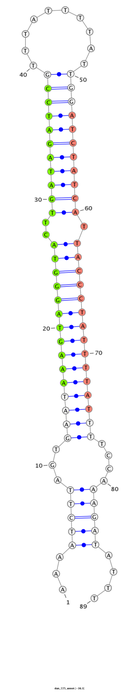
Generated: 09/08/2015 at 07:49 PM

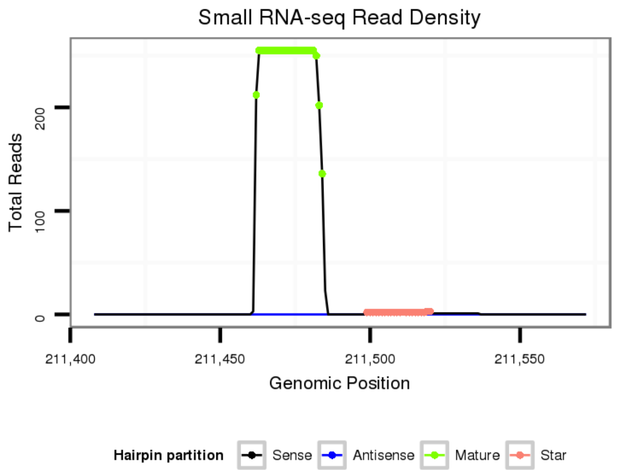
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

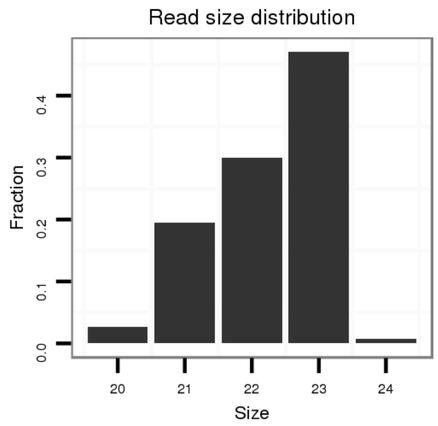
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_225	**scaffold_13335:211458-211522 +**	**confident-exception**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

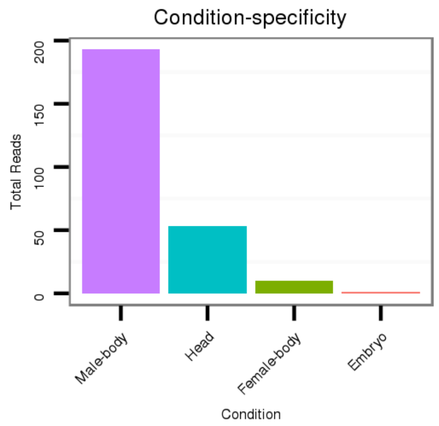
Legend: mature star mismatch in alignment mismatch in read

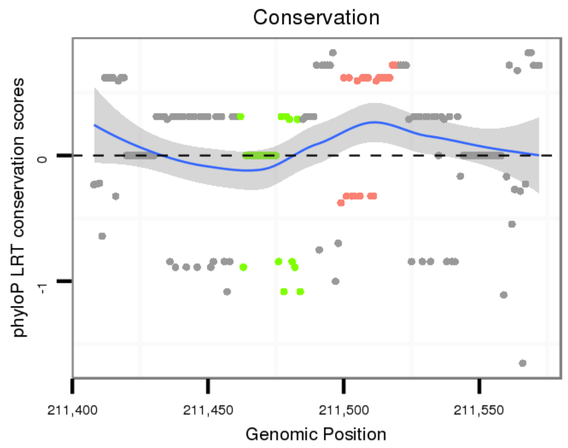
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CTTAAAATGCATGAGTGTATTTAAATTGAATATTATATAAAAATCTTAGTGAATAAAGTAGGGTACTTGATAGATCCGTTTATTTTATTGGATCTATCATTACCCTATTTTATTTTCCAAAGATATTTTCGTCCTCAGATATGTAAAATTGTAAATCCTTTTTAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V106 head	V055 head	M044 female body	V039 embryo	M058 embryo
...(((((...(((((((((((((((..(((((((((((.........)))))))))))..)))))))))))))))....)))))....********...(((((...(((((((((((((((..(((((((((((.........)))))))))))..)))))))))))))))....)))))....**********											
.....AAAGTAGGGTACTTGATAGATCC.....	23	0	1	99.00	99	67	20	10	2	0	0
.....AAAGTAGGGTACTTGATAGATC.....	22	0	1	60.00	60	47	7	3	2	0	1
.....AAAGTAGGGTACTTGATAGAT.....	21	0	1	44.00	44	38	1	3	2	0	0
.....AAGTAGGGTACTTGATAGATCCG.....	23	0	1	21.00	21	17	1	2	1	0	0
.....AAGTAGGGTACTTGATAGATCC.....	22	0	1	14.00	14	9	2	2	1	0	0
.....AAAGTAGGGTACTTGATAGATCCT.....	24	1	1	6.00	6	5	1	0	0	0	0
.....AAAGTAGGGTACTTGATAGATCT.....	23	1	1	5.00	5	3	1	1	0	0	0
.....AAGTAGGGTACTTGATAGATC.....	21	0	1	5.00	5	4	0	1	0	0	0
.....AAAGTAGGGTACTTGATAGA.....	20	0	1	4.00	4	4	0	0	0	0	0
.....AAAGTAGGGTACTTGATAGATCCA.....	24	1	1	4.00	4	4	0	0	0	0	0
.....AAGTAGGGTACTTGATAGAT.....	20	0	1	3.00	3	3	0	0	0	0	0
.....AAAGTAGGGTACTTGATAGATCCG.....	24	0	1	2.00	2	1	1	0	0	0	0
.....AAAGTAGGGTACTTGATAGATA.....	22	1	1	2.00	2	1	0	1	0	0	0
.....ATCTATCATTACCCTATTTTAT.....	22	0	1	2.00	2	0	0	0	2	0	0
.....ATTTTCCAAAGATATTTT.....	18	0	1	1.00	1	0	0	0	0	1	0
.....TAAAGTAGGGTACTTGATAGATA.....	23	1	1	1.00	1	1	0	0	0	0	0
.....AAGTAGGGTACTTGATAGATCCT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....AAGTAGGGTACTTGATAGATCCA.....	23	1	1	1.00	1	1	0	0	0	0	0
.....AAAGTAGGGTACTTGATAGATCA.....	23	1	1	1.00	1	1	0	0	0	0	0
.....AAAGTAGGGTACTTGATAGAC.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TAAAGTAGGGTACTTGATAGATCT.....	24	1	1	1.00	1	1	0	0	0	0	0
.....TAAAGTAGGGTACTTGATAGA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TAAAGTAGGGTACTTGATAGATT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....AAAGTAGGGTACTTGATAGAG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TAAAGTAGGGTACTTGATAGATC.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TAAAGTAGGGTACTTGATAGAT.....	22	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

GAATTTTACGTACTCACATAAATTTAACTTATAATATATTTTTAGAATCACTTATTTCATCCCATGAACTATCTAGGCAAATAAAATAACCTAGATAGTAATGGGATAAAATAAAAGGTTTCTATAAAAGCAGGAGTCTATACATTTTAACATTTAGGAAAAATT	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head	V039 embryo	V106 head
************************************...(((((...(((((((((((((((..(((((((((((.........)))))))))))..)))))))))))))))....)))))....**********								

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13335:211408-211572 +	dan_225	CTTAAAATGCATGAGTGTATTTAAATTGAATATTATATAAAAATCTTAGTGAATAAAGTAGGGTACTTGATAGATCCGTTTATTTTAT----------TGGATCTATCATTACCCTATTTTATTTTCCAAAGATATTTTCGTCCTCAGATATGTAAAATTGTAAATCCTTTTTAA
droBip1	scf7180000396512:27262-27394 -		TTA----------AATTGCAAATTTTATTAAAAATTTAAGAAATAT----------AAGAGGAGAGTTTATATTATTAATATAATTACATTTTAATGAATATTTATAATATTTA----------TATTTTCTAAAAATGTT-TCATTTTC----------CAAGTCCGTTTTAA
droEle1	scf7180000490564:1566833-1566852 +		TATAAAATACAT----------T----------TATTTAA
droRho1	scf7180000761098:1049-1098 +		TTTG----------TTTTAT----------TTATTTAGCGGTTATTCTATTTTATTTT----------T----------ATAGGAATTT---

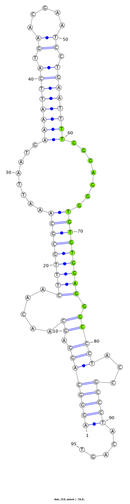
Generated: 09/08/2015 at 08:03 PM

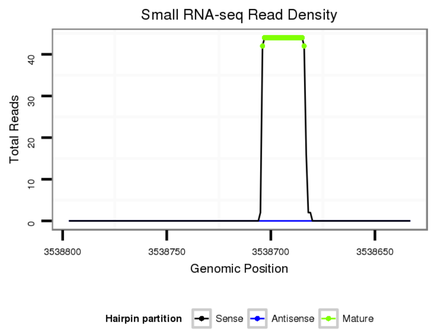
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

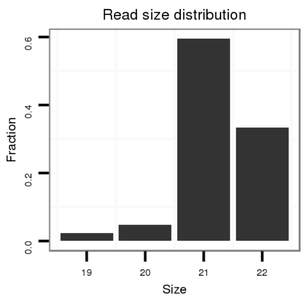
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_310	**scaffold_12943:3538683-3538747 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

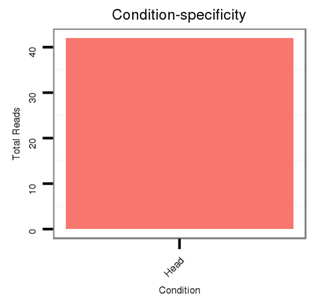
Legend: mature star mismatch in alignment mismatch in read

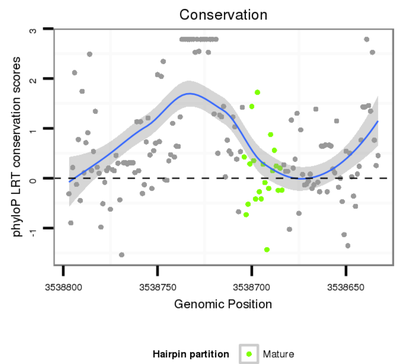
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF21117-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GCAACAACAAAAGCAATAACAGCAACAGGAACAAAAGGGCAGGAGCAACAACTTTGCGCAAATTAATGAAAATTCATGAACGAATCCTGAATTTTGGGAGGGTGTGTGGAGGGCCTACCGCCCTACAGTCCAACCTATCGTCCTTGCCCTTCACATTAATGAGC						V106	V055	M058	V039	M044
************************************(((((((((.((.....(((((((((.........(((((((((.((.....)).)))))))))........)))))))))..)))))).....************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	head	head	embryo	embryo	female body
.....TTGGGAGGGTGTGTGGAGGGC.....	21	0	1	25.00	25	25	0	0	0	0
.....TTGGGAGGGTGTGTGGAGGGCC.....	22	0	1	14.00	14	14	0	0	0	0
.....TTTGGGAGGGTGTGTGGAGGGCCCT.....	25	0	1	2.00	2	2	0	0	0	0
.....TGGGAGGGTGTGTGGAGGG.....	19	0	1	1.00	1	1	0	0	0	0
.....TTGGGAGGGTGTGTGGAGGG.....	20	0	1	1.00	1	1	0	0	0	0
.....TTGGGAGGGTGTGTGGAGGGA.....	21	1	1	1.00	1	1	0	0	0	0
.....TTGGGAGGGTGTGTGGAGGGT.....	21	1	1	1.00	1	1	0	0	0	0
.....TGGGAGGGTGTGTGGAGGGC.....	20	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

CGTTGTTGTTTTCGTTATTGTCGTTGTCCTTGTTTTCCCGTCCTCGTTGTTGAAACGCGTTTAATTACTTTTAAGTACTTGCTTAGGACTTAAAACCCTCCCACACACCTCCCGGGATGGCGGGATGTCAGGTTGGATAGCAGGAACGGGAAGTGTAATTACTCG						M044	M058	V039
************************************(((((((((.((.....(((((((((.........(((((((((.((.....)).)))))))))........)))))))))..)))))).....************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	female body	embryo	embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12943:3538633-3538797 -	dan_310	GC---------AACAACAA------A-----AGCAATAACAG----C--A---ACAGGAACAAA---------AGGG----------CAGGAG----------CAACAA---C----------TTTGCGCAAATTAATGAAAATTCATGA----ACG---AAT------CCT--GA----------ATTTTGG-GAGGGTGTGTG--GAGG--GGCCTAC---------C-G-----CCCTACAGTCCA---------ACCTATCGTCCTTGC----------CCTT---------CA-CATTAATGAGC
droBip1	scf7180000396433:429627-429782 -		GC---------AACAACAA------A-----AGCAGCAA---TAAGACGACAGCAGCAACAAA---------AGGG----------CAGGAG----------CAACAA---C----------TTTGCGCAAATTAATGAAAATTCATGAAATGACG---AAT------CCT--GA----------ATTTTGCGGTGTGTCGTA----A-----------CTGCCCCACCTATCGTCCTG----------A----------GC----------TCTT---------CA-CATTAATGAGC
droKik1	scf7180000302473:655072-655207 -		CA---------A-------CAC----A-----AACACCGTGG----C--G---GA-------------A----------CACAA---C----------TTTGCGCAAATTAATGAAAATTCATGA----CG---AAT------CCT--GT----------GG-----A---CCACTA---A-----------GCCCATCTTCGATTTT-----GCGACAGTCCTCC-----GTCC-CGC----------ACTC----------CCTGTTAATGAAC
droFic1	scf7180000454155:227391-227508 -		AC---------A-------CA----AACACCCCAC----A---A----------A----------A-----A---CCG----------CACAAA---C----------TTTGCGCAAATTAATGAAAATTCATGA----CG---AAT------CCT--GT----------TTTCGCGGCCAACA---CAGG--GTTCC--GCCCCTCTTCGATTTT----------C----------CCGC----CCGC-CCATTAATGAAC
droEle1	scf7180000491273:2488646-2488779 +		CA---------------------------GGAACG---C--G---GTC---------A----------A-----A---CAA----------CAAAAA---C----------TTTGCGCAAATTAATGAAAATTCATGA----CG---AAT------CCT--GT----------ATTTTT-GGGTGCCCA---A-----------TCCCTCTTCGATTTT----------A----------TCCCCCCAACTCCCCCTTCCTCTTGCCACGC-G-CATTAATGAGC
droRho1	scf7180000772532:3109-3222 +		CA---------A-------CA----AACACCCCAG----C--G---GTC---------A----------A-----A---CA-----A----------CAAAAA---C----------TTTGCGCAAATTAATGAAAATTCATGA----CG---AAT------CCT--GT----------ATTTCGCGGTGCCAACAATAA--G-----------CCCCCTCTTCGATTT-C----------A----------ACC-------GC---C----------GCTG----------CCATTAATGAGC
droBia1	scf7180000302188:854103-854228 +		CA---------CAACAACAA-AAAAAA------A-----AACACCCCAG----C--G---GTC---------A----------A-----A---CA-----A----------CAACAA---C----------TTGCGCAAATTAATGAAAATTCATGA----CG---AAT------CCT--GT----------TTTCGCGGTGC-----------A----------CCTCTTCGATTTT----------A----------C-CCC----------CTCG----------GG-CG-CATTAATGAGC
droTak1	scf7180000415264:370252-370356 +		GC---------AACA----------A-------GA-------A---A---A----------A----------A-----A---CA-----A----------CAACAA---C----------TTTGCGCAAATTAATGAAAATTCATGA----CG---AAT------CCT--GT----------TTTCGCGGCG--------A----------A--------GCCCTTCTTCGATTTT----------A----------C-GCC----------CCTG----------GG-CG-CATTAATGAGC
droEug1	scf7180000409005:198447-198597 +		AC---------A-------CA----AACACCCCAG----T--G---GTA-------G----------A-----A---TGGG---A----------CAACAA---C----------TTTGCGCAAATTAATGAAAATTCATGA----CG---AAT------CCT--GT----------ATTTTTCGGTGCCAATGGA-CAGG--A-------GCCCTTATTCGATTT-CTTGGTTCAC----------CCTTGTGC-----C----------CCTG----------CCCCA-TCATTAATGAGC
dm3	chr2L:1025656-1025798 -		GC---------A-------CAC----AACACCCCAG----T--G---GCA-------A----------A-----A---CA-----A----------CAACAA---C----------TGTGCGCAAATTAATGAATTCATAA----CG---AGTTCCATTTCCAT-C-T----------TTCCCC-GGGTCCATCACCCA--GCCGC----TGCTCCTTCTTCGATTT----------A----------SC----------CCTG----------C--CATTAATGAGC
droSim2	2L:973445-973583 -		GC---------A-------CAC----AACACCCCAG----T--G---GCA-------A----------A-----A---CA-----A----------CAACAA---C----------TGTGCGCAAATTAATGAATTCATAA----CG---AGTTCCATTTCCAT-C-T----------TTCCCC-GGGTCCATCACCCA--GCCGC----TGCTCCTTCTTCGATTT----------A----------SC----------CCTG----------C--CATTAATGAGC
droSec2	scaffold_14:978490-978628 +		GC---------A-------CAC----AACACCCCAG----T--G---GCA-------A----------A-----A---CA-----A----------CAACAA---C----------TGTGCGCAAATTAATGAATTCATAA----CG---AGTTCCATTTCCAT-C-T----------TTCCCC-GGGTCCATCACCCA--GCCGC----TGCTCCTTCTTCGATTT----------A----------T----------CCTG----------C--CATTAATGAGC
droYak3	2L:1001346-1001497 -		GC---------A-------CAA----AACACCCCAG----T--G---GCA-------A----------A-----A---CA-----A----------CAACAA---C----------TGTGCGCAAATTAATGAATTCATAA----CG---AGTTCTATTTCCAT-C-T----------TTCCCC-GGGTCCATCACCC--GCCGC----TTTTCATGGTGTTCATGGTTTTCATGGTTTCAC-GGGTCCATCACCC--GCCGC----TGCTCCTTCTTCGATTTT----------A----------CC----------CCTG----------C--CATTAATGAGC
droRer2	scaffold_4929:1068274-1068392 -		GC---------AACAG----A----AAA-----A-----AACACCCCAG----T--G---GCA-------A----------A-----A---CA-----A----------CAACAA---C----------AGTGCGCAAATTAATGAATTCATAA----CG---AGT----T---A----------TTCCCC-GGGTCCATCACCC--GCCGC----TGCTCCTTCTTCGATTTT----------A----------CC----------CCTG----------C--CATTAATGAGC
dp5	4_group3:9445996-9446124 -		GA---------AACAACAA------A-----AATAGCCACA---A---A---A----------A----------A-----A---CA-----A----------CAACAA---C----------TGTGCGCAAATTAATGAAAATTCATGA----ACGAGGAGT------CCT--GC----------T------A----GATGCGC--CAGC--A-------GGCCTTCTTT---TTCTTGCGCCGGGGGCCCTG----------C----------CCTG----------CG-TT-CATTAATGAGC
droPer2	scaffold_8:634713-634834 -		GA---------CACAACAA------A-----AATAGCCACA---A---A---A----------A----------A-----A---CA-----A----------CAACAA---C----------TGTGCGCAAATTAATGAAAATTCATGA----ACG---GTGCT---A---A----------TTCCCC-GGGTCCATCACCC--GCCGC----TGCTCCTTCTTCGATTT----------A----------CC----------CCTG----------CG-TT-CATTAATGAGC
droWil2	scf2_11000000004585:4317501-4317645 +		GTGGATTCGAAAGACAGCAA----AAGGACAGGAGCACGACAGCAG----C--A---A----------A----------A-----A---CA-----A----------CAACA---A----------AAACGCGCAAATTAATGAAAATTCATGA----ACG---AAA------CT---A----------TTCCCC-GGGTCCATCACCC--GCCGC----TGCTCCTTCTTCGATTT----------A----------CCTCCCCTCACCCTCTCAGCGAAAAAAAGCTT-CATTAATGAGT
droVir3	scaffold_13246:2566421-2566608 +		GC---------CAG---GGAATGAAA------A-----AACAAGCGGCAA----C--G---GCA-A---------GCGTTTGTGGGCGGGTACGAGAAGGGGACGGTGTGTAGCAGGGCGTGGGG---AA----------AAACAA---AGGGCTTG----CGCAGTGGGCAATTAATGAAAATTCATGA----ACA---AGT------CTT--TTGTCTTAAGCCAAGTG----------A----------GGCGTTGGT-CAAAGTA----------A----------TG----------GGGA----------T-CCATTAAGGAAT
droMoj3	scaffold_6500:22916595-22916801 -		GA---------AAAGGCAA------A-----AGCAGACGTGAGGCAAAG--A---GCA-------GAGATAGAAAGAGAAGAGGGAGACGA-----ACAAAGCAG--AGTTGAG---PAAAAGAGTCTAAGTAAATG---AGGGGTTGAGCAGTGCACATGGCAATTAATGAAAATTCATGA----ACA---AGT------CTT--TTGCCTTAAGGAAATTG----------A----------GGAGCGGGGGCGTG----------GTGCGCGC----------CGAG----------A-GCATTAAGGAGC
droGri2	scaffold_15126:3965691-3965862 -		AA---------AACAACGCG------A-----AATAGGGCAAG----G--G---GCA-------GGGATTGGGAGAGGGAGAAGGAGCGGGATG-----CAGTGTAGG---AG----------CAAATA---AGATGAAG-----CGCGGTGTGCAAATTAATGAAAATTCATGA----GTA---AGT------CTT--TTGTCTTAAGCGAAAGCA----------A----------GAGCTT----------A----------TT----------AGGG----------GATTGGAGCGAGT

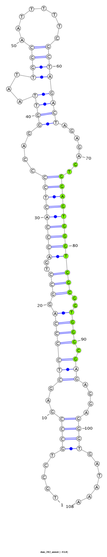
Generated: 09/08/2015 at 07:49 PM

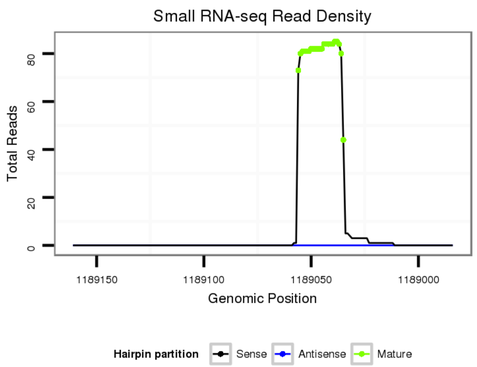
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

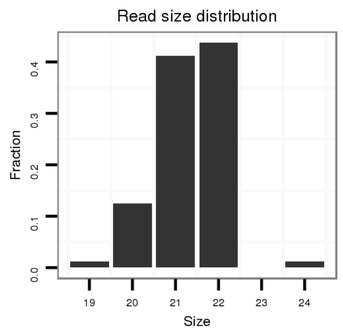
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_202	**scaffold_13047:1189034-1189111 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

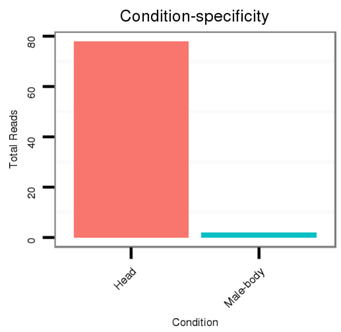
Legend: mature star mismatch in alignment mismatch in read

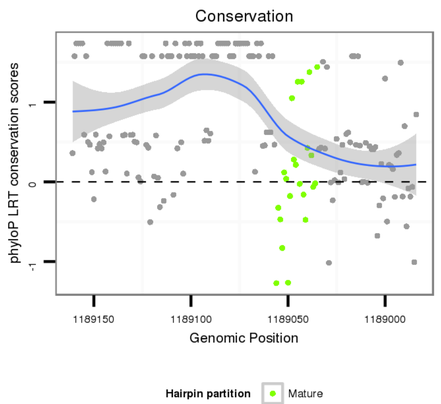
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF19077-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CGATTAACCCTAAGCGCTTATTAATACTTTTAACCTGCCTGCCCGAGCTCCCCAGGCCTGACCCACTCCCCAGGGTTAATTGGCAATTTTTCGCTAGACTAGAGAGTGGAGTGGGTGGCGGTGGGCGAGAGGAGGGTGATAAACGCCCGTCTTGGCTGCAAAAATGCACAAAATACCC											
********************************.....((((...((((((((.(((..((((((((((....((((...((((........))))))))).....))))))))))..)))))).)))....))))......*******************************	Read size	# Mismatch	Hit Count	Total Norm	Total	head	male body	head	female body	embryo
.....GTGGAGTGGGTGGCGGTGGGCG.....	22	0	1	35.00	35	35	0	0	0	0
.....GTGGAGTGGGTGGCGGTGGGC.....	21	0	1	31.00	31	31	0	0	0	0
.....TGGAGTGGGTGGCGGTGGGC.....	20	0	1	5.00	5	5	0	0	0	0
.....GTGGAGTGGGTGGCGGTGGG.....	20	0	1	4.00	4	4	0	0	0	0
.....GCGGTGGGCGAGAGGAGGGTG.....	21	0	1	2.00	2	2	0	0	0	0
.....TGGAGTGGGTGGCGGTGGGCG.....	21	0	1	2.00	2	2	0	0	0	0
.....GTGGAGTGGGTGGCGGTGGGCA.....	22	1	1	1.00	1	1	0	0	0	0
.....GGAGTGGGTGGCGGTGGGCG.....	20	0	1	1.00	1	1	0	0	0	0
.....GAGTGGAGTGGGTGGCGGTGGGCG.....	24	0	1	1.00	1	0	1	0	0	0
.....GGGCGAGAGGAGGGTGATAAACGCCCGT.....	28	0	1	1.00	1	0	1	0	0	0
.....TGGGTGGCGGTGGGCGAG.....	18	0	1	1.00	1	1	0	0	0	0
.....GTGGAGTGGGTGGCGGTGGGCGAGA.....	25	0	1	1.00	1	1	0	0	0	0
.....GTGGAGTGGGTGGCGGTGG.....	19	0	1	1.00	1	0	1	0	0	0
.....GTGGAGTGGGTGGCGGTGGGCA.....	22	1	2	0.50	1	1	0	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13047:1188984-1189161 -	dan_202	CGATTAACCCTAAGCGCTT--ATTAATACTTTTAACCTGCCTGCC-CGAGCTCCCC-AG---G------------CCTGACCCACTCCCCA----GGGTTAATTGGCAATTTTTCGCTAGAC----TAGAGAGTG----------------------------------GAGT--GGGTGGCGGTGGGCGA-GAG---GAGGG------T----------------------G-ATAAACGCCCGTCTTGGCTGCAAAA----ATGCACAAAATACCC
droBip1	scf7180000396575:219483-219708 +		CGATTAACCCTAAGCGCT--ATTAATACTCTTAACCGGCCAGCT-CGAGTTCCCC-AGACGCGTGCCCCGCCGACTTGACCCACTCC-CA----GGGTTAATTGGCAATTTTTCGCTAGAGAGGCTAGAGAGT-----GG----------------GTGCAGTGGGTTGGGGGGCAAGGGTTAATGCAAAATAAGC----------------C----------ACA-G-AGAGAGACAG------A----------------------G-AGAAACGCCCACTTGGGCTGCAGAA----ATGCACAAAATACAC
droKik1	scf7180000302798:250333-250514 +		TGATTATCGAAACCCTAT--ATTAATAACTCTGTAAGGCA---CA-TCGCTTCCGT-A---GCGTAT--ACTTGATCTGACCCACTCC-CAGGAAGGGTTAATTGGCAATTTTTCGCCAGAGTGAATAGAGCTATGT----------------------GGGGTGT----------------------C----------C---------C---CACTA---CA----------------------C-TGCAATGCACATACTTATAAA---CAAATATGTGTATATATTTC
droFic1	scf7180000453872:88967-89141 +		-GATTAACCCGGGCAGCAT--ATTAATATTTTAGCCGGCTTACT-TAAGTTCCCC-AG---GCGTAT--ACTTGACTGACCCACTCC-CA----GGGTTAATTGGCAATTTTTCGCCAGAC----TAGAGCAATCGATAGG--C-GCGTCTGTGGGCGTTAA----GCGGG------A----------------------T-GGCAACGCCCACTTGTGCAGTGCA----------CA--------
droEle1	scf7180000491193:443486-443669 -		CGATTAACACACAAGAGCATAT-TTAATATTTTAGCCGGCTTCT-TAAGTTCCCT-AG---GCGTAT--ACTTGACTGACCCACTCC-CA----GGGTTAATTGGCAATTTTTCGCTAGAC----TAGAGCCACCACTATG--C-GCGGCACTGGGCGTTAA----GAGGG------A----------------------G-AGCAACGCCCACTTTGCATTGCAT----------ACA---G-TAC
droRho1	scf7180000779986:282151-282321 +		CGATTAACCCACAGAGCATAT-GTTAATATTTTAGCCGGCTTCT-TAAGTTCCCT-AG---GCGTAT--ACTTGACTGACCCACTCC-CA----GGGTTAATTGGCAATTTTTCGCTAGAC----TAGAGCTACCGATATG--C-GCGGCACTGGGCGTTAACAGAGAGGG------A----------------------G-AGCAGCGGCCCACTTTGC-------C-----------------
droBia1	scf7180000301760:363486-363675 +		CGATTAACCCACAGAGCAT--ATTAATATTTTAGCCGGCTTACT-TAAGCTCCCC-AG---GCGTAT--ACGCGACTGACCCACTCC-CA----GGGTTAATTGGCAATTTTTCGCTAGAC----TGGAGCGCCGATGT----------------------ATGTAT--AATGGCGGCTGTGGGCGTTAA----GCGGGCG---CA----------------------G-AGCAACGCCCACTTTGCACT---C----ACACACA--------
droTak1	scf7180000415843:237459-237647 +		-GATTAACCCAAAGAGCAT--ATTAATATTTTAGCCGGCTTACT-TAAGTTCCCT-AG---GCGTAT--ACTTGACTGACCCACTCC-CA----GGGTTAATTGGCAATTTTTCGCTAGAC----TAGAGCGTCGATA----------AT----------GTGTAGC--GGCGGCTGTGGGCGTTAA----GGGGGCT---AA----------------------GAACACAACGCCCACTTTGCACTGCA----------ACA--------
droEug1	scf7180000408176:454447-454651 +		CGATTAACCCAAAGAGCAT--ATTAATATTTTAGCCGGCTGCTTACTTCCCTTAG---GCGTAT--ACTTATCTGACCCACTCCCCA----GGGTTAATTGGCAATTTTTCGCTAGAC----AAGAGCAACCGATATGGCAATATATAGAT-----ATATACAGA----------------------------------TAGATATATATGTAATGTATGTATAT-----TGTGGCGTTAA----GGCAA------A----------------------G-AGAAACGCCC----------------------------------
dm3	chrX:11287595-11287803 +		CGATTAACCCAAAGAGCATATTAATATTTTAGCTGGCTGCTTACGCTCCCTT-AG---GCGTAT--ACTTGACTGACCCACTCC-CA----GGGTTAATTGGCAATTTTTCGCTAGAC----AAGAGCGTCCGATATGGGAATTTATGGGT--GCGCTATGGCGGCGTTAA----GTGGGCTGGGG---AGGGC----------TGG-AGCGCAGCCCACTTTGCATGCATAA--TGTAC---------
droSim2	x:10713552-10713760 +		CGATTAACCCAAAGAGCATATTAATATTTTAGCCGGCTGCTTACGCTCCCTT-AG---GCGTAT--ACTTGACTGACCCACTCC-CA----GGGTTAATTGGCAATTTTTCGCTAGAC----AAGAGCGTCCGATATGGGAATTTATGGGT--GCGGGCTGCGGCGGTTAA----GTGGGTGC---GAGG-AGGCT----------TGG-AGCGCAGCCCACTTTGCATGCATAA--TGTAC---------
droSec2	scaffold_36:10928-11139		CGATTAACCCAAAGAGCATATTAATATTTTAGCCGGCTGCTTTACGCTCCCTT-AG---GCGTAT--ACTTGACTGACCCACTCC-CA----GGGTTAATTGGCAATTTTTCGCTAGAC----AAGAGCGTCCGATATGGAATTTATGGGT--TGCGGCTGCGGCGGTTAA----GTGGGTGC---GAGGGAGGGT----------TGG-AGCGCAGCCCACTTTGCATGCATAA--TGTAC---------
droYak3	X:10865494-10865700 -		CGATTAACCCAAAGAGCATT-ATTAATATTTTAGCCGGCTGCTTACGCTCCCTT-AG---GCGTAC--ACTTGACTGACCCACTCC-CA----GGGTTAATTGGCAATTTTTCGCTAGAC----AAGAGCGTCCGATATGGGAATTTAT----------CTGCAGC--GCGGGCTGTGGCGGTTAA----GTGGG----A---GC----------ATTGGTG-AGCGCAGCCCACTTTGCAGTGCATA---ATGTACA---------
droEre2	scaffold_4690:3867010-3867246 -		CGATTAACCCAAAGAGCATT-ATTAATATTTTAGCCGGCTGCTTACGCTCCCTT-AG---GCGAAC--CACTTGACTGACCCACTCC-CA----GGGTTAATTGGCAATTTTTCGCTAGAC----AAGAGCGTCCGATATGGGAATTTATGGGTGGGGTTATCTGCAGC--GGCGGCTGTGGCTGGTTAA----GTGGG-G---GAGG----GGGTTGCGTTGGGGATTCGTG-AGCGCAGCCCACTTTGCAGGCATA---ATGTACA---------

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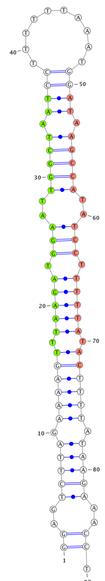
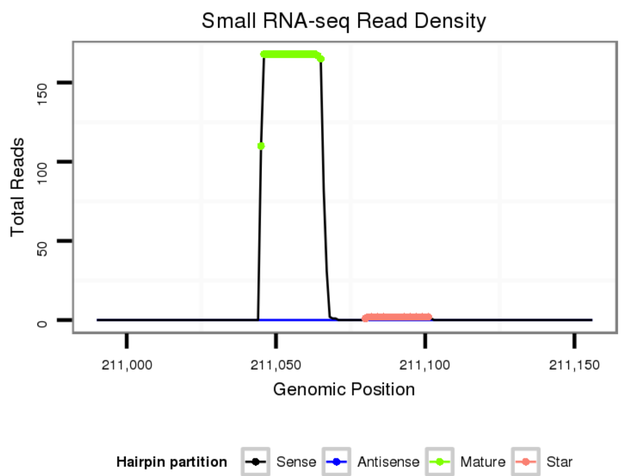
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

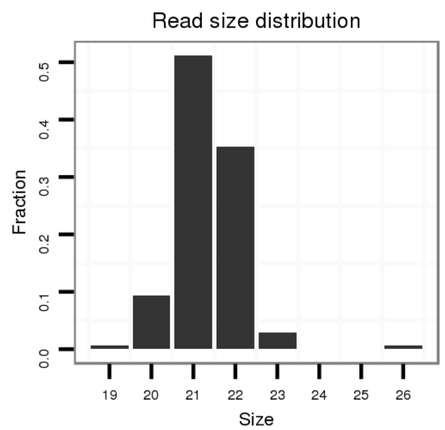
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_223	**scaffold_13335:211040-211106 +**	**confident-exception**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

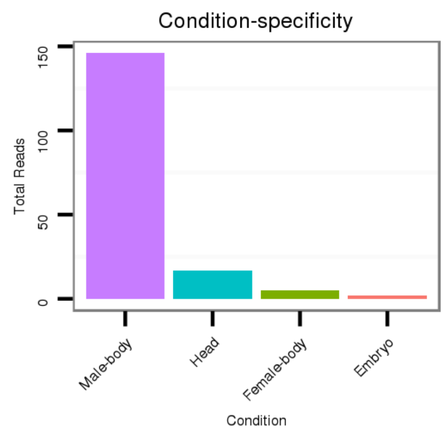
Legend: mature star mismatch in alignment mismatch in read

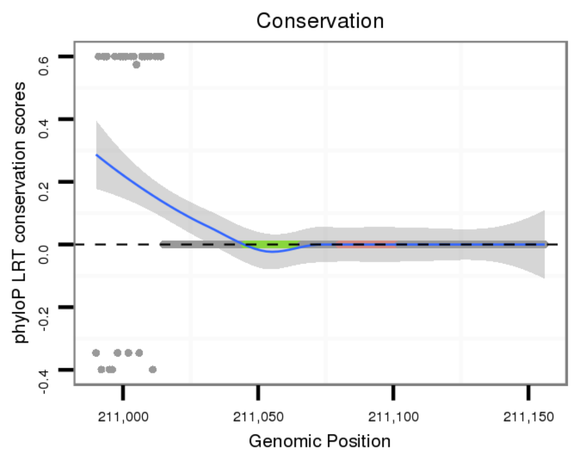
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GATTATTACATTCTACGAAATATATGTTATATATATTTAAGGAGTCTTAGAAAAGTTTAAGATGGAATTGGCTAATCCTTTTTTAAATGGATAAGCCATATCCTTTTTATACTTTTATAAGAAACCTTCTCCTCGAAATGTGTGTGGAAATTGTGAAATATAAATAT **************************************((..(((((.(((((((.(((((.(((..(((((.((((.........)))).)))))..)))..)))))..)))))).)))))..)).**************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V106 head	M044 female body	V055 head	M058 embryo
..........TTTAAGATGGAATTGGCTAAT..........	21	0	1	69.00	69	62	5	2	0	0
..........TTTAAGATGGAATTGGCTAATC..........	22	0	1	33.00	33	27	4	1	1	0
..........TTAAGATGGAATTGGCTAATCC..........	22	0	1	25.00	25	20	4	1	0	0
..........TTAAGATGGAATTGGCTAATC..........	21	0	1	18.00	18	18	0	0	0	0
..........TTAAGATGGAATTGGCTAAT..........	20	0	1	14.00	14	13	0	0	1	0
..........TTTAAGATGGAATTGGCTAATCC..........	23	0	1	4.00	4	3	1	0	0	0
..........TTTAAGATGGAATTGGCTAATT..........	22	1	1	3.00	3	2	1	0	0	0
..........TTTAAGATGGAATTGGCTAATA..........	22	1	1	2.00	2	2	0	0	0	0
..........TTTAAGATGGAATTGGCTAA..........	20	0	1	2.00	2	1	0	1	0	0
..........ATAAGCCATATCCTTTTTATAC..........	22	0	1	1.00	1	0	0	0	0	1
..........TAAGCCATATCCTTTTTATACT..........	22	0	1	1.00	1	0	0	0	0	1
..........TTTAAGATGGAATTGGCTAAA..........	21	1	1	1.00	1	1	0	0	0	0
..........TTTAAGATGGAATTGGCTAATCT..........	23	1	1	1.00	1	1	0	0	0	0
..........TTTAAGATGGAATTGGCTAATCCTTT..........	26	0	1	1.00	1	1	0	0	0	0
..........TTAAGATGGAATTGGCTAATA..........	21	1	1	1.00	1	1	0	0	0	0
..........TTAAGATGGAATTGGCTAATCT..........	22	1	1	1.00	1	0	0	1	0	0
..........TTTAAGATGGAATTGGCTA..........	19	0	1	1.00	1	1	0	0	0	0
..........TTAAGATGGAATTGGCTAATCCA..........	23	1	1	1.00	1	1	0	0	0	0
..........TTAAGATGGAATTGGCTAATCCT..........	23	0	1	1.00	1	0	0	0	1	0

Anti-sense strand reads

CTAATAATGTAAGATGCTTTATATACAATATATATAAATTCCTCAGAATCTTTTCAAATTCTACCTTAACCGATTAGGAAAAAATTTACCTATTCGGTATAGGAAAAATATGAAAATATTCTTTGGAAGAGGAGCTTTACACACACCTTTAACACTTTATATTTATA **************************************((..(((((.(((((((.(((((.(((..((((((.((((.........)))).)))))..)))..)))))).)))))).)))))..)).**************************************	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_13335:210990-211156 +	dan_223	GATTATTACATTCTACGAAATATATGTTATATATATTTAAGGAGTCTTAGAAAAGTTTAAGATGGAATTGGCTAATCCTTTTTTAAATGGATAAGCCATATCCTTTTTATACTTTTATAAGAAACCTTCTCCTCGAAATGTGTGTGGAAATTGTGAAATATAAATAT
droKik1	scf7180000302610:1797142-1797166 +		AAATAAAAATATTTTACAAAATTTAT----------

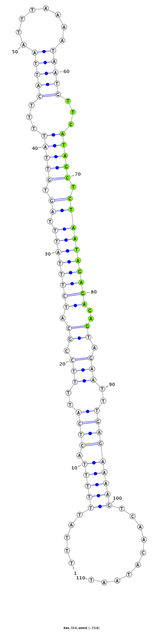
Generated: 07.15.2015 at 08:03 PM

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

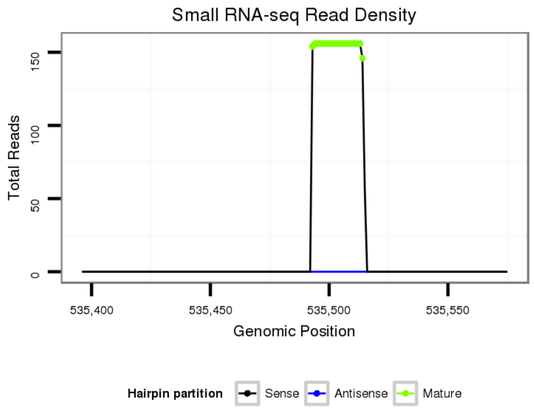
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_314	**scaffold_12903:535446-535525 +**	**candidate**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

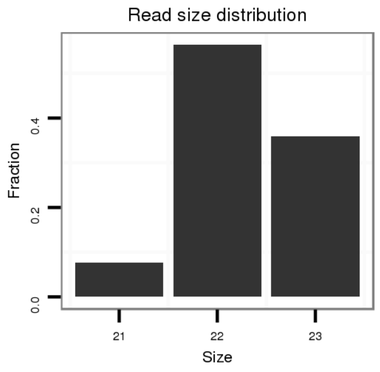
Legend: mature star mismatch in alignment mismatch in read

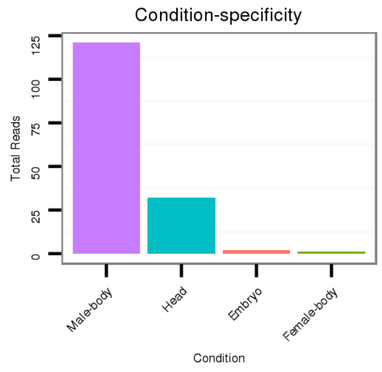
Predicted structure

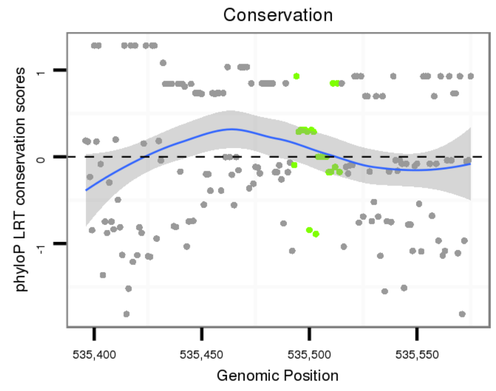


Show Alternate Folds









Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACAGTCTACAAAATAAAGTGGTGTTTATATATATTTTTATTTTTTACTCATTTTCCGCATCTTTATTTAGTGTTATTTTCATTAATTTAAAATAATGTTCATAGCTCTAATAGAGAGAGTAGAATTTGAGAAAAGTCAACATAATTCACAGACTAGCTTTTAAATAACATTTTTAGATAA **********.....(((((.(((((..(((.((..(((((((((.((.(((((...(((((........)))))...)))))).)))))))))..)).)))..)))))))))).....********** Legend: mature star mismatch in alignment mismatch in read	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V106 head	V055 head	M058 embryo	V039 embryo	M044 female body
.....TTCATAGCTCTAATAGAGAGAG.....	22	0	1	88.00	88	67	15	6	0	0	0
.....TTCATAGCTCTAATAGAGAGAGT.....	23	0	1	56.00	56	48	0	7	1	0	0
.....TTCATAGCTCTAATAGAGAGA.....	21	0	1	10.00	10	5	1	2	0	1	1
.....TCATAGCTCTAATAGAGAGAG.....	21	0	1	2.00	2	1	1	0	0	0	0
.....TTCATAGCTCTAATAGAGAGAGTT.....	24	1	1	2.00	2	2	0	0	0	0	0
.....TTCATAGCTCTAATAGAGAGAGA.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TTCATAGCTCTAATAGAGAGAT.....	22	1	1	1.00	1	0	0	1	0	0	0
.....TCATAGCTCTAATAGAGAGAGTT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....TTCATAGCTCTAATAGAGAGAG.....	23	1	1	1.00	1	0	0	0	1	0	0

Anti-sense strand reads

TGTCAGATGTTTTATTTCACCACAAATATATATAAAAATAAAAAATGAGTAAAAGGCGTAGAAATAAATCACAATAAAAGTAATTAAATTTTATTACAAGTATCGAGATTATCTCTCTCATCTTAAACTCTTTTCAGTTGTATTAAGTGTCTGATCGAAAATTTATTGTAAAAATCTATT **********.....(((((.(((((..(((.((..(((((((((.((.(((((...(((((........)))))...)))))).)))))))))..)).)))..)))))))))).....********** Legend: mature star mismatch in alignment mismatch in read	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M058 embryo	V039 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:535396-535575 +	dan_314	ACAGTCTAC----------AAAATAAA----------GTGGTGTTTA-TA----------TA--TATTTTTATTT----TTTACTCATTTTCCGCATCTTTATTTAGTGTTATT-------TTCATTAATTTAAAATAATGTTCATAGCTCTAATAGAG-AGAGTAGAATTTGAGAAAAGTCAACATAATTCACAGAC------TAGC-----TTTTAAATAACA----------TTTTTAGATAA
droBipl	scf7180000395952:825-1024 -		TTATTTTAAGGATTTAATCTTTGATTATCTTTCTTAACTACAATATATATT-TATTTAATGTATTTTATTCGTTTGAT-TA----------CG--TACATTTATTAACGTATTACGTAC----------AAGTCATAGTCA-------T---------TTTAAAAAATATTTAGTTTATTCAGAAGT------TAATTACAATTTTGAAAATTAGGTTATGCACTCTTTAGTGCTTTTAACTTAA
droKikl	scf7180000302798:211426-211573 -		ATAATTTGT----------AACATATA----------ATAATATTTAAGATATATCTTGAGGCCTTAATTTGGCATAAAAT------ATTTTAATTTAAGGAAATATT----------AA-AAAATGACGGTTGAAACAGTTGAAACTATGCTTGAAT------TG-C-----TTTAAAGAAGTAAA----------TT---ATTAAA
droTakl	scf7180000415843:977885-978041 -		ATTGTTTGA----------ATAACGGTGTATATTTTATATATTATATTTAATTGTTT-AT-TA----------TA--TATA------ATTTTAATTTGGGAGAGTTTT----------G-CAAAGTCACGGTTAA----------ACTTACAGGAACCTTCGAGA-----TTTT--ATAAAT----------TCTTCAAAAGA
droGri2	scaffold_14822:226453-226532 -		ATGGTTTAT----------TTTTTAAA----------TTATTTTATT-TA----------TA--TATATTTATTTACATATGACTTATTTTCGATCTCTTCAATAATAATTAT-------**********-**********----------**********----------**********----------**********----------**********

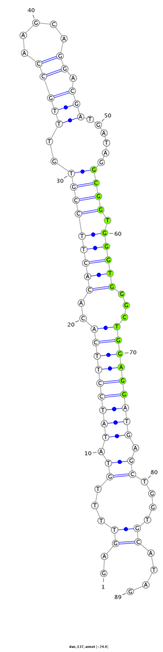
Generated: 08/8/2015 at 08:04 PM

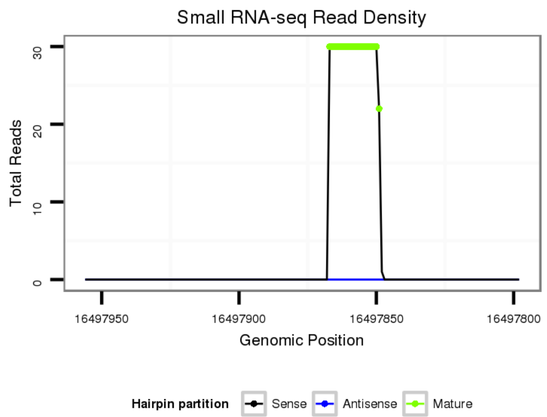
PASS/FAIL	
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

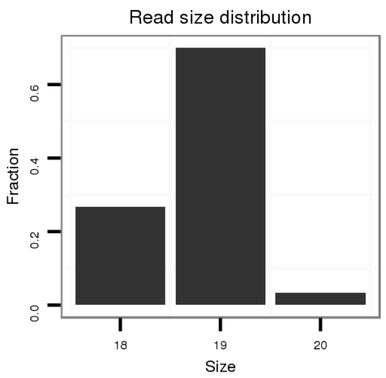
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_137	**scaffold_13337:16497848-16497906 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

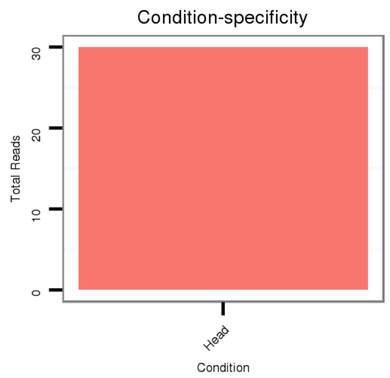
Legend: mature star mismatch in alignment mismatch in read

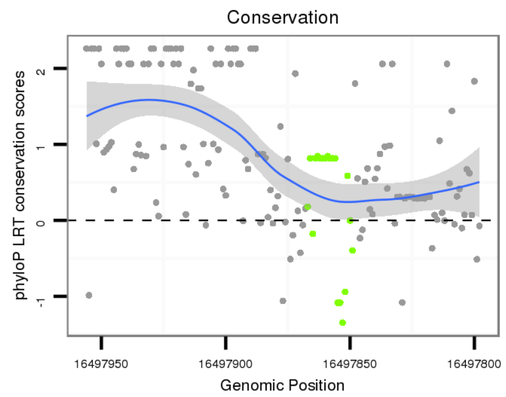
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF23770-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGAAATCGTGTGTGTATGCCCGGGTCATTTGAAATGAGTTTTGTATATCCTTCACACACTTCCGTGTTTGCCAAGCAGGACGATGATAGGCGGTGGGTGGGCTGGAGGATGAGCTGGTGCATAGAATAGTTTGGGGCATTGGATGGTGAGGACTTGAGT	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V055 head	V105 male body	M058 embryo
....................................GCGGTGGGTGGGCTGGAGG....	19	0	1	21.00	21	20	1	0	0
....................................GCGGTGGGTGGGCTGGAG.....	18	0	1	8.00	8	8	0	0	0
....................................GCGGTGGGTGGGCTGGAGGAA....	21	1	1	1.00	1	1	0	0	0
....................................GCGGTGGGTGGGCTGGAGGA.....	20	0	1	1.00	1	1	0	0	0
....................................GCGGTGGGTGGGCTGGAGGAAA....	22	2	2	0.50	1	1	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13337:16497798-16497956 -	dan_137	TGAAATCGT----------GTGTG----TATGCCCGGGTCATTTGAAATGAGTTT----------TGTATATCCTTCACACACTTCCGTGTTTGCCAAGC-AGGAC----------GATGATAGG----------CGGTGGGTGGGCTGG-------AGGA----------TG----------AGCTGG-TG-CATAG-A----------ATAGTTTGGGGCATTGGATGG----------TGAGGACTTGAGT
droBip1	scf7180000396641:24354-24515 -		TGAAATCGT----------**--**ATGTGTATGCCCGGGCATTTGAAATGAGTTT----------TGTATATCCTTCACACACTTCCGTGTTTGCCAAGC-AGGGC----------GGAGTGTA----------GGCGGTGGGTGGGAGCG-------TGA----------TGC----------C----------**--**CTGG-TG-CATTG-C----------ATCGTTTGGGGCATTGGATGG----------TGAGGATTTGAGT
droKik1	scf7180000302274:22511-22629 -		TCAATTCGT----------**--**ATG----TATGCCCAGGGCATATGAAATGAGTTCTT-TTATTGGGCCGCTTCTGTATATCCTTCACACACTTCGTGTTTGCCAAGC-AGGGC----------G-------**-**----------**-**----------**-**----------**-**----------**-**----------**-**----------**-**------**-**G-CATTG-C----------**-**----------ATGGGG---------**----**GCTTTAGA
droFic1	scf7180000454065:21464-21628 -		TGAATTCGT----------**--**ATG----TATGCCCAGGGCATGTGAAATGAGTTTTC-GTTTTTGGCCGCTTGTGTATATCCTTCACACACTTCGTGTTTGCCAAGC-GG--C----------GTGGGTGTTGAATAG-----**-**----------A-------TAGA----------**---**TGGAT----------GGGT-GGTGG-TG-CATTG-C----------**-**----------ATTGGGTGGAT-TGGAGGGAACTTAACG
droEle1	scf7180000491193:2962717-2962880 -		TGAATTCGT----------**--**ATG----TATGCCCAGGGCATGAGAAATGAGTTTTC-TTTTTTGTCCGCTTGTGTATATCCTTCACACACTTCGTGTTTGCCAAAC-GA--C----------GGTGGATGGGTGGATGG-----**-**----------G-------TGGATGGAC------**-**GC----------A-TGTGGGTGTGGGTGG-TG-CATTG-C----------**-**----------AGTGGGCGGACATGGAG**-**----------
droRho1	scf7180000780039:80572-80738 +		TCAATTCGT----------**--**ATG----TATGCCCAGGGCATGTGAAATGAGTTTTC-TTTTTGGTCCGCTTTGTATATCCTTCACACACTTCGTGTTTGCCAAGC-GG--C----------GTGGGTGGA----TG------**-**----------**-**-------TGGA----------TAGAT-------GGG----TGGGTGTTGGTGG-TG-CATTG-C----------**-**----------ATTGGGCGGAAATGGAGGGGACTTAACG
droBia1	scf7180000302428:23926-24090 -		TGAAATCGT----------**--**GTG----TATGCCCAGGGCATGTGAAATGAGTTTTTCCTTTTGAGCCGCCTGTGTCTATGCTTCACACACTTCGTGTTTGCCACAG-GG--C----------GTGGGTGTATTGGTGG-----**-**----------GTGGGTGG-----**---**TTGGTTGAAT**-**----------**-**----------GCGTGTGGCAG-TG-CATTG-C----------**-**----------ATTGGCGGATATGAAG**-**----------
droTak1	scf7180000415352:27265-27423 -		TCAATTCGT----------**--**ATG----TATGCCCAGGGCATGTGAAATGAGTTTTC-GTTTTTGGCTGCTTTGTATATCCTTCACACACTTCGTGTTTGCCAAGC-GG--C----------GGTGGGTGGA----TGG-----**-**----------C-------TGA----------TGC----------A----------TGGGCGG-TG-CATTG-C----------**-**----------ATTGGGCGGATATGAAGGGGTCTTAACG
droEug1	scf7180000409524:937268-937434 +		TGAATTCGT----------**--**ATG----TATGCCCATGGCATGTGAAATGAGTTCTTCCTTTTTGGCCGCTTGTGTATATGCTTCACACACTTCGTGTTTGCCAAGC-GG--C----------GTGGG-TGAGTGGGTGG-----**-**----------T-------TGTA----------TAGAT----------GGGTGGGTGG-TG-CATTG-C----------**-**----------ATTGGATGGATATGGAGGGGACTTAATG
dm3	chr3L:7704880-7705048 -		TGAATTGAT----------**--**ATG----TATGCCCAGGGCATGTGAAATGAGTTTTC-GTTTTTGGCCGCTTGTGTATATCCTTCACACACTTCGTGTTTGTCATGG-GG--C----------GTGGGTGGA----TGG-----**-**----------C-------TGA----------TGC----------T-TTTTGCGGGTGGGTGG-TG-CATTGGC----------**-**----------ATTGGGTTAATGTGGAGAGGATTAATG
droSim2	3L:7542167-7542339 -		TGAATTCGT----------**--**ATG----TATGCCCAGGGCATGTGAAATGAGTTTTCCTTTTTGCGGCCGCTTGTGTATATCCTTCACACACTTCGTGTTTGCCATGA-GG--C----------GTGGGTGCATGGATGG-----**-**----------C-------TGA----------TGC----------T-TTTTGCGGGTGGGTGG-TG-CATTG-C----------**-**----------ATTGGGTGAATGTGGAGGGGAGTTAATG
droSec2	scaffold_0:18037-18206 -		TGAATTCGT----------**--**ATG----TATGCCCAGGGCATGTGAAATGAGTTTTCCTTTTTCGGCCGCTTGTGTATATCCTTCACACACTTCGTGTTTGCCATGA-GG--C----------GTGGGTGCA----TGG-----**-**----------C-------TGA----------TGC----------TATTTTGCGGGTGGGTGG-TG-CATTG-C----------**-**----------GCTGGGTGAATGTGGAGGGGAGTTAATG
droYak3	3L:8301890-8302064 -		TCAATTCGT----------**--**ATG----TATGCCCAGGGCATGTGAAATGAGTTTTC-GTTTTTGGCCGCTTGTGTATATCCTTCACACACTTCGTGTTTGTCATGG-GGGGGGGGGGGGGGGC-GTGGGTGGA----T-------**-**----------**----**-GC----------T-TTTTGCGGGTGGGTGG-TG-CATTG-C----------**-**----------ACTGGGTGGTTGTGGAGGAGATTAATG
droEre2	scaffold_4784:3643637-3643807 +	der_126	TGAATTCGT----------**--**ATG----TATGCCCAGGGCATGGGAAATGAGTTTTC-GTTTTTGGCCGCTTGTGTATATCCTTCACACACTTCGTGTTTGCCATGGGG--C----------GGTGGGTGCGTGGATGG-----**-**----------C-------TGA----------TGC----------T-TTTT-CGGGTGGGTGG-TG-CATTG-C----------**-**----------ATGGGGTGGATGTGGAGGGGAGTTAAT**-**
dp5	XR_group6:1712516-1712696		TGAATTCGTCTTCCTACGATATG----TATGCTAGGCCATACGGAATGAGTCTG-----AAAGGCGGCTTTGGT---TCGTTCCCCACATTCCGCATTTGCGGGAG-GA--G----------GAGGACAACC---TAG-----**-**----------GAGCAGAG-----**-**----------**--**TCGGGGAAATGGT---------CGAGCCCTCGCCTTTG-AATTGCAACAGCTT----------CGAATGGAAC--------**-----**GCAGAAG
droPer2	scaffold_9:5269-5449 -		TGAATTCGTCTTCCTACGATATG----TATGCTAGGCCATACGGAATGAGTCTG-----AAAGGCGGCTTTGGT---TCGTTCCCCACATTCCGCATTTGCGGGAG-GA--G----------GAGGACGAGC---TAG-----**-**----------GAGCAGAG-----**-**----------**--**TCGGGGAAATGGT---------CGAGCCCTCGCCTTTG-AATTGCAACAGCTT----------CGAATGGAAC--------**-----**GCAGAAG
droWil2	scf2_1100000004837:938075-938255 +		TCAATTCGT------ATGAGTATG----TATGGTTAAGGCCATATGAAATGAGTTAAA-AGAAAAGAACTC---**------**AACTACAGTTACTTCCT-ATTTACTGAAG-AGG-T--TC---------TAGGACTATA----TAGGTAGGGTGTGGGTGGG----CATGATTCGA----------CA-------A---G-CCTT-TAAGCAAGCCC-CA-CATTG-C----AACAGCTT----------AAAATTG----CTTTGG----------A

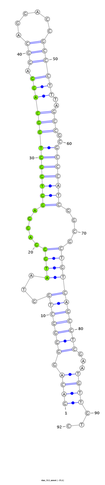
Generated: 09/08/2015 at 07:50 PM

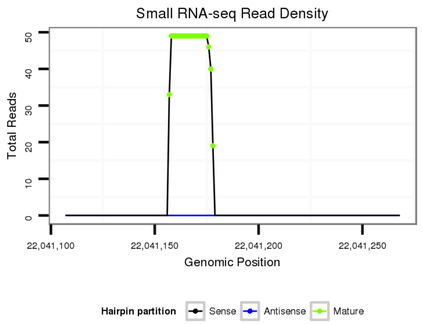
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

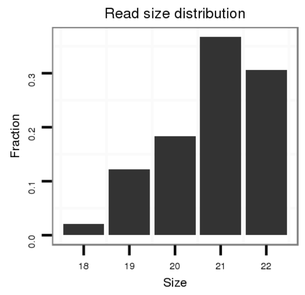
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_213	**scaffold_13340:22041157-22041218 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

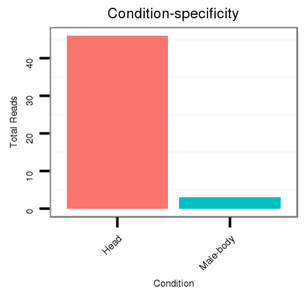
Legend: mature star mismatch in alignment mismatch in read

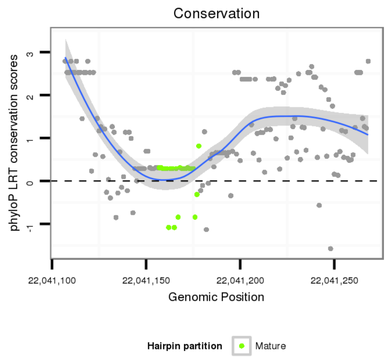
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dana\GF18875-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGCACGTGCAGCAGGCAAGGACACCGGTCGAAGGCGACAGGGGGCTGGTAATGGGAGGAGGTGGGTGGCAGGAGGCAGGACCGCCCTTTAGCCGCGCCCATCGGCGCTGTCAGCCTCGAATGTTGTCGTCGTCGTAGTCGTCGTCAGTGGGCCCCAGCT	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	V055 head	M044 female body	V039 embryo
********************************((((.(((((((...((((.....(((((((((((((.(((.....)))))))..)))..)))))))....))))))))))...)))))...*********************************										
..........ATGGGAGGAGGTGGGTGGCAGG	22	0	1	15.00	15	13	0	2	0	0
..........ATGGGAGGAGGTGGGTGGCAG	21	0	1	14.00	14	13	0	1	0	0
..........TGGGAGGAGGTGGGTGGCAG	20	0	1	7.00	7	6	1	0	0	0
..........TGGGAGGAGGTGGGTGGCA	19	0	1	4.00	4	4	0	0	0	0
..........TGGGAGGAGGTGGGTGGCAGG	21	0	1	4.00	4	3	1	0	0	0
..........ATGGGAGGAGGTGGGTGGCA	20	0	1	2.00	2	2	0	0	0	0
..........ATGGGAGGAGGTGGGTGGC	19	0	1	2.00	2	1	1	0	0	0
..........TGGGAGGAGGTGGGTGGC	18	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

ACGTGCACGTCGTCCGTTCCTGTGGCCAGCTTCCGCTGTCCCCGACCATTACCCTCCTCCACCCACCGTCCTCCGTCCTGGCGGGAAATCGGCGCGGGTAGCCGCGACAGTCGGAGCTTACAACAGCAGCAGCATCAGCAGCAGCATCACCCGGGGTCGA	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head	M058 embryo	M044 female body	V039 embryo
********************************((((.(((((((...((((.....(((((((((((((.(((.....)))))))..)))..)))))))....))))))))))...)))))...*********************************									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13340:22041107-22041268 +	dan_213	TGCACGTGCAGCAGGCAA--GGACACCGGTCGAAGGCG----------ACAGGGGGCTGGTAATGGGAGGAGGTGGGTGGCAGG----------AGG----CAG----------GACCGCCCTTTAGCCGCGCCCATCGGCGC----TGTCAGCCTCGAATGTTGT---CGTCG---TCGTAGTC----------GTCGTCGTCAGTGGG-CCCCAGCT
droBip1	scf7180000396583:142887-143050 -		TGCACGTGCAGCAGGCAA--GGACCCGGTCGAAGGCG----------C-TGGGGGCTGGTAATGGCGGCCATGGGTGGCCGG----------AGG----CAG----------GCCGCCCTTTAGCCGCGCCCATCGGCGC----TGTCAGCCTCGAATGTTGT---CGTCG---TCGTCGTC-T----------TGTCGTGTCGTCAGTGGG-CCCCAGCT
droKik1	scf7180000302475:923351-923495 -		TGCACGTGCAGCAGGCAA--GGCCGTCGGCCGG-----------------------------------GGGGAAAAGGA----------TGATGA----GGTTGTTTTGGGGGTTGCCGCCCATAGCCGCGCCCAGGCGA----TGTCAGCCTCGAATGTGT---CGTCG---TCGTCGCGTC----------TGTCGTGTCGTCAGTGGG-CCCCAGCT
droFic1	scf7180000453826:37572-37712 -		TGCACGTGCAGCAGACAA--GGCCATTGGCCGG-----------------------------------GGCGGTGGGTGGTTACTGCTTGATGGCTGCCC----------GTCGG----AGG----------GTC----CGGCCGCGCCCATCGGCGA----TGTCAGCCTCGAATGTTGT---CGTCG---TCG---TCGTCGT----------TGTCGTGTCGTCAGTGGG-CCCCAGCT
droEle1	scf7180000491280:4114386-4114506 -		TGCACGTGCAGCAGACAA--GGCCGTTGGATGG-----------C---------------------------C--GAT----------GGTAGG----TGG----------TT-----CTTGCCACGCCCATCGGCGA----TGTCAGCCTCGAATGTTGT---CGTCGTCGTCGTCGTCGT----------TGTCGTGTCGTCAGTGGG-CCCCAGCT
droRho1	scf7180000779538:352518-352651 -		TGCACGTGCAGCAGACAA--GGCCGCGGGTGG-----------C---------------------------GGTTTGCT----------GGGTGGGTGGATC----------GGTGG----TGG----------CT-----C-TTGCCCGCCCATCGGCGA----TGTCAGCCTCGAATGTTGT---CGTCG---TCGTAGTCGT----------TGTCGTGTCGTCAGTGGG-CCCCAGCT
droBia1	scf7180000302075:2913673-2913817 -		TGCACGTGCAGCAGACAA--GGCCATTGGCCGG-----------A---------GG---------------------TGGGTGGTGGGTGGT----------G--G----------TGATGCGTTGT---CG----------GT-----CGGCCACGCCCATCGGCGA----TGTCAGCCTCGAATGTTGT---CGTCG---TCGTCGT----------TGTCGTGTCGTCAGTGGG-CCCCAGCT
droTak1	scf7180000414670:31355-31491 -		TGCACGTGCAGCAGACAA--GGCCATTGGCCGG-----------------------------------TGGGCGGTGGGTGGT----------G----------TGCTGGGGGGTCAGG----------GT-----CGGCCACGCCCATCGGCA-A----TGTCAGCCTCGAATGTTGT---CGTCG---TCGTCGTC----------TGTCGTGTCGTCAGTGGG-CCCCAGCT
droEug1	scf7180000409787:1703044-1703197 -		TGCACGTGCAGCAGACAA--GGCCATTGGACGG-----------C---------------------------A--GGTGGTGGGAGGT----------A---GATGC----------GTGCA----TGG----------GT-----CGGCAAACGCCCATCGGCGA----TGTCAGCCTCGAATGTTGT--TGTCG---TCGA-------------------------TTTTCGTCGTCGTCGTCGTAGTCGTACTCGTCAGTGGG-CCCCAGCT
dm3	chr3R:23899906-23900057 +		TGCACGTGCAGCAGCAA--GGCCGTTGGGTTG-----------------------------------TGGGCAGTGGGCGGT----------A-GGCG--GTGTGCGATGGGTTATGGGTGATCGG----TGG----------GT-----CGGCCACGCCCACGGCGA----TGTCAGCCTCGAATGTTGT---CGTCG---TCGCAGTCGT----------TGTCGTGTCGTCAGTGGG-CCCCAGCT
droSim2	3r:23292782-23292905 +		TGCACGTGCAGCAGCAA--GGCCGTAGGGTTG-----------------------------------TGGGCAGTGGG----------TGATCGG----TGG----------GT-----CGGCCACGCCCACGGCGA----TGTCAGCCTCGAATGTTGT---CGTCG---TCGCAGTCGT----------TGTCGTGTCGTCAGTGGG-CCCCAGCT
droSec2	scaffold_22:517492-517615 +		TGCACGTGCAGCAGCAA--GGCCGTTGGGTTG-----------------------------------TGGGCAGTGGG----------TGATCGG----TGG----------GT-----CGGCCACGCCCACGGCGA----TGTCAGCCTCGAATGTTGT---CGTCG---TCGCAGTCGT----------TGTCGTGTCGTCAGTGGG-CCCCAGCT
droYak3	3R:22597979-22598132 -		TGCACGTGCAGCAGACAA--GGCCGTTGGGCGT-----------------------------------TGGGCGTTGGGCGGT----------G--GGCGGTGGGCGTTGGG----------TGATCGG----TGG----------GT-----CGGCCACGCCCACGGCGA----TGTCAGCCTCGAATGTTGT---CGTCG---TCGTCGC----------CAGT----------CGC----------AGTCGTGTCGTCATCAGTGGG-CCCCAGCT
droEre2	scaffold_4820:4146111-4146225 -		TGCACGTGCAGCAGACAA--GGCCGTTGGGTTG-----------------------------------TGGGTGGTA----------TAATGG----TGG----------GT-----CGGCCACGCCCACGGCGA----TGTCAGCCTCGAATGT----------GG---CG---TCGCAGTCGT----------TGTCGTGTCGTCAGTGGG-CCCCAGCT
dp5	2:8185500-8185640 -		TGCACGTGCAGCAGGCAA--GGCCGAGGATAT-----------------------------------GCAGCAGTGGGGC----------AGGCAAGTCGGTCGC----------GT-----CGAAGGT----------GA--ACGCG--CAGCGG---TCGTAGTCGTCAGAGCAAGTCCCTCGCCCCAGAACCAGT----------CCC----------AG-CT-AG-ACCTAT
droPer2	scaffold_0:2021740-2021886 -		TGCACGTGCAGCAGGCAA--GGCCGAAGGATAT-----------------------------------GCAGCAGTGGGGC----------AGGCAAGTCGGTCGC----------GT-----CGAAGGT----------GA--ACGCG--CAGCGG---TCGTAGTCGTCAGAGCAAGTCCCTCGCCCTAGCCCCAGT----------CCC----------ACCCTAGCT-----CCAG-CCCCTAT
droWil2	scf2_1100000004921:1126467-1126658 +		TGCACGTGCAGCAGCAGCACATGAAGAAA-----------------------CAAGCACGAAGGACGAAGGAC----------CATGCAGCAGTC----------TCAGG----CAA----------GT-----CAAAGCCGCGCCCATCACAAAGCGTCGC-------ATGTGT---CGTCG---TCGTCGTCGTTC----------CCGTAGTTCTTGCTGTTGTTTTGTTGTTGTTTT---TGTTGTTGTTGTTATA-CCCCAGCT
droVir3	scaffold_13047:15668088-15668240 -		TGCACGTGCAGCAGCAGACGACGACGA----CAGCGACAGCGACAAG----------GATGACAAGGACACAGGACGCA----------C-ACACAGGACATGCAGCAGTC----------GAGCTG----GCA----------GT-----CAAAGCCGCGCCCATCAACG----CGCGAA-------GTGCG---CGTCG---TCGTCGTC----------G-CCCCAGTT
droMoj3	scaffold_6540:19163756-19163948 -		TGCACGTGCAGCAGCAGACGACGA-----CGGCGACAGCGACAGCGACGACAGCGACGACTATGATGACAAGGACACAGGACGTAG----------GACATGCCGCAGTC----------GAGCG----GCA----------GT-----CAGAGCCGCGCCCGTCAACGT----GCGCAA-GTCGCAA-TGTG-CCGTCGCGG---TCG-----------CCGT----------TGCCGTCGTCGTCGTCATT-CCCCAGTT
droGri2	scaffold_14830:4338373-4338527 +		TGCACGTGCAGCAGCAGACAACGACGA----CAGC----GATGACAAGGACACAGGACACAC----------GACATGCAGCAGTC----------TGTCGA----CTG----------GCA----GT-----CAAAGCCGCGCCCATCAACG----CGCGAA-ATCGC-CGTCGT---CGTCGTCGTCGTCGTCGT----------TGCCGTCGTCGTCGTCATT-CCCCAGTT

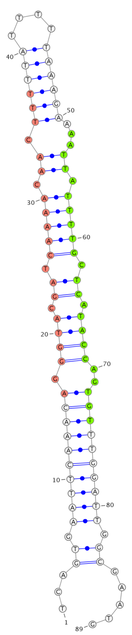
Generated: 09/08/2015 at 07:50 PM

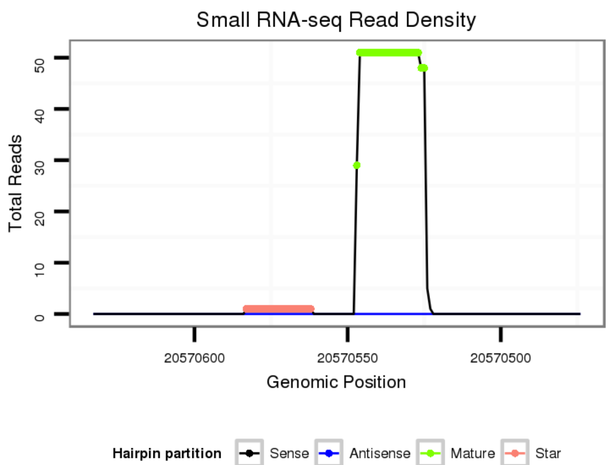
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mer	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

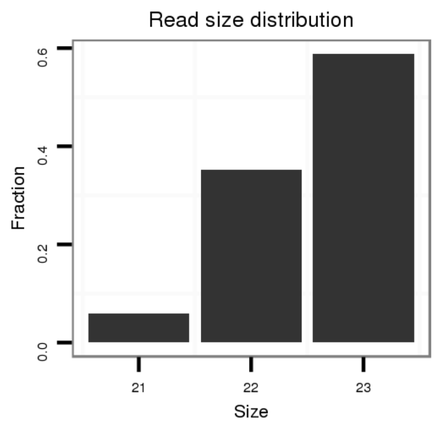
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_97	**scaffold_13337:20570524-20570583 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

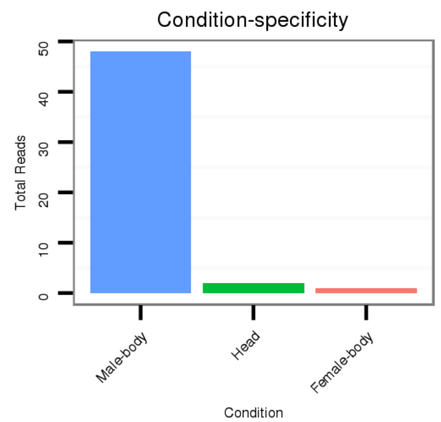
Legend: mature star mismatch in alignment mismatch in read

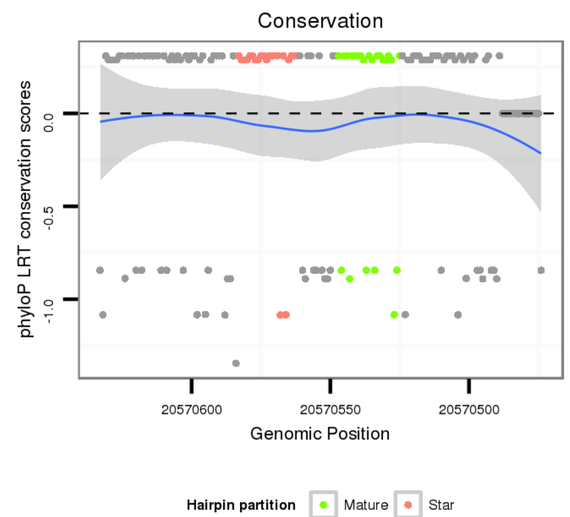
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GAAGCCCAATATATTCTATTAAGTTCTGAGATCTTTCAGTGAATTCAAACAGGGTACGATCAAAACAACTTTTTATTTTTAAAGAAAATTATTTTGCTCATACCAGTGTTTGGATTGGCGAATGGAAACAAGTTGAATACTAGATATGAAGTTATTGCTA **********...((.((((((((((.((((.((.(((((.((.((((((....))))))...)).)))))).)).))))..))))))))))).)).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V055 head	M044 female body
.....AATTATTTTGCTCATACCAGTGT.....	23	0	1	26.00	26	26	0	0
.....ATTATTTTGCTCATACCAGTGT.....	22	0	1	17.00	17	16	0	1
.....ATTATTTTGCTCATACCAGTGTT.....	23	0	1	4.00	4	3	1	0
.....AATTATTTTGCTCATACCAGT.....	21	0	1	3.00	3	2	1	0
.....ATTATTTTGCTCATACCAGTGTTT.....	24	0	1	1.00	1	0	0	1
.....AGGGTACGATCAAAACAACTTT.....	22	0	1	1.00	1	1	0	0

Anti-sense strand reads

CTTCGGGTTATATAAGATAATTCAAGACTCTAGAAAGTCACTTAAGTTTGTCCCATGCTAGTTTTGTTGAAAAATAAAAATTTCTTTTAATAAAACGAGTATGGTCACAAACCTAACCGCTTACCTTTGTTCAACTTATGATCTATACTTCAATAACGAT **********...((.((((((((((.((((.((.(((((.((.((((((....))))))...)).)))))).)).))))..))))))))))).)).....**********	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_13337:20570474-20570633 -	dan_97	GAAGCC-CAATATATTCTATTAAGTTCTGAGATCTTTCAGTGAATTCAAACAGGGTACGATCAAAACAACTTTTTATT------TTTAAAGAAAATTATTTTGCTCATACCAGTGTTTGGATTGGCGAATGGAAACAAGTTGAATACTAGATATGAAGTTATTGCTA
droBip1	scf7180000396707:859994-860146 +		ACAGCCTCAAAATACTTTATTAAATCCTGAGGTCTTGCATCGAATTATTAGAGGGTACGATCAAAAAACCTTTTCTTTACATATCCTGTTAAAAGTTTTTTTGTTCGTACCAGGATTGGGATTGGCGAATAGAAACCAGATGAGCTCTGATT----------G

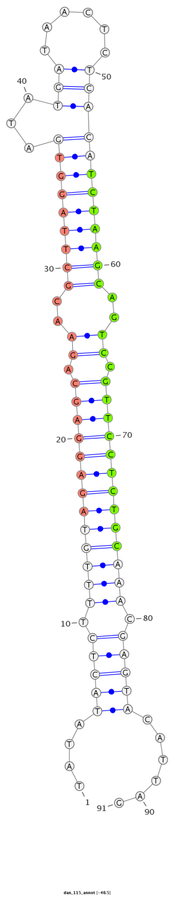
Generated: 09/18/2015 at 07:50 PM

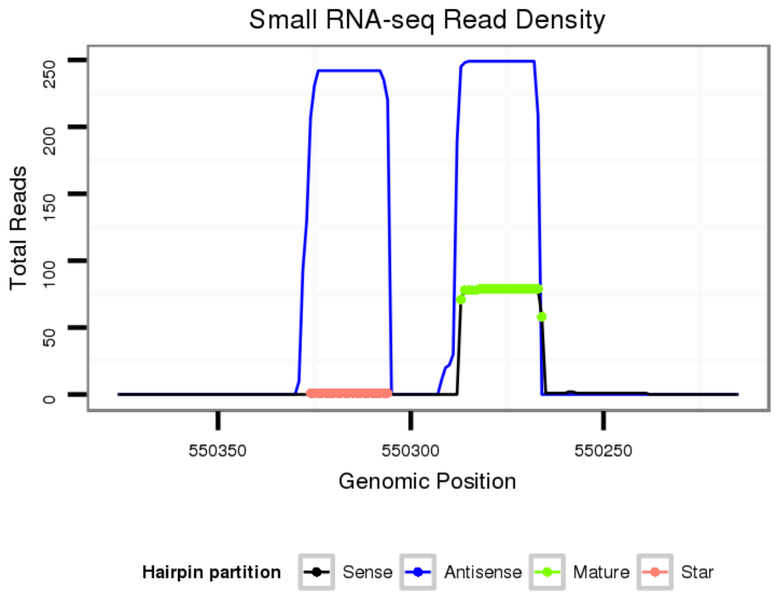
PASS/FAIL	
crit.star	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

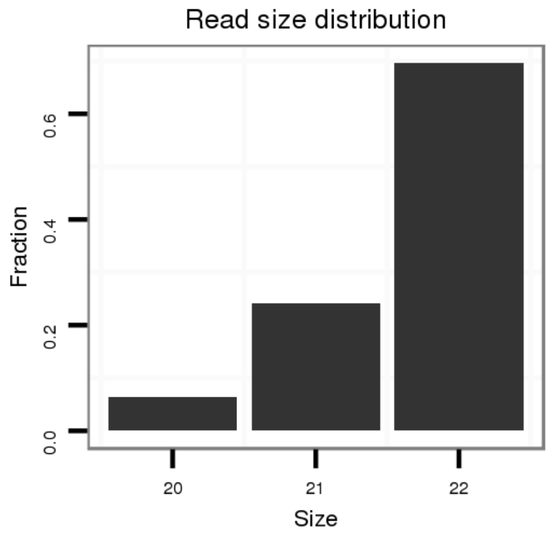
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_115	**scaffold_12903:550265-550326 -**	**candidate**	**Testes-restricted**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

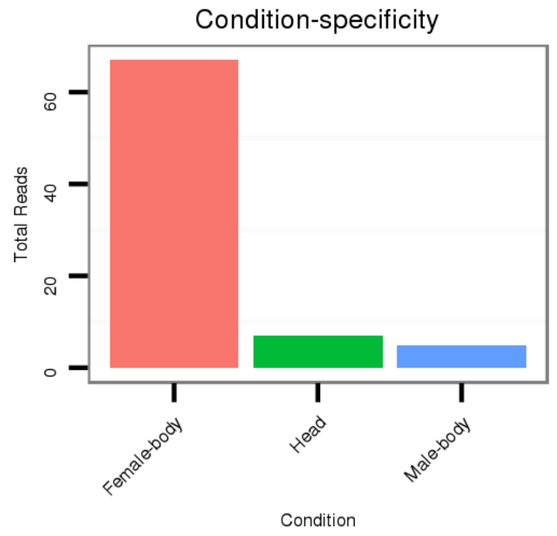
Legend: mature star **mismatch in alignment** mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

intron [Dana\GF15947-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATGTGATTTATGAAGTTGTGATGATCGACTGGCGATATATACTCTTTTGTAGAGGAGCAGAACGCTTAGGTGATATGATAACTCTCACATCTAAGCAGTCCGTTCCTCTGCAAACGAGTACATTAGTCTCTGGAACCCCTCACAGATAGAAGATCCTGAAGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V106 head	V105 male body	M058 embryo	V055 head	V039 embryo
**********************************....(((((.(((((((((((((.((..(((((((((...(((.....)))))))))))))..)).)))))))))))))).)))))......**********											
.....TCTAAGCAGTCCGTTCCTCTGC.....	22	0	1	55.00	55	48	3	4	0	0	0
.....TCTAAGCAGTCCGTTCCTCTG.....	21	0	1	16.00	16	13	3	0	0	0	0
.....CTAAGCAGTCCGTTCCTCTG.....	20	0	1	5.00	5	4	1	0	0	0	0
.....TCTAAGCAGTCCGTTCCTCTGT.....	22	1	1	4.00	4	2	2	0	0	0	0
.....CTAAGCAGTCCGTTCCTCTGC.....	21	0	1	2.00	2	2	0	0	0	0	0
.....GCAGTCCGTTCCTCTGCAAACGAGT.....	25	0	1	1.00	1	0	0	0	1	0	0
.....GTACATTAGTCTCTGGAACCC.....	21	0	1	1.00	1	0	0	0	1	0	0
.....AGAGGAGCAGAACGCTTAGGT.....	21	0	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

TACACTAAATACTTCAACACTACTAGCTGACCGCTATATATGAGAAAACATCTCCTCGTCTTGCGAATCCACTATACTATTGAGAGTGTAGATTCGTCAGGCAAGGAGACGTTTGCTCATGTAATCAGAGACCTTGGGGAGTGTCTATCTTCTAGGACTTCT	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V055 head	M044 female body	V106 head	M058 embryo	V039 embryo
**********************************....(((((.(((((((((((((.((..(((((((((...(((.....)))))))))))))..)).)))))))))))))).)))))......**********											
.....TAGATTCGTCAGGCAAGGAGAC.....	22	0	1	155.00	155	122	13	4	15	1	0
.....TCTCCTCGTCTTGCGAATCCA.....	21	0	1	76.00	76	47	12	10	7	0	0
.....CATCTCCTCGTCTTGCGAATCCA.....	23	0	1	71.00	71	39	10	11	4	6	1
.....AGATTCGTCAGGCAAGGAGAC.....	21	0	1	50.00	50	34	4	5	7	0	0
.....ATCTCCTCGTCTTGCGAATCCA.....	22	0	1	34.00	34	22	6	6	0	0	0
.....CTCCTCGTCTTGCGAATCCA.....	20	0	1	24.00	24	19	1	0	3	1	0
.....AGTGTAGATTCGTCAGGCAAGGAGA.....	25	0	1	11.00	11	5	1	3	2	0	0
.....TCCTCGTCTTGCGAATCCA.....	19	0	1	11.00	11	3	5	1	2	0	0
.....GTGTAGATTCGTCAGGCAAGGAGA.....	24	0	1	9.00	9	6	0	1	2	0	0
.....TCATCTCCTCGTCTTGCGAATCCA.....	24	1	1	8.00	8	5	0	2	1	0	0
.....GTAGATTCGTCAGGCAAGGAGA.....	22	0	1	8.00	8	4	0	2	2	0	0
.....CATCTCCTCGTCTTGCGAATCC.....	22	0	1	8.00	8	7	0	0	0	1	0
.....TTCTCCTCGTCTTGCGAATCCA.....	22	1	1	7.00	7	4	0	2	1	0	0
.....AGATTCGTCAGGCAAGGAGA.....	20	0	1	6.00	6	5	0	1	0	0	0
.....TATCTCCTCGTCTTGCGAATCCA.....	23	1	1	5.00	5	3	0	1	0	0	1
.....CATCTCCTCGTCTTGCGAATC.....	21	0	1	4.00	4	3	0	1	0	0	0
.....TAGATTCGTCAGGCAAGGAGA.....	21	0	1	4.00	4	3	1	0	0	0	0
.....ACATCTCCTCGTCTTGCGAATCCA.....	24	0	1	4.00	4	2	0	0	2	0	0
.....ATCTCCTCGTCTTGCGAATCC.....	21	0	1	3.00	3	1	1	1	0	0	0
.....GATTCGTCAGGCAAGGAGAC.....	20	0	1	3.00	3	2	1	0	0	0	0
.....ACATCTCCTCGTCTTGCGAATC.....	22	0	1	3.00	3	3	0	0	0	0	0
.....ACATCTCCTCGTCTTGCGAATCC.....	23	0	1	3.00	3	0	0	3	0	0	0
.....TGTAGATTCGTCAGGCAAGGAGA.....	23	0	1	2.00	2	0	1	0	1	0	0
.....ATAGATTCGTCAGGCAAGGAGAC.....	23	1	1	2.00	2	2	0	0	0	0	0
.....TTAGATTCGTCAGGCAAGGAGAC.....	23	1	1	2.00	2	2	0	0	0	0	0
.....ACTCCTCGTCTTGCGAATCCA.....	21	1	1	2.00	2	2	0	0	0	0	0
.....CCATCTCCTCGTCTTGCGAATCCA.....	24	1	1	2.00	2	1	0	1	0	0	0
.....AAGTGTAGATTCGTCAGGCAAGGAGA.....	26	1	1	1.00	1	1	0	0	0	0	0
.....TTAGATTCGTCAGGCAAGGAGA.....	22	1	1	1.00	1	0	0	1	0	0	0
.....ATTAGATTCGTCAGGCAAGGAGA.....	23	2	1	1.00	1	1	0	0	0	0	0
.....TTAGATTCGTCAGGCAAGGAGA.....	22	1	1	1.00	1	0	0	1	0	0	0
.....ATTAGATTCGTCAGGCAAGGAGA.....	23	2	1	1.00	1	1	0	0	0	0	0
.....CGTAGATTCGTCAGGCAAGGAGA.....	23	1	1	1.00	1	0	0	1	0	0	0
.....ATTCGTCAGGCAAGGAGAC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....GATTCTCCTCGTCTTGCGAATCCA.....	24	3	1	1.00	1	1	0	0	0	0	0
.....ATGATTCGTCAGGCAAGGAGAC.....	22	2	1	1.00	1	1	0	0	0	0	0
.....AAAGATTCGTCAGGCAAGGAGAC.....	23	2	1	1.00	1	1	0	0	0	0	0
.....ATGTAGATTCGTCAGGCAAGGAGA.....	24	1	1	1.00	1	0	0	1	0	0	0
.....TGATTCGTCAGGCAAGGAGAC.....	21	1	1	1.00	1	1	0	0	0	0	0
.....AATCTCCTCGTCTTGCGAATCCA.....	23	1	1	1.00	1	0	0	1	0	0	0
.....TGTCTCCTCGTCTTGCGAATCCA.....	23	2	1	1.00	1	1	0	0	0	0	0
.....TCTCCTCGTCTTGCGAATCC.....	20	0	1	1.00	1	0	0	1	0	0	0
.....TTTCTCCTCGTCTTGCGAATCCA.....	23	2	1	1.00	1	0	1	0	0	0	0
.....TTCCTCGTCTTGCGAATCCA.....	20	1	1	1.00	1	1	0	0	0	0	0
.....CCTCCTCGTCTTGCGAATCCA.....	21	1	1	1.00	1	0	0	0	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:550215-550376 -	dan_115	ATGTGATTTATGAAGTTGTGATGATCGACTGGCGATATATACTCTTTTGTAGAGGAGCAGAACGCTTAGGTGATATGATAACTCTCACATCTAAGCAGTCCGTTCCTCTGCAAACGAGTACATTAGTCTCTGGAACCCCTCACAGATAGAAGATCCTGAAGA

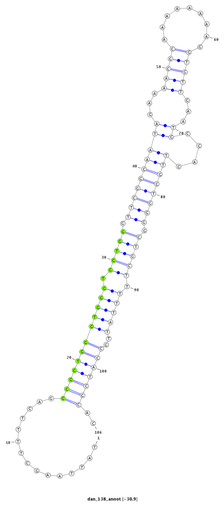
Generated: 09/08/2015 at 08:04 PM

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

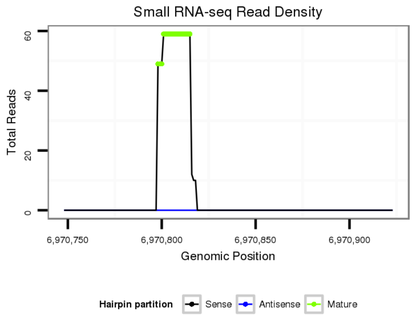
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_138	**scaffold_12916:6970798-6970873 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

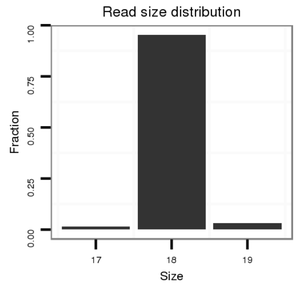
Legend: mature star mismatch in alignment mismatch in read

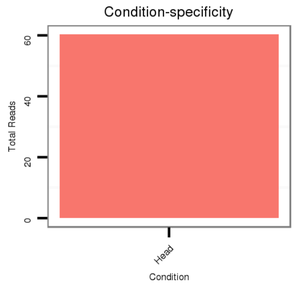
Predicted structure

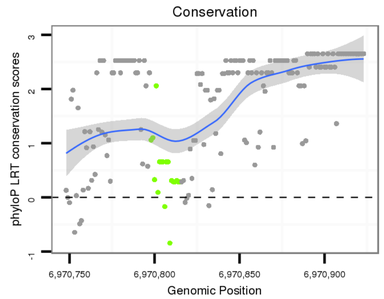


Show Alternate Folds









Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dan_132 scaffold_12916:6367567-6367584 + 2. dan_138 scaffold_12916:6970798-6970815 +	

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CCCCAGGCACTTCGAGACCATTTTCGGCGTTTGTTTATTAAGCTTTTCAGGCGGTGGGTGGGTGGGTGGTTCGGCAATAGAAAACGCAAAAAAAAGGTGTTGAATGCCACTTGCTGGGGCTGCTTTTTATTGCCATCGCACATCTAAGTGCAGCAGCTGTAAAATAAATATATATT						V106	V055	M044 female	V039	V105
********************************..............((((((((((((.(((((.((((((((((...(((((.........)))))...))...)))))))))).)))))).))))))..))))))))..********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	head	head	body	embryo	male body
.....GCGGTGGGTGGGTGGTGG.....	18	0	2	47.50	95	95	0	0	0	0
.....GTGGGTGGGTGGTGGGTT.....	18	0	1	10.00	10	9	1	0	0	0
.....GCGGTGGGTGGGTGGTGGG.....	19	0	1	2.00	2	2	0	0	0	0
.....GTGGGTGGGTGGTGGGT.....	17	0	6	0.83	5	0	5	0	0	0
.....GTGGGTGGGTGGTGGGTA.....	18	1	12	0.42	5	4	0	0	0	1
.....GTGGGTGGGTGGTGGGTT.....	19	1	7	0.14	1	0	0	1	0	0

Anti-sense strand reads

GGGGTCCGTGAAGCTCTGGTAAAAGCCGCAAACAAATAATTCGAAAAGTCCGCCACCCACCCACCACCCAAGCCGTTATCTTTTGCGTTTTTTTCCACAACTTACGGTGAACGACCCCGACGAAAAATAACGGTAGCGTGTAGATTCACGTCGTCGACATTTTATTTATATATAA						V039	M058	V055	M044 female
********************************..............((((((((((((.(((((.((((((((((...(((((.........)))))...))...)))))))))).)))))).))))))..))))))))..********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	embryo	embryo	head	body

Show Alignment With Reads

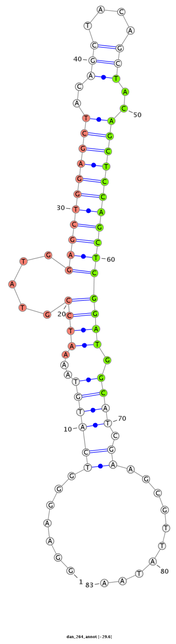
Re-alignment of all predicted orthologs

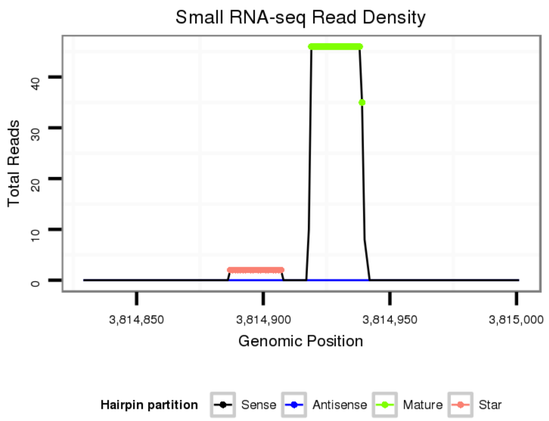
Species	Coordinate	ID	Alignment
droAna3	scaffold_12916:6970748-6970923 +	dan_138	C-----CCCAGGCACTTCGAGACCATTTTCGGCGTTTGTTTATTAAGCTTTT-CAGGC----------GGT---GGGTGGGTGG-TGGG------T-TCGGCAATAGAAAAC------G------CAA--AAAAAAGGTGTTGAATGCCACTTGCTGGGGC-TGCTTTTTATTGCC----------ATCGCA------CATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
droBip1	scf7180000396566:151384-151566 +		C-----CCCAGCCACTTCGAGACCATTTTCGGCGTTTGTTTATTAAGCTTTT-CAGGC----------GGT---GGGTGGTGGCTGGGATGGGGGTCTCGGCAATAGAAAAC------G------CAA--AAAAAAGGTGTTGAATGCCACTTGCTGGGGC-TGCTTTTTATTGCC----------ATCGCA------CATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
droKik1	scf7180000302408:661448-661624 +		C------CTCAGCCATTTCTCCACATTTTCGGCGTTTGTTTATTAAGCTTTT-CAGGC----------GGGACTGGCGGC----C----G-T--T---GAATAGAAAAGC------GCAAA--AA--AAAAAAGGTGTTGAATGCCACTTGCTGGGGC-TGCTTTTTATTGCC----------ATCGCCCATGGCCCATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
droFic1	scf7180000453883:45929-46081 -		T-----C----CAACTCTAGACGCTTTTCGGCGTTTGTTTATTAAGCTCCTGCAGGC----------GGA---------C----G-T--T---GATAGAAAAC------G------CA--AAAAAAGGTGTTGAATGCCACTTGCTGGGC-TGCTTTTTATTGCC----------ATCGCA------CATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
droEle1	scf7180000491186:448864-449018 +		C-----C----CAACTCTAGACCATTTTCGGCGTTTGTTTATTAAGCTTTT-CAGGC----------GGA---------C----G-T--T---GAATAGAAAAC------G------AA--AAAAAAGGTGTTGAATGCCACTTGCTGGGC-TGCTTTTTATTGCC----------ATCGCA------CATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
droRho1	scf7180000759732:402-555 -		C-----ACCA---ACTCTAGACCATTTTCGGCGTTTGTTTATTAAGCTTTT-CAGGC----------GGA---------C----G-T--T---GAATAGAAAAC------G------AA--AAAAAAGGTGTTGAATGCCACTTGCTGGGC-TGCTTTTTATTGCC----------ATCGCA------CATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
droBia1	scf7180000302422:7617836-7617986 +		C-----A-------CTCTAGACCATTTTCGGCGTTTGTTTATTAAGCTTTC-CAGGC----------GGA---------C----G-T--T---GAATAGAAAAC------G------AA--AAAAAAGGTGTTGAATGCCACTTGCTGGGC-TGCTTTTTATTGCC----------ATCGCA------CATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
droTak1	scf7180000415115:86600-86754 -		C-----A-----CAACTCTAGACCATTTTCGGCGTTTGTTTATTAAGCTTTT-CAGGC----------GGA---------C----G-T--T---GAATAGAAAAC------G------AA--AAGAAAGGTGTTGAATGCCACTTGCTGGGC-TGCTTTTTATTGCC----------ATCGCA------CATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
droEug1	scf7180000409767:830416-830571 -		C-----C-------AACTCTAGACCATTTTCGGCGTTTGTTTATTAAGCTTTT-CAGGC----------GGA---------C----G-T--T---GAAGGAATAGAAAAC------G------AAA-GAAAAAAGGTGTTGAATGCCACTTGCTGGGC-TGCTTTTTATTGCC----------ATCGCA------CATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
dm3	chr2L:20471133-20471290 +		C-----A-----CAACTCTAGACCATTTTCGGCGTTTGTTTATTAAGCTTTT-CAGGCA---------GGA---------C----G-T--T---GAATAGAAAAC------G------AAGCGAAAAAAGGTGTTGAATGCCACTTGCTGGGC-TGCTTTTTATTGCC----------ATCGCA------CATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
droSim2	2L:19927642-19927802 +		A-----ACCAGCCAACTCTAGACCATTTTCGGCGTTTGTTTATTAAGCTTTT-CAGGCA---------GGA---------C----G-T--T---GAATAGAAAAC------G------AAGCGAAAAAAGGTGTTGAATGCCACTTGCTGGGC-TGCTTTTTATTGCC----------ATCGCA------CATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
droSec2	scaffold_18:349422-349582 +		A-----ACCAGCCAACTCTAGACCATTTTCGGCGTTTGTTTATTAAGCTTTT-CAGGCA---------GGA---------C----G-T--T---GAATAGAAAAC------G------AAGCGAAAAAAGGTGTTGAATGCCACTTGCTGGGC-TGCTTTTTATTGCC----------ATCGCA------CATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
droYak3	2R:6827396-6827544 +		C-----A-------AACTCTAGACCATTTTCGGCGTTTGTTTATTAAGCTTTT-CAGGCA---------GGA---------C----G-T--T---GAATAGAAAAC------G------AAA--AAAAAAGGTGTTGAATGCCACTTAGCTGGGC-TGCTTTTTATTGCC----------ATCGCA------CATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
droEre2	scaffold_4845:3970294-3970449 -		A-----ACCACCCAACTCTAGACCATTTTCGGCGTTTGTTTATTAAGCTTTT-CAGGCA---------GGA---------C----G-T--T---GAATAGAAAAA-C------G------AAA--AAAAAAGGTGTTGAATGCCACTTGCTGGGC-TGCTTTTTATTGCC----------ATCGCA------CATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
dp5	4_group3:7864028-7864203 -		CGTGGCACCACCCACTCTAGACCATTTTCGTTTTGTTTATTAAGCTTTT-CAGGC----------TCC---------C----G-T--T-CAGAATAGACAAACGGGTGGCCA----AAA--AAAAAAGGTGTTGAATGCCACTTGCTGGGC-TGCTTTTTATTGCC----------ATCGCA------CATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
droPer2	scaffold_1:9310642-9310820 -		CGTGGCACCACCCGACTCTAGACCATTTTCGTTTTGTTTATTAAGCTTTT-CAGGC----------TCC---------C----G-T--T-CAGAATAGACAAACGGGTGGCCAAAAAAA--AAAAAAGGTGTTGAATGCCACTTGCTGGGC-TGCTTTTTATTGCC----------ATCGCA------CATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
droWil2	scf2_1100000004521:1822404-1822641 +		C-----CACAGCCTTCAGCCATATTCGGCGTTTGTTTATTAAGCTTTT-CTTCATACAACCAAAAAAGGGAAAATTCAAGTAGGGAAAAATACAGGAGTACAAATAAAGAAGAAAGCCAACAAAGGAGCACAAAAAAAAATATATATA-C----------C----G-T--T-------------AGGTGTTGAATACCATTGCGGGGGCATGGTTTTTATTGCC----------ATCGCA------CATCTAAGTGC---AGCAGCTGTAAAATAAATATATATT
droVir3	scaffold_12963:13636207-13636243 -		G-----C----CAACTCTAGACCATTTTCGGCGTTTGTTTATTAAGCTTTT-CAGGC----------TCC---------C----G-T--T-------------------

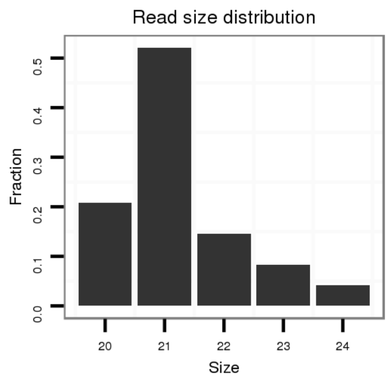
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_264	**scaffold_13266:3814879-3814951 +**	**candidate**	**Canonical miRNA**	**3pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

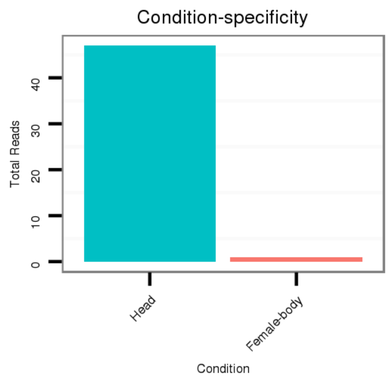
Legend: mature star mismatch in alignment mismatch in read

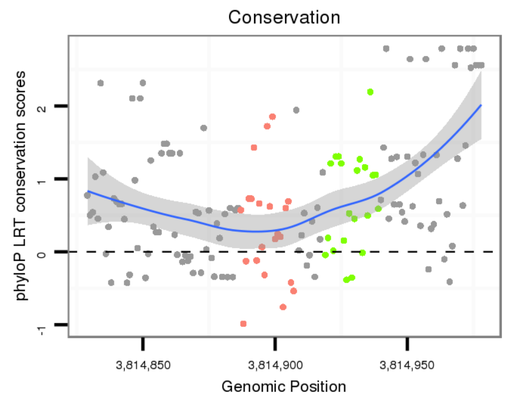
Predicted structure











Show Alternate Folds

Flybase annnotation

utr3 [utr3_minus_3275]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACGGGTTCTCCAACTGTGGAGCTGGCGCCCACGACTTGGGCTAGGAAGGGTCATGTAAAATCCGTATGGAGCTGGAGCTACAGCTACAGCTACAGCTCCAGCTCGGATGGCATCGATCGAAGCGTTATAAGATAACCAAAACCTATGTTTAAATTATTGTACAATTTATGTGTTTGC	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V055 head	M044 female body	V105 male body	M058 embryo	V039 embryo
.....((((((...((((.....((((((((((..(((....)))..)))))))))))))).)))))..))).....											
.....TACAGCTCCAGCTCGGATGGC.....	21	0	1	22.00	22	22	0	0	0	0	0
.....TACAGCTCCAGCTCGGATGG.....	20	0	1	10.00	10	10	0	0	0	0	0
.....CTACAGCTCCAGCTCGGATGGC.....	22	0	1	5.00	5	5	0	0	0	0	0
.....CTACAGCTCCAGCTCGGATGGCT.....	23	1	1	3.00	3	2	0	0	1	0	0
.....TACAGCTCCAGCTCGGATGGT.....	21	1	1	3.00	3	2	1	0	0	0	0
.....CTACAGCTCCAGCTCGGATGGCA.....	23	0	1	2.00	2	2	0	0	0	0	0
.....TACAGCTCCAGCTCGGATGGCA.....	22	0	1	2.00	2	1	1	0	0	0	0
.....AATCCGTATGGAGCTGGAGCT.....	21	0	1	2.00	2	2	0	0	0	0	0
.....CTACAGCTCCAGCTCGGATGGCAT.....	24	0	1	2.00	2	2	0	0	0	0	0
.....TACAGCTCCAGCTCGGATGGCAT.....	23	0	1	2.00	2	2	0	0	0	0	0
.....CTACAGCTCCAGCTCGGATGG.....	21	0	1	1.00	1	0	0	1	0	0	0
.....TACAGCTCCAGCTCGGATGGA.....	21	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

TGCCCAAGAGGTTGACACCTCGACCGCGGGTGCTGAACCCGATCCTTCCCAGTACATTTTAGGCATACCTCGACCTCGATGTCGATGTCGATGTCGAGGTCGAGCCTACCGTAGCTTCGCAATATTCTATTGGTTTTGGATACAAATTTAATAACATGTTAAATACACAAACG	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	M058 embryo	V055 head
**********.....((((((...((((.....((((((((((..(((....)))..)))))))))))))).)))))..))).....**********								

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13266:3814841-3814990 +	dan_264	ACTGTGGAGCTGGCGCCCACGACTTGGGCTAGGAAGG----------GTCA----------TGTAAAATCC------G-----TATGGAG--------CTGGA--G--CTACAGCTACAGCTACAGCTCC---AG----------CT----------CGGATGGCATCG-AAGCGTTATAAGATAACCAAAACCT--------ATGTTTAAATT-ATTGTACAATT
droBip1	scf7180000396427:2281681-2281815 +		ACTGTGGAGCTGGCGCCCACGACTTGGGCTAGGTTGG----------GTCG----------TGTAAAGT-C------A-----T------G---GTAAATGGA--G--C------CA--GTG----CTCC---AG----------CT----------TGGATGGCATCG-AAGCGTTATAAGATAACCAAAACCT--------ATGTTTAAATT-ATTGTACAATT
droKik1	scf7180000302471:1261214-1261348 -		ACTGCGGCG---GCACCCACGACCTGGGCTAGG-TG----------CGCAAAGTCC------G-----TGTAGAGTCGGGCGGA-----T--T---AGGAGGAGGGACTCTTCCC---GG----------CGGATGG-AAGG-AAGCGTTATAAGATAACCAAAAC-T--------AGCGTTAAATT-ACTGTACAATT
droFic1	scf7180000454044:204143-204282 -		ACTGCGGAG------GTCCTGACATGGGCTAGGATGTACA----------GC----------CTGTACAGCTC------A-----T------GC----AAAA--CGGCGCGTTG--GGGATTCAAATTGCG-AAA----------TT--TCGGC----------CGGATGG-AAGG-AAGCGTTATAAGATAACCAAAACCT--------AGCGTTAGGGC-ATTGTACAATT
droEle1	scf7180000491240:292092-292230 +		ACTGCGGAG------GTCCTGACTTGGGCTAGGATGTTGT----------AA----------TTGTAAAGTTC------G-----T------GT----AACGGGCGGTTG--GGGATTCAAATTGCG-AAA----------CT--CGCGGC----------CGGATGG-AAGCGTTATAAGATAACCAAAACCT--------AGCGTTAGGGC-ATTGTACAATT
droRho1	scf7180000779508:4974-5115 +		ACTGCGGAG------GTCCTGATTGGGCTAGGATGTTGT----------AA----------TTGTAAAGTTC------G-----T------GT----AATAGCCGGCCGTTG--GGGATTCCGATTGCG-AAA----------CT--CGCGGC----------CGGATGG-AAGCGTTATAAGATAACCAAAACCT--------AGCGTTAGGGC-ATTGTACAATT
droBia1	scf7180000301754:756766-756944 +		GC---GGAG------GTCCCGACATGAACTAGGATGCGGAGCGCAGGAAGCAGA-------AAGCAGGATGCAGGACGAGGCGTGGTGAAAGCTTCAGCCGACG----------GACGGAGCGTTG--GGCATTCAAATGCG-AGT----------GT--CGCGGC----------CGGATGG-AAGCGTTATAAGATAACCAAAACCT--------AGCGTTAGGGC-ATTGTACAATT
droTak1	scf7180000414560:5704-5837 +		ACTGCGGAGTG---GGCCCGATTTAAACTAGGACGT----------AGGATGTGGAGTGGTGAAAGCTC------GCATTCG----------AACAGATAAGCGTTG--G----------T----------CT--TT----------CGGATGG-AAGCGTTATAAGATAACCAAAACCT--------AGCGTTAGGGC-ATTGTACAATT
droEug1	scf7180000409474:1182750-1182886 +		ACTGCGGAG------CTCCGACATGAACTAGGATGTGG----------GC----------T-ATCGGT----------GC--AGGA--A--CGGCGCGTTG--CAGATTCAAATGGCG-G----------CTAACTGCGAGGGCC----------CGGATGG-AAGCGTTATAAGATAACCAAAACCT--------AGCGTTAGGGC-ATTGTACAATT
dm3	chr2R:16771858-16771956 -		G----------GC----------GC----------GC----------T-----T----------AAAAGCGGAGCGTTG--GGAATTCAAATTGCG-AGG----------CT--CGCGCT----------CGGATGG-ATGCGTTATAAGATAACCAAAACCT--AGGCCCAGCGTTAGGGCAATTGTACAATT
droSim2	2r:17329964-17330062 -		G----------GC----------GC----------GC----------T-----T----------AAAAGCGGACGCGTTG--GGGATTCAAATTGCG-AGG----------CT--CGCGCC----------CGGATGG-AAGCGTTATAAGATAACCAAAACCT--AGGCCCAGCGTTAGGGCAATTGTACAATT
droSec2	scaffold_9:97493-97591 -		G----------GC----------GC----------GC----------T-----T----------AAAAGCGGACGCGTTG--GGAATTCAAATTGCG-AGG----------CT--CGCGCC----------CGGATGG-AAGCGTTATAAGATAACCAAAACCT--AGGCCCAGCGTTAGGGCAATTGTACAATT
droYak3	2R:12427491-12427590 +		G----------GC----------GC----------GC----------T-----T----------AAAAGCGGACGCGTTG--GGAATTCAAATTGCG-AGG----------CT--CGCGCC----------CGGATGG-AAGCGTTATAAGATAACCAAAACTTATAGGCCTAGCGTTAGGGC-ATTGTACAATT
droEre2	scaffold_4845:10914022-10914119 -		G----------GC----------GC----------GC----------T-----T----------AAAAGCGGACGCGTTG--GGAATTCAAATTGCG-AGG----------CT--CGCGCC----------CGGATGG-AAGCGTTATAAGATAACCAAAACAT--AGGCCTAGCGTTAGGGC-ATTGTACAATT
dp5	3:8384523-8384645 +		ATTGCGGG------AACCATGACTT----------CTA----------A----------GGC----------CCGAACCCC----------T--T----------AA-CAATTTGACAACCACTGGCAA----------TGGAAG---CGAATGGAAGCGG-AAGCGTTATAAGATAACCAAAACCT--------ATGTTTAGAAT-ATTGTACAATT
droPer2	scaffold_4:2266055-2266177 +		ATTGCGGG------AACCATGACTT----------CTA----------A----------GGC----------CCGAACCCC----------T--T----------AA-CAATTTGACAACCACTGGCAA----------TGGAAG---CGAATGGAAGCGG-AAGCGTTATAAGATAACCAAAACCT--------ATGTTTAGAAT-ATTGTACAATT
droWil2	scf2_1100000004954:4992220-4992334 -		ACCATGAG----------TT----------TTAGACAGCCGA----------GAC----------ACGAATCGAC------AC----------T--T----------AG----------CCACAGACTTTGGAGAAAGGGAACTTCCGAATGTTAAGG-AATAT---AGAAAAAATTGAATACCC--------ATACATATATA-TTATACA---
droVir3	scaffold_12823:1910994-1911081 +		ATTGCGGC------AGTCACGAGTT----------CTA----------A----------T----------T----------T--T----------AA-CAGTTTGACAGC----------CCAAGGGCGCAGCAACAAGTTTTAGTTTT--------AACTTTAACAT-ATTGTACAATT
droMoj3	scaffold_6496:1209004-1209099 +		ATTGCGGC------AGCACGACTT----------TTGAAGCGA----------T----------CTGTACGCACC----CCACA----------T--T----------CACGGACAGTTT-GAGAGCCAA----------CCCGGGAAGAGTTTTCA----------AGCCA-ATTGTACAATT
droGri2	scaffold_15245:16146988-16147108 -		ATAGCGGC------AGTCACGAGTA----------TTGAATAAACTG----------A----------AC----------T--T----------A-CAGTTTGACAGCCACCCG----CTCGGGCCAACCGAGCTTTAGA----------T----------TAAGCTAACCAAATTT--AATTTTAGATTTAAAGA-ATTAACAATT

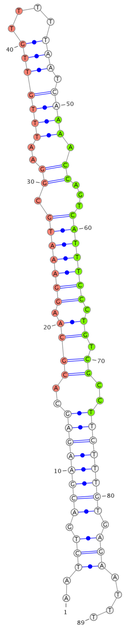
Generated: 09/08/2015 at 07:51 PM

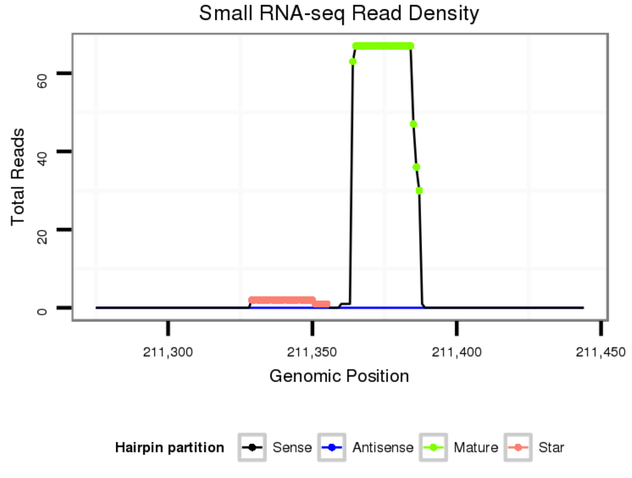
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

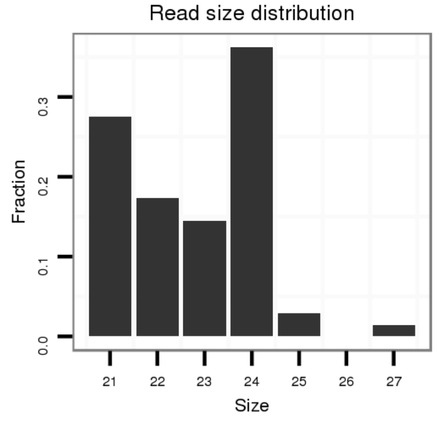
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_224	**scaffold_13335:211325-211394 +**	**candidate**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

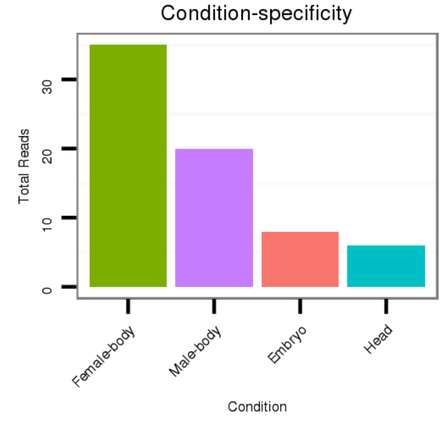
Legend: mature star mismatch in alignment mismatch in read

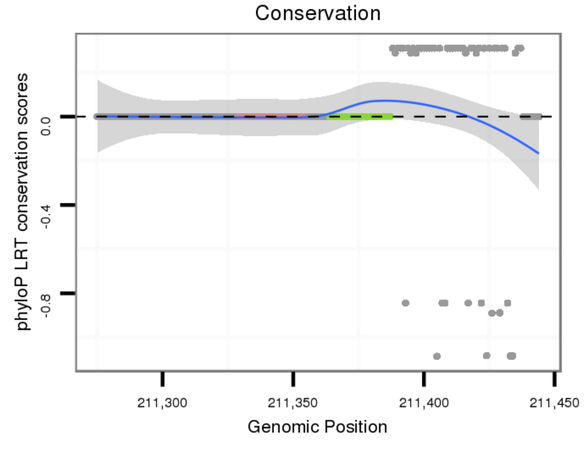
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATTCAACAATATTAAATTTTCAAGTGTGTGCGTTTTTAAAATCTGACGAAGAGCACGCAAGGAAATGCGGAATTTGTTGTTTTTAATCAAAACCAGTCATTTCCCTGTCGCCTTCTTTGTGAGAATTTTTCTCCTTAAAATGCATGAGTGTATTTAAATTGAATATTATA	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V105 male body	M058 embryo	V055 head	V106 head
**********..(((.(((((((((..(((((.(((((((.((..(((((((....))).)))))..))...)))))))).))..))..)))))))).)))....**********										
.....AAACCAGTCATTTCCCTGTCGCCT.....	24	0	1	25.00	25	20	1	3	1	0
.....AAACCAGTCATTTCCCTGTCG.....	21	0	1	19.00	19	3	13	0	2	1
.....AAACCAGTCATTTCCCTGTCGC.....	22	0	1	11.00	11	5	4	1	0	1
.....AAACCAGTCATTTCCCTGTCGCC.....	23	0	1	6.00	6	1	0	4	0	1
.....AACCAGTCATTTCCCTGTCGCCT.....	23	0	1	4.00	4	4	0	0	0	0
.....AAACCAGTCATTTCCCTGTCGCCC.....	24	1	1	2.00	2	0	0	2	0	0
.....ATCAAAACCAGTCATTTCCCTGTCG.....	25	0	1	1.00	1	1	0	0	0	0
.....AAACCAGTCATTTCCCTGTCGCCTT.....	25	0	1	1.00	1	1	0	0	0	0
.....ACGCAAGGAAATGCGGAATTTGTTGTT.....	27	0	1	1.00	1	0	1	0	0	0
.....AAACCAGTCATTTCCCTGTCGCCA.....	24	1	1	1.00	1	0	0	1	0	0
.....AAACCAGTCATTTCCCTGTCGCT.....	23	1	1	1.00	1	0	1	0	0	0
.....ACGCAAGGAAATGCGGAATTTG.....	22	0	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13335:211275-211444 +	dan_224	ATTCAACAATATTAAATTTTCAAGTGTGTGCGTTTTTAAAATCTGACGAAGAGCACGCAAGGAAATGCGGAATTTGTTGTTTTTAATCAAAACCAGTCATTTCCCTGTCGCCTTCTTTGTG-AGAATTTTTCTCCTTAAAATGCATGAGTGTATTTAAATTGAATATTATA
droBip1	scf7180000396427:573843-573893 -		---------- TCTTTATGAAGAATTTTTATTTTTAAAATGATGATTTTTTAAAGGGGAA------

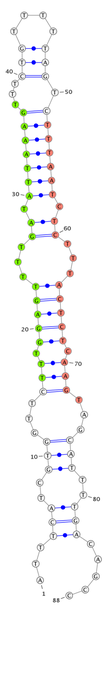
Generated: 06/5/2015 at 08:04 PM

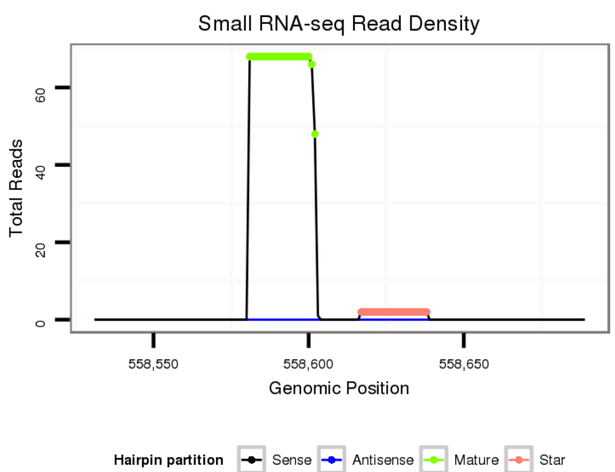
PASS/FAIL	
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

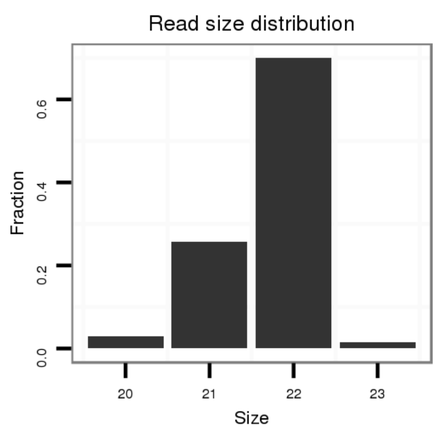
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_95	**scaffold_12903:558581-558639 +**	**candidate**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

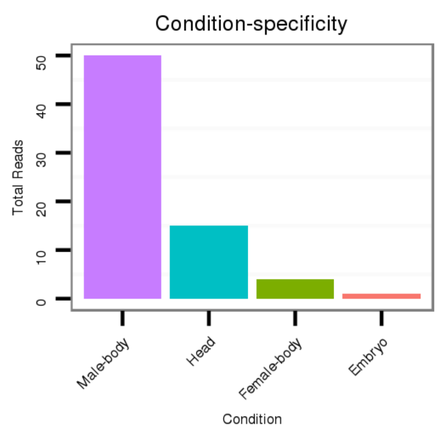
Legend: mature star mismatch in alignment mismatch in read

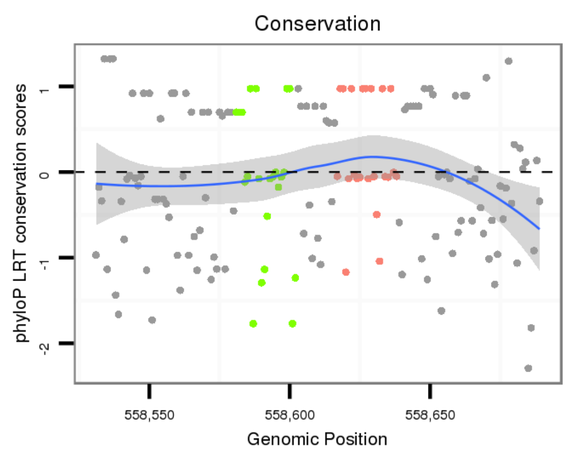
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATCTGTTCTCCATTTTATTTCAATCATTTTATTTTATTTCATCGTGGTTCTTTGGAGTTTTGATATTAAAGTTTCTGTTTTTAGTCTTTAATCTCTTTACTCTCAAGTAGCATTTTGACAGCCAGCCATCTTTGTGATTTGGGATATTTTTAAAATTTG **********...(((..(((...(((.(((((...((.(((((((...(((....))).)))))))).))...)))))...)))...)))..))).....	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V106 head	M044 female body	V055 head	M058 embryo
..........TTTGGAGTTTTGATATTAAAGT..........	22	0	1	47.00	47	38	5	1	2	1
..........TTTGGAGTTTTGATATTAAAG...........	21	0	1	18.00	18	10	5	2	1	0
..........TTTGGAGTTTTGATATTAAA............	20	0	1	2.00	2	0	2	0	0	0
..........TTTAATCTCTTTACTCTCAAGT..........	22	0	1	2.00	2	1	0	1	0	0
..........TTTGGAGTTTTGATATTAAAGTT.........	23	0	1	1.00	1	1	0	0	0	0
..........TTTGGAGTTTTGATATTAAAA...........	21	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

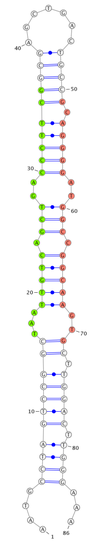
Re-alignment of all predicted orthologs

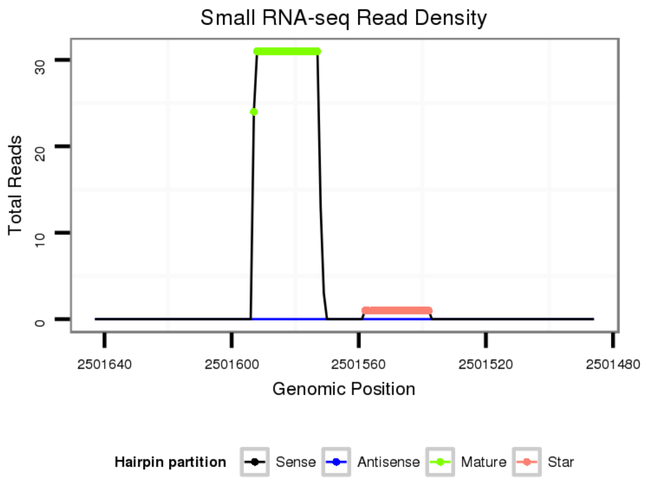
Species	Coordinate	ID	Alignment
droAna3	scaffold_12903:558531-558689 +	dan_95	ATCTGTTCTCCATTTTATTTCAATCATTTTATT-----TTATTTCATCGTGGTTCTTTGGAGTTTTGATA--TTAAAGTTCTGTTTTT----------AGTCTTTAATCTC---TTTACT-CTC-AAGTAGCATTTTGACAGCCAGCCATCTTTGTGA-------TTTGGGATATTTTTAAAA------TTTG
droBip1	scf7180000395912:27405-27563 +		ATCTAATTACTTATTATATCTA------TTACTT-----ATTACTCAGAATGATTCTTTGGACTTAAGAAA--TAAACGTTTTGCTAATTATCTTAATATTA----------ATTTATTCTC---TTTACT-ATC-GAGACCCATTTTAAAAGTCAC----------CTTTGAAATTTTTTTTCTTCTGACAT------TTGC
droKik1	scf7180000302798:184023-184230 -		ATTTGTTTTTGCTTGATATG------TTAGTTTAATATTGTTAAAATTGTTTGTTTTAATTAGCTTAA--GAAAATTT--------GTTAGTTTATTTGTCAAGTCATTAAGTTCTAATTGTAATTTTAGTGTAAAACAATCCAGCCTTTATTCCC---TTCATAATTT-AAGTA-------AAAAGTTGCCGTTGTTAGGACTTTAAAATGTATTTGATTCTTAATT------CCTG
droFic1	scf7180000451789:223383-223422 +		CTTTTTTGCCCACTTTTTTTGGTTTGTTTAAT-----T----------**----------**----------**

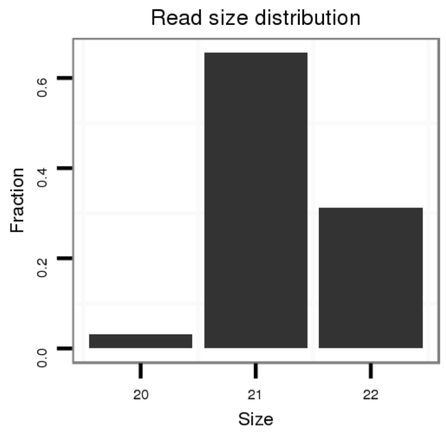
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_207	**scaffold_13417:2501536-2501593 -**	**candidate**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

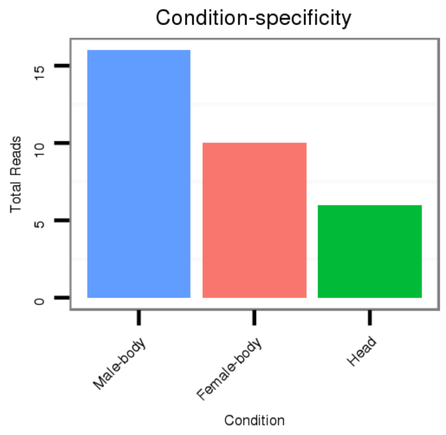
Legend: mature star mismatch in alignment mismatch in read

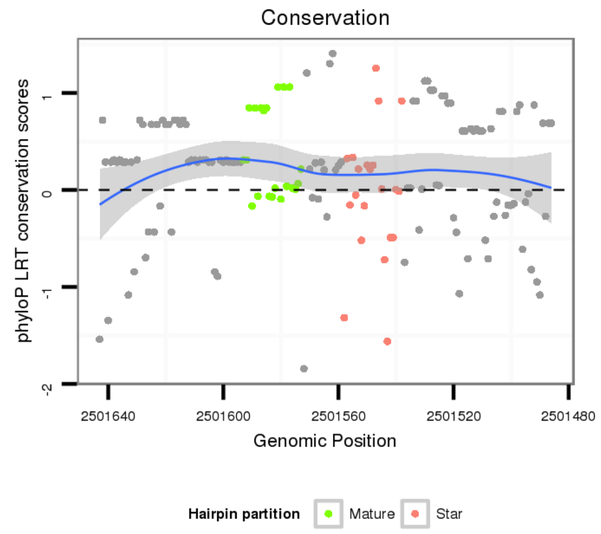
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dana\GF20486-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTGCCTCACCCGATTCGCCCGGTGCGTTGACCTACAATGCCTAGTCCGGCTAATTGTCAGCTGACCCTTCGGCGAGCTGACTGCCGCAGGGGATGGCCGGCAAGTGCTTGGACTTGGGAAACGGACCCGACACCGCACCGGACAACAACATATCGCGG	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	M044 female body	V106 head	V055 head	M058 embryo
....(((((((((((...(((((.(((..(((((((((((.......)))))).)))))..))).))))))..)).)))))).))))...**********										
..........TAATTGTCAGCTGACCCTTCG..........	21	0	1	17.00	17	12	3	2	0	0
..........TAATTGTCAGCTGACCCTTCGG.........	22	0	1	7.00	7	0	5	1	1	0
..........AATTGTCAGCTGACCCTTCGGTT........	23	2	1	5.00	5	2	1	2	0	0
..........AATTGTCAGCTGACCCTTCGG..........	21	0	1	3.00	3	1	1	1	0	0
..........AATTGTCAGCTGACCCTTCGGC.........	22	0	1	3.00	3	1	1	0	1	0
..........TAATTGTCAGCTGACCCTTCGT.........	22	1	1	2.00	2	1	0	1	0	0
..........TAATTGTCAGCTGACCCTTCGGTT.......	24	2	1	2.00	2	1	0	1	0	0
..........AATTGTCAGCTGACCCTTCG...........	20	0	1	1.00	1	1	0	0	0	0
..........TAATTGTCAGCTGACCCTTCGGCTTT.....	26	3	1	1.00	1	0	0	1	0	0
..........TAATTGTCAGCTGACCCTTCT..........	21	1	1	1.00	1	1	0	0	0	0
..........TAATTGTCAGCTGACCCTTCA..........	21	1	1	1.00	1	1	0	0	0	0
..........GCAGGGGATGGCCGGCAAGTGT.........	22	1	1	1.00	1	1	0	0	0	0
..........AATTGTCAGCTGACCCTTCGGT.........	22	1	1	1.00	1	0	1	0	0	0
..........GCAGGGGATGGCCGGCAAGTG..........	21	0	1	1.00	1	1	0	0	0	0
..........AATTGTCAGCTGACCCTTCGGCT........	23	1	1	1.00	1	0	0	1	0	0

Anti-sense strand reads

GACGGAGTGGGCTAAGCGGGCCACGCAACTGGATGTTACGGATCAGGCCGATTAACAGTCGACTGGGAAGCCGCTCGACTGACGGCGTCCCCTACCGGCCGTTCACGAACCTGAACCCTTTGCCTGGGCTGTGGCGTGGCCTGTTGTTGTATAGCGCC	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_13417:2501486-2501643 -	dan_207	CTGCCTCACCCGATTCGCCCGGTGCGTTGACCTACAATGCCTAGTCCGGCTAATTGTCAGCTGACCCTTCGGCGAGCTGACTGCCGCAGGGGATGGCCGGCAAGTGCTTGGACTTGGGAAACGGACCCGACACCGCACCGGACAACAACATATCGCGG
droBip1	scf7180000395874:75808-75947 -		CTGGCTCACCAGGTTCACCCGGTGCGTTGACCTACAATGCTAAGTCCGGCTAATTGTCAGCTGACCCTTCGCCGAGCTGACTGCCGCAGGTGATTGCCGAAAAGTGCTTGGACTTGGGA----------CCGGACAGCAACACACAGCGG
droKik1	scf7180000302677:223154-223208 +		T----------CGGCGGATGCTCTCACCGGGGCATGGCCGGATTGGGATTGGGCTTGGGAAACG----------
droEle1	scf7180000490967:672227-672269 +		A----------GCTGACTGCCAGAAAGGCGGGCCAACAATGGTGGGATTTGG----------
droRho1	scf7180000779234:293650-293724 +		CT----------TCAGGGATGCCTTGAC----------CAGGGGAATGGCCGGATTGGCTTGGGTTTGGGCAACGAGG----------TGGCCCACATTGGAC-----
droBia1	scf7180000299728:248-278 +		G----------CTGCCTCTCCGCCGGGCTGGCTGCCGCAGG----------
droTak1	scf7180000415878:263138-263184 -		G----------ACTTGGAAAACGGAACCCACACCTGAACGGAAAACACCGGAT-GAGG
droWil2	scf2_1100000004958:376322-376367 +		A----------AGTATCAAGGGACCCCTGAACAAGTTGACTGGTGCAGAGGGTGAG----------

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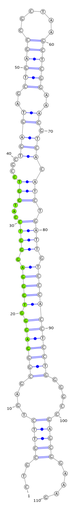
PASS/FAIL

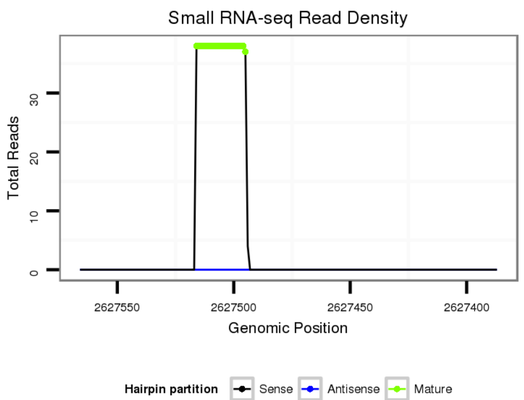
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

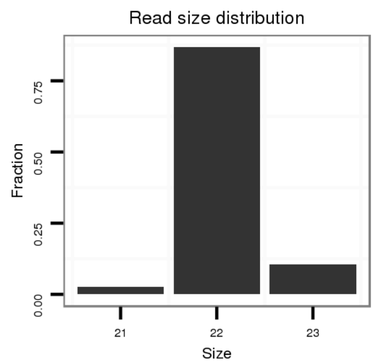
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_183	**scaffold_13417:2627437-2627516 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

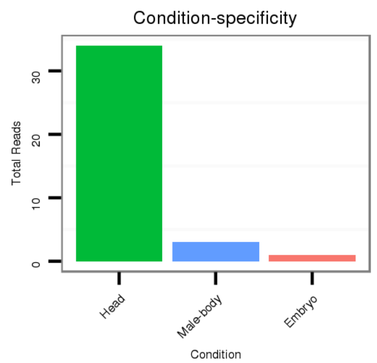
Legend: mature star mismatch in alignment mismatch in read

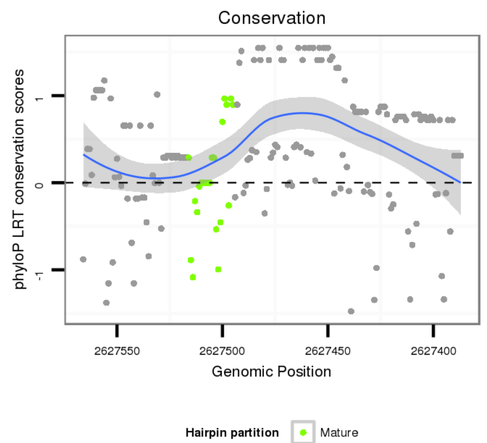
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AGCCCCTTTTTTCGGAGCTCCCCCGGGGAACGGAACTGCGTTCTGAGCGGGAGGGTGGGAGGGTCCATGGTCCGCTGAGTAGCTGAGCCGCTAAGCTCGGAAACGTCACATCTGATTGTCCCACCTCCTGGGGCCGAGCGGAAAGGACGATTAGGCGGAGGATGCACTGCCCTGCGATAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	M058 embryo	V055 head	M044 female body
**********...(((((....(((((((.(((((.((((...(((....(((((..(((((((.....))))))..))).))).))))).)))))))))))).....))))).....**********										
.....GAGGGTGGGAGGGTCCATGGTC.....	22	0	1	33.00	33	30	2	1	0	0
.....GAGGGTGGGAGGGTCCATGGTCC.....	23	0	1	4.00	4	4	0	0	0	0
.....GAGGGTGGGAGGGTCCATGGT.....	21	0	1	1.00	1	0	1	0	0	0
.....GAGGGTGGGAGGGTCCATGGTCA.....	23	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

TCGGGGAAAAAAGCCTCGAGGGGGCCCCTTGCCTTGACGCAAGACTCGCCCTCCCACCCTCCCAGGTACCAGGCGACTCATCGACTCGGCGATTCGAGCCTTTGCAGTGTAGACTAACAGGGTGGAGGACCCCGGCTCGCCTTTCCTGCTAATCCGCCTCCTACGTGACGGGACGCTATA	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head	M044 female body	V106 head	M058 embryo
**********...(((((....(((((((.(((((.((((...(((....(((((..(((((((.....))))))..))).))).))))).)))))))))))).....))))).....**********									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13417:2627387-2627566 -	dan_183	AGCC----------CCTTTTTTC------GGAGCTCCCCCGGGGAACGG----AACTGCGTTCTGAGCGGGAGGGTGGGAGGGTCCATGGTCCGCTGAGTAGCTGAGCCGCTAAGCTCGGAAACGTCACA-TCTGATTGTCCCACCT----CCTGGGG-CCGAGCGGAAAGGA----------CGATTAGGCGGAGGATG---CACTGCCCTGCGATAT
droBip1	scf7180000394954:57188-57361 +		AGCC----------CCTTTTTCC------GGAGCTCCCCTCGGGAACAG----AACTGCGTTCTGAGCGGGTTG------GGCACATGGTCCGGCTGAGTAGCTGAACCGCTAAGCTCGGAAAAGTCACA-TCTGATTGTCCCACCTC---TTGGGGCCCGAGCGGAAAGGA----------CGATTAGAAAGAGGATG---CACTGCTATGTGATAT
droKik1	scf7180000302685:486777-486880 +		GGCCT---CCTTTTTTTTTT----------GGAGTTCCTGTCAAGGGG-G---GACTG----------CAGATGCTCCGGCTGAGTCGCTGAGCGCCCAGCTCAGCGAAGTCAAA-ACTGATTGTCCCGC----------
droRho1	scf7180000761121:312603-312669 -		GGCC----------TCTTTTTAG-CTG--GGTGT----------GTCTCGGGTTGAAGCGATAAGCCTAGAAAAGTTACA-TCTGATTG----------
droBia1	scf7180000302069:1258934-1259055 -		GGTGT---CCTGTTTTTCTCTTTTAATATATACATATAGCCAGTAG--G-------CTG----------TAG-CCG--GTAGTC----------AGTAG-GCC----------GTCGTCGGGTTGAGAGCGATAAGCCTAGAAAAGTTACAAACTGATTGTCCCACC----------
droTak1	scf7180000415843:809843-809935 -		CTGT---CCTTTTTTTTTTTGT----------TAGCCAG----------TAGCCAGT---A----------GTCGTCGGGTTGAACCGATAAGCCTAGAAAAGTTACAAACTGATTGTCCCGTCGC----------
droEug1	scf7180000409109:113004-113107 -		AACCA----------ACCAAGTCCTGGTTGTCCCCAGAGCTCATGTCAGCGTGG---------- GTCCA----------AGC----------GTCTGGGGTTGAACCGATAAGCCTAGAAAAGTTACA-ACTGATTGTCCCGCCT----------
dm3	chrX:19329838-19329933 +		GGCC----------TCTTTTTCGGCTGCT---G----------GCC----------GTCTGGGGTTGAACCGATAAGCCAGCAAAAGTTACA-ACTGATTGTCCCGCCTGTATTTTGGGG-AGACA-CGAAA---
droSim2	x:18228604-18228748 +		GCCC----------TCTTTTTCGG----------CTGGGGTTGAACCGATAAGCCTGCAAAAGTTACA-ACTGATTGTCCCGCCTGTATTTTGGGG-AGAC--TGAAAGTGGAAGTTGAAATGTGGGAATCACGGGGAGATTAGGGAGCGGATGTGGCACAAAAGCGCG---
droSec2	scaffold_8:1621757-1621820 +		GGCC----------TCTTTTTCGG----------CTGGGGTTGAACCGATAAGCCTGCAAAAGTTACA-ACTGATTGTCCCGCCT----------
droYak3	X:11997858-11998054 -		AGCCTACATCCTAGAGACCACTTCCCACATGGCCACATGGCCACCACGTCCTGC---TCCCCAGAGCTCATGTCAGCGTGGGCCTCTTTTTCGGCTGGT---G----------GGC----------TGGTCGGCTTCTGGGTTGAACCGATAAGCCTGCAAAAGTTACA-ACTGATTGTCCCGCCTGTATTTTGGGG-AGAC--CGAAAGTAGGAGTAGAAGTG----------GAG----
droEre2	scaffold_4690:9578586-9578660 +		GGCC----------TCTTTTTCAGCTGGC---G----------GGC----------GTCAGGGTTGAACCGATAAGCCTGGAAAAGTTACA-ACTGATTGTACCGCCT----------

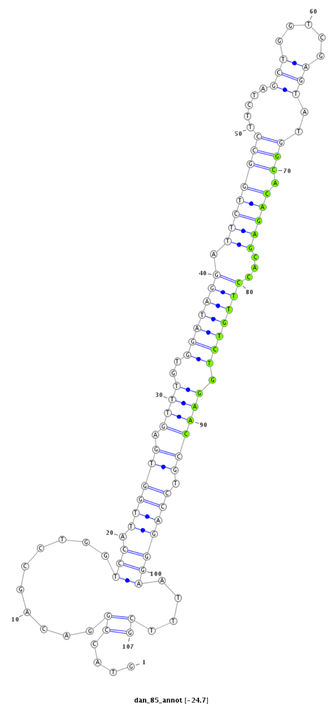
Generated: 09 Sep 2015 at 07:52 PM

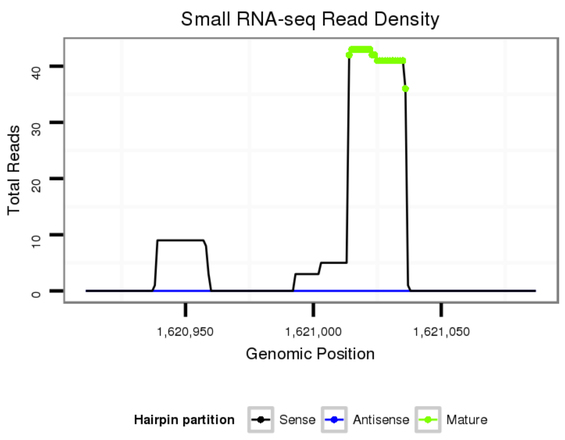
PASS/FAIL	
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

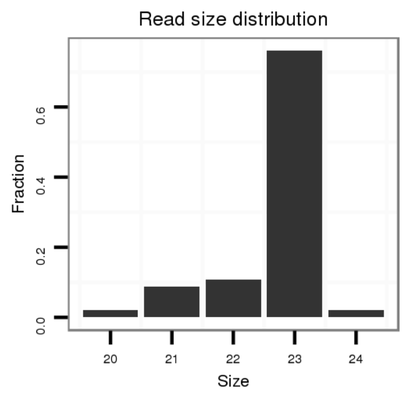
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_85	**scaffold_13417:1620961-1621037 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

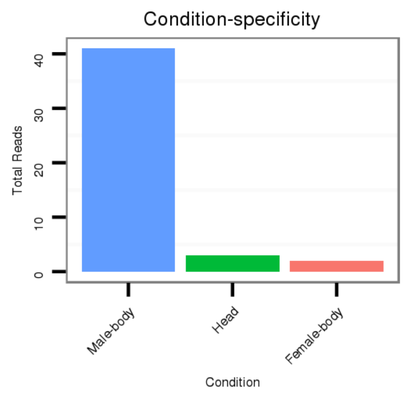
Legend: mature star mismatch in alignment mismatch in read

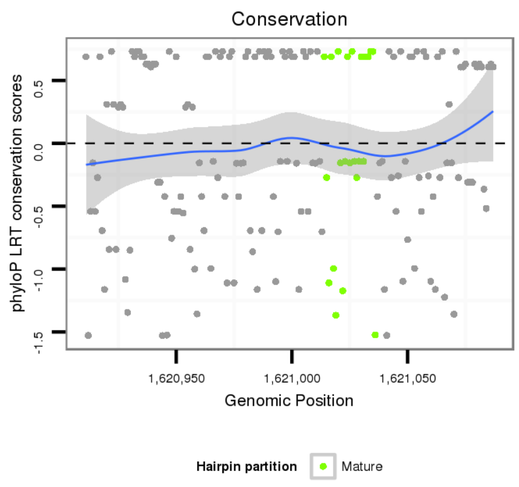
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CCCCCCCTGAGTTCCTGCCCACATGGATCTAAAGCGTACCGGACAGCCTGGTCCATTGGTGAGTTTGTGGATAGGATTCTGGCCTTCTAGCTGGTCGAGTATGGCACAGAGCACCTTGTCTGGAACCGTCCAGGGAATTTCGAAGGAGATGCGGAAGTGAAGCGAGGGAGTGTGGAG **********....((.........(((.(((((((.((((..(((((((.(((((((((.....(((.....))))..))))..))))))...)))))))..)))))))..)))))))....))**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	V055 head	V106 head	M044 female body	V039 embryo
.....GCACAGAGCACCTTGTCTGGAAC.....	23	0	1	35.00	35	31	1	1	2	0
.....CTAAAGCGTACCGGACAGCC.....	20	0	1	4.00	4	4	0	0	0	0
.....GCACAGAGCACCTTGTCTGGAA.....	22	0	1	4.00	4	3	1	0	0	0
.....CCTTCTAGCTGGTCGAGTATG.....	21	0	1	3.00	3	3	0	0	0	0
.....CTAAAGCGTACCGGACAGCCT.....	21	0	1	3.00	3	3	0	0	0	0
.....TCTAAAGCGTACCGGACAGCC.....	21	0	1	1.00	1	1	0	0	0	0
.....GCACAGAGCACCTTGTCTGGAACC.....	24	0	1	1.00	1	1	0	0	0	0
.....GGTCGAGTATGGCACAGAGC.....	20	0	1	1.00	1	1	0	0	0	0
.....GGTCGAGTATGGCACAGAGCAC.....	22	0	1	1.00	1	1	0	0	0	0
.....CACAGAGCACCTTGTCTGGAA.....	21	0	1	1.00	1	1	0	0	0	0
.....CTAAAGCGTACCGGACAGC.....	19	0	1	1.00	1	1	0	0	0	0
.....CTAAAGCGTACCGGACAGT.....	19	1	2	1.00	2	2	0	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13417:1620911-1621087 +	dan_85	CCCCCCCTGAGTTCCTGCCCACATGGATCTAAAG-----CGTACCG-----GACAGCCTGGTCCATTGGTGAGTTTGTGGATAG-GATTCTGGCCTTCTAGCTGGTCGAGTATGGCACAGAGCACCTTGTCTGGAACCGTCCAGGG---AATTTCGAAGGAGATGCGGAAGTGAAGCGAGGGAGT-GTGGA----------G
droBip1	scf7180000396805:6932-7095 +		C-GTGTCGCCCACATTTCTGAGAACATGG-------CTAAATCGTTCA-----GCAACAGAGCCCCTTGGTGTGTATGTGGACCGCCACTCTGGTTTTCTAGCTCATCAAGTATAGCTCCAGCACCTTGTCTGGAAGCGTGGAGACGAAACTACGCAGAAGACGCGGACGTGCAG----------------------
droTak1	scf7180000414450:137216-137405 +		CACTCACTG--T--------CACATGGATCTAGGT-----GATACCGTTCCACG----ACACTCCACTTGTCGGTCACAAGATCGGATTCTGCATCTCCAGCAGGTCGAAAACAGAGCACAAGGGTTCTCCGGAATGACCAATGG---CAACACGAATGAGCACCGTATA-AGATGGAAAAAGTTGATGAATGTCTGTGCCATATGGGGGG

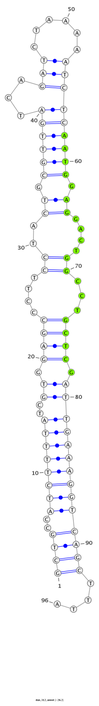
Generated: 09/08/2015 at 07:52 PM

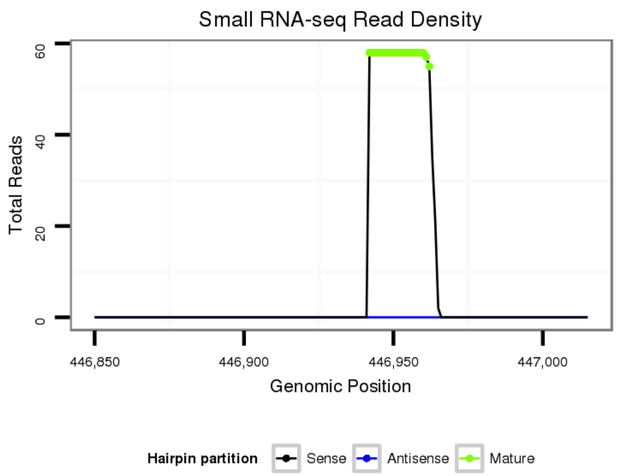
PASSFAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

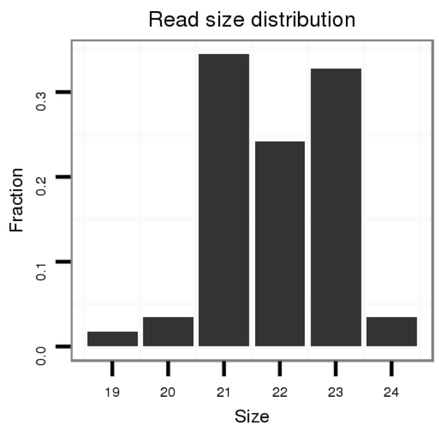
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_312	**scaffold_13258:446900-446965 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

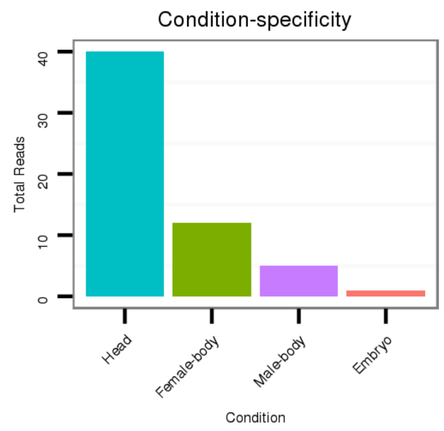
Legend: mature star mismatch in alignment mismatch in read

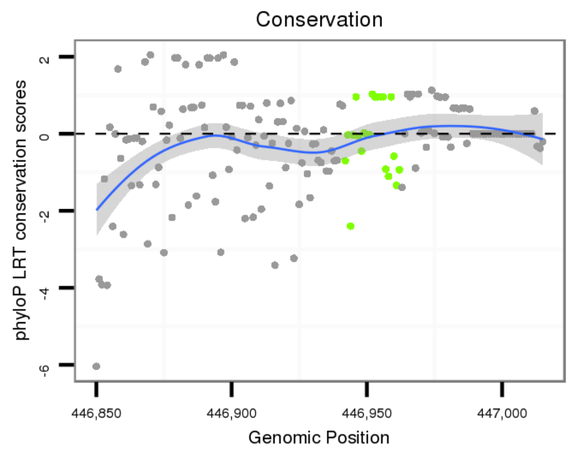
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

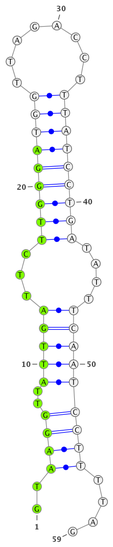
hide 3p reads | show mid mismatch reads

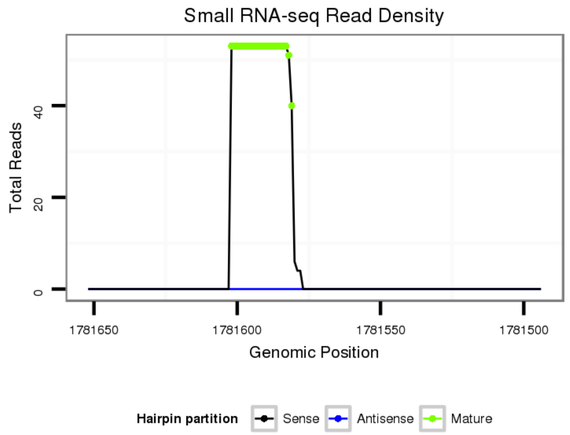
| | | |

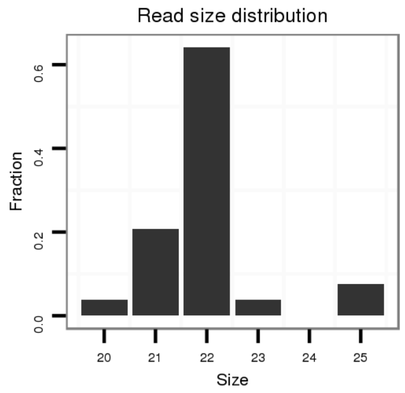
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_488	**scaffold_12916:1781544-1781602 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

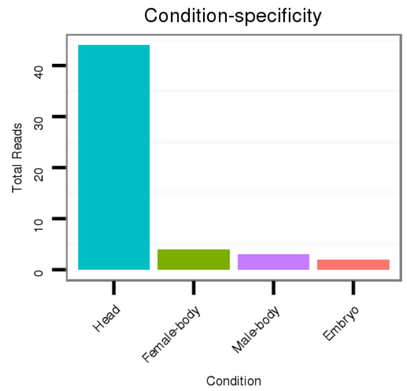
Legend: mature star mismatch in alignment mismatch in read

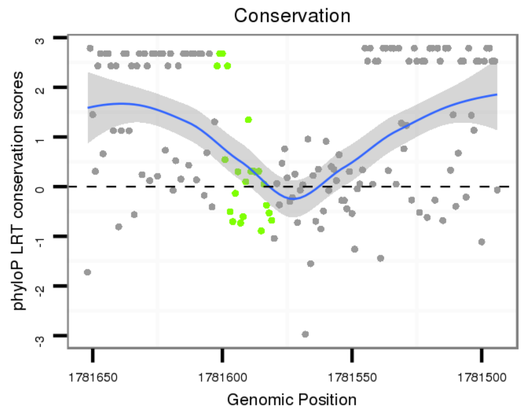
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF14871-in]; CDS [Dana\GF14871-cds]; CDS [Dana\GF14871-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTACGAGATGCGGCATCGGGAAACCTACTTTGAGCGGAACTTCAACCTAAGTAAGGTTATTGATTCTTGGGATGGTTAGACCTTTATCCTGATATTTCAATCCTTTTAGAGCGATTTATTTACGCCACCCCCTTCACGAAGAATGGCAAGGCACATGGC	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V055 head	V105 male body	M044 female body	M058 embryo	V039 embryo
**********..(((((..(((((...(((((((((.(.....).)))))))))....)))))))))....**********											
.....GTAAGGTTATTGATTCTTGGGA.....	22	0	1	34.00	34	22	6	3	2	1	0
.....GTAAGGTTATTGATTCTTGGG.....	21	0	1	11.00	11	9	1	0	0	0	1
.....GTAAGGTTATTGATTCTTGGGATGG.....	25	0	1	4.00	4	3	0	0	1	0	0
.....GTAAGGTTATTGATTCTTGGGAT.....	23	0	1	2.00	2	2	0	0	0	0	0
.....GTAAGGTTATTGATTCTTGG.....	20	0	1	2.00	2	1	0	0	1	0	0
.....GTAAGGTTATTGATTCTTGGGT.....	22	1	1	1.00	1	0	1	0	0	0	0
.....GTAAGGTTATTGATTCTTGGG.....	21	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

GATGCTCTACGCCGTAGCCCTTTGGATGAAACTCGCCTTGAAGTTGGATTCATTCCAATAACTAAGAACCCTACCAATCTGGAAATAGGACTATAAAGTTAGGAAAATCTCGCTAAATAAATGCGGTGGGGGAAGTGCTTCTTACCGTTCCGTGTACCG	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_12916:1781494-1781652 -	dan_488	CTACGAGATGCGGCATCGGGAAACCTACTTTGAGCGGAACTTCAACCTAAGTAAGGTTATTG--ATTCTTGGGATGG----------T----------TAG----------ACCTTT----------ATC--C----------TG-ATATTTCAATCCTTTTAGAGCGATTTATTTACGCCACCCCCTTCACGAAGAATGGCAAGGCACATGGC
droBip1	scf7180000396728:443914-444072 -		CTACGAATGCGGCATCGGGAAACCTACTTTGAGCGGAACTTCAAGATAAGTAAGCTTCCTA--ATTCTAATGGCGC----------A----------TTG----------ACCGTG----------ACC--C----------TG-GTGTTTCGAATCGTTTAGAGCGGTTCATCTATGCCACAGCCTTCACGAAGACTGGCAAGGCACATGGC
droKik1	scf7180000302807:11261-11424 +		GTACGAGATGCGTCATCGGGAAACATACTTTGAGAGAACTTCAAGATCAGTAAGCATTAGAT------TGCTCTT----------|----------|---------AATACGGTCTTAATTTAGCTACATATAA--|||--|----------TG-GT----TTTTTTTAAGAGACGGTTTATATATGGCACGCCTTCACGAAAAACGGAAAGGCCATGGC
droFic1	scf7180000454111:805494-805653 +		CTATGAAATGCGTCATCGTGAAACATACTTTGAACGGAATTTCAAGATAAGTAACAACTAGA--A----------|----------|----------TTAA------GATTTTATATTGCTC----------AAT--CTGA----------TTTTTGTTCGTTATTGTTAGAACGATTCATCTATGCAACGCCTTTACGAAAAATGGTAAGGCTCATGGC
droEle1	scf7180000490770:15064-15224 +		TTATTGAAATGCGTCATCGGGAAACATATTTGAGCGGAATTTTAAGATTAGTATGAACAGAA--|----------|----------TTGC------TAGATATGTGATAGTT----------A---|---|---------TTCTAACATG-TTATTTTTGTTACCTTAGAACGGTTTATATATGCAACACCTTCACGAAGAATGGTAGGGCACATGGC
droRho1	scf7180000779252:12924-13082 -		GTATTGAAATGCGGCATCGTGAAACATACTTTGAGCGGAATTTTAATATTAGTATTGAACTAAA--|----------|----------TTGA------TAGTTATTTGATGTGA----------ATT--CTGA----------TG-TTATTTTTTATAAATTTAGAACGATTTATATATGGCAACGCCTTCACGAAAAGTGGTTAGGGCACATGGC
droBia1	scf7180000301455:109418-109580 +		CTATGAAATGCGACATCGTGAAACATACTTTGAGCGGAATTTCAATATAAGTATTGAACTGGA--A-----TATTATTTC----------|----------AA----------|---|----------AGTGGTTA----------AGTTTCACA----------AGGTA-TTTTTTTTTATAATTTAGAACGATTTATATATGGCAACGCCCTTTACGAAAAATGGTAAGGCTCATGGA
droTak1	scf7180000413017:460520-460686 -		TTATTGAAATGCGGCATCGTGAAACATACTTTGAGCGGAATTTCAATTTAAGTATTGAATTTGA--A-----TGTTACTTT----------|----------AAAGGAAT----------|---|----------C----------GTGTTC----------AGTCTGACA----------A--TC-ATTTTTTTTATAATATAGAGCGATTTATATACGGAACGCCTTCACGAAAAATGGTAAGGCACATGGC
droEug1	scf7180000409154:93752-93910 +		ATATTGAAATGCGGCATCGTGAAACATATTTCGAACGGAATTTTAATATAAGTATTGAACTGGA--|----------|----------TTAA------CATTTGTATAGTTTTG----------GTT--CTGA----------AG-TTTGTTTTTTTTAATTTAGAGCGATTTATATATGGCAACTGCTTTACAAAAAGTGGTTAAGGCACATGGC
dm3	chr2L:100893-101065 +		ATATTGAAATGCGTCATCGTGAGACATACTTTGAGCGGAATTTCAAGTATAAGTATTGATATGAA--|----------|----------TTAAA-----CAGATAATTT------|------AAATCGA---AAT--TTAAAATTATAATTTTAACATTT-TT---TGGTTTATGGCAGAACGGTTTATATATGCCACGCCTTTACTAAAATGGAAAGGCACATGGC
droSim2	2l:87055-87227 +		ATATTGAAATGCGTCATCGTGAGACATACTTTGAGCGGAATTTCAAGTAAGTATTGAGATGAA--|----------|----------TTAAA-----CAGATAATTG------|------AAATCGA---AAT--TTAAAATTAAAATTTTAACATT-TT---TGTTTTATGGCAGAACGGTTTATATATGCCACGCCTTTACCAAAATGGAAAGGCCATGGC
droSec2	scaffold_14:100166-100338 +		ATATTGAAATGCGTCATCGTGAGACATACTTTGAGCGGAATTTCAAGTAAGTATTGAGATGAA--|----------|----------TTAAA-----CAGATAATTG------|------AAATTGA---AAT--TTAAAATTAAAATTTTAACATT-TT---TGTTTTATGGCAGAACGGTTTATATATGCCACGCCTTTACCAAAATGGAAAGGCCATGGC
droYak3	2L:90239-90411 +		ATATTGAAATGCGTCATCGTGAGACATACTTCGAGCGGAATTTCAATATAAGTATTGAGATGAA--|----------|----------TTACA-----AATTTAATTG------|------AAACCGA---AAA--TTAAAATTATAATTTAAACATT-TT---TTGTTTATGGCAGAACGGTTTATATATGCCACGCCTTTACCAAAATGGTAAGGCCCATGGA
droEre2	scaffold_4929:128932-129104 +	der_1234	ATATTGAAATGCGTCATCGTGAGACATACTTTGAACGGAATTTCAATATAAGTATTGAGATGAA--|----------|----------TTACA-----AATTTAATTG------|------AAATCGA---AAA--CTAAAATTATTATTTAAACATT-TT---TGTATTATGGCAGAACGGTTTATATATGCCACGCCTTTACCAAAATGGTAAGGCCCATGGC
dp5	4_group2:26888-27048 -		ATATTGAAATGCGTCATCGGAAACCTACTTTGAGAGGAACTTAAGATTAGTACTGTTTATT-------TGTATTT----------|----------ATAGCATT----------|---|----------TA----------|----TATTATATTAACACCTATTG----|ATC----------|--|---------AAATTTAGAACGTTTATATATGCCACACCTTTACAAAAAGTGGTAAGGCCCATGGA
droPer2	scaffold_8:3868768-3868928 +		ATATTGAAATGCGTCATCGCGAAACCTACTTTGAGAGGAACTTAAGATTAGTACGTGTTTATT-------TGTATTT----------|----------ATAGCATT----------|---|----------TA----------|----TATTATATTAACACCTATTG----|ATC----------|--|---------AAATTTAGAACGTTTATATATGCCACACCTTTACAAAAAGTGGTAAGGCCCATGGA
droWil2	scf2_1100000004851:60636-60806 -		CTATTGAAATGAGAATCGTGAGACATATATTTGAGCGTAATTTAATATCCGTAAGACTTTAT--|----------|----------CCCAAGTAATTAAATTTACTTA------|------AAAACTA---ATT--CTAAAATTCGC----------|--|--ATATTCATACTTCCAGAACGTTCATATTTGGCACACCTTCACTAAGACTGGCAAAGCTCATGGT
droVir3	scaffold_13246:88050-88127 -		TTTA----------|----------|----TC----------|---|----TA----------|-----|----------|---|-|----------TTTCATACTTTTTCCCTTAGAACGTTTTATTATTGCAACACCTTCACTAAAGGCGGAAAAGGTCATGGA
droMoj3	scaffold_6500:141847-142038 -		CTATTGAAATGCGTCATCGTGAAACTTACTTTGAACGAAATTTTAATATAAGTAACCGATTTATT-------AAGAATG----------A--GCATGTATATATGCCATGTAGAGTTGA------ACGTAATCCAATGTAT----------|---|-|-----ATATATATATAT--||--ATTTTTTTTTTATTAGAACGATTTATATTTTGAACGCCGTTCACTAAAAGCGGAAAAGCTCATGGA
droGri2	scaffold_15252:17144114-17144304 +		CTATTGAAATGCGTCATAGAGAGACTTACTTTGAACGAAATTTTAATATTAGTAACTAATTCCAAA-----TATTTTTCTCGACAAGCCCAACTATAAAACAACCAAAAAA----------|----------AATGTCA----------AT--AAT--TTCC----------CG-TTATCTTTTTCCATTAGAGCGTTTATTTTTGGAACACCTTTACAAAAAGCGGAAAAGGTCATGGA

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

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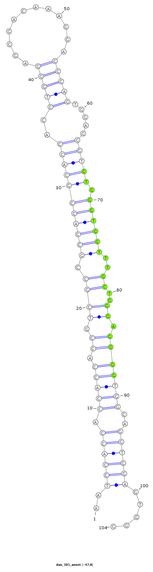
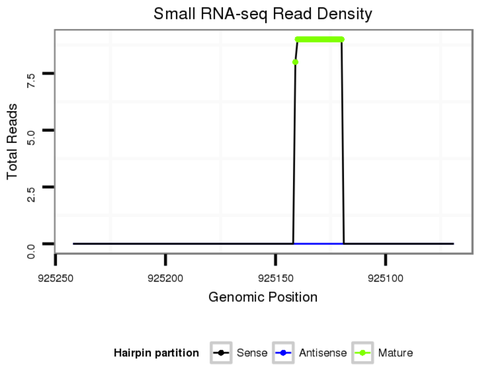
rescue.known	0
rescue.confident	0
rescue.candidate	1

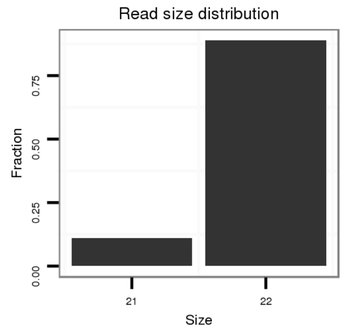
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_305	**scaffold_13340:925119-925192 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

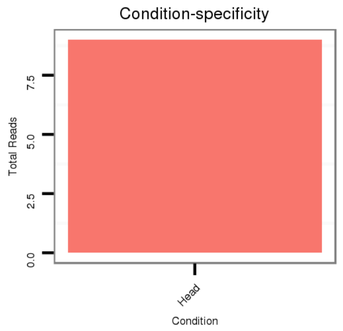
Legend: mature star mismatch in alignment mismatch in read

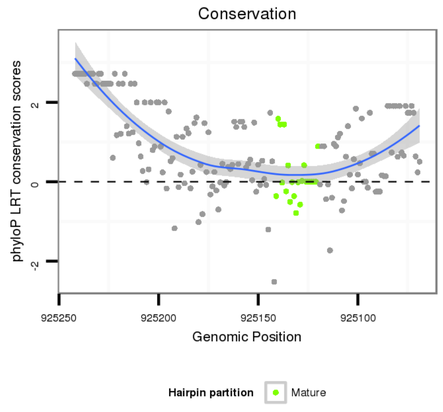
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TAATTTCATAGCAACGCCCTAGCGGAAGCAGCAGAAATCCACCACCACCACCGTCGCCGCCACCGCACCACCTGGGAGCGACAAAGGACCCAGTGGAGGGTGTGGGTGGTTTGCTGGGAGGGGGTGGCAGGTGGAGTGGGCGACCAAACGCCTCCCTATTATTGAAGACCTGCTC	Read size	# Mismatch	Hit Count	Total Norm	Total	female body	V106 head	V105 male body	V055 head	V039 embryo	M058 embryo
**********..(((((((.(((((.((.((((.(((((((((((..(((((.....))))).....)))))..)))))).))))))..))..))..)))))))..)))))))).....**********											
..... GTGGGTGGTTTGCTGGGAGGGG	22	0	1	8.00	8	0	8	0	0	0	0
..... TGGGTGGTTTGCTGGGAGGGG	21	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

ATTAAAGTATCGTTGCGGGATCGCCTTCGTCGTCTTTAGGTGGTGGTGGCAGCGGCGGTGGCGTGGTGGACCCTCGCTGTTTCCTGGGTCACCTCCCACACCCACCAAACGACCCTCCCCACCGTCCACCTCACCCGCTGGTTTGCGGAGGGATAATAACTTCTGGACGAG	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M058 embryo	M044 female body
**********..(((((((.(((((.((.((((.(((((((((((..(((((.....))))).....)))))..)))))).))))))..))..))..)))))))..)))))))).....**********								

Show Alignment With Reads

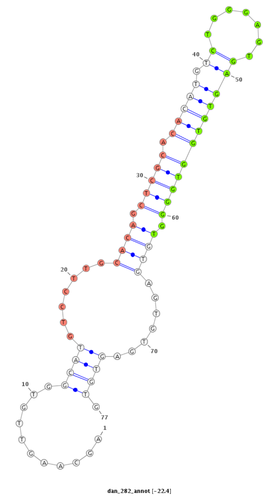
Re-alignment of all predicted orthologs

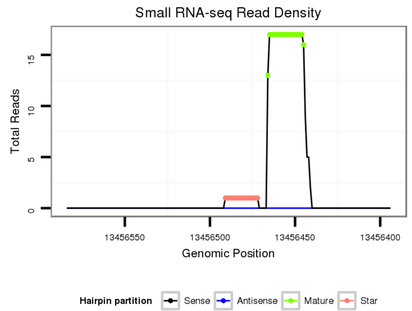
Species	Coordinate	ID	Alignment
droAna3	scaffold_13340:925069-925242 -	dan_305	TAATTTCATAGCAACGCCCTAGCGGAAGCAGCAGAAATCCACCA---CCAC--CA--------CCGTCGC---CGCCAC-CGC----------ACCACCTG---GGAGCGACAAAGGA----------CCCA-----GTGGAG----------GG----------T------GTGGGTG--------GTTTGCTGGGAGGGGTGGCAGGTGGAGTG---G-----GCGACCAAACGC---C-TCCCTATTATTGAA--------GACCTGCTC
droBip1	scf7180000394085:72007-72152 +		TAATTTCATAGCAACGCCCTAGCGGAAGCAGCAGAAATCACCA---CC--------------AC---CGCCAC-CGC----------ACCACCTG---GGAGCGACAAAGGA----------CCCA-----GTGGAA----------GGGGGA-GGC----------AGGTGGATGGGCG--------GCGAACG----------------------------GCCAC---CGATTATTGAA--------GACCTGCTC
droKik1	scf7180000302475:1385327-1385497 -		TAATTTCATAGCAACGCCCAGCGGAAGCAGCG-AAG-CCACCA---CGTCCA-----GC---CGCCAT-TGC----------ACACCGCGG----------GGGTGGGGATAACAAGGGCTGGGGAGAGGG----------AGTGAC-GTGTGTG-TTTGC-CACAC-AATG----------------------G-----GGATAG--TGTTGCT---TCCTTATTAAAGAAGACCAAGACCTGCTC
droFic1	scf7180000453800:2278545-2278721 -		TAATTTCATAGCAACGCCCAGCGGAAGCAGCAAAG-CCACCA---CCCC--------------T---GGCGCACAAAGGA----------TCCA-----TGGGGTGGAAGGAAGCGGCGGTGGT---GGTG---GTGGTGGAGTGGGAGTAGGATGGAAAGTGGGTGTGGGTG--------GTTGCGCTG----------------------G-----ATGATAG--TGTTGAT---TCCTTATTGAA--------TACCTGCGC
droEle1	scf7180000491080:31580-31749 +		TAATTTCATAGCAACGCCCAGCGGAAGCAGCAAAT-CCACCA---CCAGAGCA--------GCAGCAC-------GA---GCGCACACAAAGGA----------TCCA-----TGGAAA---G-----GGGATGAGGATGGGTGGGTCT-GGG----------ACTGGGATGTGGCG--------GTTGCAAA----------------------GAT--GATGATAG--CGTTGAT---TCCTTGTTGAA--------TACCTGTTC
droBia1	scf7180000302402:8286997-8287181 -		TAATTTCATAGCAACGCCCAGCGGAAGCAGCAGAG-CCACCA---CCAGAGCAGCAGAGGCAG-AC-AC---CACCAA-CAGCACCACCC-CACCACGC--GAGGCGGAACAAAGGA----------TCCA-----TGTC-----------CATAGCA---------GGGGGAAG-----------------------GCGGCGCTGGA-C--G---AT--GATTATAG--TGTTGAT---TCCTTATTGAA--------TACCTGCGC
droTak1	scf7180000415380:1442766-1442917 +		TAATTTCATAGCAACGCCCAGCGGAAGCAGCAAAG-CCACCA---CCAGG--------------T---GGCGCACAAAGGA----------TCCGGATCCTTGGGA-----------------------TGGGGGA-AGG----------TGCCGCATGGGCG--------GTTGCGCTG----------GAT--G---ATGCTGATGATAG--TGTTGAT---TCCTTATTGAA--------TACCTGCTC
droEug1	scf7180000409881:463700-463877 +		TAATTTCATAGCAACGCCCAGCGGAAGCAGCAGAG-CCACCA---CCAGAGTGACAGG---AGCAGCAC---CACCAA-CAC----------ACAATCAG---GGGCGCACGAAGGA----------TG--------GC---GTAGA-G-ATGG----------CGTAGGATGGGCG--------TCTTTGCTG----------GAT--G---ATGATGACGATAG--TGTTGAT---TCCTTATTGAA--------TACCTGCTC
dm3	chr3R:6198982-6199167 -		TAATTTCATAGCAACGCCCAGCGGAAGCTGCACAAG-CCACCA---CCAGAGCA--------CCGCGCAC---CAC-CACACCACCACCGC-------A---GCACACACAAAGGA----------TCCA-----TGGGAG----------AGGGGGACCAT----TGGG----ATAGGGGAATGG----------AGTGGGATTGACG--------CTCGCGTG----------------------G-----ATGATAG--TGTTGAT---TCCTTATTGAA--------TACCTGCTC
droSim2	3r:14876512-14876703 +		TAATTTCATAGCAACGCCCAGCGGAAGCAGCAAAG-CCACCA---CCAGAGCA--------CCAGCAC-CAC-CACACCACCATCCGC-------A---GCACACACAAAGGA----------TCCA-----TGCGAG----------GCGGGGGGCCAT----TGGG----ATAGGGGAATGG----------AGTGGGATTGACG--------CTCGCGTG----------------------G-----ATGATAG--TGTTGAT---TCCTTATTGAA--------TACCTGCTC
droSec2	scaffold_0:15742965-15743156 +		TAATTTCATAGCAACGCCCAGCGGAAGCAGCAAAG-CCACCA---CCAGAGCA--------CCAGCAC-CAC-CACACCACCATCCGC-------A---GCACACACAAAGGA----------TCCA-----TGCGAG----------GCGGGGGGCCAT----TGGG----ATAGGGGAACGG----------GGTGGGATTGACG--------CTCGCGTG----------------------G-----ATGATAG--TGTTGAT---TCCTTATTGAA--------TACCTGCTC
droYak3	3R:10226752-10226942 -		TAATTTCATAGCAACGCCCAGCGGAAGCAGCAAAG-CCACCA---CCAGAGCA--------GCAGCAC---CACCAC-CGCACCACCACCGC-------A---CGACACACAAAGGA----------TCCT-----TGGGAG----------G-----GGGATGGGC---GGATAGGGGA-GGG----------AGTGGGATGGGCT-TTAGCCCGCTCGCGTG----------------------G-----ATGATAG--TGTTGAT---TCCTTATTGAA--------TACCTGCTC
droEre2	scaffold_4770:15417961-15418135 +		TAATTTCATAGCAACGCCCAGCGGAAGCAGCAAAG-CCACCA---CCAGCGCACCAC---ACCAGCAC-CAC-CACACCACCACCAC-------A---CCACACACAAAAGAC---------TCCT-----TGGAG----------GG----------GGTGGGATTGGCC-C-----CGC-CGCGTG----------------------G-----ATGACG--TGTTGAT---TCCTTATTGAA--------TACCTGCTC
dp5	2:7267625-7267788 +		TAATTTCATAGCAACGCCCAGCGGAAGCAGCAC----CCACCACCAGC---C---------------GAG-CGC----------TGGGGAGGGAT-----------GGGGCGGTGGGTGGTGGGGCAGGCAACAAAAGATTGC----TGGGGG----------G----------G-----------------------GCGGGAGTGGAGGCGCGG-----ATGATAG--GGTTGATGCTTGCTTATTGAG--------GACCTGCTG
droPer2	scaffold_0:1128420-1128582 +		TAATTTCATAGCAACGCCCAGCGGAAGCAGCAC----CCACCACCAGC---C---------------GAG-CGC----------ACGGGAGGGGAT-----------GGGGTGG-GGGTGGTGGGGGTAGGCAACAAAAGATTGC----TGGGGG----------GG----------G-----------------------GCGGGGTGTGGAG--GCGG-----ATGATAG--GGTTGATGCTTGCTTATTGAG--------GACCTGCTG
droWil2	scf2_1100000004902:107225-107275 +		TAATTTCATAGCAACGCCCTAGCGGAAACTGCACAAAGCGCGC---TCGAGCA--------C------------------------

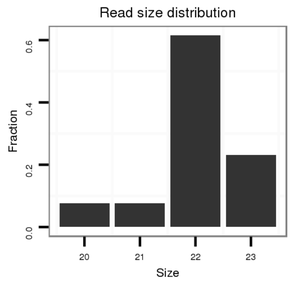
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_282	**scaffold_13266:13456444-13456534 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

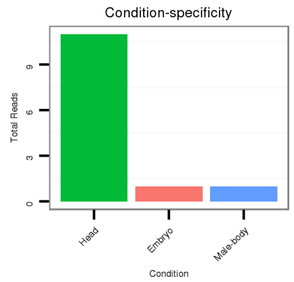
Legend: mature star mismatch in alignment mismatch in read

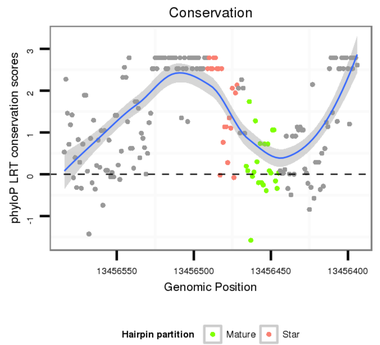
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dana\GF11449-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

						V106	V055	V105	V039	M058
GCAACTCCTCCAACCAGCCACCCAGTCAACCAGCCAGCAGGATATTTCTCCCACCAGCACTTAATGCATTATGCAACAGCAAGTTGTGGCATGTCCTTGCACAGCTCGCACATGTCTGGGAGTGAGTGTGGTGGGGTGTGAGTGTGAGTGTGCTTCTTGGGGGCTGAGCCATTTCGCAGTTGCTGAAA	Read size	# Mismatch	Hit Count	Total Norm	Total	head	head	male body	embryo	embryo
..........((((.....((((.(((((.(((((.((.....)))))))))))).)))).....)))).**********										
.....CTGGGAGTGAGTGTGGTGGGGT.....	22	0	1	7.00	7	6	1	0	0	0
.....CTGGGAGTGAGTGTGGTGGGGTG.....	23	0	1	3.00	3	2	0	1	0	0
.....CTGGGAGTGAGTGTGGTGGGGTGA.	25	1	1	2.00	2	1	1	0	0	0
.....TGGGAGTGAGTGTGGTGGGGTGTG.....	24	0	1	2.00	2	2	0	0	0	0
.....CTGGGAGTGAGTGTGGTGGGGTGTGA.....	26	0	1	1.00	1	1	0	0	0	0
.....TGGGAGTGAGTGTGGTGGGGTG.....	22	0	1	1.00	1	1	0	0	0	0
.....GTCCTTGCACAGCTCGCACA.....	20	0	1	1.00	1	0	0	0	1	0
.....TGGGAGTGAGTGTGGTGGGGTGTGA.....	26	2	1	1.00	1	1	0	0	0	0
.....TGGGAGTGAGTGTGGTGGGGTGTGA.....	25	0	1	1.00	1	1	0	0	0	0
.....CTGGGAGTGAGTGTGGTGGGG.....	21	0	1	1.00	1	1	0	0	0	0
.....CTGGGAGTGAGTGTGGTGGGGTGTG.....	25	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

						M044 female body	M058 embryo	V055 head	V039 embryo
CGTTGAGGAGGTTGGTCGGTGGGTCAGTTGGTCGGTCAGTCCTATAAAGAGGGTGGTCGTGAATTACGTAATACGTTGTCGTTCAACACCGTACAGGAACGTGTCGAGCGTGTGTACAGACCCTCACTCACACCACCCACACTCACACTCACACGAAGAACCCCCGACTCGGTAAAGCGTCAACGACTTT	Read size	# Mismatch	Hit Count	Total Norm	Total				
..........((((.....((((.(((((.((.....)))))))))))).)))).**********										

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13266:13456394-13456584 -	dan_282	GCAACTCC----------TCCAACCAG-----CCACCCAGTCAACCAGCCAG----------TCAGGATATTTCTCCCACCAGCACTTAATGCATTATGCAACAGCAAGTTGTGGCATGTCCTTGCACAGC----------T--------CGCAC----------A----------CATGTCTGGGAGTGAGTGTGGTGGGGTG----------TGAGTGTGAG----------TGTGCT----------TC----------T-----TGGGGGCT---GAGCCATTTCG-----CAGTTGCTGAAA
droBip1	scf7180000396759:2680733-2680914 +		GCAACTCC----------TCAACCAAGCCAGCCAGCAACCAGCCAG----------TCAGGATATTTCTCCCACCAGCACTTAATGCATTATGCAACAGCAAGTTGTGGCATGTCCTTGCACAGC----------T--------C-----G-----GCAC----------CATGCTC----CTTGCGTGCA----------A----------A----------A-----AGTG----------CGAGT----------GTGAGTAGGGGGGTT---GAACCATTTCG-----CAGTTGCTGAAA
droKik1	scf7180000302476:3043925-3044057 -		GCAACTCC----------TCACCAG----------G----------CAGGATATTTCTCCCACCAGCACTTAATGCATTATGCAACAGCAAGTTGTGGCATGTCCTTGCACA----------TGCTC--------CAC----------A-TC----------A----------CATGTTGTC----------A----------A----------A-----A----------A--PA--GT---GTGCCATTTCG-----CAGTTGCTGAAA
droFic1	scf7180000453948:2282657-2282808 -		GCAACTTGC---G---ATTCCG-CG---G----------GG----------CAGGATACTTCCCCACCAGCACTTAATGCATTATGCAACAGCAAGTTGTGGCATGTCCTTGCACA----------TAGTC--------CACA----------CAC----------CATACT--TGCATGTGT----------A----------A----------A-----A----------A----------TGTTCGC---G---GTGCCATTTCG-----CAGTTGCTGAAA
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droBia1	scf7180000301754:5416910-5417065 +		GCAACTCC----------CG-TGCG-----G----------A----------CAGGATCGCTTCGCCCACCAGCACTTAATGCATTATGCAACAGCAAGTTGTGGCATGTCCTTGCCA----------TAGTC--------CACA----------CATC----------N----------CATGTGCGGGGTGT----------A----------A----------A-----A----------A----------GCGGGGTGTGCGGGTGTAC---GA---GTGCCATTTCG-----CAGTTGCTGAAA
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droEug1	scf7180000409672:1953383-1953556 -		GCAACTCC----------CGGTGCGT----CCACCAA-----TGCCA----------CAGGATATTTCTCCCACCAGCACTTAATGCATTATGCAACAGCAAGTTGTGGCATGTCCTTGCACA----------TAGAGCACATAGCCACAC---CGAACACAAGC----------A----------CCAATCA-CATGTGTGC----------A----------A----------A-----TGTC----------CCA----------A----------A-----CGCCATTTCG-----CAGTTGCTGAAA
dm3	chr2R:13168705-13168876 +		GCAACTCC----------CG-TGCG-----G----------A----------CAGGATATTTCTCCCACCAGCACTTAATGCATTATGCAACAGCAAGTTGTGGCATGTCCTTGCCA----------TGGTC--------CACAC-CACACTCAAGTC----------A----------CATGTGTGC----------A----------A----------A-----ACTA----------CGATGTGCGAGTGAAGTGGGGTTCA---GT---GGCCATTTCG-----CAGTTGCTGAAA
droSim2	2r:13820967-13821121 +		GCAACTCC----------CG-TGCG-----G----------A----------CAGGATATTTCTCCCACCAGCACTTAATGCATTATGCAACAGCAAGTTGTGGCATGTCCTTGCCA----------TGGTC--------CACAC-----CAAGTC----------A----------CATGTGTGC----------A----------A----------A-----ACTC----------CGATC----------TGCGTTCA---GT---GGCCATTTCG-----CAGTTGCTGAAA
droSec2	scaffold_1:10670088-10670242 +		GCAACTCC----------CG-TGCG-----G----------A----------CAGGATATTTCTCCCACCAGCACTTAATGCATTATGCAACAGCAAGTTGTGGCATGTCCTTGCCA----------TGGTC--------CACAC-----CAAGTC----------A----------CATGTGTGC----------A----------A----------A-----ACTA----------CGATC----------TGCGTTCA---GT---GGCCATTTCG-----CAGTTGCTGAAA
droYak3	2R:18304912-18305099 -		ACAACTCC----------CG-TGCG-----G----------CCA----------CAGGATATTTCTCCCACCAGCACTTAATGCATTATGCAACAGCAAGTTGTGGCATGTCCTTGCCA----------TGGTC--------CACAC-CAAACTCAAGTC----------A----------CATGTGTGCC----------A----------A----------A-----ACTGCCACTGCCACTGCGATGCGAGCGAGTTTGAGTTCA---GT---GGCCATTTCG-----CAGTTGCTGAAA
droEre2	scaffold_4845:12686784-12686955 -		GCAACTCC----------CG-TGCG-----G----------A----------CAGGATATTTCTCCCACCAGCACTTAATGCATTATGCAACAGCAAGTTGTGGCATGTCCTTGCCA----------TGGTC--------CACAC-CAAACTCAAGTC----------A----------CATGTGTGCC----------A----------A----------A-----ACTG----------CGATGCGAGCGGGTTTGAGTTCA---GT---GGCCATTTCG-----CAGTTGCTGAAA
dp5	3:16734653-16734796 +		GCAAGCGA-C----------GG-TGCG-----G----------A----------CCTCG---ACTTCGAGGA----------TTGCCAGCACTTAATGCATTATGCAACAGCAAGTTGTGGCATGTCCTTGCACA----------TGGTC--------CAGC----------A----------CATGTCTTGTGTC----------A----------A----------A-----A----------A----GTGTGTGTTGTGTGTGCTC---GGCGGCAGCCATTTCG-----CAGTTGCTGAA
droPer2	scaffold_4:35352-35491 -		GCAAGCGA-C----------GG-TGCG-----G----------A----------CCTCG---ACTTCGAGGA----------TTGCCAGCACTTAATGCATTATGCAACAGCAAGTTGTGGCATGTCCTTGCACA----------TGGTC--------CAGC----------A----------CATGTCTTGTGTC----------A----------A----------A-----A----------A----GTGTGTGTTGTGT----GTGCTC---GGTGGAGCCATTTCG-----CAGTTGCTGAAA
droWil2	scf2_1100000004822:639228-639419 +		GCAACTCGCTTACGG---CGTCGG-G---TATTGGTCGGCGACCAGCGAACCCCTTTGCTGGCTTCTTC-AGCGTCAC----GA----------TCCAGCACTTAATGCATTATGCAACAGCAAGTTGTGGCATGTCCTTGCACT----------CGCTA--------CAC----ACAGTCTC-ATTCTTGCCTGGCACACA----------A----------CATGTGC----------A----------A----------A-----A----------A----------AGCATTTCG-----CAGTTGCTGAAA
droVir3	scaffold_12875:7864094-7864274 +		A-ACGTGGT---TGTCA---------G----------GGAGACGCCCGCAGAA-------G-TCCAGCACTTAATGCATTATGCA-CAGCAAGTTGTGGCATGTCCTTGCCAGC-AGAAGTAAGTACTGTGC----------G-A----------A----------CTGCAA-CAGAAGAGGAGAAGTCGTAACGGACAGAACACAAGTGCA----------A----------A----------A-----A----------A----GTGTGAGCATTTCG-----CAGTTGCTGAAA
droMoj3	scaffold_6496:19436426-19436618 -		GCAGGTT----GTCA---------G----------GGAGGCGCCCGCAGGA-------G-TCCAGCACTTAATGCATTATGCA-CAGCAAGTTGTGGCATGTCCTTGCGTGC-AAATGTAAGTACTCTGCGAGGCGAAGCAGAGGCAACGGCAATGGCC----------AGC----------A----------A----------A-----A----------A----------AGGAGTA----------TCG-CATGCGC---CCACACAAGTGCA----------A----------A----------A-----A----------A----GTGCAGCATTTCG-----CAGTTGCTGAAA
droGri2	scaffold_15245:1363284-1363450 +		ACACGTGGT---TGTCA---------G----------GGA---GCCCGCAGGA-------G-TCCAGCACTTAATGCATTATGCA-CAGCAAGTTGTGGCATGTCCTTGCCAGCCAAAAGTATGTACA----------A----------A----------A----------CAAAGGAGGAGGCAAG----------CTG-------CTGCACACAAGTGCAAGT----------A----------A----------A-----A----------A----CGCCATGTTCG-----CAGTTGCTGAAA

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

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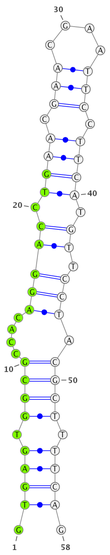
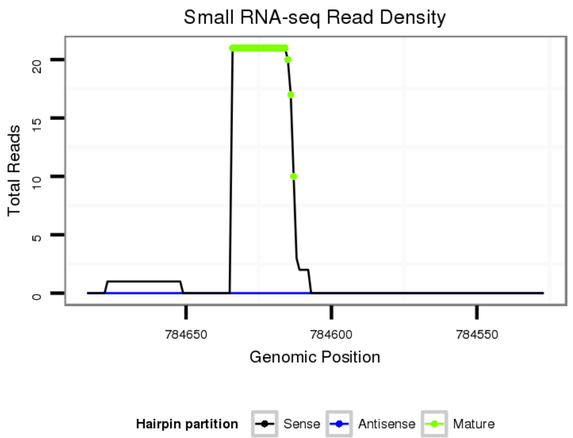
rescue.known	0
rescue.confident	0
rescue.candidate	1

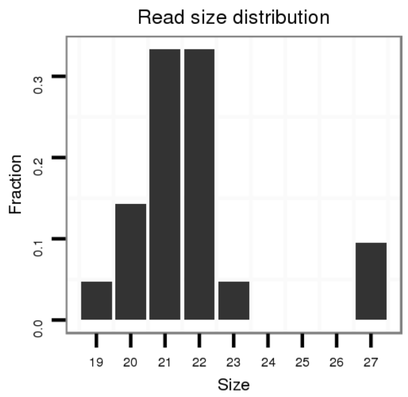
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_1288	**scaffold_13117:784577-784634 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

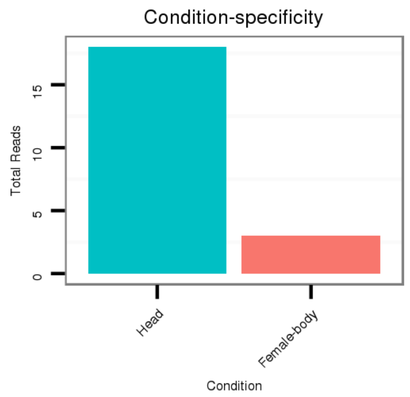
Legend: mature star mismatch in alignment mismatch in read

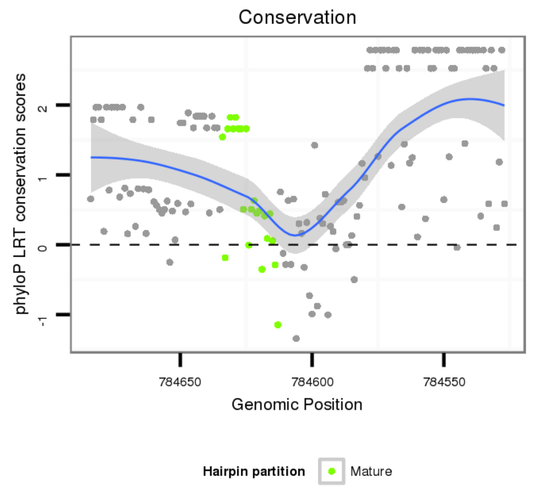
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF21092-in]; CDS [Dana\GF21092-cds]; CDS [Dana\GF21092-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GGATCGATATAGAACAGATTACAGGCGCGTGTCTATGTGCATATCCTGCGGTGAGTGGCGCCACAGGACCTGAACGAACGAATTCCTTCATGTTCCTACGCTTTTCAGTGATGAGATCGAGACTATTTTGGATACTGGCTATTATATACTCCTCACTC **********.((((.((((.....((((((.((((.(((....))).))))).)).))))..))))).))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	V055 head	M058 embryo	V105 male body
.....GTGAGTGGCGCCACAGGACCTG.....	22	0	1	7.00	7	7	0	0	0	0
.....GTGAGTGGCGCCACAGGACCT.....	21	0	1	7.00	7	5	2	0	0	0
.....GTGAGTGGCGCCACAGGACC.....	20	0	1	3.00	3	2	1	0	0	0
.....GTGAGTGGCGCCACAGGACCTGAACGA.....	27	0	1	2.00	2	2	0	0	0	0
.....GTGAGTGGCGCCACAGGACCTGA.....	23	0	1	1.00	1	1	0	0	0	0
.....TATAGAACAGATTACAGGCGCGTGTC.....	26	0	1	1.00	1	0	0	0	1	0
.....GTGAGTGGCGCCACAGGACT.....	20	1	1	1.00	1	1	0	0	0	0
.....GTGAGTGGCGCCACAGGACCG.....	21	1	1	1.00	1	1	0	0	0	0
.....GTGAGTGGCGCCACAGGACCG.....	21	1	1	1.00	1	1	0	0	0	0
.....GTGAGTGGCGCCACAGGAC.....	19	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

CCTAGCTATATCTTGTCTAATGTCCGCGCACAGATACACGTATAGGACGCCACTCACCGCGGTGTCCTGGACTTGCTTGCTTAAGGAAGTACAAGGATGCGAAAAGTCACTACTCTAGCTCTGATAAAACCTATGACCGATAATATATGAGGAGTGAG **********.((((.((((....((((((.((((.(((....))).))))).)).))))..))))).))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body

Show Alignment With Reads

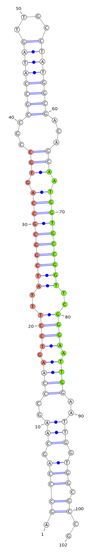
Re-alignment of all predicted orthologs

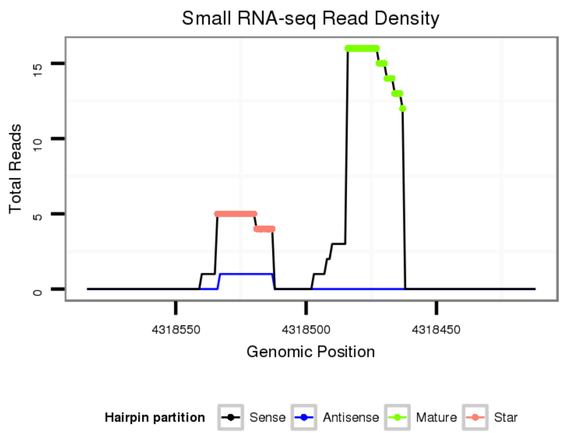
Species	Coordinate	ID	Alignment
droAna3	scaffold_13117:784527-784684 -	dan_1288	G----------GATCGATATAGAACAGATT------ACAGGCGC-----GTGTCTATG-TGC--ATATCCTGCGGTGAGTGGCGCCACAGGA-----CCTGAACGAAC------GAATTCC----------TTCATGTTCCTACGCTTTTCAGTGATGAGATCGAGACTATTTTGGATACTGGCTATTATATACTCCTCACTC
droBip1	scf7180000396412:696620-696780 -		G----------GATCGATATAGAACAGATT------ACAGGCGC-----GTTTATATG-TGC--ATATCCTGCGGTGAGTGGCGTCAGGA-----CTCAAA----A------G------AAT----------CC----------TTTCCCCCTACACATTC---GTAC-----GTTTTCAGTGATGAGATCGAGACTATTTTGGATACTGGCAATTATATACTCCTCACTC
droKik1	scf7180000302696:1665163-1665287 -		G----------GATCGATATAGAACAGATT------ACGGG---------------TGC--ATATCCTGGC----------------ACCCAAC----------------------ATCCCGGGATACGGTCATACT-----CGGTTGCAGTGATGAGATCGCGCTGTTTTGGATACTGGCAATTATATACTCCTCGCTC
droFic1	scf7180000454045:1264529-1264702 -		G----------GATGAATATAGAACAGATT------ACAGGCGC-----GTTCATATG-TGC--ATATCCTGCGGTGAGTGGCGCCAGTTGCTGTG-CATCT-------CATATCCT-----GTGT----------CC----------CGTATCTCGGCATATGAAGAACT-----CTGTTGCAGTGATGAGATCGAGCTGTTTTGGATACTGGCGATTATATACTCCTCACTC
droEle1	scf7180000491044:651232-651396 +		G----------GATCGATATAGAACAGATT------TCAGGCGC-----GTTCATATG-TGC--ATATCCTGCGGCGAGTGGCGCCAGTTGGTGTATC----------------------CATAT----------CC----------TGTATCTCGGCATACCCAGATACC-----CTGTTGCAGTGATGAGATCGAGCTGTTTTGGATACTGGCAATTATATACTCCTCACTC
droRho1	scf7180000779479:17670-17834 +		G----------GATCGATATAGAACAGATT------ACAGGCGC-----GTTCATATG-TGC--ATATCCTGCGGTGAGTGGCGCCAGTTGGTGTATC----------------------CATAT----------CC----------TGTATCTCGGCATACCCAGATACT-----CTGTTGCAGTGATGAGATCGAGCTGTTTTGGATACTGGCGATTATATACTCCTCACTC
droBia1	scf7180000301774:15945-16149 +		G----------GATCGATATAGAACAGATT------ACAGGC---------------GC--ATATCCTGCGGTGAGTGGCGCCAGTGGATGCCTCATCT-------CGCACCC-GCACCGGCATCCGCATCCGTGTCCCGCGTCTGTGCCCCCGCATCGTATCG--TCTCGGCCTATGAACATACTCCT--CTGCTGCAGTGATGAGATCGAGCCTGTTCTGGATACTGGCGATTATATACTCCTCACTC
droTak1	scf7180000415262:114112-114330 -		GGATTTGGATTTCGATTTGGATTTGGATCGATATAGAACAGATT------ACAGGCGGTCGGGGCGTCATATCCTGCATATATCCTGCGGTGAGTGGCGCCAGTTGATGCATCATCC-------CGTATCC------GCATCCCGAT------CC----------CATCGTATCGTA--CTGGCCTATGCAGACACT-----CGGTTGCAGTGATGAGATCGAGCTGTTTTGGATACTGGCGATTATATACTCCTCACTC
droEug1	scf7180000409830:52083-52255 -		GGACT----------TGGATCGATATAGAATAGATT------ACAGGCGC-----GTCCATATG-T--------GAGTGGCGCCAGTTAATGCATCATCC-------CGAATCCTGTATGTGTAT----------CC----------CGTATCTCAGCATATGAACATACT-----CGGTCCCAGTGATGAGATCGAGCCTGTTCTGGATACTGGCGATTATATACTCCTCACTC
dm3	chrX:7801324-7801514 -		GGACT----------TGGATCGATATAGAACAGTTT-----AGAGGGGC--GTTCGTTCATATG-TGC--ATATCCTGCGGCGAGTGGCGCCAGTCGATGCATCATCC-------CGCATCCTGTTAGCGTAT----------CC----------CGTAAGTCGGCATATGAAGACACT-----CGGTTGCAGTGATGAGATCGAGCCTGTTTTGGATACTGGCGATTATATACTCCTCACTC
droSim2	x:7365105-7365295 -		GGACT----------TGGATCGATATAGAACAGTTT-----AGAGGGGC--GTTCGTTCATATG-TGC--ATATCCTGCGGCGAGTGGCGCCAGTCGATGCATCATCC-------CGCATCCTGTTAGCGTAT----------CC----------CGTAAGTCGGCATATGAAGACACT-----CGGTTGCAGTGATGAGATCGAGCCTGTTTTGGATACTGGCGATTATATACTCCTCACTC
droSec2	scaffold_50:88082-88272 -		GGACT----------TGGATCGATATAAAACAGTTT-----AGAGGGGC--GTTCGTTCATATG-TGC--ATATCCTGCGGCGAGTGGCGCCAGTCGATGCATCATCT-------CGCATCCTGTTAGCGTAT----------CC----------CGTAAGTCGGCATATGAAGACACT-----CGGTTGCAGTGATGAGATCGAGCCTGTTTTGGATACTGGCGATTATATACTCCTCACTC
droYak3	X:13511996-13512189 +		GCACT----------TGGATCGATATAGAACAGAGTTAACAGAGAGGCGC------GTTCATATG-TGC--ATATCCTGCGGCGAGTGGCGCCAGTCGATGCATCATCC-------CGCATCCTCTTAGCGTAT----------CC----------CGTAAGTCGGCGTATGAAGACACT-----CGGTTGCAGTGATGAGATCGAGCCTGTTCTGGATACTGGCGATTATATACTCCTCACTC
droEre2	scaffold_4690:16712850-16713036 -		GGACT----------TGGATCGATATAGAGCAGATT------ACAGGCGC-----GTTCATATG-TTC-ATATCCTGCGGTGAGTGGCGCCAGTCGATGCATCATCC-------CGCATCCTCTAAGCGTAT----------CC----------CGTAAGTCGGCATATGAAGACACT-----CGGTTGCAGTGATGAGATCGAGCCTGTTTTGGATACTGGCGATTATATACTCCTCACTC
dp5	XL_grouple:401653-401820 +		G----------GATGAAAATAGAAAACGGTT------ACAGTGAA--GTGAATACGAATG-TGC--ATATCGTGCGGTGAGTGGAGAG-----CATCACTGAGTGGAGTTTGAGTGGAATTGCATAT----------T----------------------

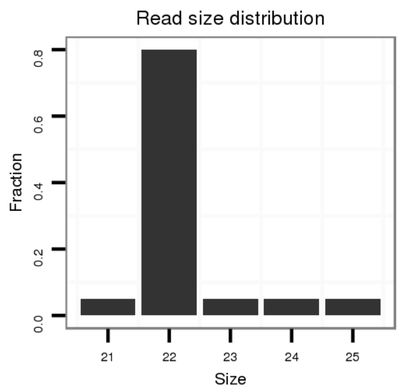
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_117	**scaffold_13117:4318462-4318534 -**	**candidate**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

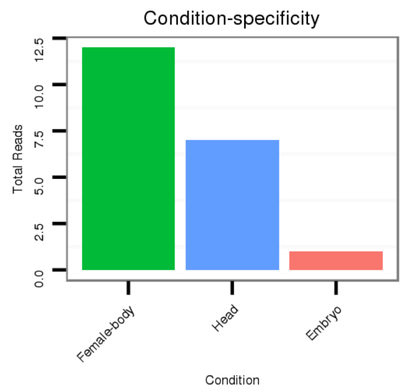
Legend: mature star mismatch in alignment mismatch in read

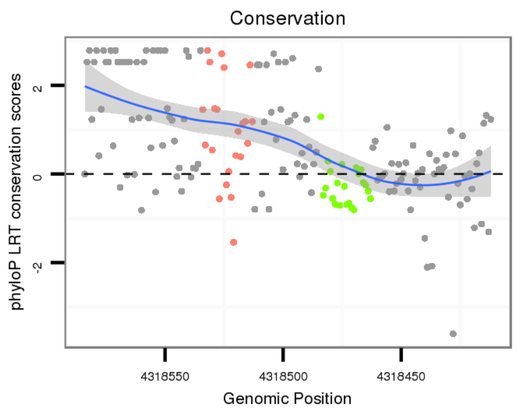
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dana\GF20849-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TCAGCACATGCAGACCCGCCGACGCCAGATGTTCAAGCCCAGCAAGCCCAAGTCCTTTATCGGCGCCAGTGCCGCCGCCATAGTTGCCTATGGCGACAGCAATGGTGCCGGTTCGGGAATTGGAATTGGTGGCGCCGGCGGAACATCCAGCCATCCAGTGGAGGGTCGAGTTG	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V106 head	V105 male body	V055 head	V039 embryo	M058 embryo
**********.(((((.(((..((((.((((..((((((((((.(((...(((((((((....)))))))))...))).))))))))))..))))).))))..))).))).))..**********											
.....AATGGTGCCGGTTCGGGAATTG.....	22	0	1	12.00	12	7	3	0	1	1	0
.....AGTCCTTTATCGGCGCCAGTGC.....	22	0	1	4.00	4	2	2	0	0	0	0
.....AATGGTGCCGGTTCGGGAATTGT.....	23	1	1	2.00	2	0	2	0	0	0	0
.....AATGGTGCCGGTTCGGGAATTT.....	22	1	1	1.00	1	0	1	0	0	0	0
.....GCACAGCAATGGTGCCGGTTCG.....	23	0	1	1.00	1	1	0	0	0	0	0
.....AATGGTGCCGGTTCGGGAATTA.....	22	1	1	1.00	1	0	1	0	0	0	0
.....AATGGTGCCGGTTCGGGAATT.....	21	0	1	1.00	1	0	1	0	0	0	0
.....CTATGGCGACAGCAATGGTGCCGGT.....	25	0	1	1.00	1	1	0	0	0	0	0
.....AGCCCAAGTCCTTTATCGGCG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GACAGCAATGGTGCCGGTTCGGGA.....	24	0	1	1.00	1	1	0	0	0	0	0
.....AATGGTGCCGGTTCGGGTT.....	19	2	2	0.50	1	1	0	0	0	0	0

Anti-sense strand reads

AGTCGTGTACGTCTGGGCGGCTGCGGTCTACAAGTTCGGGTCGTTCGGGTTCAGGAAATAGCCGCGGTCACGGCGGCGGTATCAACGGATACCGCTGTCGTTACCACGGCCAAGCCCTTAACCTTAACCACCGCGGCCGCCTTGTAGGTCGGTAGGTCACCTCCCAGCTCAAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V055 head	V106 head	V039 embryo
**********.(((((.(((..((((.((((..((((((((((.(((...(((((((((....)))))))))...))).))))))))))..))))).))))..))).))).))..**********									
.....CAGGAAATAGCCGCGGTCACG.....	21	0	1	1.00	1	0	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13117:4318412-4318584 -	dan_117	TCAGCACATGCAGACCCGCC---GACGCCAGATGTTCAAGCCCAGCAAGCCCAAGT----CCTTTATCGGCGCCAGTGC---CGCCGC---CAT----------AGTTGCCTATGGCGACAGCAAT----------GG---TG----------CC---------GGTTCGGGA---------ATT-------GG-AATTGGTGGCGCCG-----GC----------GGAACATCCAGC---CATCCAGTGGAGGGTCGAGTTG
droBip1	scf7180000396383:87271-87428 +		CCAGCACATGCAGACGCGCC---GCCGCCAGATGTTCAAGCACAGCAAGCCCAAGT----CCTTCATCGGCGCCAGTGC---CGCCGC---CAT----------AGTTGCCTATGGCGACAGCAGT----------GG---AG----------CC---------GGC------------G------CGG-------AATTG-----GA----------GCCAGCGCGTAGC---CACAGGGTGGAGGGAGCGGTGG
droKik1	scf7180000302469:85450-85622 -		TCAGCACATGCAGACGCGTC---GCCGTCAGATCTTCAAGCATGCAACCCAAGT----CCTTTATCAATGCCAGTGC---CGCCGC---CAT----------TGTCGCCTATAGTGATAGCAGTAGTAGCAGTGG---AGGAGTAGGAG---GA----------GT------------G------GAGG-------AGAG-----CT----------AGTGGTTCCACT---AATACCATAG---ATCGTGTGG
droFic1	scf7180000453775:112524-112687 +		CCAGCACATGCAGACGCGTC---GCGCCAGATCTTCAAGCACGTCAAGCCCAAGT----CCTTCATGCGTCCAGTGC---GGCGGC---GAT----------TGTCGCCTACAGCGATGCCAAT----------GG---AT----------CA---------CCA------------G------GCAT-GG-------AGCAG-----TC----------GGCTCCGCGGGCTCAAATTCCGTTGAAGGAGGAGTGG
droEle1	scf7180000491011:1731641-1731798 +		CCAGCACATGCAGACGCGTC---GCCGCCAGATGTTCAAGCACGCAAGCCCAAGT----CCTTCATAGCATCGAGTGC---AGCGGC---CAT----------TGTCGCCTTGGCGACAGCAGT----------GG---CT----------CC---------GTC------------G------GCGG-------AGCAG-----CA----------GGATCGACTGGC---AGTCCGCGCGAAGGTCGTGTGG
droRho1	scf7180000778083:140380-140537 -		CCAGCACATGCAGACGCGTC---GCGCCAGATGTTCAAGCATGCAAGCCCAAAT----CCTTCATAGCATCCGCTGC---AGCGGC---CAT----------TGTCGCCTATGGCGATAGCAGT----------GG---CT----------CC---------GTC------------G------GAGG-------AGCAG-----CA----------GGCTCGGCTGGC---AGTCCGCGATGGCAGGAGGACGGTGTGG
droBia1	scf7180000301703:121498-121664 +		CCAGCACATGCAGACGCGTC---GTCGCCAGATGTTCAAGCACGCAAGCCCAAGT----CCTTCATTGCGTCCAGTGC---AGCGGC---CAT----------TGTCGCCTATGGCGATAGCAGC----------GGTGGAC----------CA---------GTT------------G------GTGG-------AGCAGGCGCATCC----------GGATCGCCGGGT---AATCCGCGCAGAGGGACGAGTGG
droTak1	scf7180000414746:59401-59528 -		CCAGCACATGCAGACGCGTC---GTCGCCAGATGTTCAGGCACGCAAGCCCAAGT----CCCT----------------------------GTCGCCTATGGCGATGCCAGT----------GG---AG----------CA---------GT------------G------GCAG-------CC----------GGATCATCGGGT---AATCCGCGCAGAGAATCGAGTGG
droEug1	scf7180000409548:350981-351141 -		CCAGCACATGCAGACACGTC---GCCGCCAGATGTTCAAGCATAGCAACCCAAAGT----CCTTTATAGCAGACAGTGC---AGCGGC---TAT----------TGTTGCCTATGGCGATAGCAGT----------GG---CA----------CA---------GTC------------G------GAGG-----AGGAGCAA-----TC----------GGATCGCCGGGT---AATTCATCCGAAGGACGAGTAG
dm3	chrX:4575564-4575721 -		TCAGCACATGCAGACGCGTC---GTCGTCAGATCTTCAAGCATGTCAAGCCAAAGT----CCTTCATACAGTCCAGTGC---TGCGGC---GAT----------TGTCGCCTATGGAGACAGCACC----------GA---AA----------CG---------GTC------------G------GAGG-------AAGAG-----CC----------GGAGCATCTGCC---ACACCTGCAGCTGGCGCGTGTAG
droSim2	x:4266413-4266570 -		TCAGCACATGCAGACGCGTC---GTCGCCAGATCTTCAAGCATGCAAGCCCAAGT----CCTTCATACAATCCAGTGC---TGCGGC---GAT----------TGTCGCCTATGGAGACAGCAGT----------GA---AA----------CG---------GTC------------G------GAGG-------AAGAG-----CC----------GGAGCATCTGCC---ACACCGGCAGCTGGCGCGTGTAG
droSec2	scaffold_4:2154109-2154266 +		TCAGCACATGCAGACGCGTC---GTCGCCAGATCTTCAAGCATGCAAGCCCAAGT----CCTTCATACAATCCAGTGC---TGCGGC---GAT----------TGTCGCCTATGGAGACAGCAGT----------GA---AA----------CG---------GTC------------G------GAGG-------AAGAG-----CC----------GGAGCATCCGCC---ACACCGGCAGCTGGCGCGTGTAG
droYak3	X:3864632-3864789 +		TCAGCACATGCAGACGCGTC---GCCGCCAGATATTCAAACATGTCAAGCCCAAGT----CCTTCATACAATCCAGTGC---TGCGGC---CAT----------TGTCGCCTATGGAGACAGCAGT----------GA---AA----------CG---------GTC------------G------GCGG-------CAGAG-----CC----------GGACCATCTGCC---AATCCAGCAGCTGGCGCGTGTAG
droEre2	scaffold_4690:1952862-1953019 -		TCAGCACATGCAGACGCGTC---GTCGCCAGATATTCAAGCATGTCAAGCCCAAGT----CCTTCATACAATGGAGTGC---TGCGGC---CAT----------TGTCGCCTATGGAGACAGCAGC----------GA---AA----------CG---------GTC------------G------GAGG-------AAGAG-----CC----------GGATCATCTGCC---AATCCTGCAGTTGGCGCGTGTTG
dp5	XL_grouple:7674718-7674851 +		CCAGCACATGCAGACGCGCC---TCCGACAGCGTGTTAAGCACTGCAAGAACAGGT----CCTTGA---------GTGC---GGCGTC---CATCAGAGATGCTGCTGTTGGC------G-C------------------AGGAGCAGGAGCAAT-------TCCAATC------------G------GAGG-------AGCAG-----CT----------GTAG--------------------CCG
droPer2	scaffold_13:881461-881609 -		CCAGCACATGCAGACACGCC---TCCGACAGCGTGTTAAGCACTGTAAGAACAGGT----CCTTGA---------GTGC---CGCGTC---CATCAGAGATGCTGCTGTTGGC------G-C------------------AGGAGCAGGAGCGAT-------TGCAATC------------G------GAGG-------AGCAG-----CT----------GCAG--------------------CCGCAGGTGCAGGAGTAG
droWil2	scf2_1100000004909:7414558-7414724 -		CCAGCATATGCAGACAGCAGCGACGCCATCAATCTTCAAGAGCACCAAGCCCAAGT----CCTTTATCACAGCCAGTGC---TGCTGC---AAT----------TGTCGGCATACATGTGAAGGCGCAG----------CA---AA----------TT------GAGTGCC---AGA---------GAG---------GA-ATCTGGTGCTGACA-----AC----------AGATGCGAACCCC---GATACGC---------TCGTAG
droVir3	scaffold_12970:4162788-4162942 +		CCAACACATGCAAACACGAC---GCCGCAGCTGTTCAAGCACAGCAAAACGAAGT----CCTTTATTGGCGCCAGCGC---AGCTGC---CAT----------TGTTGCCTATGCCACACAGCAGC----------AG---CA----------GC---------AGCAGCCAGGCATTGCCCA---GCGGCAGCAGC---------AACAG-----CA----------GCATTAAG----------------------A
droMoj3	scaffold_6473:8735999-8736180 +		TCAACATTTGCAGACGCGTC---GCCGACAGCTGTTCAAGCACACAAAACGAAGT----CGTTTATTGCTGCCAGTGC---AGCAGC---AAT----------TGTTGCCTATAACAGTAACAAC----------G---AGCAGCAATAGCAAC-------AGCAATA-----------T-----TAAT-ATCAGCAACAGCA-----GCGGCAGCATCAGCACAGCGAAGCGC---TG----------CCCAGCGGTCA
droGri2	scaffold_14853:8452055-8452236 +		CCAACATATGCAAACGCGTC---GCCGACAGATGTTCAAGCATAGCA-GCAAAAGTAAGGGTACA---------GCGCTGCAGGAGCGTTTGT----------TGCTGCCTACAGCAGCAGCAACC----------AA---CA----------ACAGCAGCAGC-AGCGCTCAGTTTTGCCTA---G------CAGC---------AACAG-----CA----------GCAGCAGC-AGC---AATAATGTCAAAAGCGACATCA

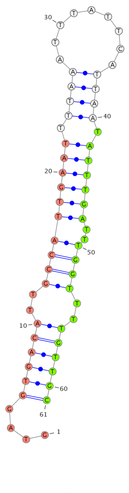
Generated: 09/08/2015 at 07:52 PM

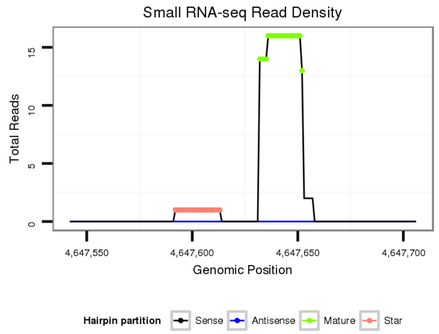
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

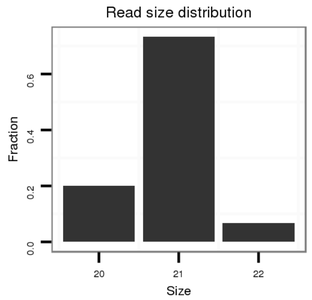
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_967	**scaffold_12943:4647592-4647656 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

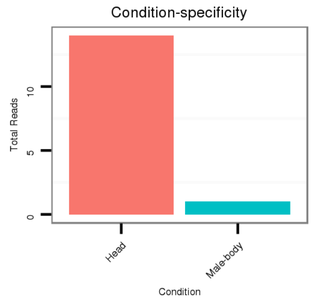
Legend: mature star mismatch in alignment mismatch in read

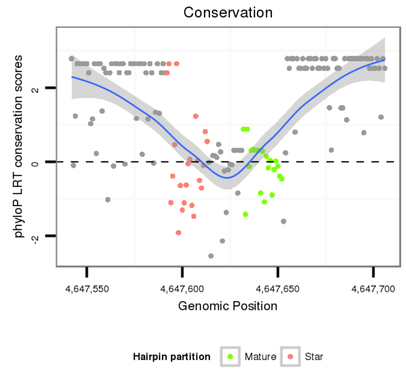
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dana\GF24654-in]; CDS [Dana\GF24654-cds]; CDS [Dana\GF24654-cds]

No Repeatable elements found

Sense Strand Reads

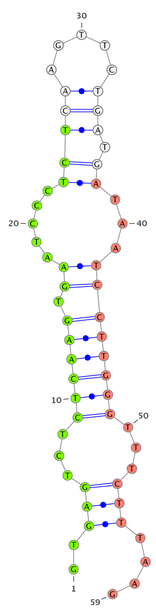
hide 3p reads | show mid mismatch reads

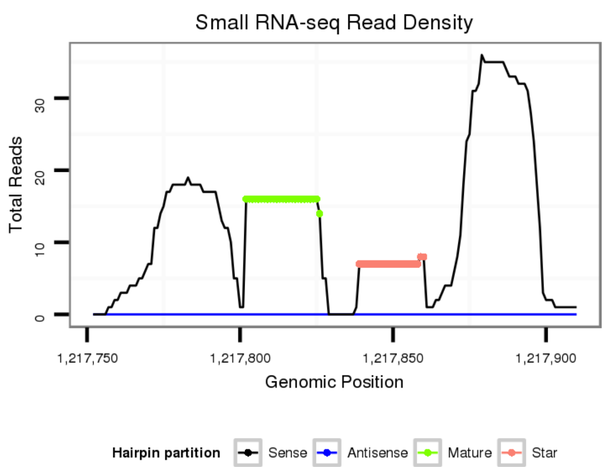
```
                                                
```

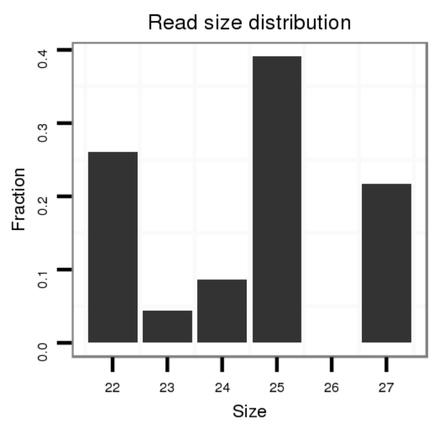
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_1714	**scaffold_13266:1217802-1217860 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

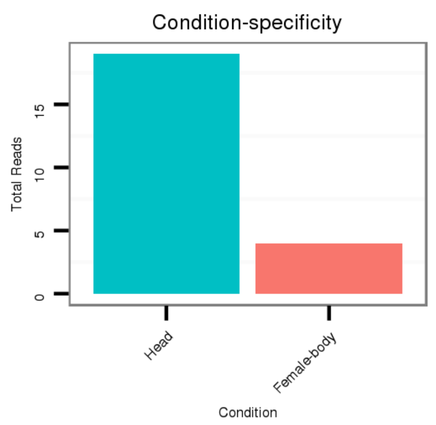
Legend: mature star mismatch in alignment mismatch in read

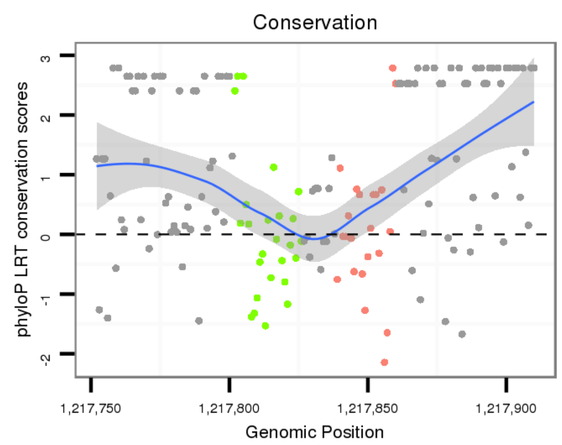
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF12560-in]; CDS [Dana\GF12560-cds]; CDS [Dana\GF12560-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GCGCTCACTACATGGATAATCACTTCAAGACGATGCCCTTCGAGAAGAATGTGAGTCTCTCAAGTGAATCCCTCTCAAGTTCTGATGATAATCCTTGGGTTTCTTTAAGGCTCCTGTCATTTTGGCCGTTCTTGGAGTGTGGTACTCGAACTTCTTCAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	V105 male body	V055 head	M058 embryo	V039 embryo
**********..(((...(((((((.((.....(((((.....))))).))...)))))))))...))).**********											
.....GTGAGTCTCTCAAGTGAATCCCTCT.....	25	0	1	9.00	9	7	2	0	0	0	0
.....ATAATCCTTGGGTTTCTTTAAG.....	22	0	1	6.00	6	3	1	0	2	0	0
.....GTGAGTCTCTCAAGTGAATCCCTCTCA.....	27	0	1	5.00	5	5	0	0	0	0	0
.....TGGCCGTTCTTGGAGTGTGGTACTC.....	25	0	1	4.00	4	4	0	0	0	0	0
.....CACTTCAAGACGATGCCCTTCGAGAA.....	26	0	1	3.00	3	3	0	0	0	0	0
.....GATGCCCTTCGAGAAGAATGCT.....	22	2	1	2.00	2	1	0	1	0	0	0
.....ATAATCCTTGGGTTTCTTTAAGT.....	23	1	1	2.00	2	0	0	1	1	0	0
.....GTTCTTGGAGTGTGGTAC.....	18	0	1	2.00	2	2	0	0	0	0	0
.....TTGGCCGTTCTTGGAGTGTGGT.....	22	0	1	2.00	2	1	0	1	0	0	0
.....GTGAGTCTCTCAAGTGAATCCCTC.....	24	0	1	2.00	2	1	0	0	1	0	0
.....GCCGTTCTTGGAGTGTGGTACTC.....	23	0	1	2.00	2	2	0	0	0	0	0
.....GCCGTTCTTGGAGTGTGGTACT.....	22	0	1	2.00	2	2	0	0	0	0	0
.....TTGGCCGTTCTTGGAGTGTGGTA.....	23	0	1	1.00	1	0	1	0	0	0	0
.....AAGACGATGCCCTTCGAGAAGA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TCAAGACGATGCCCTTCGAGAAGA.....	24	0	1	1.00	1	1	0	0	0	0	0
.....CACTTCAAGACGATGCCCTTCGA.....	23	0	1	1.00	1	0	1	0	0	0	0
.....ATTTTGGCCGTTCTTGGAGTGTGGTA.....	26	0	1	1.00	1	1	0	0	0	0	0
.....AATCACTTCAAGACGATGCCCTTC.....	24	0	1	1.00	1	0	1	0	0	0	0
.....CACTTCAAGACGATGCCCTTCGAGA.....	25	0	1	1.00	1	0	0	0	0	1	0
.....TTGGCCGTTCTTGGAGTGTGG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TCAAGACGATGCCCTTCG.....	18	0	1	1.00	1	0	1	0	0	0	0
.....AGGCTCCTGTCATTTTGGCCG.....	21	0	1	1.00	1	0	1	0	0	0	0
.....ATCACTTCAAGACGATGCCCTTCGAGA.....	27	0	1	1.00	1	1	0	0	0	0	0
.....TTTGGCCGTTCTTGGAGTGTGGTA.....	24	0	1	1.00	1	0	1	0	0	0	0
.....CTTCAAGACGATGCCCTTCGAGAAGA.....	26	0	1	1.00	1	0	1	0	0	0	0
.....CCTGTCATTTTGGCCGTTCTTGGA.....	24	0	1	1.00	1	0	0	0	0	1	0
.....CGTTCTTGGAGTGTGGTA.....	18	0	1	1.00	1	0	1	0	0	0	0
.....AGACGATGCCCTTCGAGAC.....	19	1	1	1.00	1	0	0	0	0	1	0
.....CTACATGGATAATCACTTCAA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....GATAATCCTTGGGTTTCTTTAAG.....	23	0	1	1.00	1	0	1	0	0	0	0
.....TTGGCCGTTCTTGGAGTGTGGTACT.....	25	0	1	1.00	1	0	1	0	0	0	0
.....TCAAGACGATGCCCTTCGAGAAGAG.....	25	1	1	1.00	1	1	0	0	0	0	0
.....TTTTGGCCGTTCTTGGAGTGTGGTAC.....	26	0	1	1.00	1	0	1	0	0	0	0
.....TGGCCGTTCTTGGAGTGTGGTACT.....	24	0	1	1.00	1	1	0	0	0	0	0
.....GCCGTTCTTGGAGTGTGGTACTCGAAC.....	27	0	1	1.00	1	0	1	0	0	0	0
.....ATTTTGGCCGTTCTTGGAGTGTGGT.....	25	0	1	1.00	1	0	1	0	0	0	0
.....ACATGGATAATCACTTCAAGACGATGC.....	27	0	1	1.00	1	1	0	0	0	0	0
.....TTGGCCGTTCTTGGAGTG.....	18	0	1	1.00	1	0	1	0	0	0	0
.....TGGATAATCACTTCAAGACGATGCCCTTC.....	29	0	1	1.00	1	0	1	0	0	0	0
.....GCCGTTCTTGGAGTGTGGTAC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....GTTCTTGGAGTGTGGTACT.....	19	0	1	1.00	1	1	0	0	0	0	0
.....GTTCTTGGAGTGTGGTACTC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GTGTGGTACTCGAACTTCTTCAA	23	0	1	1.00	1	0	1	0	0	0	0
.....TTGGCCGTTCTTGGAGTGTGGTAC.....	24	0	1	1.00	1	0	1	0	0	0	0
.....GATGCCCTTCGAGAAGAAT.....	19	0	1	1.00	1	0	0	1	0	0	0
.....GTCATTTTGGCCGTTCTTGGA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GGCCGTTCTTGGAGTGTGGTACTC.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TTCAAGACGATGCCCTTCGAGAA.....	23	0	1	1.00	1	0	1	0	0	0	0
.....TTTTGGCCGTTCTTGGAGTGTGGTACTC.....	28	0	1	1.00	1	1	0	0	0	0	0
.....TGGCCGTTCTTGGAGTGTGGTACTCG.....	26	0	1	1.00	1	1	0	0	0	0	0
.....TGTCATTTTGGCCGTTCTTGG.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TTTGGCCGTTCTTGGAGTGTGGTAC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TTTGGCCGTTCTTGGAGTGTGGTACT.....	26	0	1	1.00	1	1	0	0	0	0	0
.....GACGATGCCCTTCGAGAAGA.....	20	0	1	1.00	1	0	0	1	0	0	0
.....CTTCAAGACGATGCCCTTCGAGAA.....	24	0	1	1.00	1	0	1	0	0	0	0
.....ATAATCACTTCAAGACGATGCCCTTCG.....	27	0	1	1.00	1	1	0	0	0	0	0
.....CACTACATGGATAATCACTTCAAGACG.....	27	0	1	1.00	1	0	0	0	0	0	1

Anti-sense strand reads

CGCGAGTGATGTACCTATTAGTGAAGTTCTGCTACGGGAAGCTCTTCTTACACTCAGAGAGTTCACTTAGGGAGAGTTCAAGACTACTATTAGGAACCCAAAGAAATTCCGAGGACAGTAAAACCGGCAAGAACCTCACACCATGAGCTTGAAGAAGTT	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M058 embryo
**********..(((...(((((((.((.....(((((.....))))).))...)))))))))...))).**********							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13266:1217752-1217910 +	dan_1714	GCGCTCACTACATGGATAATCACTTCAAGACGATGCCCTTCGAGAAGAATGTGAGTC-TCT--C-------------------------AAGTGA-A-----------TC-------CCTCTCAA----GTTCTGA---------TGAT--AATCCTTGGGTTT--CT----TTAAGGCTCCTGTCATTTTGGCCGTTCTTGGAGTGTGGTACTCGAACTTCTTCAA
droBip1	scf7180000396730:2217350-2217504 +		GCGCCCACTACATGGACAACCACTTCAAGACGCTGCCCTTCGAGAAGAACGTAAGTC-ATGC--AA----------------------AGTAA-A-----------TC--------CCCAA----GTTTTGA---------TGTTAAAATCC-TGG-T---A----TTTAGGCTCCCGTCATTTTAGCCGTCCTGGGAGTGTGGTACTCGAATTCTTAA
droKik1	scf7180000302682:1362582-1362742 -		GCGCCCATTATATGGATAACCACTTCAGGTCAACGCCGTTGAGAAAAATGTAAGTT-AAGGCCA-----GTTCCATGAAATTATT---------------GATCCTTACCGAGTCCC--------C-----------TCCAA---TG----GCTAGGCACCTGTTATCCTGGCGTTGCTTGGTGTCTGGTACTCCAACTTCTTCAA
droFic1	scf7180000453851:1498476-1498635 +		GTGCCCACTACATGGACAACCACTTCAGGTCACGCCATTCGAGAAAAATGTAACAT-TAC--------------------------AGCTTTATT---TACTGAATTAA--GTCACATTATTTAACGGTCCA--------T-----------TTT----A----TGTAGGCTCCAGTTAATCCTGGCCTTGCTTGGCATTTGGTACTCCAACTTCTTCAA
droEle1	scf7180000490483:55891-56047 +		GCGCTCACTACATGGATAATCATTTCCGATCGACGCCATTCGAGAAAAATGTAAGAT-TTAA--------------------------G---GCTCAAGTGAC--AAGCTTAAAGTTAACAATTTCA--------A-----------ATG-T---T----GTTAGGCTCCCGTTGTCCTGGCCTTGCTCGGCGTTTGGTACTCCAACTTCTTCAA
droRho1	scf7180000780108:161375-161536 -		GTGCTCACTATATGGATAATCATTTAGGACGACGCCATTCGAGAAAAATGTAAGAA-TTCATGG--------------------------TCGT--GTGACATCGA--AAGCTTCAACTTAACCATTACA--------AT----------TTG----A----TTTAGGCTCCTGTGGTCCTGGCGTTGCTTGGCGTTTGGTACTGAACTTCTTTAA
droBia1	scf7180000302291:2743548-2743710 -		GAGCACATTACATGGATAACCACTTCAGGTCGACGCCGTTCGAGAAGAATGTAAGAC-CGAGTG--------------------------AAGT---GTGTTTTTAAATGATTTTGTTGTTAACCATTCCG--------T-----------TTG-C---T----ACTAGGCTCCTGTGGTCCTGGCCCTACTCGGAGTTTGGTACTCCAACTTCTTCAA
droTak1	scf7180000415386:441677-441839 +		GAGCCCATTACATGGATAACCACTTCAGGTCACGCCGTTCGAGAAGAATGTAAGAT-CAAGCG--------------------------TAATC-AGCTATTGAAA---GCTATTCTTGTTTACCATCCAA--------C-----------TAC-C---T----TTAGGCTCCTGTCATCCTGGCGCTGCTCGGCGTTTGGTACTCCAACTTCTTCAA
droEug1	scf7180000409183:453422-453584 -		GTGCCCATTACATGGATAACCATTTCAGGACGACACCATTCGAGAAAAATGTAAATAC-CGAGCT--------------------------TAGTG-TGTTATTA---ATAGCTAATATTATTGACATTCCAA--------T-----------TTC-A---T----ATTAGGCTCCTGTAGTCCTGGCTTTGCTGGGTGTTTGGTACTCCAACTTCTTCAA
dm3	chr2R:4799410-4799571 -		GAGCTCACTTCATGGACAACCATTTCAAGACGACACCATTCGAGAAGAATGTAAGAC-TCAACT--------------------------GAG---AGTTAAGTAAA---ATGATTATAGTTAACCATTTTA--------T-----------TGGCT---T----CCTAGGCTCCTGTTATCCTGGCGTTGCTTAGGCGTTTGGTACTCCAACTTCTTCAA
droSim2	2r:5608285-5608446 -		GAGCTCACTTCATGGACAACCATTTCAAGACGACACCATTCGAGAAGAATGTAAGAC-TCAACT--------------------------GAG---AGTTAAGGAAA---ATGAGTGTAGTTAACCATGCTA--------T-----------TGGCT---T----CCTAGGCTCCTGTTATCCTGGCGTTGCTTGGCGTTTGGTACTCCAACTTCTTCAA
droSec2	scaffold_1:2437275-2437436 -		GAGCTCACTTCATGGACAACCATTTCAAGACGACACCATTCGAGAAGAATGTAAGAC-TCAACT--------------------------GAG---AGTTAAGGAAA---ATGAGTGTAGTTAACCATGCTA--------T-----------TGGCT---T----CCTAGGCTCCTGTTATCCTGGCGTTGCTTGGCGTTTGGTACTCCAACTTCTTCAA
droYak3	2L:17457437-17457594 -		GAGCTCATTACATGGACAACCATTTCAGGACGACACCATTCGAGAAAAATGTAAGGT-TCAACTAAAG--------------------------G---AGTTAAACAAA---A---ATAGTTAACCACGTTA--------T-----------TGGCT---T----CTCAGGCTCCGTTATCCTGGCGTTGCTTGGCGTTTGGTACTCGAACTTTTCAA
droEre2	scaffold_4929:17850415-17850578 +		GAGCTCATTTCATGGACAACCATTTCAGGACGACACCATTCGAGAAAAATGTAAGTT-TCAACTGAAG--------------------------A---AGTTTACCCAA---ATGATTATAGTTAATCACTTCA--------T-----------TGGAT---T----TCAAGGCTCCGTTATCCTGGCTTTGCTTGGCGTTTGGTACTCCAACTTCTTCAA
dp5	3:13598417-13598583 +		GTGCCCATTACATGGATAATCACTTCAAGACATCGCCGCTGGACAAAAATGTAAGTC-GAGATT--------------------------GAT---ATTTGTGG--GCAGCT-------CCTACCAT----GTTTAAA--------TATTTGGT--------TTTT-TGGCTATCAGGCACCTGTCATTCTGGCTCTGCTGGCCGTCTGGTATTCGAACTTCTACAA
droPer2	scaffold_2:8021259-8021425 -		GTGCCCATTACATGGATAATCACTTCAAGACATCGCCGCTGGACAAAAATGTAAGTC-GAGATT--------------------------AAT---ATTTGTGG--GCAGCT-------CCTACCAT----GTTTAAA--------TATTTGGT--------TTTT-TGGCTATCAGGCACCTGTCATTCTGGCTCTGCTGGCCGTCTGGTATTCGAACTTCTACAA
droWil2	scf2_1100000004513:5282500-5282660 +		GTGCTCACTATATGGATAATCATTTCAAGACAAGTCCCTTGGAGAAAAATGTGAGTT-GTGTTTGAAAA-AA---------ATTATC---------------GATT---T---ATTTGTTATGT----------------------AATTGAA-T--TTGCT---G----TATAGGCACCGTTATTCTGGCTCTATTGGGAGTCTGGTACTCGAATTTCTATAA
droVir3	scaffold_12875:1782528-1782693 -		GCGCCCATTTTATGGATACCCATTTTAAAACTGCACCACTGACCAAAAATGTGAGTGCATTTTGAAAA-AT---------TTAAAT---------------GTT---TGATTATAATAAAA----------TAATGCAAAT---------G-T-AATT---TC----CTTAGGCACTGTTATTCTGGCACTACTTGGCATTTGGTATTCGAATTTTTATAA
droMoj3	scaffold_6496:13708460-13708627 +		GTGCATACTATATGGATACTCATTTCCGCACTGCACCACTGGCGAAAAATGTAAGCG-TTGA---AAATCT---------TTACAT---GTA---A---------T---TAAATATAAATTAACA----------TAGTGCAATT---------TTCACAT---TT----CGTAGGCACCGTTATTCTGGCTCTGCTTGGCATTTGGTATTCAATTTTTATAA
droGri2	scaffold_15112:3878045-3878133 -		AAATGTATT---TATCTGTGACTCTTATC--------T-----------TAAAT---TT----TGTAGGCACCTGTTGTGCTGGCGTTGCTTGGCATTTGGTATTCGAATTTTTATAA

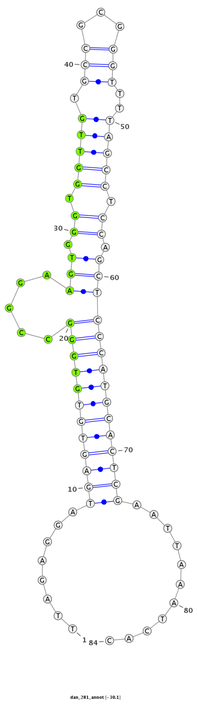
Generated: 09/08/2015 at 07:05 PM

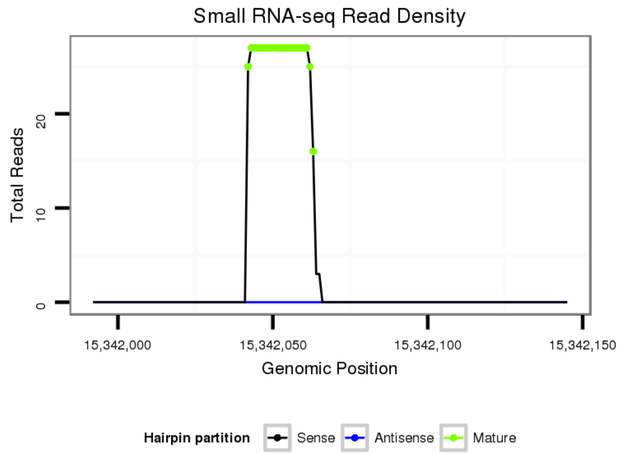
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	0
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

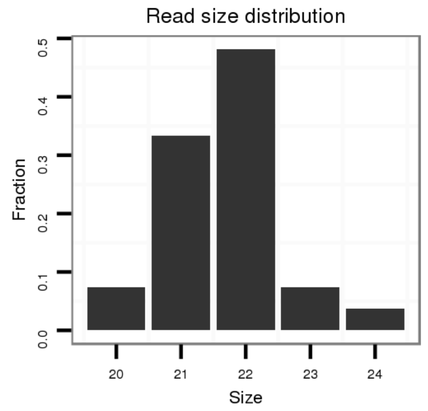
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_281	**scaffold_13340:15342042-15342095 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

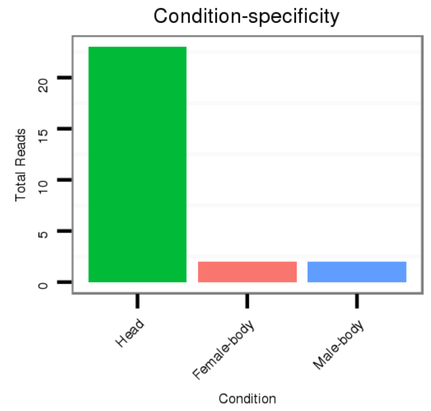
Legend: mature star mismatch in alignment mismatch in read

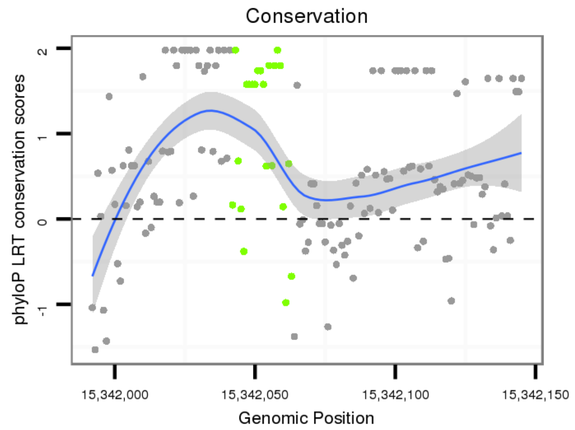
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF18473-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TCCCCCCAGGGGTTGCCTGGCGACCTTTTTGGTAATTAGAGGATGAGTGTGTGGGCCGGAAGTGGGTGGTTGTGCCGCGGGTTTTAGCCTCCAGCTCCCATGCACTCGAATTAAATCACAAAACGCAGTAAACTTTTGCGTTCTCAACGTTTTT **********.....(((((((((((.....(((.((.(((((.(((...))))..)))))).)).)))))))))))).....**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V106 head**	**V105 male body**	**M044 female body**	**V039 embryo**
.....GTGGGCCGGAAGTGGGTGGTTG.....	22	0	1	13.00	13	12	1	0	0
.....GTGGGCCGGAAGTGGGTGGTT.....	21	0	1	9.00	9	8	1	0	0
.....GTGGGCCGGAAGTGGGTGGT.....	20	0	1	2.00	2	2	0	0	0
.....TGGGCCGGAAGTGGGTGGTTGTG.....	23	0	1	2.00	2	1	0	1	0
.....GTGGGCCGGAAGTGGGTGGTTGTG.....	24	0	1	1.00	1	0	0	1	0
.....GTGGGCCGGAAGTGGGTGGTTGA.....	23	1	1	1.00	1	1	0	0	0

Anti-sense strand reads

AGGGGGGTCCCCAACGGACCGCTGGAAAAACCATTAATCTCCTACTCACACACCCGGCCTTCACCCACCAACACGGCGCCCAAAATCGGAGGTCGAGGGTACGTGAGCTTAATTTAGTGTTTTGCGTCATTTGAAAACGCAAGAGTTGCAAAAA **********.....(((((((((((.....(((.((.(((((.(((...))))..)))))).)).)))))))))))).....**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V055 head**	**M058 embryo**	**V039 embryo**	**V106 head**

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13340:15341992-15342145 +	dan_281	TCCCCCCAG-----GGGTT-GCCTGGCGACC----------TT-TTTGGTAATTAGAGGATGAGTGTGT--GGGCCGGAAGTGGGTGGTT-GT-GC-CGCGGG------TTTTAGCCT-CCA------GCTCCCA---------TGCACTCGAATTAAATCACAAAACGC--AGTAAACTTTTG-CGTT--CTCAACGTTTTT
droBip1	scf7180000396708:4692179-4692335 -		CCCCCCCAG-----TTGTT-GCCAGGCGACC----------TT-TTTGGTAATTAGAGGATGAGTGTGT--GGGCCGGAAGTGGGTGGGT-TGTGC-CATAA-------TTTCAGCCT-CAA------GCCCACA---------TGCATTCCAATAAAATCAGAAAACGA--AGTAAACTTTTGGTTTTAATTTAATATTTTT
droKik1	scf7180000302707:258925-259085 -		TACCTACAG--CTTCCGTT-GCTT-GCGACC--------A---TTTTTATT-TTTGGTAATAAGAGGATGAGTGTTTTTGGGCCGGAAGTGGGTGGCT-AGCG-T--C---------------AGTT-GAA------GCCCGTGTATAT-TTATGCATGCAAATAAAATTAGAAACGACTGGCAAAACTTTTA-T-TT--GCAGCATTT--T
droFic1	scf7180000454126:21398-21549 -		TTC-----ACTCTTCCGCT-GCCTGCCATTTTTTC---CTTTTTTTTTTT-GTTGATAATTAGAGGATGAGTGTGT--GCCCCGGAAGAGGTGTTT---T--------------GC-AAA------ACTCATA---------TGCATGCAAATAAATTCAGAGAAGGCTTGTGGAACTTTCA-TGTT--GCCAGCATTTTT
droEle1	scf7180000490994:813042-813179 -		T--------T--CTTCCGCT-GCCTGTCGACC----------TTTTTTT-TGTGTAATAAGAGGATGAGTGTTT--GGCCCGGAAGTGGGTGGCT-GG--T--------------GC-AAA------ACTCATA---------TGCATGCAAATAAATCAGAAAAGGCTTGGAAACTTTCA-TGTT--GCTAGCAGTTTT
droRho1	scf7180000777405:27940-28100 +		TGTCCTCAACTCTTTTGCT-GCCTGGCGACC----------TT-TTTGGTAATTAGAGGATGAGTGTGT--GGCCCGGAAGTGGGTGGTT-GTGGG-CTTGG-------TTGGGTGCT-CAA------ACTTATA---------TGAATGCAAATAACATTAAAAAGGCTTGTGAAACTGTCA-TGTT--GCCAGCATTTTT
droBia1	scf7180000302402:806032-806191 -		CG-----AACCCTTTCGCA-GCCGGCGACC----------TTTTTTGGTAATTAGAGGATGAGTATGT--GGTCCGGAAGTGGGTGGCT-TGGGG-TCTGGG-------CATCCCAGATCCCCCTGCGATA---------TGCATGCAAATAAATCAGAAAAGGCTGTTAAAACTTTCA-TGTT--GCCACCACTTTT
droTak1	scf7180000410451:67521-67684 -		TTCCTGCAACT-TTTCGCTGCCCGGCGACC----------TTTTTTT-TTTGGTAATTAGT-GATGAGTATGT--GGCCCGGAAGTGGGTGGTT-T---------GGG-------CA-CCC-CAA------ACTCATATACAACATGTATATGGAAATAAATCAGAAAAGGCTTGTGAAATTTGCA-TGTT--GCCAGCATTTTT
droEug1	scf7180000409804:1308775-1308945 -		GCCCCTCAACTCTTTCGTT-GCCTGGCGACCTTTCATATTTTTTTTCTTT-TTTGGTAATTAGAGGATGAGTATGT--GGTCCGGAAGTGGGTGGTT-TG-GG-TTTGGGGTCCTGGCA--GAGTC-CAA------ACTCATG---------TGCATGCAAATAAAATGAGAAA----------CTTTTA-TGGT--GCCAGCATTTTT
dm3	chr3R:15046205-15046319 -	dme_420	T--------------TGCT-GCCTGGCAACC----------TT-TTTGGTAATTAGAGGATGAGTATGT--GGCCCGGAAGTGGGTGGTTTTCGG-TTTGGC-------CA-GTGTT-CAA------ACTCATA---------TGCATGCAAATAAAATGCAAAAAGGC---------------------
droSim2	3r:6216213-6216339 +		TTCCC--CACTCTTTTGCT-GCCTGGCGACC----------TT-TTTGGTAATTAGAGGATGAGTATGT--GGCCCGGAAGTGGGTGGTT-TTCGGCTTCGGG-------CA-GAGTT-CAA------ACTCATA---------TGCATGCAAATAAAATGCAAAAAGGC---------------------
droSec2	scaffold_25:719471-719594 +		TCCC----ACTCTTTTGCT-GCCTGGCGACC----------TT-TTTGGTAATTAGAGGATGAGTATGT--GG-CCGGAAGTGGGTGGTT-TTCGGCTTTGGG-------CA-GAGTT-CAA------ACTCATA---------TGCATGCAAATAAAATGCAAAAAGGC---------------------
droYak3	3R:3747832-3747969 -		T--------T--CTTTTGCT-GCCTGGCGACC----------TT-TTTGGTAATTAGAGGATGAGTATGT--TGCCCGGAAGTGGGTGGTT-TCCGG-TTTGGG-------CA-GAGTT-CCT------ACTCATA---------TGCATGCAAATAAATGCAAAAGG--T------CTTTCA-TGCT--GGCAACCCTTTT
droEre2	scaffold_4770:6585639-6585790 +		GCCCTCCAACTCTTTTGCT-GCCTGGCGACC----------TT-TTTGGTAATTAGAGGATGAGTATGT--GGCCCGGAAGTGGGTGGTT-TC-GG-TTTGGG-------CA-GAGTT-CAA------GCTCATA---------TGCATGCAAATAAAATGCAAAAGGCTTTTGAAGC-----TGCT--GGCAACACTTTT
dp5	2:29492151-29492230 -		ATCTG-CAACCCT-TTTTT-TAATGTTTTTT----------TTTTTTT-TTTGGTAATTAGAGGACGAATGTGT--GT---------GTGTGTTG-CACGT-TTTGG-------CA--
droPer2	scaffold_6:4862826-4862897 -		TGCA----ACCCT-TTTTT-TAATGTTTTTT----------TT-TTTGGTAATTAGAGGACGAATGTGT--GT---------GTGTGTTG-CACGT-TTTGG-------CA--

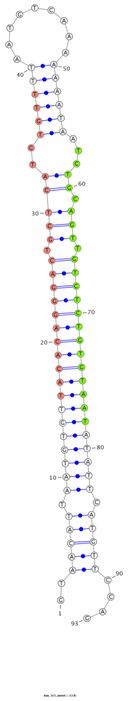
Generated: 09/08/2015 at 07:53 PM

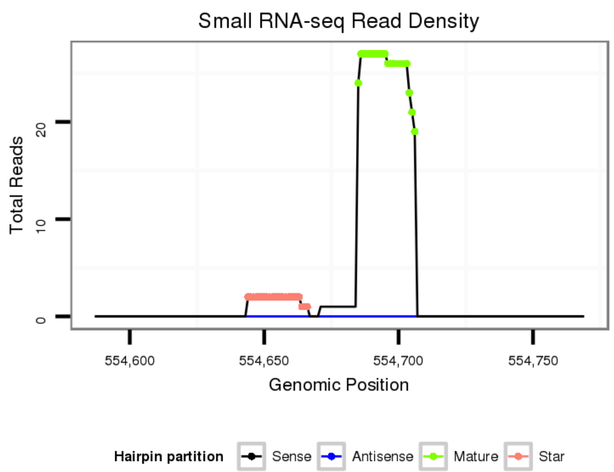
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

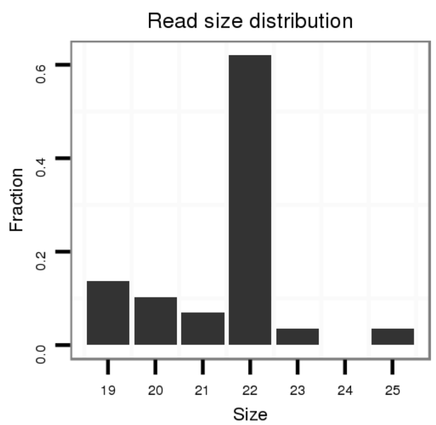
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_315	**scaffold_12903:554637-554719 +**	**candidate**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

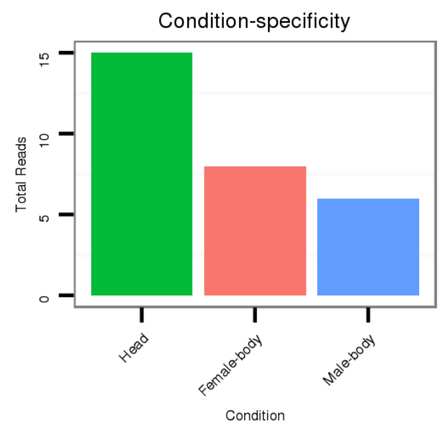
Legend: mature star mismatch in alignment mismatch in read

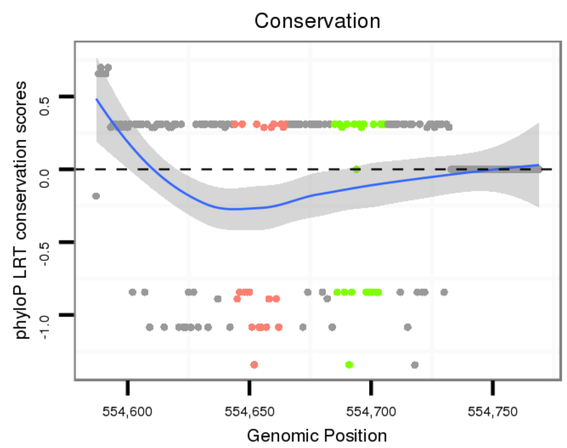
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TCAGCTGATCACAGTGAATACTCCCTAACACCAACAGTCTAAGTAACATTAATGTGTTACACAGGGACTGCTCATCTGTTTTAATGTCAAAAAAATAATCTGCAGTTGTCTCTGTGTAATATATTCATGTTCCAGTCATCATAGTGGTTTTTTTCAGTGTTTTTTTTAAGATAATAATTTTGT **********..(((((.((((((((((((((((((.(((((..((((((.........))))))...))).))).))))))))))))))))).)))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	V105 male body	V055 head	V039 embryo
.....TCTGCAGTTGTCTCTGTGTAAT.....	22	0	1	18.00	18	6	4	5	3	0
.....TCTGCAGTTGTCTCTGTGT.....	19	0	1	3.00	3	1	0	0	2	0
.....TCTGCAGTTGTCTCTGTGTAA.....	21	0	1	1.00	1	0	1	0	0	0
.....TACACAGGGACTGCTCATCTGTT.....	23	0	1	1.00	1	0	1	0	0	0
.....CTGCAGTTGTCTCTGTGTAAT.....	21	0	1	1.00	1	0	1	0	0	0
.....CTGCAGTTGTCTCTGTGTA.....	19	0	1	1.00	1	1	0	0	0	0
.....TGTCAAAAAAATAATCTGCAGTTGT.....	25	0	1	1.00	1	0	0	1	0	0
.....TCTGCAGTTGTCTCTGTGTAATT.....	23	1	1	1.00	1	0	0	1	0	0
.....TCTGCAGTTGTCTCTGTGTA.....	20	0	1	1.00	1	0	0	0	1	0
.....CTGCAGTTGTCTCTGTGTAA.....	20	0	1	1.00	1	0	1	0	0	0
.....TACACAGGGACTGCTCATCT.....	20	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

AGTCGACTAGTGTCACTTATGAGGGATTGTGGTTGTCAGATTCATTGTAATTACACAATGTGTCCCTGACGAGTAGACAAAATTACAGTTTTTTTATTAGACGTCAACAGAGACACATTATATAAGTACAAGGTCAGTAGTATCACCAAAAAAAGTCACAAAAAAAATTCTATTATTAAAACA **********..(((((.((((((((((((((((((.(((((..((((((.........))))))...))).))).))))))))))))))))).)))))....**********	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_12903:554587-554769 +	dan_315	TCAGCTGATCACAGTGAATACTCCCTAACACCAACAGTCTAA----------GTAACATTAATGTGTTACACAGGGACTGCTCATCTGTTTTAATGTCAAAAAAATAATCTGCAGTTGTCTCTGTGTAATATATTCATGTTCCAGTCATCATAGTGGTTTTTTTCAGTGTTTTTTTAAGATAATAATTTTGT
droBip1	scf7180000395912:23596-23752 +		TCAGCTGATCACAGTAAATATTACCTAAAACCAAAATGTGGACCTTATTAAATCTTAAAATTTATGTTTTTATGATCAAGAACAAATGTTTAATTTTAAAAAGAAACTTTGTACCT-TCTTCATACAATATATTTATTTGTAACCATCATAATG----------
droKik1	scf7180000302798:187108-187113 -		ACAGCT----------

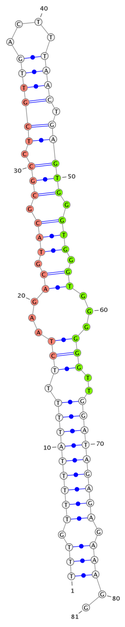
Generated: 09/03/2015 at 08:04 PM

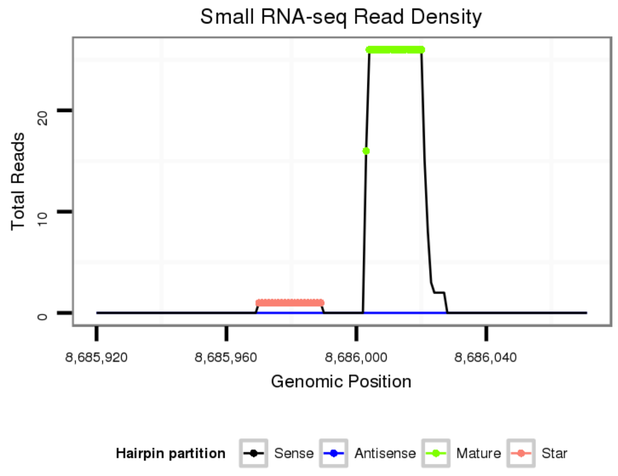
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

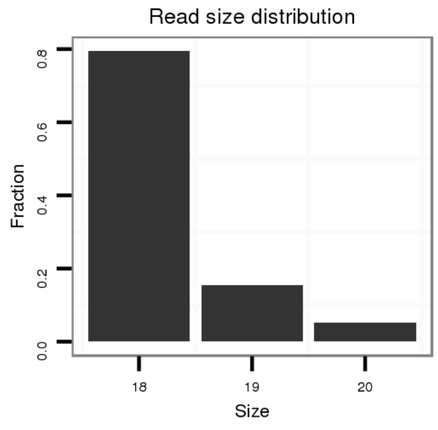
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_102	**scaffold_13337:8685970-8686021 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

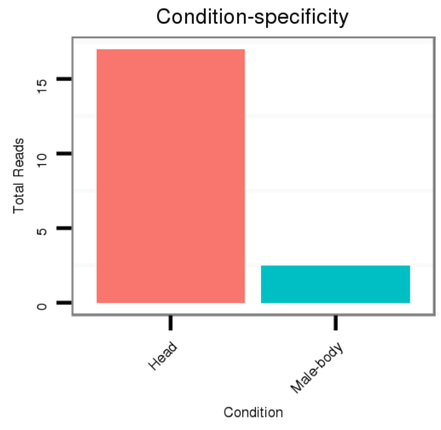
Legend: mature star mismatch in alignment mismatch in read

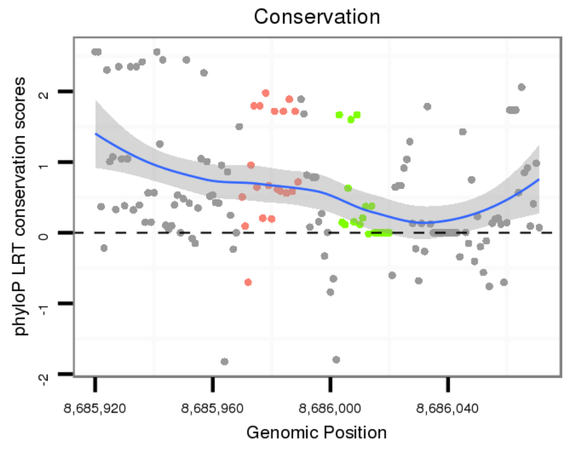
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF10192-in]

No Repeatable elements found

mature	star
1. scaffold_12929:2163244-2163261 + 2. dan_102 scaffold_13337:8686003-8686020 +	

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAGAAAACAAAAACATAAATAAATTGCCTTAATATTTTGTTTTTATTTTTCTAAGACGTACGCGCCTCGTTGACTTTAACTGAGTGGGTGGGTGGGGGGTTGGATAGAGAGAAAGGGGAGAGTGTGCGAGAGAGATGGGCTATTGTTTTGCG	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V055 head	V105 male body	M044 female body	M058 embryo	V039 embryo
************************************(((.((((((((((.(((...((.(((.((((.((((((....)))))).)))))).)))).))...)))).))..)))))))))..))).************************************											
..........GTGGGTGGGTGGGGGGTT..........	18	0	2	11.50	23	20	0	3	0	0	0
..........TGGGTGGGTGGGGGGTTGG..........	19	0	1	5.00	5	5	0	0	0	0	0
..........TGGGTGGGTGGGGGGTTG..........	18	0	1	4.00	4	4	0	0	0	0	0
..........GTGGGTGGGTGGGGGGTTG..........	19	0	1	3.00	3	3	0	0	0	0	0
..........GTGGGTGGGTGGGGGGTTGGATAGA....	25	0	1	2.00	2	2	0	0	0	0	0
..................CTAAGACGTACGCGCCTCGT..........	20	0	1	1.00	1	0	0	1	0	0	0
..........TGGGTGGGTGGGGGGTTGGA..........	20	0	1	1.00	1	0	0	0	1	0	0
..........GTGGGTGGGTGGGGGGTC..........	18	1	8	0.13	1	1	0	0	0	0	0
..........GTGGGTGGGTGGGGGGTAA..........	19	2	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

TTCTTTTGTTTTTGTATTTATTTAACGGAATTATAAAACAAAAATAAAAAGATTCTGCATGCGCGGAGCAACTGAAATTGACTCACCCACCCACCCCCCAACCTATCTCTCTTTCCCCTCTCACACGCTCTCTCTACCCGATAACAAAACGC	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	V106 head
************************************(((.(((((((((.(((...((.(((.(((.((((((....)))))).)))))).)))).))...)))).))..)))))))))..))).************************************							
..........GTGGGTGGGTGGGGGGTC..........	18	1	8	0.13	1	1	0
..........GTGGGTGGGTGGGGGGTAA..........	19	2	20	0.05	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13337:8685920-8686071 +	dan_102	AAGAAAAC-----AAAAACATAAA-TAAATTGCCTTAATA-TTTTGTTT----------TTATTTTTC----TAAGACGTACGC-GCCTCGTTGACTTTAACTG----AGTGGGTGGGT---GGGGGGTTGGATAG----------AGAGAAAGGGGAGAGTGTGC----------GAGAGAGATGGGC-TATTGTTTTGCG
droBip1	scf7180000396541:827440-827589 +		AACAAAAC-----AAAAACATAAA-TAAATTGCCTTCATA-TTTTGTTGCTTTTTGTTTTTTTTTGTTTTTTC-TC-TC----TAAGCGGTACGC-GCCTCGTTGACTTTGGTGGGGTGGTGAGAG-----------AGAGACAG----------AGAGAGAGAAAGGGGGC-TATTGTTTTGCG
droKik1	scf7180000302601:142869-143029 -		AACAAAAC-----AATAACAAAAA-TAAATTTCCTCAAAAGCGGTTGATT----------TTT-GG-TT----GTAGGCGTGTGC-AGCTCGTTGGAGGATACGAT-----------AGAGGAAAATAGGGGAGATTGGAAAGCAGAAAGCATGAAGACGAGGAA----------C----------GAGAGAGAGTGGGAGGATTATTGTTTTGCG
droFic1	scf7180000453929:159658-159778 -		AA----AC-----AATAACAAAAA-TAAATACCTTAAAAGTTTTGTTT----------TTCTTT-TT----TGAGCGTGCGC-GCGTCGTTGACTTCTCTTTTGCGGGAAAGAGA----------GGGTGAAGAAAAGAGGTTGATTGTTTTGCG
droEle1	scf7180000491193:2353336-2353465 +		AACCAAA-----AAAACAAAAATAAATAGCTTAAAAAGTTTTGTTT----------TTT----TT----TGAGCGTGCGC-GCGTCGTTGACTTCTCTTTTGCGAAAGAGA----GG----------AAAAG---------TGCT---------AGAGAAAAAACGAGAAGTGGATTGTTTTTGCG
droRho1	scf7180000779801:43598-43729 -		AACAAAAC-----AA------AAA-TAAATAGTCTAAAAGATTTTGTTT----------TTT-TT-TT----CGAGGCGTGTGC-GCGTGGTTGACTTCTCTTTGGCGAGAAGAGAGA----GG----------AAAG---------TGC----GAAAGAG-----AAAATAAGATGTTGATTGTTTTGCG
droBia1	scf7180000302193:5034020-5034175 +		AACAAAAC-----AAATAACAAAAA-TGAATACCCTTAAACAATTTGTTT----------TT-------T----TAGCGGTGCGC-GCGTCGTTGACTTCTCTGTTGCGTGAACAGAGAGGTG----------AATAGTTGGCGGG-GGAAGAAAGAGAGGATG----------GGGGAGAGAAAGAGAGGTTGATTGTTTTGCG
droTak1	scf7180000415319:73433-73558 -		AACAAAAC-----AAATAATAAAAA-TGAATAGCCTTAAAAAGATTTTTTT----------TTG-TT-TT----TGAGCGTGCGC-GCGTCGTTGACTTCTCTTCTGCGGGAAA-AGT----------G----------AGAGAG-----G---------AGC----GAAATAC-----------A--GGATTGTTTTGCG
droEug1	scf7180000409711:4991678-4991831 +		AACAAAAC-----AAATAACAAAAA-TGAATAGCCTTAAAAGATTTGTTT----------TTTTTT--TTTGGTGAGGCGTGCGC-GCGTCGTTGACTTCTCTTTTGCGGGAAAGAGA----GT----------GG----------AAAAG---------TGCGGGGGAAAGAGATGGAGAAGAGTGAGGTTGATTGTTTTGCG
dm3	chr3L:21000381-21000501 -		AACAAAAC-----AAATAACAAATA-TGAATAGCCTTAAAAGTTTTGTTT----------TTC-----C----TAAGCGGTGCG--------------------AAGAAACAGAGA----AG----------AAAAG---------TGGATGGGAAAGAGAGGGCAAAAATGTGAGATTGATTGTTTTAGTT
droSim2	31:20561148-20561268 -		AACAAAAC-----AAATAACAAATA-TGAATAGCCTTAAAAGTTTTGTTT----------TTC-----T----TAAGCGTTGCG--------------------AACACAGAGAGA----AG----------AAAAG---------TGGGTGGGAAAGAGAGGGCAAAAATGAGAGGTTGATTGTTTTACG
droSec2	scaffold_11:896825-896945 -		AACAAAAC-----AAATAACAAATA-TGAATAGCCTTAAAAGTTTTGTTT----------TTC-----T----TAAGCGCTGCG--------------------AACACAGAGAGA----AG----------AAAAG---------TGGGTGGGAAAGAGAGGGCAAAAATGTGAGGTTGATTGTTTTACG
droYak3	3L:19522417-19522554 +		AACAAAACAAAACAATAACAAATT-GGAATATTCCTAAAAGTTATGTTT----------TTC-----T----TAAGCGGTGCGC-GCGTCGCT----------ACAAGAAAGAGAGA----AG----------AAAAG---------TGGTTGTGAAAGAGAGGGGGGTCATTTGAGGGTTGATTGTTTTACG
droEre2	scaffold_4784:20689691-20689819 -		AACAAAAC-----AAATAACAAATT-TGAATAGCCTTAAAAGTTTTGTTT----------TTC-----T----TAAGCGGTGCGC--GCGTCGTTG----------CGCGA-AGGGAGA----AG----------AAAG---------TGGGTGGAAAAGAGGGG-CGAAAATGTAAGGGTTGATTGTTTCACG
dp5	XR_group6:1139433-1139575 +		AACCAAAC-----AAATAACAAAAA-TAAATTGCCTCAAAAGT---GTTT----------TTT----TT----CGAGCGCGTGCGTTGCGTCGTTGACTTTTCCCC----AGAAAGAGACACA---GA------CGATAG----------AGAGAGGAAGAG---------GGAGAGAGCGAGGGAGGCCAAAAGAGAGGGAAAG-------AGCG
droPer2	scaffold_12:1827464-1827588 +		AACCAAAC-----AAATAACAAAAA-TAAATTGCCTCAAAAGT---GTTT----------TTT----TT----CGAGCGCGTGCGTTGCGTCGTTGACTTTTCCC----AGAAAGAGACACA---GA------CGATAG----------AGAGAGCGACAG---------AGCAAGAGCGAGG------------GAGGC----------GA
droVir3	scaffold_12875:15313416-15313438 +		AAATAAAA-----AAAAAATAAAA-AAA---
droMoj3	scaffold_6500:8739538-8739592 -		AAAAATCG-----AGATACAAATA-CAAATATTAATGAGCCACTTGAAT----------ACA-----T----TGC---GATA
droGri2	scaffold_15110:3008891-3008938 -		AAAG-----------CG-CGAGTGCTT-AA-TTTTTTGTCG----------CTG-----T----TC---------A-------AGTTTT--CTAGCA

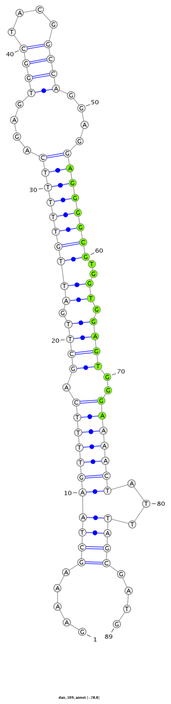
Generated: 09/08/2015 at 07:57 PM

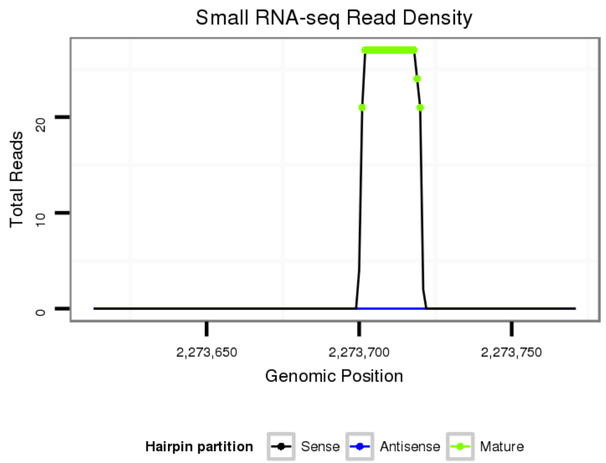
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

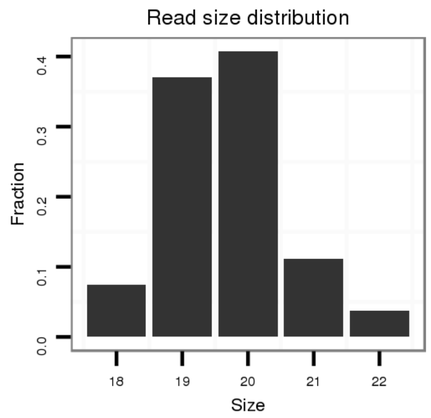
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_309	**scaffold_12916:2273663-2273721 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

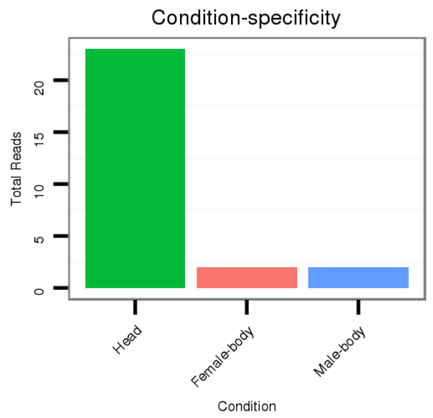
Legend: mature star **mismatch in alignment** mismatch in read

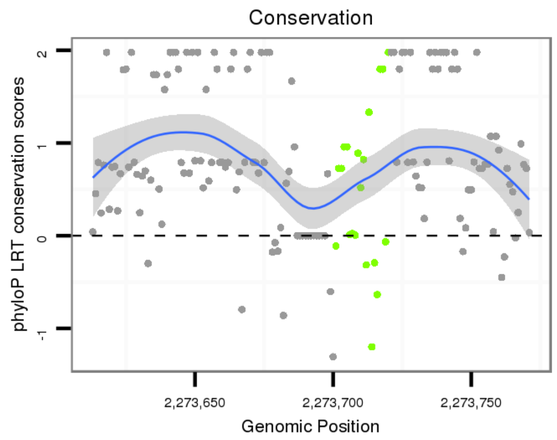
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GCTGCATTTTCCGAAAATGTGTTTACGTAATGTGAGAAAAGCTAAGTTTTCAGCTTGATTGTTTTTCAGAGTGGCTACGGCCAGGAGGAGGGGCGTGGTGGAGTGGGAAAACTATTTAGCGATGACAAAAGTCGGCAATTGCAATCAGAGGCCCGGAGA	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	female body	V055 head	M058 embryo	V039 embryo
**********.....((((((((((.((((.((((((((((....((((....))))....))))))))).))).))).))))))).....**********.....((((((((((.((((.((((((((((....((((....))))....))))))))).))).))).))))))).....**********											
.....AGGGGCGTGGTGGAGTGGGA.....	20	0	1	11.00	11	11	0	0	0	0	0
.....GGGGCGTGGTGGAGTGGGA.....	19	0	1	6.00	6	5	0	0	1	0	0
.....AGGGGCGTGGTGGAGTGGG.....	19	0	1	3.00	3	3	0	0	0	0	0
.....AGGGGCGTGGTGGAGTGG.....	18	0	1	2.00	2	1	0	1	0	0	0
.....GAGGGGCGTGGTGGAGTGGGA.....	21	0	1	2.00	2	1	1	0	0	0	0
.....GAGGGGCGTGGTGGAGTGGGAA.....	22	0	1	1.00	1	0	0	1	0	0	0
.....AGGGGCGTGGTGGAGTGGGAA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....GAGGGGCGTGGTGGAGTGG.....	19	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

CGACGTAAAAGGCTTTTACACAAATGCATTACACTCTTTTCGATTCAAAAGTCGAACTAACAAAAAGTCTCACCGATGCCGGTCCTCCTCCCCGCACCACCTCACCCTTTTGATAAATCGCTACTGTTTTCAGCCGTTAACGTTAGTCTCCGGGCCTCT	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	V055 head
**********							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12916:2273613-2273771 +	dan_309	GCTGC--ATTTTCC-GAAAATGTGT-TTA-----CGTAATGTGA--GAAAAGCTAAGTTTTCAGCTTGATTGTTTTT---CA----G--------AGTG-----------------GCTACGGCCAGGAGGAGGGGCGTGGT--GGAGTGGGAAAACTAT---TTAGCGATGACAAAAGTCGGCA------A--TTGCAATCAG--------AGGCCCGGAGA
droBip1	scf7180000396430:223317-223477 +		GCTGC--ATTTTCC-GAAAATGTGT-TTA-----CGTAATGTGA--GAAAAGCTAAGTTTTCAGCTTGATTGTTTTT---CA----G--------AGTGGTCGGAGTGGCCGTAGTGG----------CAGGGGCGT---GGAGTGGGAAACTAT---TTGGCGATGACAAAAGTCGGCA------A--TTGCAATCAG--------GGGCCCGGAGA
droKik1	scf7180000302401:198148-198278 -		AATAT--ATTTTCCTGAAAAAGTTTTTTGTTGATTGTAATGTGAGAAAAAGCAAAGTTTTCAGCTGATTGTTTTTGTTT--GGAAAACTAT---TCGCGATGACAAAAGTCGCTTGGCGTTTGTCT-------G---TCG----CC-G----
droFic1	scf7180000454059:583384-583500 -		AATAT--ATTTTCC-GAAACTG--T-TTG-----CGTAATGTGA--GAAACGGCAAGTTTTCAGCTTGATTGTTTTGTGTTT----G--------TGTG----------------------------------G---T--GAGGGAAAACTAT---TTGGCGATGACAAAAGTCAGTT------T-TTT--------------G----C--------
droEle1	scf7180000491338:2322701-2322819 +		AATAT--ATTTTCC-GAAACTC--T-TTG-----TGTAATGTGA--GAAAAGCAAAGTTTTCAGCGTGATTGTTTTGGGTTC----G--------TGTG----------------------------------G---T-CCAGGGAAAACTAT---TTGGCGATGACAAATGTCAGTT------T--TT--------------A----CC------
droRho1	scf7180000779703:30230-30347 -		GATAT--ATTTTCC-GAAACTG--T-TTG-----TGTAATGTGA--GAAAAGCAAAGTTTTCAGCGTGATTGTTTTGTGTTC----------------GTG----------------------------T--GGTGAGGGAAAACTAT---TTGGCGATGACAAAAGTCAGTT------T-TTT--------------G----CC------
droBia1	scf7180000302422:5330429-5330551 -		AATATATATTTTCC-GAACCTG--T-TTG-----TGTAATGTGA--GAGAAGCAAAGTTTTCAGCTTGATTGTTTTTAGCC----TG--------CGTG----------------------------G---GGTGCGGGAAAACTATT--TTGGCGCTGACAAAAGTCAGTT------T-TTT--------------G----CC------
droTak1	scf7180000415867:614499-614626 +		--TAT--ATTTTCC-GAAACTG--T-TTG-----TGTAATGTGA--GAAAAGCAAAGTTTTCAGCATGATTGTTTTGCGTTT----G--------AGTG----------------G----------------GGTGAGGTGAGGAGCGGGAAAACTAT---TTGGCTATGACAAAAGTCACTT------T-TTT--------------G----CC------
droEug1	scf7180000409447:304847-304972 +		AATAT--ATTTTCC-GAAACTG--T-TTG-----TGTAATGTGA--GAAAAGCAAAGTTTTCAGCCTGATTGTTTTGAGTTT----TA--------TGCG----------------------------G---GCCAAGGGAAAACTAT---TTGCGATGACAAAAGTCAGAT------TTTTT----TTA-----G----CC-A----
dm3	chr2L:18359627-18359753 +		AATATAAATTTTCC-GAAACTG--C-TTG-----TGTAATGTGA--GAAAAGCAAAGTTTTCAGCCTGATTGTTTTGAGTTTGCCTG----------CGTG----------------------------G---GGAGCGGCAAAAACTAT---TTGATGATGACAAAAGTCGGTT------TTTTT--------------G----CC------
droSim2	2L:17924725-17924850 +		AATATAAATTTTCC-GAAACTG--C-TTG-----TGTAATGTGA--GAAAAGCAAAGTTTTCAGCCTGATTGTTTTGAGTTTGCTTG----------CGTG----------------------------G---GGAAGCGGGAAAACTAT---TTGGTGATGACAAAAGTCGGTT------T-TTT--------------G----CC------
droSec2	scaffold_7:1986292-1986421 +		AATATAAATTTTCC-GAAACTG--C-TTG-----TGTAATGTGA--GAAAAGCAAAGTTTTCAGCCTGATTGTTTTGAGTTTGCTTG----------CGTG----------------------------GTGCGGAGCGGGAAAACTAT---TTGGCTGATGACAAAAGTCGGTT------TTTTT--------------G----CC------
droYak3	2R:4876750-4876878 +		AATATAAATTTTCC-GAAACTG--C-TTG-----TGTAATGTGA--GAAAAGCAAAGTTTTCAGTCTGATTGTTTTGAGTT-GCCTG----------CGTG----------------------------G---GGAGCGGGAAAACTAT---TTGGCGATGACAAAAGTCGGTT------T-TTT--------------A----CCCGG--T
droEre2	scaffold_4845:5909047-5909172 -		AATATAAATTTTCC-GAAACTG--C-TTG-----TGTAATGTGA--GAAAAGCAAAGTTTTCAGCCTGATTGTTTTGAGTTTGCTTG----------CGTG----------------------------G---GGAGCGGGAAAACTAT---TTGGCGATGACAAAAGTCGCTT------T-TTT--------------G----CC------
dp5	4_group3:4450586-4450751 -		GCATTAAACGTC--GCAAACG---------------AATGAAA--AAAAA---GAGCCGACA-CTCGACAATATTCGGGGGGAAAATGTGAGAAAATGGGGG-AATGGTG------G----------ACTGGGGGCATGC---C---GGAAAAACTACCATTTG--AATGACAAAAGTCGGCA------A--TTGCAATCAGTTATTGTTGTGGAGGAGA
droPer2	scaffold_1:5933758-5933916 -		GGATT--AAGCGTC-GCAAACG---------------AATGAAA--AAAAA---GAGCCGACA-CTCGACAATATTCGGGGGGAAAATGTGAGAAAATGGGGG----------G----------ACTGGGGGCATGC---C---GGAAAAACTACCATTTG--AATGACAAAAGTCGGCA------A--TTGCAATCAGTTATTGTTGTGGAGGAGA

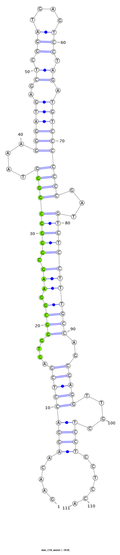
Generated: 09/08/2015 at 07:53 PM

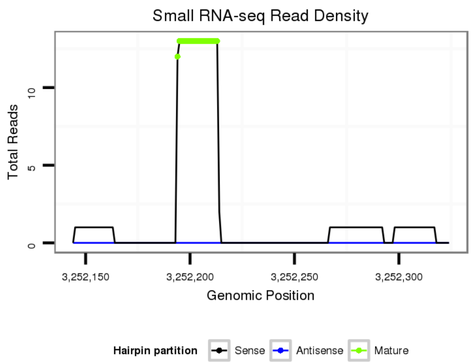
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

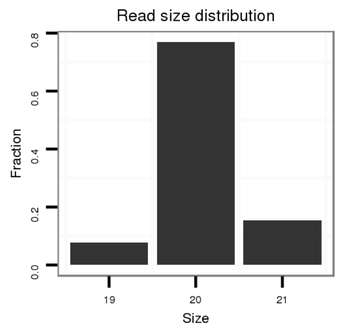
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_220	**scaffold_12911:3252194-3252274 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

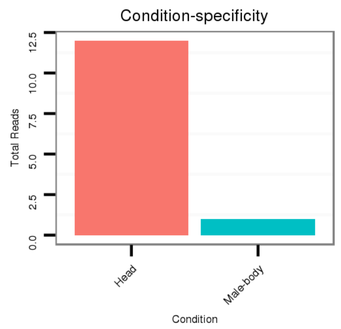
Legend: mature star mismatch in alignment mismatch in read

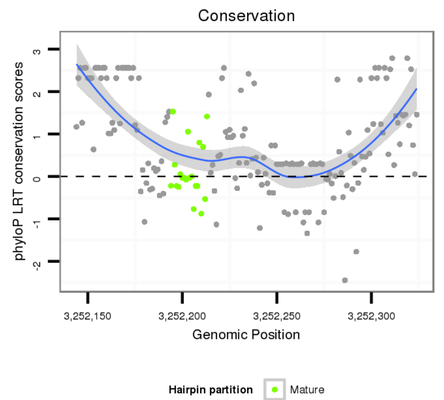
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TCAAATCGCATAAGTTGGCTGCTTTTAATGAAGGAGAACAAGGACCTCGAGTGGGCGGAAGCGGGGCGGGGTAAAGGGATGAGCTCGGATGAGTCCTAGATGTCCCCCCCGATGTCTCCTTTGCCAGCGAGGTTGCTCCTCCTCCAGCGTCCGCCACTTCATCAGGCATTCAAAATCCCTA	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M058 embryo	M044 female body	V055 head	V105 male body	V039 embryo
**********.....(((((((((.....((((.(((.((((((((((.....((((((..((.(((.....))).)).)))))))))...)))))))))))..)))))....)))).....**********											
.....GTGGGCGGAAGCGGGGCGGG.....	20	0	1	10.00	10	9	0	0	0	1	0
.....GTGGGCGGAAGCGGGGCGGGG.....	21	0	1	2.00	2	2	0	0	0	0	0
.....CCAGCGAGGTTGCTCCTCCTCCAGCG.....	26	0	1	1.00	1	0	0	1	0	0	0
.....CACTTCATCAGGCATTCAAA.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TGGGCGGAAGCGGGGCGGG.....	19	0	1	1.00	1	1	0	0	0	0	0
.CAAATCGCATAAGTTGGCT.....	19	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12911:3252144-3252324 +	dan_220	TCAAATCGCATAAGTTGGCTGCTTTTAATGAAGGAGAAC----------AAGGACC----------TCGAGTGGGCGGAAGCGGGGC----------G-GG----GTAAAGGGATGAG--CTC-GGATGAGTCCT----------A----------GATGTCCCCCCCGATGTCTCCTTTGCCAGCGAGGTTGCTCCTC----------CT-----CCAG------CGTC---CGCCACTTCATCA----------GGCATTCAAAATCCCTA
droBip1	scf7180000396640:116221-116396 +		TCAAATCGCATAAGTTGGCTGCTTTTAATGAAGGAGAAC----------AAGGA--------C----------GCCGAGTGGGCGGAAG------------G---G-G---CGTAAAGGGATGAG--CTC-GGATGAGTCCT----------G----------AATGTCCCCCCCAAAGTCCCCTGCCTGAGAATGGCCCTC----------C-----CCAG------CGTC---TGCCACTTCATCA----------GGCATTCAAAATCCCGA
droKik1	scf7180000302778:307931-308083 -		TCAAATCGCATAAGTTGGCAGCTTTTAATGAAGCCCTAC----------G-------ACGCGGCGGGGTTA----------------------------G-AG----GAACTGGGATGAG--ACC-GGCTAAGCCTA----------A----------GGAGA----------------------------GCCTCCGGCGCCGCCATCTC--TCTTCCG------CGTCCGGCCGCCACTTCATCA----------GGCATTCAAAATCCTGA
droFic1	scf7180000453912:1065837-1065991 -		TCAAATCGCATAAGTTGGCAGCTTTTAATGAAGGAGAAC----------GG------ATGCG---GGGTTAAAAAAAGG----------------AAAGGAAAGGAAA----G-G---GGAACCGGGATGAG--CTC-GGCTCAGCCT----------T----------AGAGG----------------------------GCCTC----------CT-----TGG------CGTC---CGCCACTTCATCA----------GGCATTCAAAATCCTGA
droEle1	scf7180000491008:201094-201205 -		TCAAATCGCATAAGTTGGCAGCTTTTAATGAAGGAG--
droRho1	scf7180000766203:1067-1199 +		TCAAATCGCATAAGTTGGCAGCTTTTAATGAAGGAAAC----------G------ATGGG---GGGCCA----------------------------G-AG----GAAAGATGAG--CTCAGGCTCAGCCT----------T----------GGAGA----------------------------GCCTC----------CA-----TGG------CGTC---CGCCACTTCATCA----------GGCATTCAAAATCCTGA
droBia1	scf7180000302136:245370-245504 -		TCAAATCGCATAAGTTGGCAGCTTTTAATGAAGGACGC----------G--G-AG----GAACAGGGATGAG--CTC-GGCTCAGCCT----------TGGAGCAGAGATGAGAT----------G---GATG----------------------------GCCTC----------CT-----TGG------CGTC---CGCCACTTCATCA----------GGCATTCAAAATCCTGA
droTak1	scf7180000414373:150625-150736 +		TCAAATCGCATAAGTTGGCAGCTTTTAATGAAGCCGAAC----------G--G-AG----AACGGGGATGAG--CTC-GGCTCAGCCTC----------T----------------------------TCCTC----------CT-----TGGG-----CGTC---CGCCACTTCATCA----------GGCATTCAAAATCCTCA
droEug1	scf7180000409798:492396-492535 +		TCAAATCGCATAAGTTGGCAGCTTTTAATGAAGGAAGAG----------CA-------ATGTG---GGG----------GATCCT----------G-GG----GAACGGGATGAG--CTC-GGCTCAGCCT----------T----------GGACACG----------------------------GCCC----------C-----TGG------CGC---CGCCACTTCATCA----------GGCATTCAAAATCCTGA
dm3	chr3R:19899991-19900148 -		TCACATCGCATAAGTTGGCAGCTTTTAATGAAGGACA----------G----GGC---GATGGG---GGGCCAGA---GG-------AGCCGATGGTG----------G-AG----GAGCTGGGATGAG--CTCGGCTCAAGCCT----------A----------TCC---GAGG----------------------------GCCTC----------C-----TGG------CGTC---CGCCGCTTCATCAGGC----------GGCATCAAAATCCTCA
droSim2	3r:19438845-19438991 -		TCACATCGCATAAGTTGGCAGCTTTTAATGAAGGACA----------G----GGT---GATAGG---GA----------GCCGATGGTG----------G-AG----GAGCTGGGATGAG--CTCGGCTCAAGCCT----------C----------C---GAGA----------------------------GCCTC----------C-----CGA------CGTC---CGCCGCTTCATCAGGC----------GCATCAAAATCCTCA
droSec2	scaffold_0:20240502-20240645 -		TCACATCGCATAAGTTGGCAGCTTTTAATGAAGGACA----------G----GGT---GATAAG---GA----------GCCGATGTC----------G-AG----GAGCTGGGATGAG--CTCGGCTCAAGCCT----------C----------C---GAGA----------------------------GCCTT----------C-----TGA------CGTC---CGCCGCTTCATCAGGC----------GCATCAAAATCCTCA
droYak3	3R:26601880-26602009 +		TCACATCGCATAAGTTGGCAGCTTTTAATGAAGGACGCC----------CAGGAGC-A--GAT----------A---GAA----------GC----------TGGCAGCTGGAAA----CTGG----GAGCTGGGATGAG--CTCGGCTCAAGCCT----------A--GCA----------C-----TGA------CGC---CGCCGCTTCATCA----------GACATCAAAATCCTGA
droEre2	scaffold_4820:8157558-8157691 +		TCACATCGCTAAGTTGGCAGCTTTTAATGAAGGACGCC----------G------ATGCG---GGGCCA----------------------------G-AG----GAGCTGGGATGAG--CTCGGCTCAAGCCT----------C----------C---GAGA----------------------------GCCTC----------C-----TGG------CGTC---CGCCGCTTCATCA----------GGCATCAAAATCCTGA
dp5	2:14425760-14425925 -		TCAAATCGCATAAGTTGGCAGCTCTTAATGACGGTACAC----------GCAC----------A-----GAAGGAGG----------------------AGCAGGAACAGCACAGGAGTCGGCAGGATGAG--C---ACAGGCTTGGCTCTGGCTCT----------GGCTA----------TG-----CGGACCTGCTTC----TTGCACTTCATCA----------GGCATTCAAAATCCCTA
droPer2	scaffold_0:6000317-6000476 +		TCAAATCGCATAAGTTGGCAGCTGCTTAATGACGGTACAC----------GCAC----------A-----GAAGGAGG----------------------AGCAGGAGCAGCACAGGAGTCGGCAGGATGAG--C---CACAGGCTT----------G----------GGCAC----------------------------TGGCTC----------TG--GCTCTGCGGGACCTGCTTC----TTGCACTTCATCA----------GGCATTCAAAATCCCTA
droWil2	scf2_11000000004902:6007424-6007438 +		---
droVir3	scaffold_12822:3057701-3057865 +		GCAAATCGCATAAGTTGGCAACTTTTAATGAAGCGCAC----------ACACAGCGAAAGAGCGA---GA----GAGTGAG----------GGCGATGCAGCAGA-----------T----G-A---GTATAGAGGAGAAGGGTT-AGCTCACGCCC----------C----------GGCAA----------------------------AGTGCTG----------GG-----TCAA------C--C---CATTC-GTCAAGA----------GGCATCAACATGCTGA
droMoj3	scaffold_6540:7341587-7341710 -		GCAAATCGCTAAGTTGCGAACTTTTAATGAATCTGG----------CA--GTGT---GATA--G-AG----GCGAAGAGGG--CGA-TGCTCACCCCT----------T----------GAGGA----------------------------AGTCAG----------TG-----CCAC------AAGC---CATTCCTTCAACA----------GGCATCAAAGTCCTCA
droGri2	scaffold_14906:4598086-4598284 +		GCAAATCGCATAAGTTGGCAACTTTTAATGAAGCGCCTCGCCTCGCACAACGCCGACAGATACA---GA----GAAAGAGAGCCTGCGGAGGCGAGTGGAGAGAAG----------G-----GGGA----------T----------GTGGTAACCGATACTTCTCTGGCCGAGA----------CAAGTCCTG----------CT-----GCAA------CC---CATTCCTTCAAGAGGCGGCGGCTGGCAGGCAGGCAGCGCAAATCGGTA

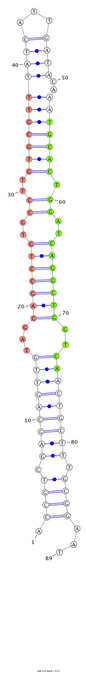
Generated: 09/08/2015 at 07:54 PM

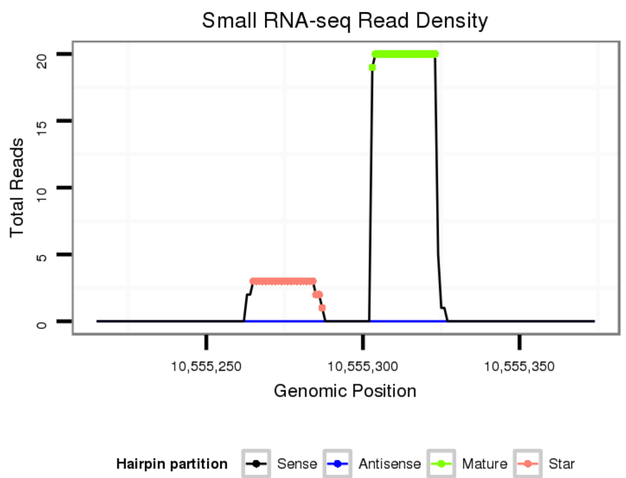
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

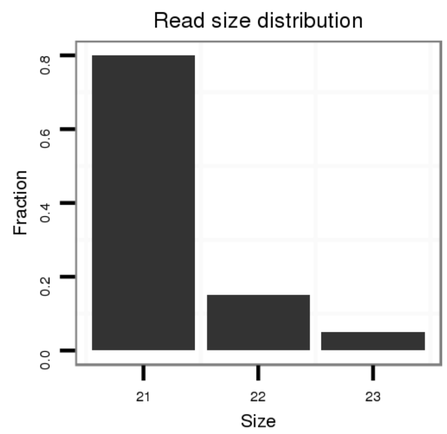
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_114	**scaffold_13266:10555265-10555324 +**	**candidate**	**Canonical miRNA**	**antisense_to_CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

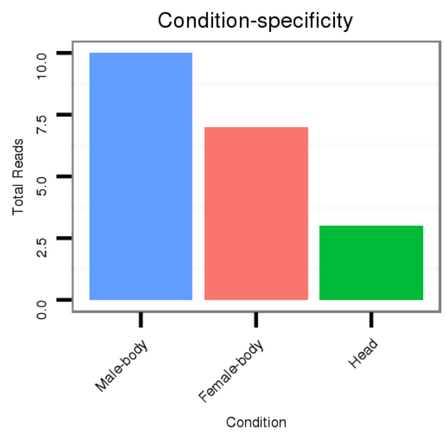
Legend: mature star mismatch in alignment mismatch in read

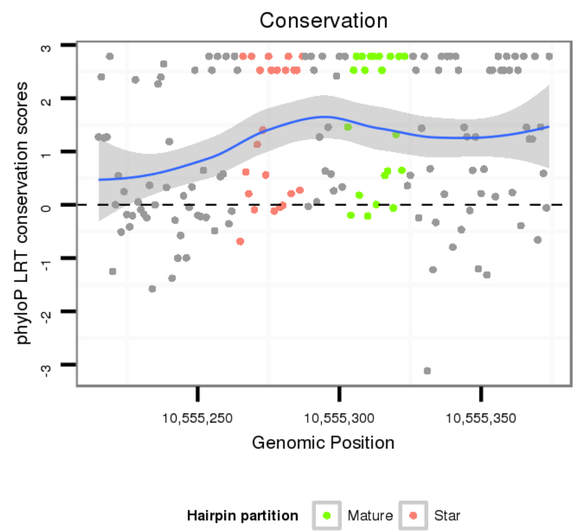
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to CDS [Dana\GF11668-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GGCGTAGAGGACATGATTAACCCATTAACCGATCCACCGTCGAGCAGTTGTAGCAGCCTGTGCCTTGTGCGTTTATCATTGATACAAATGCACTGGATCAGGCTGGTCAACTGCTTTGCGGAATACTCGTCGCTTTGTCGTTGCTGCTCGATCCATTGCT	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	M044 female body	V106 head	V055 head	V039 embryo	M058 embryo
**********.(((((.(((((((((...(((((((..((..((((((((((...))))..))))))).))..))))))).))))))))).))))...**********											
.....TGCACTGGATCAGGCTGGTCA.....	21	0	1	15.00	15	8	4	3	0	0	0
.....TGCACTGGATCAGGCTGGTCT.....	21	1	1	3.00	3	2	1	0	0	0	0
.....TGCACTGGATCAGGCTGGTCAA.....	22	0	1	3.00	3	1	2	0	0	0	0
.....TGTAGCAGCCTGTGCCTTGTGC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TAGCAGCCTGTGCCTTGTGCGTT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GCACTGGATCAGGCTGGTCAA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TGTAGCAGCCTGTGCCTTGTGCGT.....	24	0	1	1.00	1	0	1	0	0	0	0
.....TGCACTGGATCAGGCTGGTCAACT.....	24	0	1	1.00	1	0	0	0	1	0	0

Anti-sense strand reads

CCGCATCTCCTGTACTAATTGGGTAATTGGCTAGGTGGCAGCTCGTCAACATCGTCGGACACGGAACACGCAAATAGTAACTATGTTTACGTGACCTAGTCCGACCAGTTGACGAAACGCCTTATGAGCAGCGAAACAGCAACGACGAGCTAGGTAACGA	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head	V106 head	M058 embryo	V039 embryo
**********.((((.((((((((...(((((((..((..(((((((((...)))))..)))))))).))..))))))).))))))))...**********									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13266:10555215-10555374 +	dan_114	GGCGTAGAGGA--CA-TGATTAACCCATTAACCGATCC---ACCGTCGAGCAGTTGTAGCAGCCTGTGCCTTGTGCGTTTATCATTGATACAAATGCACTGGATCAGGCTGGTCAACTGCTTTGCGGAATACTCGT---CGCTTTGTCGTTGCTGCTCGATCCATTGCT
droBip1	scf7180000396428:977296-977455 +		GGCGTCGTGGA--CA-TGATTAGCCCATTGACCGATCC---ACCATCGAGCAGTTGCAGCAGCCTGTGCCTTGTGCGTTTATCATTGATGCAAATGCACTGAATCAGGCTGGTCAACTGCTTTGCGGAATATTCGT---CGCTTTGTCGTTGCTGCTCGATCCATTGCT
droKik1	scf7180000302385:386504-386665 -		A-CATGTTTAAGCCATTGCCATTGCCATTGCCTTATACC---GCCATCTAGCAGTTGCAGCAACCTTTGGCGCTCGCTTGTCGCTGACACAGATGCACTGAATCAGGCTGGTCAGCTGCTTCGTGGAGTACTCAT---CGCCCAGGCGCTGCTGCTCGATCCACTGCT
droFic1	scf7180000453948:1816748-1816907 +		GGCGTCGTCGA--TG-TGGCTATCCCATTAGGTAATCC---CGTATCGAGCAATTGCAGCAACCTTTGCCTTGTGCGTTTGTCGCTTACGCAAATGCACTGAATAAGGCTGGTCAGCTGCTTAACGGAGTACTCGT---CGCCAAGGCGCTGCTGTTCAATCCACTGTT
droEle1	scf7180000491214:620798-620957 +		GGCGTCGTCGT--TG-TGGTGACCCATTGGCCATTCC---AAGATCCAGCAGCTGCAGAAGCCTTTGCCTTGTTGGCTTGTCGCTGATGCAAATGCACTGAATAAGGCTGGTCAACTGCCTCGGCAGAGTATTCAT---GCCCCAGGCGCTGCTGTTCGATCCACTGCT
droRho1	scf7180000777956:159688-159847 +		GGCGTGGTCGA--GG-TGGTTACCCCATTGGCCAATCC---AAGATCCAGCAATTGCAGAAGCCTTTGGCGTGTGCGCTTGTCGCTAACACAAATACACTGAATAAGGCTGGTCAACTGCCTTGCGGAGTATTCGT---CGCCAAGGCGCTGCTGTTCGATCCATTGCT
droBia1	scf7180000301754:2945101-2945260 +		GGCGTCGTCGA--CG-TGGTCACCCCATTAGCCACTCC---ACCATCGAGCAACTGCAGCAACCTTTGCCGCGTGCGCTTGTCACTGACACAAATACACTGTATCAGGTTGTTCAGCTGCTTCAGGGAGTACTCAT---CGCCGAAGCGCCTGCTGTTCCTATCCATTCTT
droTak1	scf7180000415313:60600-60759 +		GGCGTCGTCGA--CG-TGGTCACCCCATTTGCTATCCC---AAGATCGAGCAATTGCAGCAACCTTTGCCGCGTGCGCTTGTCGCTGACACAAATTGCACTGGATGAGGTTATTTAACTGCTTGAGGGAGTACTCAT---GCCCCAGTCGCTGCTGTTCAATCCATTGCT
droEug1	scf7180000409672:1474959-1475118 +		GGCGTCGTCGA--CG-TGGTTACCCCATTGGGTGTTCC---AAGATCTAGCAAGTGTAGCAGTCCTTTGCCGAGTAGGCTTGTCGCTGA---ATATACATTGAATAAGGTTGTTCAACTGTTTAAGGGAATACTCATGCGTGCCTAATCGCTGCTGTTCAATCCACTGCT
dm3	chr2R:13630724-13630883 -		GGCGTCGTTGA--CA-TTGGCTATTCCATTTTGTATTCC---AGCGTCAAGCAACTGTAGCAACCTTTGTCGCGTGCGTTTATCGCTGACACAAATACAATGCAATAAGGTTGTTCAATTGCTTGAGAGAGTATTCAT---CGCCCGTACGCTGCTGTTCAATCCATTGCT
droSim2	2r:14322780-14322939 -		GGCGTTGTGGA--CA-TGGCTATTCCATTTGGTATTCC---AGCGTCAAGCAACTGCAGCAACCTTTGTCGCGTGCGTTTATCGCTGACACAAATGCACTGAATAAGGTTGTTCAATTGCTTGAGAGAGTATTCAT---CGCCCGTACGCTGCTGTTCAATCCATTGCT
droSec2	scaffold_1:11129356-11129515 -		GGCGTCGTGGA--CA-TGGCTATTCCATTTGGTATTCC---AGCGTCAAGCAACTGCAGCAACCTTTGTCGCGTGCGTTTATCGCTGACACAAATGCACTGAATAAGGTTGTTCAATTGCTTGAGAGAGTATTCAT---CGCCCGTACGCTGCTGTTCAATCCATTGCT
droYak3	2R:15550800-15550959 +		GGCGTAGTTGT--CA-TGGTTATTCCATTTGGTATTCC---CACGTCAAGCAGCTGCAATCAACCTTTGTCGAGTGCGTTTATCGCTGACACAAATGCACTGAATAAGGTTGTTCAATTGTTTGAGTTGAGTATTCAT---CGCCCATACGCTGCTGTTCAATCCATTGCT
droEre2	scaffold_4845:7859769-7859928 -		GGCGTCGTTGT--CA-TGGTTATTCCATTTGATATCCC---AAGGTCAAGCAAGTGCATCAACCTTTGTCGAGTGCGTTTATCGCTGACACAAATGCACTGAATAAGGTTGTTCAATTGTTTGATAAGATTATTCAT---CGCCCATACGCTGCTGTTCAATCCATTGCT
dp5	3:16442425-16442575 -		GGCGTCCC---TT---T-------CCCATTGGCCATTGCTGGCACCGTCCAGTAACTGCAAAAGCCTTTGCCTTGTGCGCTTGTCACTGGCACACGATGCACTGTATTAGGTTGTCAACTGTTTGGCGGAGTAGTCGT---CCTCCTGCCGCTGCTGCTCGATCCACAGTT
droPer2	scaffold_4:319886-320036 +		GGCGTCCC---TT---T-------CCCATTGGCCATTGCTGGCACCGTCCAGTAACTGCAAAAGCCTTTGCCTTGTGCGCTTGTCACTGGCACACGATGCACTGTATTAGGTTGTCAACTGTTTGGCGGAGTAGTCGT---CCTCCTGCCGCTGCTGCTCGATCCACAGTT
droWil2	scf2_1100000004512:2080162-2080321 -		GGCGTTCCACC--AT-TATTTCCTCCAGAACTTGCTCC---ATTTTCCACCACTGTAGCAAGCGCTGTGGTGTGCGCTTATCACTGACACAAATACATTGCAATCAGATTCGTTAATTGCTTTGGGAATATTCCA---CATCCTGACGCTGCTGATCAATCCATTGTT
droVir3	scaffold_12875:7594508-7594652 +		GGTGTAA----T---T---------CACTTGATGCCAC---ACCCTCCAGCAGCTGCAGTAGCCTCTGTCGTGTGCGCTTATCGCTGACACAAATGCATTGTATCAGATTCGTCAATTGTTTGCGGAATATTCAT---CGCCTTGTCGTTGCTGTTCAATCCAGTTTT
droMoj3	scaffold_6496:14355587-14355731 +		GGCGTAACAGT--AC-TGCCA----------C---GCCCTCCAGCAGCTGCAGCAGCCTCTGTCGTGTGCGCTTATGGCTGACACAAACGCATTGTATCAGATTTGTCAATTGCTTAGCTGAATACTCAT---CGCCCAGTCGCTGCTGTTCGATCCACTGCT
droGri2	scaffold_15245:1122594-1122738 +		GGCGTAACA---T---T--------CCAG---CGGCAC---GCCCTCCAACAGCTGCAGCAGCCTCTGTCGTGTGCGCTTGTCGCTGACACAAATGCATTGTATCAGGTTCGTCAATTGTTTCGTCGAATATTCGT---CGCCATGCCGCTGCTGTTCAACAAACTGTT

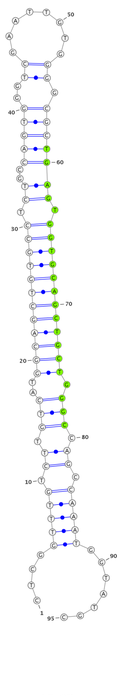
Generated: 09/08/2015 at 07:54 PM

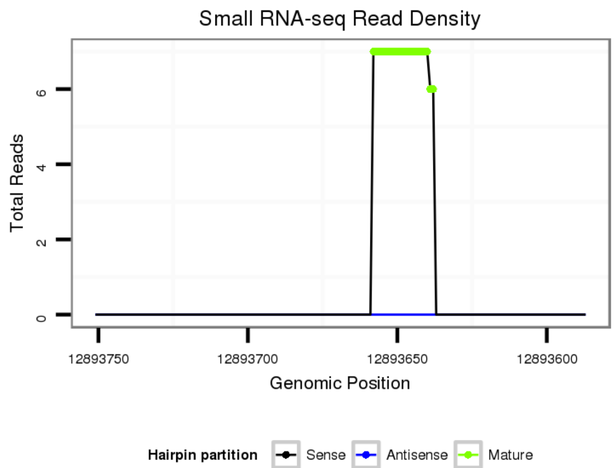
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

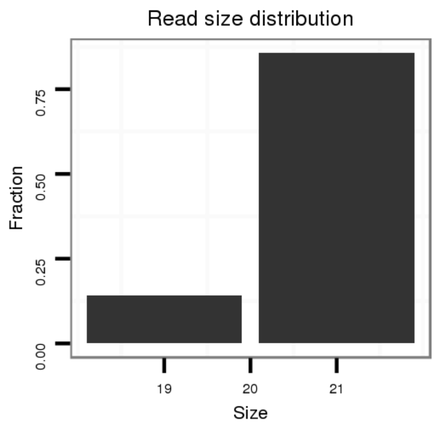
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_181	**scaffold_13340:12893637-12893701 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

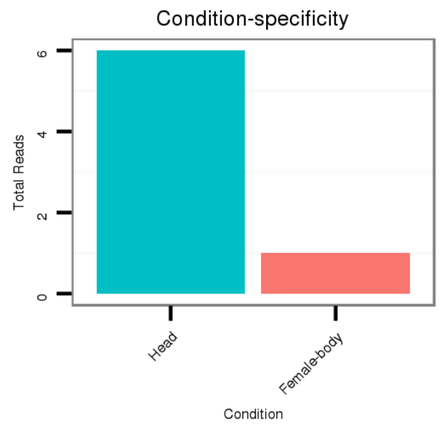
Legend: mature star mismatch in alignment mismatch in read

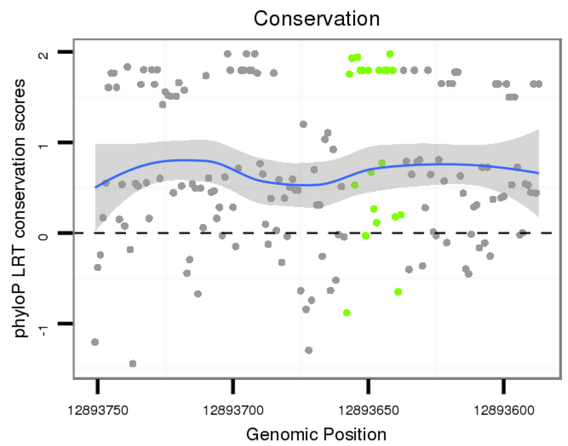
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGCACCTTCTCGAGATTCAGATGATCTTCGCACCACTCGGTTTGTCTTGTCATGGCAGCTGTGCCTCTGCCAGTGGGTCGAATTGTGGGGCGCTGAGTGGTGCAGCTGCTGGGCCAGCCAAATGGTATGCTGCAATCGTTGATCACCGATCGAGTGGTTTACATT	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V039 embryo	M044 female body	V055 head	M058 embryo	V105 male body
**********....(((((.((.(((..(((((((((((((.((..((((((..((........)).)))))))..)))))))))))))).))).)).))))).....**********											
.....TGAGTGGTGCAGCTGCTGGGCA.....	22	1	1	6.00	6	6	0	0	0	0	0
.....TGAGTGGTGCAGCTGCTGGGC.....	21	0	1	6.00	6	6	0	0	0	0	0
.....TGAGTGGTGCAGCTGCTGGGT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TGAGTGGTGCAGCTGCTGG.....	19	0	1	1.00	1	0	0	1	0	0	0
.....TGAGTGGTGCAGCTGCTGGGA.....	21	1	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13340:12893587-12893751 -	dan_181	TGCACCTTCT-CGAGA----------TTCAGATGATCTTCGCACCAC--T-CGG----TTTGTCTT---GTCATGGCAGCTGTGCCTCTGCCAGTGG-------GT-CGAATTGTGGGGCGCTGAGTGGTGCAGCTGCTGGGC-CA------GCCAAATG--GTATGCTGCAATCGTTGAT------CACCGATCGAGTGGTTTACATT
droBip1	scf7180000396691:1775768-1775932 -		TGCACCTTCT-CGAGA----------TCCAGATGATCTTCGCACCAC--T-CGG----TTTGCTTT---GTCATGGCAGCTGTGCCTCTGCCGGTGG-------GT-TATATTGTGGGGCGCTGAGTGGTGCAGCTGCTGGGC-CA------GCCAAATG--GTATGCTGCAATCGTTGAT------CACCGATCGAGTGGTATACATT
droKik1	scf7180000302639:1374366-1374522 +		----------------------ACGCAGCGTGATCTTCACACCGC--T-TAAGAGCTTTGCTTT---GTCATGGCAGCTGCAGTGGAGCGCGCTTAGAATGGCTC-CAA----GTGCCGCAGGAGTGGAGCAGCACGCTGGTCCA-------GCCAAATGTGTTGTGCTGCAATCGAC---GCC-------TCATCGAGAG-ATTACACT
droFic1	scf7180000452523:662186-662341 -		CCAATCTTCT-CGATCCGCAGAA---CCACGCAGATGATCTTCGCACCAC--T-CGG----TTTCCCGT---CTCACTGCAGCTGTGGTGCAGCCGGTGG-------CT-------------CTCAGAGTGGTGCAGCAGCTGGTC-CA-------ACCAGGCG--G--GTTGCTGCAATCCCA--AGAC-------TGATGGAGTG-CTTACACT
droEle1	scf7180000491080:1075109-1075222 -		TGAG------CAAATGGAGAA---CCACGCAGATGATCTTCGCACCAA--T-CGG----ATGCGATT---GTCGCTGCAGCTGTGGTGCAGCCGGTGG-------CT-------------CTCAGAGTGGTGCAACACGCTGCTT-CA-------GTCAAGTG--G--GTT---------------------------------
droRho1	scf7180000779250:21275-21393 +		---ATCTTCT-CGAGCCGCAGAA---CCACGCAGCGTGATCTTCGCACCAA--T-CGG----TTTGGATT---GTCACTGCAGCTGTGGTGCAACCGGTGG-------CT-------------CTCAGAGTGGCGCAACACGCTGCGC-CA-------GTCAAGTG--G--GTT---------------------------------
droBia1	scf7180000302136:901691-901828 -		CACATCTTGC-GCAGA----------------GGCACCGA--T-GAG----ATTGGATT---GTCACTGCAGCTGTGGTGCAGCCGGTGG-------TT------CTG--GTTCCGAGTGGTGCAACACGCTGGGC-CA-------ACCAAGTG--G--GTGCGCAAGCCCA---GCC-------GGATCAAGTG-CTCACACT
droTak1	scf7180000415769:1857770-1857904 +		AACATCTTCT-CAAGACGCA---------------------CCGATCTTCAG----ATTGGATC---GTCACTGCAGCTGTGGTGCAGCCGGTGG-------CT-------------TTCCGAGTGGTGCAACACGCTGGGC-CA-------TCCAAGTG--G--GTTGCTGCAATCACA---GCC-------GGATCAAGTG-CTTACACT
droEug1	scf7180000409281:43297-43426 +		AACATCTTCT-TGAGGTGGAGAA---CCACGCAGATGATCTTCGCACCGT--T-CAG----ATTGGATA---GTCATTGCAGCTGTGGTGCAGCCGGTGG-------CT-------------TTCCGAGTGGTGCTACACGCTGGGC-CA-------GCCAAAAG--G--CGCTGCAAT--------------------------------
dm3	chr3R:11306486-11306624 -		GGCAACTTCCACGAG----------CCACGCAGATGATCTTCGCACCCA--T-CGG----ATTGGATCGTCGTCAGTGCAGCTGTGGAGC---------------------TGAGTGGTGGCACACGCTGGGA-CA-------GCCGATTG--G--GTGTTGCAATCAGA---GTC-------GGATCAAGTG-CTTACACT
droSim2	3r:9922501-9922637 +		GGCAACTTCT-CGAG----------CCACGCAGATGATCTTCGCACCCA--T-CGG----ATTGGGTCGTCGTCAGTGCAGCTGTGGAGCTG-------------------------GTGGTGGCACACGCTGGGC-CA-------GCCGATTG--G--GTGCTGCAATCAGA---GCC-------GGATCAAGTG-CTTACACT
droSec2	scaffold_0:10638094-10638231 +		GGCAACTTCTT-CGAG----------CCACGCAGATGATCTTCGCACCCA--T-CGG----ATTGGGTCGTCGTCAGTGCAGCTGTGGAGC---------------------TGAGTGGCGCACACGCTGTGC-CA-------GCCGATTG--G--GTGCTGCAATCAGA---GCC-------GGATCAAGTG-CTTACACT
droYak3	3R:15122146-15122291 +		GGCATCTTCT-CGAGCCGCAGAACCGCCACGCAGATGATCTTCGCATGCG--C-CAG----ATTGGATT---GTCACTGCAGCTGTGGTGCA---------------------GAGTGGTGCCACACGCTGGGC-CA-------GCCGATTG--G--GTGCTGCAATAAGA---GCC-------GGATCAAGTG-CTTACACT
droEre2	scaffold_4770:10833276-10833379 -		GGCATCTTCT-CGAGCCGCAGAACCACCACGCAGATGATCT-CGCACCCA--C-CGG----ATTGGAGT---GTCGCTGCAGCT----------------------GGTGCCACACGCTGGGC-CA-------CCCGATTG--G--GTGCTGC-----------------------------------
dp5	2:6322783-6322942 +		TGTGTCTTCT-CGAAGAACAGCA---CCACGCAAATGAG----------T-C---------CTT---GTCATGGCAGCTGTGTGTCTGAGCATGG-------ATT------CTGCGAAGGTGACTGGTGCAACACGCTGGCC-CGAACCTGCACCAAGTG--GCATGCCGCAATCGCT---GCCTGCCCCGATCGAGTGGCGTGTACT
droPer2	scaffold_0:146926-147080 +		-----CTTCT-CGAAGAACAGCA---CCACGCAAATGAG----------T-C---------CTT---GTCATGGCAGCTGTGTGTCTGTGCATGG-------ATT------CTGCGAAGGTGACTGGTGCAACACGCTGGCC-CGAACCTGCACCAAGTG--GCATGCCGCAATCGCT---GCCTGCCCCGATCGAGTGGCGTGTACT

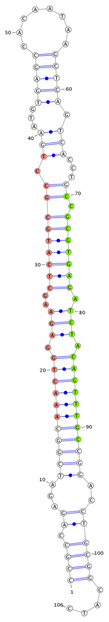
Generated: 09/08/2015 at 07:54 PM

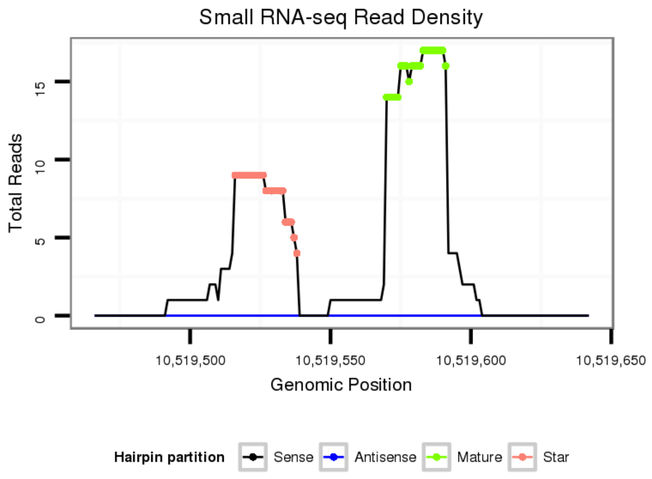
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

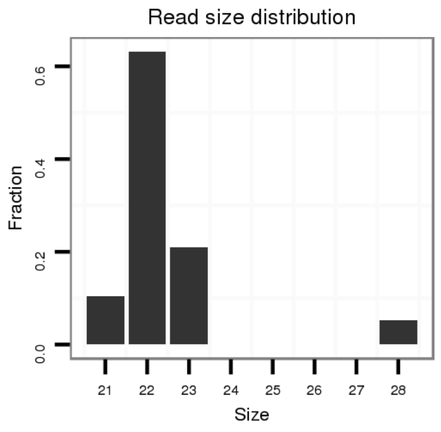
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_119	**scaffold_13340:10519516-10519592 +**	**candidate**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

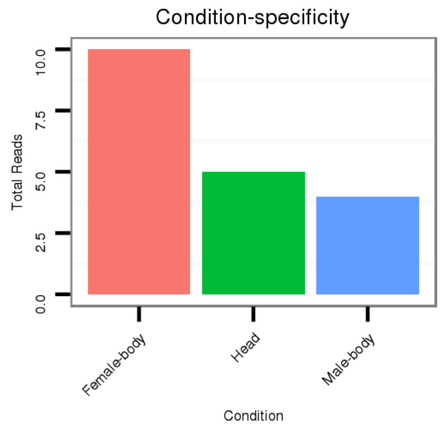
Legend: mature star mismatch in alignment mismatch in read

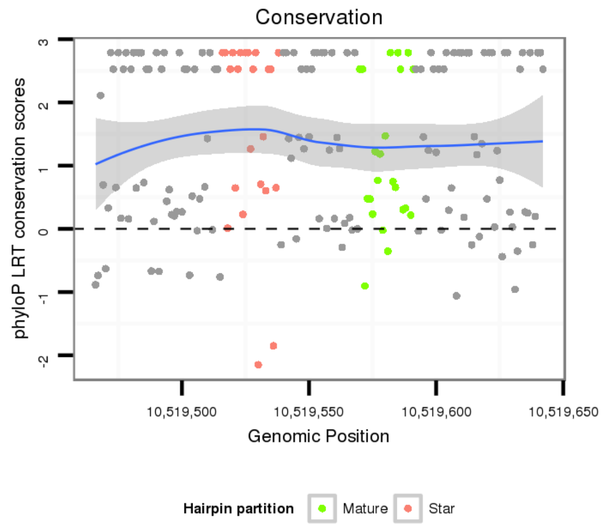
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dana\GF18150-cds]; utr5 [utr5_minus_8885]; intron [Dana\GF18150-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTTTAAAGCTGCATGATAACGCCTTAGTGGAGCTGCCGCCAGAGATCGGCAAACTGGAGAAGCTCATGCGCCTGAATGTGAGCCACAATAAGCTCAGTCACCTGCCGCGTGAGATCTACAGTTTGCCGGACCTGCGGCATCTCAACATTTCATACAACGAGTTCAAGGAACTTGATC **********(((((.((...((((((((((.(((..((((((((((.(((...(((((.....)))))).)))...)).)))))))..)))).)))))))))))..)))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V106 head	V105 male body	V055 head	M058 embryo
..........CCGCGTGAGATCTACAGTTTGC..........	22	0	1	11.00	11	6	3	1	1	0
..........AAACTGGAGAAGCTCATGCGCCT..........	23	0	1	3.00	3	1	1	1	0	0
..........CCGCGTGAGATCTACAGTTTGT..........	22	1	1	2.00	2	1	1	0	0	0
..........TCGGCAAACTGGAGAAGCTCATG..........	23	0	1	2.00	2	2	0	0	0	0
..........ACAGTTTGCCGGACCTGCG..........	19	0	1	1.00	1	1	0	0	0	0
..........AAACTGGAGAAGCTCATGCGC..........	21	0	1	1.00	1	0	0	1	0	0
..........ATCTACAGTTTGCCGGACCTGCGGC..........	25	0	1	1.00	1	1	0	0	0	0
..........CCGCGTGAGATCTACAGTTTG..........	21	0	1	1.00	1	1	0	0	0	0
..........TGAGATCTACAGTTTGCCGGAC..........	22	0	1	1.00	1	0	1	0	0	0
..........GAGATCGGCAAACTGGAGAA..........	20	0	1	1.00	1	1	0	0	0	0
..........CAAACTGGAGAAGCTCATGCGCCT..........	24	0	1	1.00	1	0	0	0	0	1
..........GCCGCGTGAGATCTACAGTTTGC..........	23	0	1	1.00	1	1	0	0	0	0
..........ACAATAAGCTCAGTCACCTGCCGCGTGA..........	28	0	1	1.00	1	1	0	0	0	0
..........GTGGAGCTGCCGCCAGAG..........	18	0	1	1.00	1	1	0	0	0	0
..........AAACTGGAGAAGCTCATGCGCC..........	22	0	1	1.00	1	0	0	1	0	0
..........TGAGATCTACAGTTTGCCGGA..........	21	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

GAAATTTCGACGTACTATTGCGGAATCACCTCGACGGCGGTCTCTAGCCGTTTGACCTCTTCGAGTACGCGGACTTACACTCGGTGTTATTCGAGTCAGTGGACGGCGCACTCTAGATGTCAAACGGCCTGGACGCCGTAGAGTTGTAAAGTATGTTGCTCAAGTTCCTTGAACTAG **********(((((.((...((((((((((.(((..((((((((((.(((...(((((.....)))))).)))...)).)))))))..)))).)))))))))))..)))))))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head	M058 embryo
..........GCCGCGTGAGATCTACAGTTTGC..........	23	0	1	1.00	1	1	0	0	0
..........ACAATAAGCTCAGTCACCTGCCGCGTGA..........	28	0	1	1.00	1	1	0	0	0
..........CAAACTGGAGAAGCTCATGCGCCT..........	24	0	1	1.00	1	0	0	0	1
..........GAGATCGGCAAACTGGAGAA..........	20	0	1	1.00	1	1	0	0	0
..........TGAGATCTACAGTTTGCCGGAC..........	22	0	1	1.00	1	0	1	0	0
..........ATCTACAGTTTGCCGGACCTGCGGC..........	25	0	1	1.00	1	1	0	0	0
..........AAACTGGAGAAGCTCATGCGC..........	21	0	1	1.00	1	0	0	1	0
..........ACAGTTTGCCGGACCTGCG..........	19	0	1	1.00	1	1	0	0	0
..........TCGGCAAACTGGAGAAGCTCATG..........	23	0	1	2.00	2	2	0	0	0
..........CCGCGTGAGATCTACAGTTTGT..........	22	1	1	2.00	2	1	1	0	0
..........AAACTGGAGAAGCTCATGCGCCT..........	23	0	1	3.00	3	1	1	1	0
..........CCGCGTGAGATCTACAGTTTGC..........	22	0	1	11.00	11	6	3	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13340:10519466-10519642 +	dan_119	CT----------TTAAAGCTGCATGATAACGCCTTAGTGGAGCTGCCGCCAGAGATCGGCAAACTGGAGAAGCTCATGCGCCTGAATGTGAGCCACAATAAGCTCAGTCACCTGCCGCGTGAGATCTACAGTTTGCCGGACCTGCGGCATCTCAACATTTCATACAACGAGTTCAAGGAACTTGATC
droBip1	scf7180000396708:5534811-5534987 +		CT----------TTAAAGCTACATGACAATGCCCTAGTGGAGCTGCCGCCAGAGCTCGGCAAACTGGAGAAGCTAATGCGTCTGAACGTGAGCCACAACAAACTCAGTCAGTTGCCCCGTGAGCTCTACAGTTTGCCGGACTTGCGGCACCTCAACATTTCGTACAACGAGTTCACCGAACTTGATC
droKik1	scf7180000302706:533854-534030 -		GC----------TTATAGTTGCACGATAATGGTTTGGTGGAGCTGCCACCAGAGATCGGCAACGTGGAGAAGCTGATGCGCCTGAATGTGAGCCACAACAAGCTTAGCCAGCTTCCCCGTGAGACTATAGTTTACCTGACGCTGCGCCATTTCAACATCTCCTACAACGCCTTAAGGAACTTGATC
droFic1	scf7180000453912:22893-23069 -		TT----------TTGTAGCTTCACGATAATGGTTTAGTGGAGTTGCCACCAGAAATTGGGAAACTGGAAAAGCTTATTCGGTTGAATGTCAGCCACAACAAGCTCAGCCAGCTGCCCCGTGAGATCTACAGTTTGCCGGAGCTGCGACATCTCAATTATTCGTACAATGAATTCGACGAAATCCATC
droEle1	scf7180000491047:1668171-1668347 +		CT----------TTTTAGCTGCACGATAATGGTTTGGTGGAACTGCCGCCAGAAATCGGGAAGCTGGAGAAGCTAATGCGGCGTAAATGTAAGCCACAACAAGCTTAGCCAGTTGCCCCGTGAGTTGTACAGTTTGCCGGACGCTGCGGCATCTCAACATCTCGTACAATTCAGTTCAACGAAATCGATC
droRho1	scf7180000769095:38654-38830 +		TT----------TTGTAGCTGCACGATAATGGTTTGGTGAAACTGCCGCCAGAAATCGGAAGCTAGAGAAGCTAATGCGCCTCAATGTAAGCCACAACAAGCTCAGTCAGCTACGGCGCGAGATCTACAGTTTGCCGGACGCTGCGACATCTCAACATCTGCTACAATGGGTTCACCGAAATCGATC
droBia1	scf7180000302402:2260312-2260488 -		CG----------TTTTAGCTGCACGATAATGGTTTGGTGGAGCTGCCTTCGGAAATCGGGAAACTGGAAAAGCTGATGCGCCTCAATGTGAGCCACAACAAACTCAGCCAGCTGCCCCGTTCGATCTACAGTCTGCCGGAGCTGCGACACCTCGAACATTTCGTACAATGAGTTCAACGAAATCGATC
droTak1	scf7180000415380:351620-351790 -		--**----------**----AGTTGCACGATAATGGCTTAGTGGAGCTACCATTGCGAAATCGGGAAGCTGGAGAAGCTCATCCGTCTTAATGTGAGCCACAACAAGCTCAGCCAGCTGCCCCGTTCGATCTACAGTTTACCTGAGCTGCGACACCTCAACATCTCGTACAATGAATTCAACGAAGTCGATC
droEug1	scf7180000409802:450663-450839 +		TA----------TTTTAGCTGCATGATAATGGTTTAGTGGAGCTACCGTCCGCGAAATTGGCGAAGCTGGAAAAGCTTATGCGTCTGAATGTTAGCCACAACAAGATCAGCGAGCTACCCCGTGAGATCTATAGCTTACCAGAGCTGCGACATCTTAACATCTGCTACAATGAGTTCAAAGAAATCGATC
dm3	chr3R:9523592-9523764 -		T---------**---TAGCTGCACGATAATGGTTTGGTGGAGTTACCACCGGAGATCGGCAACGTGGAAAAGCTAGTGCGCCTTAATGTGAGCCACAACAAACTCAGCCAGCTGCCGCGTGCGATGTACAGTCTACGGAGCTGCGGCACCTCAACATCTGCTACAACGAGTTCGTCGAACTTAATC
droSim2	3r:11655298-11655472 +		TA----------T--TAGCTGCACGATAATGGTTTGGTGGAGTTACCACCGGAGATCGGCAAGCTGGAAAAGCTAATGCGCCTTAATGTGAGCCACAACAAACTCAGCCAGCTGCCCCGTGAGATCTACAGTCTACGGAGCTGCGGCACCTCAACATCTGCTACAACGAGTTCGACGAACTCAATC
droSec2	scaffold_0:12483552-12483724 +		T---------**---TAGCTGCACGATAATGGTTTGGTGGAGTTACCACCGGAGATCGGCAACGTGGAAAAGCTAATGCGTCTTAATGTGAGCCACAACAAGCTCAGCCAGCTGCCCCGTGAGATGTACAGTCTACGGAGCTGCGGCACCTCAACATCTGCTACAACGAGTTCGACGAACTCAATC
droYak3	3R:13832027-13832197 -		--**----------**----AGCTGCATGATAATGGTTTGGTGGAGTTGCCACCGGAGATCGGGAAGCTGGAAAAGCTAATGCGCCTTAATGTGAGCCACAACAAACTCAGCCAGTTGCCCCGTGAGATATACAGTCTACGGAGCTGCGACACCTCAACATCTGCTACAACGAGTTTAACGAGCTTAATC
droEre2	scaffold_4770:12111486-12111674 +		ATGCAAAATCCAAATATTAGCTGCATGATAATGGCTTGGTGGAGTTGCCACCGGAGATCGGAAGCTGGAAAAGCTAATGCGCCTTAATGTGAGCCACAACAAACTCAGCCAGCTGCCCCGTGAGATATACAGTCTACGGAGCTGCGACACCTCAACATCTGCTACAACGAGTTCAACGAACTTAATC
dp5	2:10074808-10074982 -		TT----------T--TAGCTCCATGACAACGCCCTGGTTGCTCTGCCGGCGGAGATCGGTAACGTGGAGAAGCTTATGCGCCTGAATGTGAGTCGCAACAAGCTCAGCGATTTGCCGCGAGAGCTGTACAGCCTGCCGGAGCTGCGGCATCTGAATATCAGCTATAATGAGTTCAGCGAACTCAATC
droPer2	scaffold_0:10406527-10406701 +		TT----------T--TAGCTCCATGACAACGCCCTGGTTGATGTCCGGCGGAGATCGGTAAGCTGGAGAAGCTTATGCGTCTGAATGTGAGTCGCAACAAGCTCTGCGATTTGCCGCGAGAGCTGTACAGCCTGCCGGAGCTGCGGCATCTGAATATCAGCTATAATGAGTTCAGCGAACTCAATC
droWil2	scf2_1100000004943:10972120-10972296 -		CC----------TTTCAGCTGCATGACAATGGGTTGGTTGAGTTGCCACCCCAGATCGGCAAACTAGAGAAGCTCACGCGCGCTGAATCTTAGCCACAATAAGCTAAGTCAATTGCCGCGTGAGCTCTTCAGTTTGCCGGTCCTGAGGCATCTCAATATTTCGTACAATGAATTTACTGACGCTAAATC
droVir3	scaffold_12822:1486135-1486305 -		--**----------**----AGCTGCATGACAATGGCCTCGTCGCGCTGCCGCCAGAGATTGGGAAACGTGGAGAAGCTGGTGCGCCTGAATCTTGGCCACAATAAGCTAAGCGAATTGCCAATCGAGCTATTCAGCTTGCCAGAGCTGCGGCATCTAAATATATCACATAATGAATTCATTGACGCTCAATC
droMoj3	scaffold_6540:11620711-11620882 +		C---------**----AGCTGCATGACAATGGTCTGGTCGAGCTGCCGCCGCAGATTGGCAAGCTGGAGAAGCTGGTGCGCCTGAATCTTAGCCACAATAAGCTAAGGAATTACCGCCGACCTCTACAGCTTGCCAGAGCTGCGGCATCTGAACATATGCGCATAACGAGTTCGAGGAGCTCAATC
droGri2	scaffold_14624:2532075-2532246 -		C---------**----AGCTGCATGACAATGGTTTAGTCTCATGCGCACCAGAGATAGGCAACGTGGAGAAACTGGTGGCATTGAATCTTAGCCACAACAAGCTAAGTGAATTGCCAGCCGAGTTCTACAGCTTGCCAGAGCTGCGGCATTTAAATATATGCGCACAATGAATTCCTCGAACTCAATC

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

	PASS/FAIL
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crit.loop	0
crit.mor	0
crit.half	0
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crit.tptop3	1
crit.uri	0
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rescue.known	0
rescue.confident	0
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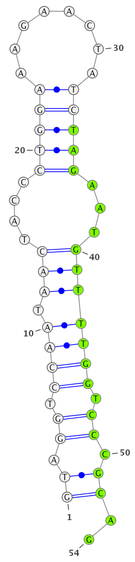
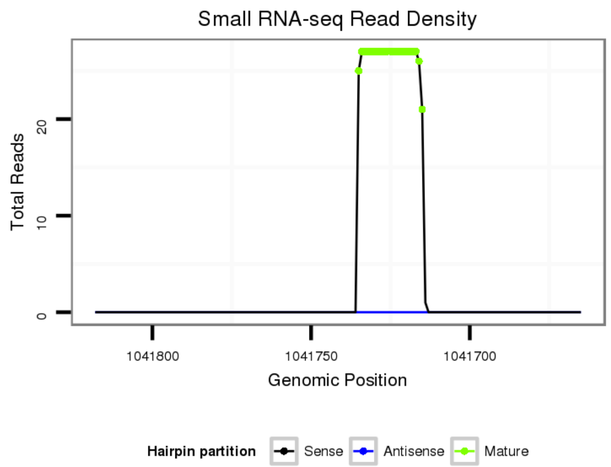
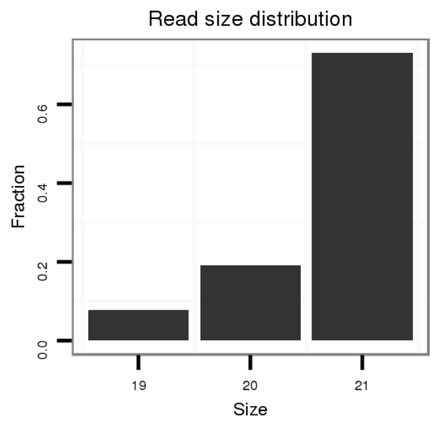
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_2331	**scaffold_13337:1041715-1041768 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

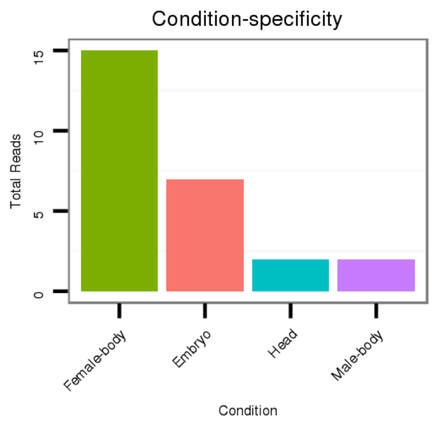
Legend: mature star mismatch in alignment mismatch in read

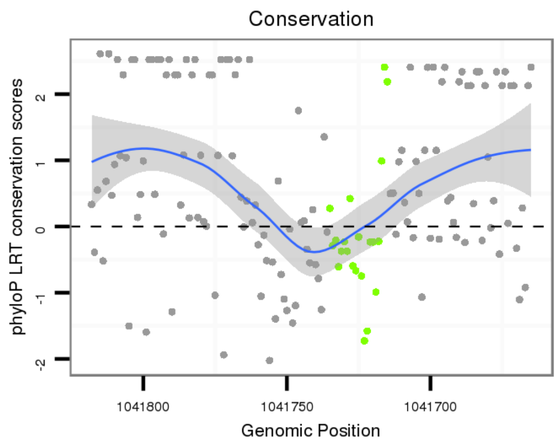
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF24836-in]; CDS [Dana\GF24836-cds]; CDS [Dana\GF24836-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATGTCAAGGAGCGCATTTCTAAGAAGGATGGAGACGAGAAGGCCTTAAAGGTAGGTCCAATAACTACCCTGGAAAGAACTATCTAGAATGTTTTGGTCCCGCAGAAAGAGTTGGAAAAAATAGAGAATGAAGGCAAGGAGTTGGACCGCGTTGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	M058 embryo	V105 male body	V055 head	V039 embryo	V106 head
**********(((.(((.(((((.(((....(((((.........)))))...)))))))).)))..)))..**********											
.....TAGAATGTTTTGGTCCCGCAG.....	21	0	1	19.00	19	9	6	2	1	1	0
.....TAGAATGTTTTGGTCCCGCAGT.....	22	1	1	5.00	5	2	1	2	0	0	0
.....TAGAATGTTTTGGTCCCGCA.....	20	0	1	4.00	4	4	0	0	0	0	0
.....TAGAATGTTTTGGTCCCGCAAT.....	22	2	1	1.00	1	0	0	1	0	0	0
.....AGAATGTTTTGGTCCCGCAG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TAGAATGTTTTGGTCCCGC.....	19	0	1	1.00	1	0	0	0	0	0	1
.....TAGAATGTTTTGGTCCCGCAA.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TAGAATGTTTTGGTCCCGCAGA.....	22	0	1	1.00	1	0	0	0	0	1	0
.....AGAATGTTTTGGTCCCGCA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TAGAATGTTTTGGTCCCGCAGC.....	22	1	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

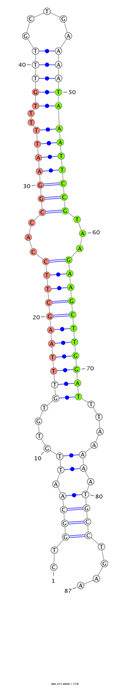
Re-alignment of all predicted orthologs

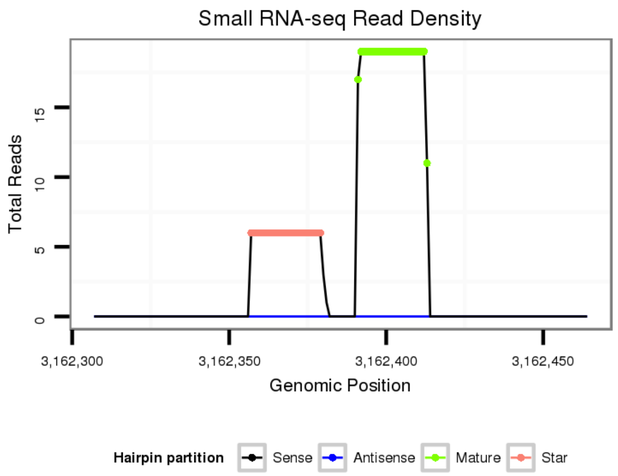
Species	Coordinate	ID	Alignment
droAna3	scaffold_13337:1041665-1041818 -	dan_2331	ATGTCAAGGAGCGCATTTCTAAGAAGGATGGAGACGAGAAGGCCTTAAAGGTAGGTCCAATAACTACCCTGGAA------AG-------AACTAT-----CTAG----AA----------TGT-T----TTGGTCCCGCAGAAAGAGTTGGAAAAAATAGAGAATGAAGGCAAGGAGTTGGACCGCGTTGA
droBip1	scf7180000396371:1372593-1372747 -		ACGTCAAGGAGCGCATATCCAAGAAAGATGGAGACGAGAAGGCCTTAAAGGTAGGTTCAATAGCTACCGTACAA-------AG-------AACCGT-----CTAG----AA----------TGTAT----TTGTTCCTGCAGAAAGAGCTAGAAAACATAGAGAATGAAGGCAAGGAGTTGGACCGAGCTGA
droKik1	scf7180000302577:284644-284805 +		ACGTCAAGGAGCGGATTTCAAAGAAGGACGGCGACGAGGAGGCCCTTAAGGTGCGTCACTGTCCAATT-GTCATGTAGACC--AA---AA-TGT--AATTTC----CTT----------GT-TA----ATTAACCCGCAGAAGAGCGTAGAGAAGCATCGAGAGCGAGGGCAAGGAGTTGGATCGCGATCGA
droFic1	scf7180000454113:276703-276757 -		C----------------------

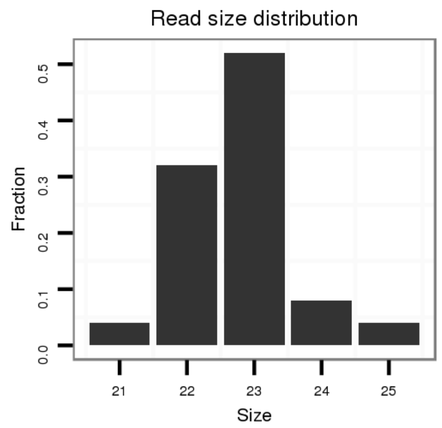
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_113	**scaffold_13340:3162357-3162414 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

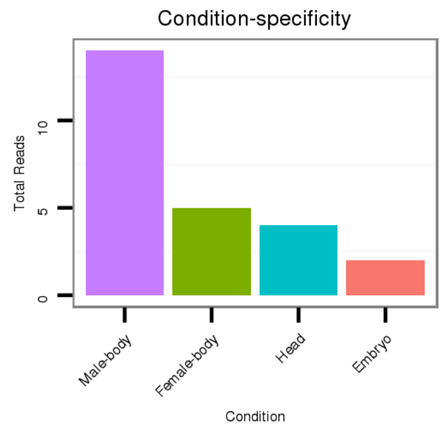
Legend: mature star mismatch in alignment mismatch in read

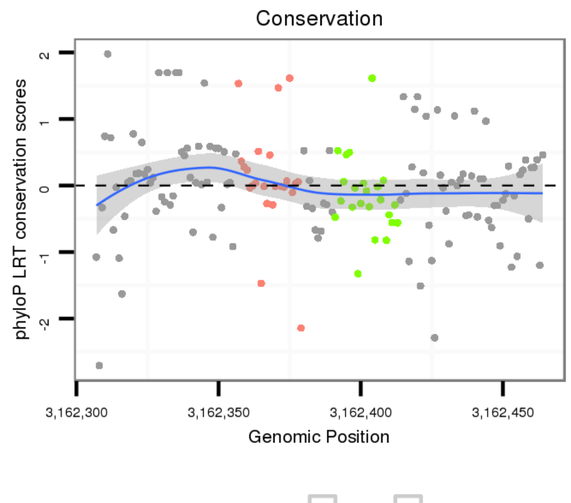
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAAAAATAAAGTGTGTGCAGTCATCAAATATTTATCTGGCAATTGTGTGTTTAAGCTTCCACCGGAATTTTTGTTTGCTGAAAATAAATTCCGTAAGAAGCTTGGATTTAAAAATGCCTGAACACCTGTATAATTATTAATTAGGTAAGTTAGACTAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	female body	V055 head	M058 embryo	V106 head	V039 embryo
************************************..(((((.((....((((((((((...(((((((..(((((.....)))))))))))))...)))))))))))....)).)))).....************************************											
.....TAAATTCCGTAAGAAGCTTGGAT.....	23	0	1	10.00	10	8	1	0	1	0	0
.....TAAATTCCGTAAGAAGCTTGGA.....	22	0	1	7.00	7	3	2	1	0	1	0
.....TTAAGCTTCCACCGGAATTTTTG.....	23	0	1	3.00	3	1	2	0	0	0	0
.....TTAAGCTTCCACCGGAATTTTTGT.....	24	0	1	2.00	2	0	0	1	1	0	0
.....AAATTCCGTAAGAAGCTTGGAT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TTAAGCTTCCACCGGAATTTTTGTT.....	25	0	1	1.00	1	0	0	1	0	0	0
.....AAATTCCGTAAGAAGCTTGGA.....	21	0	1	1.00	1	1	0	0	0	0	0
.....AAATTCCGTAAGAAGCTTGGAG.....	22	1	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13340:3162307-3162464 +	dan_113	AAAAAATAAA-GTGTGTGCAGTCATCAA--ATATTTATCTGGCAATTGTGTGTTTAAGCTTCCACCGGAATTTTTGT------T--TGCTGAAAATAAATTCCGTAAGAAGC-TTGGATTTAAAAATGCCTGAA---CACCTGTATAATTATTAATTAG----------GTAAGT----TAGACTAA
droBip1	scf7180000396712:1195882-1196075 -		AAAAAATAAA-TTGTGTGCAGTCATCAA--ATATTTACATGGCATTTGTATGTTTAAGCTTCTATCGGGATTGCTGT------T--TGTTGAAAATAAATTCCGTAAGATGC-TTGGATTTAAAAAAGCCTAAA---CACCTGTAT----------T-AAATACATAACTTAGTTTATTGCATCAGCAGATGTAGCTTGACTTTTTTTTGGAGTTTA
droKik1	scf7180000302706:166242-166456 +		AGAAAAAGCG-GTGTGTGCGTTCAGAAA--ATAATTACATGGTATTTGTATGCTTAGGCATTGTTTGGCTTTTCCTTATTTT--TATTTTAAGTAAGGTGGAACTAATGC-TTGGACCTACTAAAACCCAA---CAACTGTTTCATTTCTCTCCAAAGTACAGTGTTAAATTATATTTTATTGCATCAGCAGACTTAGTTCTGATTTTA--AAGTAAGCTAA
droFic1	scf7180000454063:245696-245804 -		TCTAAAAAAA-ACGTGTGAAAGAAAATATATATTCACATAGCCATTATAGTTT---GTGAATTTTAGGTTTATTCC------CTGAATAAGGAATTGAATGCCTTA-GAAAAT-T----------
droEle1	scf7180000491104:947953-948091 -		TCGAAAAAAC-GCATATGAGACAAAAT--ATA--TTTATGGCATTTT--------AAAATATATCGGGACTATTT------TGGTGCCAAGAGTATATTCCTCAAGATAC-TAAACTTTTTAAAGGCATTAT---TATTTGAACAATCATTTTTCA
droRho1	scf7180000779661:259383-259440 +		GAAAAACATG-GCGTGTGAAACAACATT--TTAT-TAAATGGCATTTATACTTTTAAAGCATC----------
droBia1	scf7180000302155:1208306-1208493 -		TCAAAAAACCCTCGAGTGAAACCATATTATATTTGCACAGCACATGTTGTTTT------GTCGGT-GTATTCT------TGTCCCTTAACCTATATTCCGAAGGAAA-CAG-GCT-TAGA-AAGCTCCAACT-GCT----------
droTak1	scf7180000415875:577971-578182 +		AGAAAATAAC-CCGTGTGAAACCAAAATATATTTACATAGCATTTATATGTTTAAGCATCTATCGGGATTATTATA-----GTGCGCTAA-GCCAATTTACAAGGAAAG-ATG-GCTTTTGA-ATGCAGAAACTATCTTTCAAGAATCATTTATTTAGTATT-AACATTAAATCATGTTTTATTGCATCAGCAGACTTATCTTTAGATTCTCC
droEug1	scf7180000409760:288150-288321 +		AAAAAACT--GAATGTGAAACGAGATTATTTATTTACATGGCAGTAAAATATTAAATCATGATCGGGATTATATT------TGTGCCAAGACCACATTTTGAAAGACATTCCT----------
dm3	chr3R:3389173-3389308 +		GGAAAAAAGC-GAATGGGAAACCAAAAT--GTATATACGTGGCATTTATATTT----GGATATTATTGGGATTATTAT------GTGTGCTAA-ACCAAATTTCAAAATAAA-ATGTATGCTACAAATG----------
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droSec2	scaffold_6:3480797-3480885 +		TGGAAAAAAGTGAATGGGAAACCAAAAA--ATATATATGTGGCA----------TATATCGGGATTATTAT------GTGTGCTAA-ACAAAATTTCAAAATAAA-ATT----------
droYak3	v2_chr3R_random_112:8950-8961 +		TGGAAAAAAGTC----------
droEre2	scaffold_4770:3649075-3649189 +		TAGAAAAAAGTGAATGGGAAACCAAAAA--ATATATACATGGTATTTATATGTTT--GGATATATCGGGATTAGTT------GTGTGTTA-ACAAAATTCCAAAATAAA-ATTGTTATTACAAAT----------
dp5	2:26780409-26780452 +		AAACAGTGCC-GTGTAGAAATT----------
droPer2	scaffold_6:2091958-2092001 +		AAACAATGCC-GTGTAGAAATT----------

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	PASS/FAIL
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crit.half	0
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rescue.known	0
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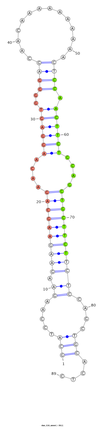
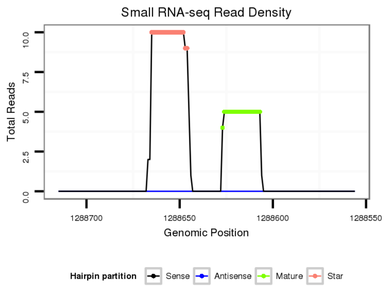
rescue.candidate	1

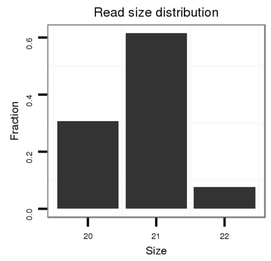
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_116	**scaffold_13334:1288606-1288665 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

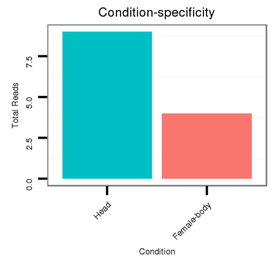
Legend: mature star mismatch in alignment mismatch in read

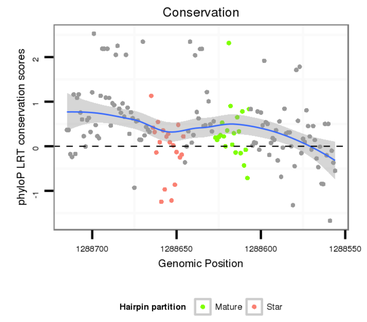
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GCAGCGGCAGCAGCAGCGATTGCAGTTGCCAGCACGCATCCAAGAAGAACAAGCAGAACAAGGAGTGGGGAGCAACAAAAAAAAAACTCCAACTTCTGCAGCTGCTTCTTCTCCAGCTGCACTCCTTCGACTATGCCCCCCCACTATATATAGTATATAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	V055 head	M058 embryo	V105 male body	V039 embryo
********************************(((.....((..(((((((((((....(((((((..(((((.....)))).)))))).....)))))))))))....))).....**********************************												
.....CCAACTTCTGCAGCTGCTTCT.....	21	0	1	4.00	4	3	0	1	0	0	0
.....AAGCAGAACAAGGAGTGGGG.....	20	0	1	4.00	4	0	3	1	0	0	0
.....AAGCAGAACAAGGAGTGGGGATT.....	23	2	1	1.00	1	1	0	0	0	0	0
.....AAGCAGAACAAGGAGTGGGGAG.....	22	0	1	1.00	1	0	1	0	0	0	0
.....AGAAGCAGAACAAGGAGTGGGGA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....AGAAGCAGAACAAGGAGTGG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....AAGCAGAACAAGGAGTGGGGCT.....	22	2	1	1.00	1	1	0	0	0	0	0
.....AAGCAGAACAAGGAGTGGGGT.....	21	1	1	1.00	1	1	0	0	0	0	0
.....AAGCAGAACAAGGAGTGGGGAT.....	22	1	1	1.00	1	0	0	0	0	1	0

Anti-sense strand reads

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

Show Alignment With Reads

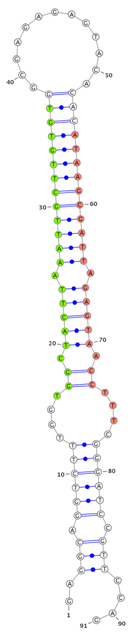
Re-alignment of all predicted orthologs

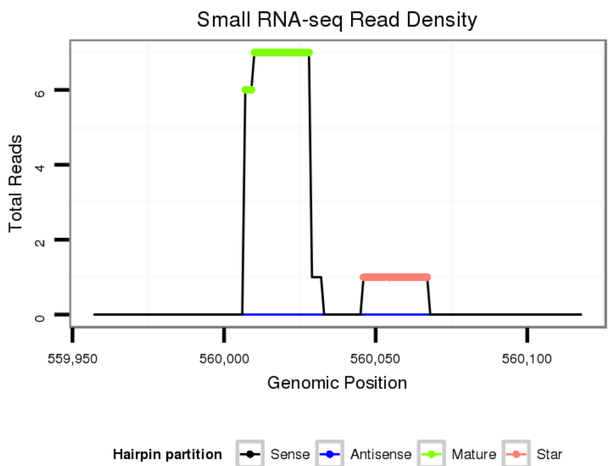
Species	Coordinate	ID	Alignment
droAna3	scaffold_13334:1288556-1288715 -	dan_116	GCAGCGGC----------AGCA----------GC--AGCGATTGCAGTTGCCAGCACGCATCCAAGAAGAAGAAG----------CAGAACAAGGA----------G----------TGGG----------G----------AG--A----------CAACAAAA--AAAAAACTCCAACT-----T----------CTGCAGCTGCTTCTTCTCCAGCTGC------ACTCCTTCGACTATGCCCCC---------CCAC----------TATATAT----------AGTATATAT
droBip1	scf7180000395198:26759-26916 -		GTAGCAGCTC----------CAGCA-GCAGCAGCTAGAACGC--AGCGATTGCAGTTGCCAGCACGCATCCAAGAAGAAGAAG----------CAGAACAAGGA----------G----------TGGG----------G----------AC-----G----------CAAGAAAAGCAAGAAACTCCAACT-----T----------CTGCAGCTG------T--TT-T---TCTCTTCTCACTA-TACCCC---------C----------CCA----------CTATATAT
droKik1	scf7180000302395:326730-326881 +		GCTTCGGC----------ACAGC----------GC--AGCGATTGCAGTTGCCAGCACGCATCAAGAAGAAGAAG----------CAGAACAAGGAAGAAGTAGTGGA----------G----------AGGG----------AGATATGGA-GTTGG-T-AAAG----------AGGAAAACAAG---AGCAAGAAACCCAGCT----------G----------CTGCAGCTC------T--TT-T---TTT-G---TCGCTT-T------GCCCC---------CCACACACCCC--ACA----------CCCCATT----------CCCTCTCCA
droFic1	scf7180000454077:428062-428225 +		---CGGC----------AGCA----------GC--AGCGTTGCAGTTGCCAGCACGCATCAAGAAGAAGAAG----------CAGCACAAGGC----------G----------AGGG----------A----------AA-AAAGG----A-AAAA----------AGAAAAACAAAAGCAAGAAACTCCAACT-----T----------CTGCAGCCT------T--TT-T---TTT-G---TCGCTT-T------GCCCC---------CCACACACCCC--ACA----------CCCCATT----------CCCTCTCCA
droEle1	scf7180000490214:962456-962627 +		A-TTCGGC----------AGAGG----------GC--AGCGATTGCAGTTGCCAGCACGCATCAAGAAGAAGAAG----------AAGTGAAGA----------ATA----A----GTGTG----GG----------AGGG----------GGG--T---GGTGT----AAGAAA----------AGGAATC-----T---GAAACTCCAACT-----T----------CTGCAGCTTA----------T----------CCCCCACACTATAACACACCC---ACACCCCCCACACTC---GTGTGTGT
droRho1	scf7180000780082:267155-267300 -		GC------AGAGG----------GC--AGCGATTGCAGTTGCCAGCACGCATCAAGAGAAGAAG----------ATGTG----------GGTGG----GGGA----------AGGG----------G----------GC----AAGAAA----------AGGAAT-----TGAAACTCCAACT-----T----------CTT----------T----TA-CCCCCACACTATAACACACCC---ACAACCACCCC---T----------TCCCCACA
droBia1	scf7180000302187:562516-562674 -		---CGGC----------AGCA----------GC--AGCGTTGCAGTTGCCAGCACGCATCAAGAAGAAGAAG----------AAGTATT----ATAGAACCC---C-CT----GG----------A----------CGG----GGGATGGGC---CC-GGGGAGGCC---CAAAAC----------GGAAAT-CAAAAGCAAGAAACTCCAACT-----T----------CTGC----------T----------CCGCACTC---T----ATGCC-CC-CCACCCCG----------C
droTak1	scf7180000415564:98388-98551 -		GC------AGCA----------GCAGCCGCATTGCAGTTGCCAGCACGCATCAAGAAGAAGAAG----------AAGAATGTGGC----------GGA----------TGGG----------GGC--T-GG--AAAAG----AGAAA----------AGGAAAACAAAAGCAAGAAACTCCAACTTCAACT----------T----------CTGCAGCTGGCCGTTCTCTTTTTGTTCTCTTTCTTT----T-CCCC---------CCAC----------A----------CCCCCC
droEug1	scf7180000408193:526510-526700 -		---CGGC----------AGCA----------GC--AGCGATTGCAGTTGCAGCACGCATCAAGAAGAAGACAC----------AAGGG-----T----------ACG----------TT-GAAGAAGGCGGGC----------GGA--T--T-AAAGG----AAGAAA----------AGGGAATCAAAAGCAAGAAACTCCAACT-----T----------CTGCAGCTGGCCGTTCTCTCTTTGTTCTCTTTCTTT----T-CCCC---------CCAC----------A----------CCCCCC
dm3	chrX:20926186-20926387 +		---CGGC----------AGCA----------GC--AGCGATTGCAGTTGCCAGCACGCATCAAGAAGAAGAAG----------AAGGG-----AATCGAATGC---T--ATGATGGGAGG----GCGTGGA----------AGGG----------GGGTAGGGG--AAAGG----AAGAAA----------AGGAAACAAAAGCAAGAAACTCCAACT-----T----------CTGCCTTCC------T--TT-TGTTCTCTCTTCCTTCGC------CCCA----------CCAC-----CCCCCCCA
droSim2	scf19652375-19652580 +		---CGGC----------AGCA----------GC--AGCGTTGCAGTTGCCAGCACGCATCCAAGAAGAAGAAG----------AAGAA-----AAGA-GGGAATCGAATT----ATGAGC----------GGA----------AGGG-GGCGGC----------G--GCAGGGG--GTAGG----AAGAAA----------AGGAAACAAAAGCAAGAAACTCCAACT-----T----------CTGCCTTCC------T--TT-TGTTCTCTCTTCCTTCGC------CCCA----------CCAC-----CCCCCCCA
droSec2	scaffold_8:3215074-3215255 +		---CGGC----------AGCA----------GC--AGCGATTGCAGTTGCCAGCACGCATCCAAGAAGAAGAAG----------AAGAA-----AAGA-GGGAATCGAATG----ATGATC----------GGA----------AGGG-TGGCCGG----------G--GCAGGGG--GTAGG----AAGAAA----------AGGAAACAAAAGCAAAAACTTTAACT-----T----------CTGCCTTCC------T--TT-TGTTCTCTCTTCCTTCGC------CCCA----------CCAC-----CCCCCCCA
droYak3	X:20134657-20134817 +		GC-CGGC----------AGCA----------GC--AGCGATTGCAGTTGCCAGCACGCATCCAAGAAGAAGAAG----------AAGGG-----G----------TT-GGCTTA----------G--GGCGGG--GAAGG----ATAAGA----------AGGAAACAAAAGCAAGAAACTCCACT-----T----------CTGCAGCTTC------T--TT-TGTTCTCTCTTCCTTCGC------CCCC----------CCAC-----CCCCCCCA
droEre2	scaffold_4690:17498468-17498650 +		---CGGC----------AGCA----------GC--AGCGATTGCAGTTGCCAGCACGCATCCAAGAAGAAGAAG----------AAGAAGG-----GAATCGAGTGAAGTCCGATGAGC----------GGA----------AGGG----------AT-GGG----GAAGG----ATAGAA----------AGGAAACAAAAGCAAGAAACTCCAACT-----T----------CTGCAGCTTC------T--TT-TGTTCTCTCTTCCTTCGC------CCCA-----CCAC-----CCCCCCCA
dp5	3:4117535-4117673 -		GCAGCAGC----------AGCA----------GC--AGCAGCACGCATTGCAGTAGC-------T----------A----------A----------A

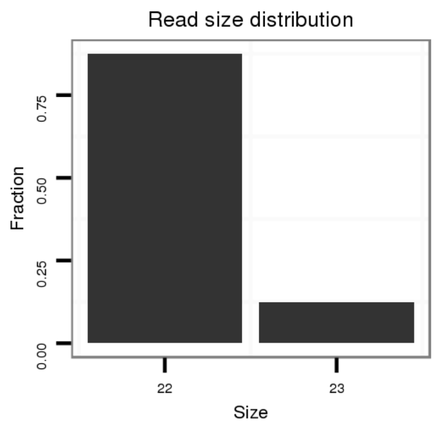
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_251	**scaffold_12903:560007-560068 +**	**candidate**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

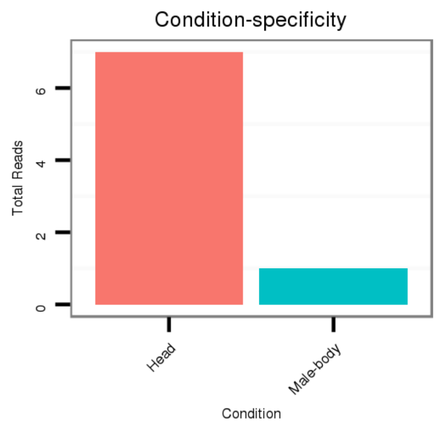
Legend: mature star mismatch in alignment mismatch in read

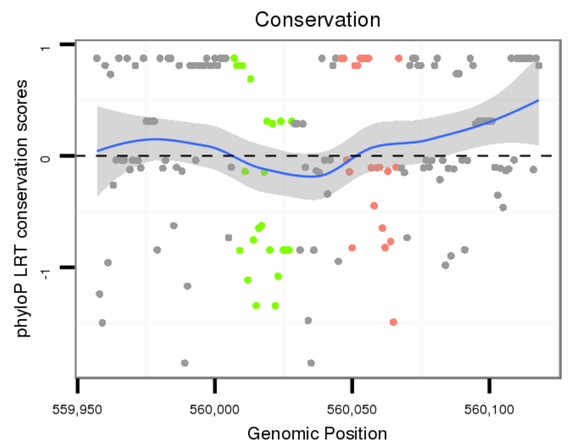
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAGCGAAAAAAAAACCGAAAAATTCCTTATCGAGGGAGGCAGGTCTTTGGTGGCTACTTAAATTGCTTGTGTGGCGAGAGAGTACACACATAAGCGATTAGAGTAACCTTTCGGGATCCGTTCCAGCAACAGCAACTGCATATATAGAGTATATTATTTATG	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V055 head	M044 female body	V105 male body
**********..(((.(((((((....((.(((((.(((((((((((((.....)))))))))))))).)))))..))....)))))))..)))....**********										
.....TGGCTACTTAAATTGCTTGTGTGT.....	24	1	1	7.00	7	3	0	4	0
.....TGGCTACTTAAATTGCTTGTGTGT.....	22	0	1	6.00	6	2	3	0	1
.....TGGCTACTTAAATTGCTTGTGTGTT.....	25	2	1	1.00	1	1	0	0	0
.....TGGCTACTTAAATTGCTTGTGTGT.....	23	1	1	1.00	1	1	0	0	0
.....CTACTTAAATTGCTTGTGTGGCT.....	23	1	1	1.00	1	1	0	0	0
.....GGCTACTTAAATTGCTTGTGTGT.....	23	1	1	1.00	1	0	0	1	0
.....ATAAGCGATTAGAGTAACCTTT.....	22	0	1	1.00	1	0	1	0	0
.....CTACTTAAATTGCTTGTGTGGCG.....	23	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

TTCGCTTTTTTTTTGGCTTTTAAGGAATAGCTCCCTCCGTCCAGAAACCACCGATGAATTTAACGAACACACCGCTCTCTCATGTGTGTATTCGCTAATCTCATTGGAAAGCCCTAGGCAAGGTCGTTGTCGTTGACGTATATATCTCATATAATAAATAC	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_12903:559957-560118 +	dan_251	AAG-CGAA---------AAAAAAACCGAAAAATTCCTTATCGAGGGAGGCAGGTCT-TTGGTGGCTACTTAAATTGCTTGTGTGGCGAGAGAGTACACACATAAGCGATTAGAGTAACCTTTCGGGATCCGTTCCAGCAAC----------AGCAACTGCATATATAGAGTATATTATTTATG
droBip1	scf7180000395925:48291-48454 -		AGTGCAAAAAACTGACAAAAAAACCGAAAAACTTCTTATCTTCGGAGGCAGGTCT-TTAGTGTCCTCACTATTCCGGTACATGGTGATTTTATACACATATACACGATTAGCGTTGAGCTTTAAGATCCGTTCCAGC-------------AC-CTGCATATATA--TAGTATTATTTATG
droEle1	scf7180000490751:845095-845240 -		AAA-CA-C---------TAGGAAGCTTA-----TCTTTGGGGTGGGGGCAGGTCTCTTTGTCCCT---AGGT----------CTGAAATGGTCACATTCCCGATTATATGGCCAAGTCATGATCCTCGTCACTGGTACTAAAAAGAAATTGGTGTTG------CCGTTGTTTATTTATG
droTak1	scf7180000415843:938913-939061 +		ATT-CGAA---------TAGGAGGCTTA-----TCTTTGGGCTGGGGGCAGGTCT-TTTATGCCTCCTCGTT----------CCCAAATGCTCATATTCCCGATTATATGGCCGTGTCATGATCCTCGTCACTTGAACGAGAAAGAAACTGGTGTTG------CCGTTGTTTATTTGTG

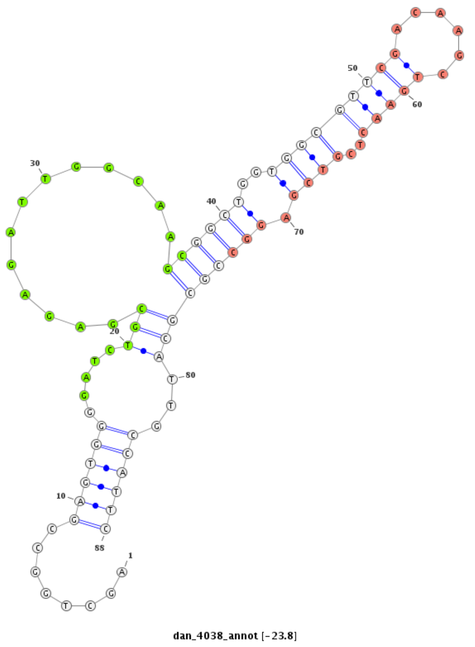
Generated: 06/08/2015 at 08:04 PM

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_4038	**scaffold_13337:4137445-4137533 +**	**candidate**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

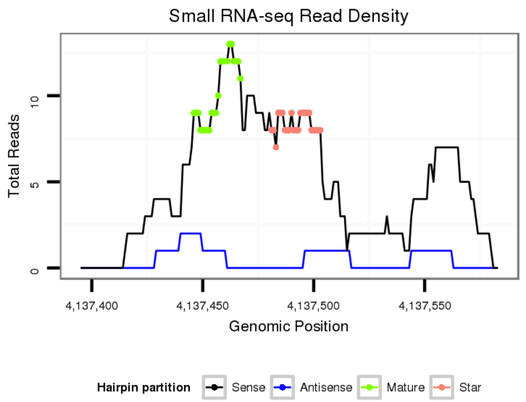
Legend: mature star mismatch in alignment mismatch in read

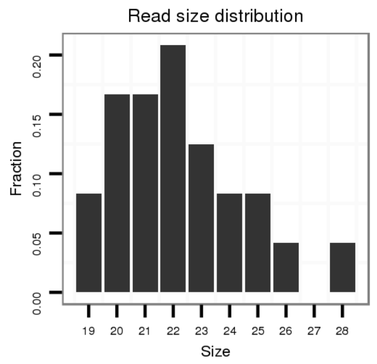
Predicted structure

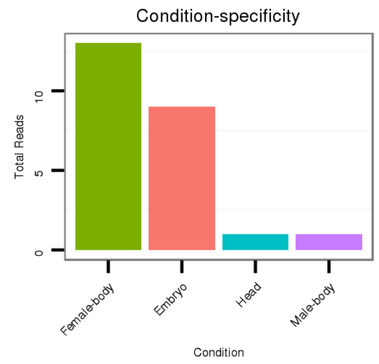


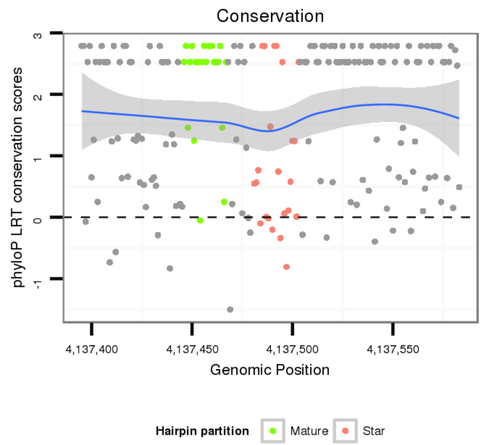
dan_4038_annot [-23.8]

Show Alternate Folds









Flybase annnotation

CDS [Dana\GF25174-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AACGAGGCGGAGGCGCAGGCCTTCGCCGAGGCCCAGAGCTGGCCGAGTGGGGATCTGCGAGAGATTGGCAAGCGGCTGGTGGCGTTCGACAAGCTGAACTCGTCGAGGCCGCGCATTGCCATTCTCACGCAGGGCTGTGATCCCGTGCTGCTCTTCCAGCAGGACTCGGTGCAGGAGTTCCCGGTCACA	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	M058 embryo	V105 male body	V106 head	V039 embryo	V055 head
..GTGGGGATCTGCGAGAGATT	20	0	1	2.00	2	0	0	1	0	1	0
....GATCTGCGAGAGATTGGCAAGC	22	0	1	2.00	2	0	1	1	0	0	0
..CGACAAGCTGAACTCGTCGAGGC	23	0	1	1.00	1	1	0	0	0	0	0
..CTGGTGGCGTTCGACAAGCTG	21	0	1	1.00	1	1	0	0	0	0	0
..GGCCCAGAGCTGGCCGAGTGGG	22	0	1	1.00	1	1	0	0	0	0	0
..GGCAAGCGGCTGGTGGCGTTCG	22	0	1	1.00	1	1	0	0	0	0	0
....GATCTGCGAGAGATTGGCAAG	21	0	1	1.00	1	0	1	0	0	0	0
..TTCGCCGAGGCCCAGAGCTGGCCG	24	0	1	1.00	1	1	0	0	0	0	0
..CAAGCTGAACTCGTCGAGGC	20	0	1	1.00	1	0	1	0	0	0	0
..AGGACTCGGTGCAGGAGTTCCCGGTC...	26	0	1	1.00	1	0	1	0	0	0	0
..AGTGGGGATCTGCGAGAGATT	21	0	1	1.00	1	0	0	1	0	0	0
..GATCCCGTGCTGCTCTTCCAG	21	0	1	1.00	1	1	0	0	0	0	0
..CTGGTGGCGTTCGACAAGCT	20	0	1	1.00	1	0	1	0	0	0	0
..CAAGCTGAACTCGTCGAGGCCGCGCATT	28	0	1	1.00	1	1	0	0	0	0	0
..CTCTTCCAGCAGGACTCGGTG	21	0	1	1.00	1	1	0	0	0	0	0
..GATTGGCAAGCGGCTGGTGGC	21	0	1	1.00	1	1	0	0	0	0	0
..GCAAGCGGCTGGTGGCGTT	19	0	1	1.00	1	1	0	0	0	0	0
..TCGTCGAGGCCGCGCATTGCC	21	0	1	1.00	1	1	0	0	0	0	0
..TTCTCACGCAGGGCTGTGATCCCGT	25	0	1	1.00	1	1	0	0	0	0	0
..GCTCTTCCAGCAGGACTCGGTG	22	0	1	1.00	1	1	0	0	0	0	0
..GGATCTGCGAGAGATTGGCAAGC	23	0	1	1.00	1	0	0	0	0	1	0
..ATTGGCAAGCGGCTGGTGGCGTT	23	0	1	1.00	1	1	0	0	0	0	0
..GGCAAGCGGCTGGTGGCGTTCGACAA	26	0	1	1.00	1	1	0	0	0	0	0
..GAACTCGTCGAGGCCGCGCATT	22	0	1	1.00	1	1	0	0	0	0	0
..GCTCTTCCAGCAGGACTCGGTGCAGGA	27	0	1	1.00	1	0	1	0	0	0	0
..AGGACTCGGTGCAGGAGTT	19	0	1	1.00	1	0	1	0	0	0	0
..AGCAGGACTCGGTGCAGGAGTTCCCGGT....	28	0	1	1.00	1	0	1	0	0	0	0
..AGCAGGACTCGGTGCAGGAGT	21	0	1	1.00	1	0	0	1	0	0	0
..GGCAAGCGGCTGGTGGCGTT	20	0	1	1.00	1	0	0	0	1	0	0
..ATTGCCATTCTCACGCAGGGCTGTG	25	0	1	1.00	1	1	0	0	0	0	0
..GACAAGCTGAACTCGTCGAGGC	22	0	1	1.00	1	1	0	0	0	0	0
..AGAGATTGGCAAGCGGCTGG	20	0	1	1.00	1	1	0	0	0	0	0
..GAACTCGTCGAGGCCGCGCATTGCC	25	0	1	1.00	1	0	1	0	0	0	0
..GTGGGGATCTGCGAGAGATTGGC	23	0	1	1.00	1	0	0	1	0	0	0
..CTTCGCCGAGGCCCAGAGCTG	21	0	1	1.00	1	1	0	0	0	0	0
..CAGAGCTGGCCGAGTGGGGAT	21	0	1	1.00	1	0	0	0	1	0	0
..TCGACAAGCTGAACTCGTC	19	0	1	1.00	1	0	1	0	0	0	0
..CGACAAGCTGAACTCGTCGAGGCC	24	0	1	1.00	1	0	1	0	0	0	0
..ATTGGCAAGCGGCTGGTGGCGTTC	24	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

TTGCTCCGCCTCCGCGTCCGGAAGCGGCTCCGGGTCTCGACCGGCTCACCCCTAGACGCTCTCTAACCGTTCGCCGACCACCGCAAGCTGTTCGACTTGAGCAGCTCCGGCGCGTAACGGTAAGAGTGCGTCCCGACACTAGGGCACGACGAGAAGGTCGTCCTGAGCCACGTCCTCAAGGGCCAGTGT	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V105 male body	V106 head	V055 head	M058 embryo
..CAGCTCCGGCGCGTAACGGTA	21	0	1	1.00	1	1	0	0	0	0
..CGAGAAGGTCGTCCTGAGC	19	0	1	1.00	1	0	0	1	0	0
..TCTCGACCGGCTCACCCCTAG	21	0	1	1.00	1	0	1	0	0	0
..TCACCCCTAGACGCTCTCTAA	21	0	1	1.00	1	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13337:4137395-4137583 +	dan_4038	AACGAGGCGGAGGCGCAGGCCTTCGCCGAGGCCCAGAGCTGGCCGAGTG---GGGATCTGCGAGAGATTGGCAAGCGGCTGGTGGCGTTCGACAAGCTGAACTCGTCGAGGCCGCGCATTGCCATTCTCACGCAGGGCTGTGATCCCGTGCTGCTCTTCCAGCAGGA---CTCGGTGCAGGAGTTCCCGGTCACA
droBipl	scf7180000395450:265900-266088 +		AACGAGGCGGAGGCGCAAGCCTTCGCCGAGGCCCAGAGCTGGCCGAGTG---GGGATCTGCGAGAGATTGGCAAGCGGCTGGTGGCGTTCGATAAGCTGAATACGTCAATGCGTCGAATTGCCATTCTCACGCAGGGATGCCGATCCCGTGCTGCTCTTCCAGCAGGA---CTCGGTGCAGGAGTTCCCGGTCAGG
droKik1	scf7180000302272:666717-666905 -		AATTGAGGCGGAGGCGCAGGCCTTGCCGAGGCCCAAAATGGCCGAGCG---AGGATCTGCGTGAGATTGGCAAAGCGCTGGTGGCAATGGACAAACGTAAATCGGTCGCGGGCGACGCATTGCCATGCTCACGCAGGGTTGTGATCCCGTCGTGCTGATCCAGCAGGA---TTCGGTGCAGGAATTCCCGGTCACA
droFic1	scf7180000454048:724234-724422 +		AATTGAGGCTGAGGCCAGGCCTTCGCCGAGAAACAGAATGGCCGAGCG---GGGATCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGACAAACGTGAATCCGGCGCGGGCGACGCATTGCCATGCTCACGCAGGGCTGCGATCCCGTCGTGCTGATCCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCACA
droEle1	scf7180000491255:1412089-1412277 -		AACGAGGCGGAGGCGACAGGCCTTCGCCGAGGCCCAGAACTGGCCGAGCG---GGGATCTGCGCGAGATTGGCAAGCGGCTGGTGGCGATGGACAAGCTGAATCCGGCGCGGGCGACGCCGCATTGCCATGCTCACGCAGGGCTGCGATCCCGTGCTGCTGATCCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCAGG
droRho1	scf7180000769477:967-1151 +		AACGAGGCGGAGGCGACAGGCCTTCGCCGAGGCCCAGAACTGGCCGAGCG---GGGATCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGACAAACGTGAATCCGGCGCGGGCCGCGCATTGCCATGCTCACGCAGGGCTGCGATCCCGTGCTGCTGATCCAGCAGGA---TTCGGTGCAGGAGTTCCCGGT----
droBia1	scf7180000302193:2253856-2254044 -		AACGAGGCGGAGGCGACAGGCCTTCGCCGAGGCCCAGAGTTGGCCGAGCG---GGGATCTGCGCGAGATTGGCAAGCGGCTGGTGGCGTTCGACAAACGTGAATCCGGCGCGGGCGGCGCATTGCCATTCTCACGCAGGGCTGCGACCCGTGCTGCTCTTCCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCAGG
droTak1	scf7180000415706:66147-66335 -		AACGAATCGGAGGCTCAGGCCTTCGCCGAGGCCCAGAGTTGGCCGAGCG---GGGATCTGCGCGAGATTGGCAAGCGCTGGTGGCGCTGGACAAGCTGAATCGGCGCGGGCGGCGCATTGCCATGCTCACGCAGGGCTGCGATCCCGTCGTGCTGATCCAGCAGGA---CTCGGTGCAGGAGTTCCCGGTCAGG
droEug1	scf7180000409711:6101265-6101453 -		AACGAGGCGGAGGCAGAGCCTTCGCCGAGGCCCAGAATTGGCCAAGTG---GGGATCTCGTGAGATTGGCAAGCGACTGGTGGCGATGGCAAATTAAATCGAGCGGGCCGCGCATTGCTATGCTCACGCAGGGCTGTGATCGTGTCGTGCTTATCCAACAGGA---CTCGGTACAGGAGTTCCCGGTCAGG
dm3	chr3L:13013576-13013764 -	dme_245	AACGAGGCGGAGGCTCAGGCGTTCGCCGAGGCCCAGCAGTGGCCGAGCG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGAGAAGAAAAACGCGAGCGGGCCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATTCAGCAGGA---TTCGGTGCAGGAATTCCCGGTCAGG
droSim2	3L:12704025-12704213 -	dsi_32458	AACGAGGCGGAGGCTCAGGCGTTCGCCGAGGCCCAGCAGTGGCCGAGCG---GGGACCTGCGCGAGATTGGCAAGCGATTGGTGGCGATGAGAAGAAAAACGCGAGCGGGCCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATTCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCAGG
droSec2	scaffold_0:5185161-5185349 -	dse_1846	AACGAGGCGGAGGCTCAGTCGCTTCGCCGAGGCCCAGCAGTGGCCGAGCG---GGGACCTGCGCGAGATTGGCAAGCGATTGGTGGCGATGAGAAGAAAAACGCGAGCGGGCCGCGCATTGCCATTCTCACGCAGGGCTGCGATCCTGTACTGCTTATTCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCAGG
droYak3	3L:13092479-13092667 -	dya_1798	AACGAGGCAGAGGCTCAGGCCTTCGCCGAGGCCCAGCAGTGGCCGAGCG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGAGAAGAAAAACGCGAGCGGGCCGCGCATTGCCATCCTCACGCAGGGCTGCGATCCTGTCGTGCTGCTTATTCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCAGG
droEre2	scaffold_4784:13021109-13021297 -	der_1523	AACGAGGCGGAGGCTCAGGCCTTCGCCGAGGCCCAGCAGTGGCCGAGCG---GGGACCTGCGCGAGATTGGCAAGCGACTGGTGGCGATGGACAAGAAAAACGCGAGCGGCGACGCGCATTGCCATGCTCACGCAGGGCTGCGATCCGTGTCGTGCTGATCCAGCAGGA---TTCGGTGCAGGAGTTCCCGGTCAGG
dp5	XR_group6:4377266-4377454 -	dps_3829	AATGAGGCGGAGGCGCAAGCCTTGCTACGGCCCAGCGCTGGCCGACGCG---AAGATCTGCGCGAGATTGGCAAGCGGCTGGTGGCGCTGGACAAACGTGAATCCGGCGCGACGCGCATTGCCATACTAACGCAGGGCTGTGATCCCGTGCTGCTGATCCAGCGGGA---CTCGGTTGAAGAGTTTCCGGTCACA
droPer2	scaffold_9:2666447-2666635 -	dpe_2483	AATGAGGCGGAGGCGCAAGCCTTGCTACGGCCCAGCGCTGGCCGACGCG---AAGATCTGCGCGAGATTGGCAAGCGGCTGGTGGCGCTGGACAAACGTGAATCCGGCGCGACGCGCATTGCCATACTAACGCAGGGCTGTGATCCCGTGCTGCTGATCCAGCGGGA---CTCGGTTGAAGAGTTTCCGGTCACA
droWil2	scf2_1100000004511:5276750-5276938 +	dwi_5417	AATGAGGCGGAGGCTCAGTCGCTTGCCACTGCCCAGCGCTGGCCGAGCG---AAGATCTGCGCGAGATTGGCAAGCGATAAGTCCGTCGTGGAGAAACGTAAATCGAAGCGGGCCGCGCATTGCCATACTAACGCAGGGCTGTGATCGCGTGTTGCTCATTCAAAATGA---TTCGGTTGAAGAGTTTCCGGTTACA
droVir3	scaffold_13049:22492152-22492341 +	dvi_158	AACGAGGCGGAGGCGGAGCGCATTGCCACTGGCGAGGTTGGCCGCCGCGACAATGATCTGCGTGAGATTGGCAAGCGGCTGGTGGCGCCGCTGGATAAAACGTCAATACGGCGCGACGCGACGCATTGCCATACTCACGCAGGGCTGTGACCCGTGCTGCTTATTACAGCAGGA---TTCGGTCCAGGAGTTTCCGAGTGACA
droMoj3	scaffold_6680:17099712-17099903 +	dmo_114	AACGAAGCAGAGGCGCAAGCCTTGCCACGGGCCAAGGCTGGCCGCCGCGATGCGGATCTGCGTGAGATTGGCAAGCGTTGGTGGCAGTGCCAAAATCAATTCAGAGCGACGCGACGCATTGCCATACTCACGCAGGGCTGTGACCCGTGCTGCTGATCCAGCAGGA---CGAAGGTCCAGGAGTTCCCGGTCACA
droGri2	scaffold_15121:203613-203807 +	dgr_465	AATGAGGCGGAGGCGAAGGCTTTGCCACGGGCAAGAGGCTGGCCGCCGCGATGAGGATCTGCGTGAGATTGGCAGGCGCAGCGACGCATTGCGATACTCACGCAGGGCTGTGATCCCGTGCTGCTGATCCAGCAGGACGGCTCCGGTCCAGGAGTTCCCAGTTACA

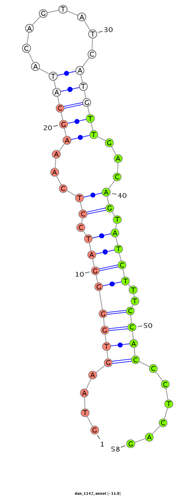
Generated: 09/08/2015 at 07:55 PM

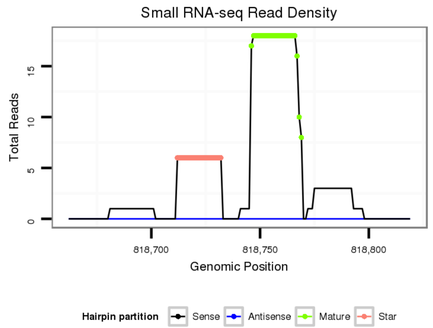
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	0
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	10

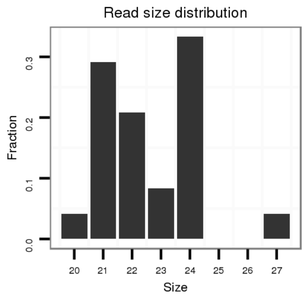
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_1142	**scaffold_13047:818712-818769 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

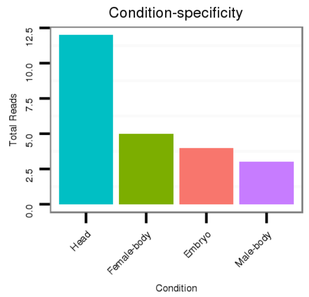
Legend: mature star mismatch in alignment mismatch in read

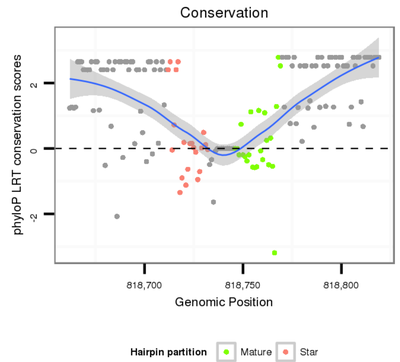
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dana\GF19194-in]; CDS [Dana\GF19194-cds]; CDS [Dana\GF19194-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GGCCATAGGCGAGTATGGCGACCTGTTCATGTACGGAGCAAACGAAGACGGTAAGTGGG-G--A----------T-C----------CTCAAA-GCAT------AC---AGTATCATGTTGACAGTATCT------TTCCACCCTCAGAGTTCGAACGGCCCACTGAGAGCGATCTGATCGCCGTGTACCATAAGTTT												
....(((((((((.((...(((((.........)))))...))..)))))..))))......	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M058 embryo	M044 female body	V055 head	V105 male body	V039 embryo
.....TTGACAGTATCTTTCCACCCTCAG.....	24	0	1	8.00	8	2	2	4	0	0	0
.....GTAAGTGGGGATCCTCAAAGC.....	21	0	1	6.00	6	3	0	0	0	3	0
.....TTGACAGTATCTTTCCACCCTC.....	22	0	1	5.00	5	3	1	0	1	0	0
.....TTGACAGTATCTTTCCACCCTCA.....	23	0	1	2.00	2	1	1	0	0	0	0
.....GAACGGCCCACTGAGAGCGATCT.....	23	0	1	1.00	1	0	1	0	0	0	0
.....ACCTGTTCATGTACGGAGCAAAA.....	23	1	1	1.00	1	0	0	1	0	0	0
.....GACCTGTTCATGTACGGAGCA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TTGACAGTATCTTTCCACCCT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TTGACAGTATCTTTCCACCCTCAA.....	24	1	1	1.00	1	0	0	0	0	0	1
.....TCATGTTGACAGTATCTTTCCACCCTC.....	27	0	1	1.00	1	1	0	0	0	0	0
.....TTCGAACGGCCCACTGAGAGC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TGACAGTATCTTTCCACCCT.....	20	0	1	1.00	1	0	0	1	0	0	0
.....GAACGGCCCACTGAGAGC.....	18	0	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

CCGGTATCCGCTCATACCGCTGGACAAGTACATGCCTCGTTTGCTTCTGCCATTCACCCCTAGGAGTTTCGTATGTCATAGTACAACTGTCATAGAAAGGTGGGAGTCTCAAGCTTGCCGGGTGACTCTCGCTAGACTAGCGGCACATGGTATTCAAA							
....(((((((((.((...(((((.........)))))...))..)))))..))))......	Read size	# Mismatch	Hit Count	Total Norm	Total	V055 head	V039 embryo
.....GTTGACAGTATCTTTCCACCCTCA.....	23	0	1	2.00	2	1	1	0	0	0	0
.....GAACGGCCCACTGAGAGCGATCT.....	23	0	1	1.00	1	0	1	0	0	0	0
.....ACCTGTTCATGTACGGAGCAAAA.....	23	1	1	1.00	1	0	0	1	0	0	0
.....GACCTGTTCATGTACGGAGCA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TTGACAGTATCTTTCCACCCT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TTGACAGTATCTTTCCACCCTCAA.....	24	1	1	1.00	1	0	0	0	0	0	1
.....TCATGTTGACAGTATCTTTCCACCCTC.....	27	0	1	1.00	1	1	0	0	0	0	0
.....TTCGAACGGCCCACTGAGAGC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TGACAGTATCTTTCCACCCT.....	20	0	1	1.00	1	0	0	1	0	0	0
.....GAACGGCCCACTGAGAGC.....	18	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_13047:818662-818819 +	dan_1142	GGCCATAGGCGAGTATGGCGACCTGTTCATGTACGGAGCAAACGAAGACGGTAAGTGGG-G--A----------T-C----------CTCAAA-GCAT------AC---AGTATCATGTTGACAGTATCT------TTCCACCCTCAGAGTTCGAACGGCCCACTGAGAGCGATCTGATCGCCGTGTACCATAAGTTT
droBip1	scf7180000396431:602852-603012 +		GGCCATAGGCGAGTATGGCGACCTGTTCATGTACGGAGCAAACGAAGACGGTGAGTGGAGT--GGGGTC----------T-C----------TGTATC----------CCAGT----------ATCTT--ATTGTTGAGC-----AGCA---T----T------T--T----------ACCT------TTCAGCCCAGAGTTCGAACGGCCCACTGAGAGCGATCTGATCGCCGTGTACATAAGTTT
droKik1	scf7180000301542:71053-71206 +		GGCCATAGGCGAGTAGGGCGATGTTTTATGTACGCGCCAATGAGAATGGTAAGTGA-TT--GCATT----------T-C----------TATTTT----------CCATATATTA----------TTTATAAATT-----A------T----T------T--T----------TTTT--T-----TTTGCAGAGTTGAACGGCCCACGGAGAGCGATCTGATCGGTGTGTACATAAGTTT
droFic1	scf7180000453829:980076-980322 +		GGCCATAGGCGAGTAGGGCGACCTGTTCATGTACGGCGCCAACGAAGAATGGTGAGTGGCTC--TAT--ACCTTCCTTGCAATTACACCATCTA--CTTTGAGCTAGAACCTTTAGTTCAAGTTCCCAATTTAGATGGGGATTCCCTCTATTTAAAAGGGAAAGCCATTTTAACATTTGTTAACATCTGGCT----------T------T----T------T--T----------TATATT--T-----TTTCAGAGTTGAAAGACCCACTGAGAGCGATCTGATCGGTGTGTACATAAGTTT
droEle1	scf7180000491006:2534643-2534827 +		GGCCATAGGCGAGTAGGGCGATGTTTCATGTACGCGCCAATGAGAATGGTGAGTCAGT--C----------T-C--CC----------CTAA----------CCGAATCATCTGCGATCTGGATGATT----A----------A----CTAAAAC----------CAAT---CATTATTGGATCT----------T------T----T------T--T----------CACTCG--T-----TTTGCAGAGTTGAACGGCCCACTGAGAGCGATCTGATCGGTGTGTACATAAGTTT
droRho1	scf7180000779841:541847-542007 +		GGCCATAGGCGAGTAGGGCGATGTTTCATGTATGCGCCGACGAGAATGGTAAGTACTG--C---G----------T-C----------CTGAATAATCTTT----------AACCCGA----------ACTCG--TTT--CTGAT----TCTG--G---T------T----T------T--T----------TCACCCT--T-----TTTCCAGAGTTGAACGGCCCACTGAGAGCGATCTGATCGGTGTGTACATAAGTTT
droBia1	scf7180000301760:1784356-1784523 +		GGCCATAGGCGAGTAGGGCGATGTTTCATGTACGGCGCCAACGAGAATGGTGAGTGGG-C--AGTGGC----------T-C--CAGTGA----------CC----------AG----------GTTAACTTT-GTAATTATTTGTATCGC---T------T----T------T--T----------CATTAA--T-----TTTGCAGAGTTGAACGGCCCACTGAGAGCGATCTGATCGGTGTGTACATAAGTTT
droTak1	scf7180000415210:248347-248512 -		GGCCATAGGCGAGTAGGGCGATGTTTCATGTACGGCGCCAACGAGAATGGTGGGTTGATCTTG---AG----------T-C--CT----------CTTTT----------AGCAGCA----------ACTTT-ATTTTTAATT----CCTTGAA-T-----T------T----T------T--T----------ATCTCTAA--T-----TTTGCAGAGTTGAACGGCCCACTGAGAGCGATCTGATCGGTGTGTACATAAGTTT
droEug1	scf7180000409032:964464-964622 -		GGCCATAGGCGAGTAGGGCGATGTTTCATGTACGGCGCCAACGAGAATGGTGAGTGA-CC--AGGATA----------T-C----------AATCTT----------TCGAG----------ATTCT-ATTATAATTT----ACTTG--T-----TTT------T----T------T--T----------TTTTGA--T-----TTTTCAGAGTTGAACGGCCCACTGAGAGCGATCTGATCGGTGTGTACATAAGTTT
dm3	chrX:9008554-9008716 +		GGCCATAGGCGAGTAGGGCGATGTTTATGTACGGCGCCAACGAGAATGGTAGTTA-TCTCGCTAAT----------T-C----------CTCCT----------TGCCTCA----------ATCCA-ATTGTTAATT----CATGG--T-----T------T----T------T--T----------TGCCAAT--T-----ATTATAAGAGTTGAACGGCCCACTGAGAGCGATCTGATCGGTGTGTATTATAAGTTT
droSim2	x:8555291-8555453 +	dsi_21526	GGCCATAGGCGAGTAGGGCGATGTTTCATGTACGGCGCCAACGAGAATGGTAAGTAC-TCTCGCTAAT----------T-C----------CTCCT----------AGCCCCA----------ATCCG-TTTGCTAATT----CCTGG--T-----T------T----T------T--T----------TCTCCAA--T-----TTGCAGAGTTGAACGGCCCACTGAGAGCGATCTGATCGGTGTGTATTATAAGTTT
droSec2	scaffold_34:368901-369063 +		GGCCATAGGCGAGTAGGGCGATGTTTCATGTACGGCGCCAACGAGAATGGTAAGTAA-TCTCGCTAAT----------T-C----------CTCCT----------AGCCCCA----------ATCCT-ATTGCTAATT----CCTGG--T-----T------T----T------T--T----------TCTCCAA--T-----ATTGCAGAGTTGAACGGCCCACTGAGAGCGATCTGATCGGTGTGTATTATAAGTTT
droYak3	X:12308229-12308387 -		GGCCATAGGCGAGTAGGGCGATGTTTCATGTACGGCGCCAACGAGAATGGTAAGTAA-TCT--GGTAGT----------T-C----------CACATT----------CCCG----------TTCCA-ATTGTTAATT----CCTGG--T-----T------T----T------T--T----------TCTCCAA--T-----TTGCAGAGTTGAACGGCCCACTGAGAGCGATCTGATCGGTGTGTATTATAAGTTT
droEre2	scaffold_4690:6108813-6108972 -		GGCCATAGGCGAGTAGGGCGATGTTTCATGTACGGCGCCAACGAGAATGGTAAGTAC-CC--GGCAAT----------T-C----------CTCATT----------CCCCA----------ATCCA-ATTGTCGATT----CCTGG--T-----T------T----T------T--T----------TCTCCAA--T-----TTGCAGAGTTGAACGGCCCACTGAGAGCGATCTGATCGGTGTGTACATAAGTTT
dp5	XL_group1e:6975478-6975654 -		GGCCATAGGCGAGTAGGGCGATGTTTCATGTATGCGCCAAATGAGAATGGTGAGTGGATA-T--A----------TC--TCGAGTGA----------TT----------AGCCGTAGATTAAGCTGGAATTTAAT----------CTAT---CAATTGC-----CT--T----------TGCCTT--T-----TTTAAGAGTTGAACGCCCCTGAGAGCGATCTGATCGCCATGTATACATAAGTTT
droPer2	scaffold_13:1579956-1580132 +		GGCCATAGGCGAGTAGGGCGATGTTTCATGTATGCGCCTAAATGAGAATGGTGAGTGGATA-T--A----------TC--TCGAATGA----------TT----------AGCCGTAGATTATGCTGGAATTTAAT----------TTAT---CAATTGC-----TT--T----------TGCCTT--T-----TTTCAGAGTTGAACGCCCCTGAGAGCGATCTGATCGCCATGTATACATAAGTTT
droWil2	scf2_1100000004909:9450302-9450473 -		GGCATAGGCGAATAGGGCGATGTTTCATGTACGCCTCAATGAGAATGGTGAGTTAAGG--A--AAT----------A----------T---GATGA----------TTGTA----------TGCGATTTACTC----------TCA--ATTGT----------TGTT--T-----T------T----T------T--T----------A-TTTCATCTA-----TTCATTTAGAGATTGAACGTCCCACGGAGAGCGATCTGATCGGTGTGTACATAAGTTT
droVir3	scaffold_12932:1865139-1865303 +		GGCCATAGGCGAGTAGGGCGATGTTTCATGTATGCGCCAACGAAGAATGGTGAGTTGATT--A--AAC----------A----CAATAC--GAGAAAGA----------AC----------AATTTAAT----------TC-----T-----T------T----T------T--T----------CTATAAACTGATTTGAGAGATTGAACGTCCCACGGAGAGCGATCTGATCGGTGTGTACATAAGTTT
droMoj3	scaffold_6473:5429117-5429284 +		GGCCATAGGCGAGTAGGGCGATGTTTCATGTACGCGCCAATGAGAATGGTGAGTGTAC--GTAGT----------T-C----------CA----------TATCATTCGTGAATCTTTT----------TTAT---CCATTCA-----C-CAA----------ATCTATT--T-----GAACAGAGTTCGACGTCCACGGAGAGCGATCTGATCGGTGTGTACATAAGTTT
droGri2	scaffold_15203:1995603-1995665 -		TAA-----T---G----------T-C----------T---T------T----T------T--T----------TT--T-----TTTGCAGAGTTGAACGTCCCACGGAGAGCGATCTGATCGGTGTGTACATAAGTTT

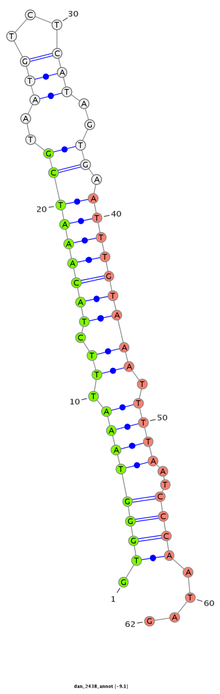
Generated: 09/08/2015 at 07:05 PM

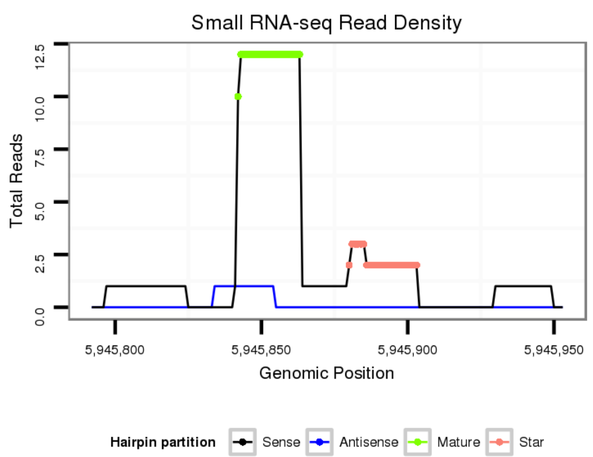
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

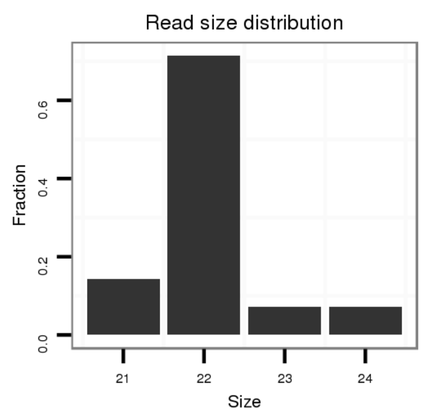
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_2438	**scaffold_13337:5945842-5945903 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

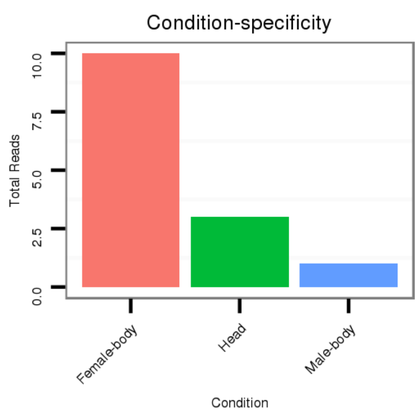
Legend: mature star mismatch in alignment mismatch in read

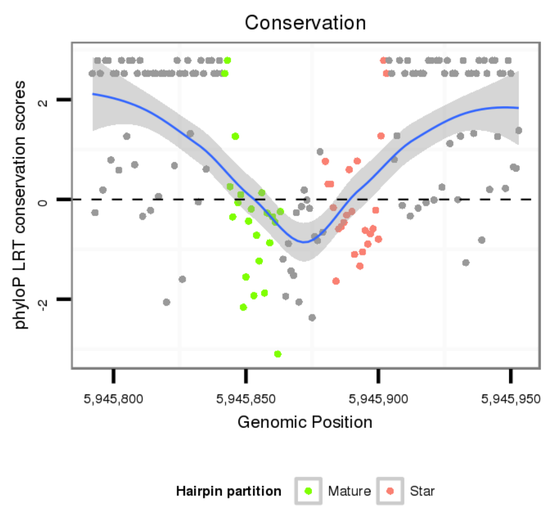
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF25282-in]; CDS [Dana\GF25282-cds]; CDS [Dana\GF25282-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CCTCCTATGCGAGCATTGTGGCTCCACCGGGCACAGAGGCCACCATGCAGGTGGGTAAATTTCTACAAATCGTAATGTCTCATAGTGAATTTGTAAATTTTAATCCCAATAGAGTCTGGTGGGTGCCATTTTTGAGGGCGTTGGCGTCTCCATGGGCAGCCT	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V055 head	V106 head	V105 male body
**********.(((((((((.((.(((((((((..(((...))))..))).)))))))))).)))))..))))....**********									
.....GTGGGTAAATTTCTACAAATCG.....	22	0	1	9.00	9	6	2	1	0
.....TGGGTAAATTTCTACAAATCG.....	22	0	1	2.00	2	2	0	0	0
.....TAATGTCTCATAGTGAATTTGT.....	22	0	1	1.00	1	0	0	0	1
.....TATGCGAGCATTGTGGCTCCACCGGGCA.....	28	0	1	1.00	1	1	0	0	0
.....CGTTGGCGTCTCCATGGGCA....	20	0	1	1.00	1	1	0	0	0
.....ATTTGTAAATTTTAATCCCAATAG.....	24	0	1	1.00	1	1	0	0	0
.....TTTGTAAATTTTAATCCCAATAG.....	23	0	1	1.00	1	1	0	0	0
.....GGTGGGTAAATTTCTACAAATCG.....	23	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

GGAGGATACGCTCGTAACACCGAGGTGGCCCGTGTCTCCGGTGGTACGTCCACCCATTTAAAGATGTTTAGCATTACAGAGTATCACTTAAACATTTAAAATTAGGGTTATCTCAGACCACCCACGGTAAAAACTCCCGCAACCGCAGAGGTACCCGTCGGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	V055 head	V039 embryo
**********.(((((((((.((.(((((((((..(((...))))..))).)))))))))).)))))..))))....**********								
.....GGTACGTCCACCCATTTAAAG.....	21	0	1	1.00	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13337:5945792-5945953 +	dan_2438	CCTCCTATGCGAGCATTGTGGCTCCACCGGGCACAGAGGCCACCATGCAGGTGGGTAAATT----TCTAC--AAATC----------GTA----------AT-----GTCTCA---TAGTGAATTT-G--TAAAT--TT-TAATCCCAATAGAGTCTGGTGGGTGCCATTTTTGAGGGCGTTGGCGTCTCCATGGGCAGCCT
droBip1	scf7180000396518:9406-9568 +		CCTCCTATGCGAGCATTGTGGCTCCACCGGGCACAGAGGCCACCATGCAGGTGGGTAAAG----GATAT--TAATA----------GTA----------AT-----GTTCCA---TGATTAATTTAA--TATAT--TT-TATCTTTAATAGAGTCTGGTGGGTGCCATTTTTGAGGGCGTTGGCGTCTCCATGGGCAGCCT
droKik1	scf7180000302391:1160297-1160468 -		CCTCCTATGCGAGCATTGTGGCGCCACCGGGCACCGAGGCCACCATGCAGGTGAGTTTCG----G----------G----------GTTCTTATAAATCTTATAATTTATATT----ATACTA---TTTATT----AT---TT--CC-CTTTTCCCACAGAGCCTTGTGGGCGCCATTTTCGAGGGCGTGGCGTCTCCATGGGCAGCCT
droFic1	scf7180000454113:3020244-3020406 -		CCTCATACGCGAGCATTGTGGCTCCACGTGGAACGGAGGCCACCATGCAGGTGGGTTTCTT----GGCC--TAAGA----------AGA----------GT-----GTCCATCAATCCATT---ATC--TTTTT--TC-TTGCTGTTTCAGAGTCTGGTGGGCGGCAATTTTCGAGGGTGTCGGTGTGTCCATGGGAAGTCT
droEle1	scf7180000490993:2115796-2115955 -		CCTCCTATGCGAGCATTGTGGCACCGCCTGGAACTGAGGCTACCATGCAGGTGGGTTGTAT----AACTT--TAAGC----------AGG----------AC-----AAACA---TTATTT----CA--TTTATGTT-TCTCGATGCAGAGTTTGGTTGGAGGCGATTTTCGAGGGTGTTGGTGTGTCCATGGGCAGCCT
droRho1	scf7180000779604:23575-23734 +		CCTCCTATGCGAGCATTGTGGCACCGCCTGGAACTGAGGCTACCATGCAGGTGGGCTTTAT----GATTT--AAAGA----------AAG----------AA-----ATTCAA---TAATTT----GA--TTTATATT-TTCTCGATTCAGAGTCTGGTTGGAGGCGATTTTCGAGGGCGTTGGTGTCTCCATGGGCAGCCT
droBia1	scf7180000302334:122159-122318 +		CCTCCTATGCGAGCATCGTGGCACCGCCAGGAACGGATGCTACCATGCAGGTGGGTTAAAT----GACTG--TAGCC----------AGT----------GG-----ATCCAT---TGCATA----AA--ATCTTATT-TGCCCACATCAGAGTCTTGTTGGAGGCATTTTCGAGGGCGTAGGTGTCTCCATGGGCAGCCT
droTak1	scf7180000414445:523516-523676 -		CCTCATATGCGAGCATTGTGGCACCGCCGGGAACGGATGCTAACGATGCAGGTGGGTTTAAT----GCCTT--TGAGG----------AGT----------GG-----CTACAA---TGGATA----ATTTCCTTT--TT-TCCCCATAACAGAGTCTGGTTGGTGGCGATTTTCGAGGGCGTTGGTGTCTCCATGGGCAGCCT
droEug1	scf7180000409711:3556633-3556792 +		CTTCCTATGCGAGCATTGTAGCACCTCCGGGAACGGATGCTACCATGCAGGTGAGTTGCT----CGGTC--CGGGT----------ACA----------AA-----ATCCAA---TAGCTA----AT--TTTATT-CT-TTCTATAACAGAGCCTTGTTGGAGGCGATTTTCGAAGGAGTAGGTGTATCCATGGGCAGCCT
dm3	chr3L:11681141-11681301 +		CCTCCTATGCAAGCATTGTGGCACCGCCAGGCACCGATGCTACCATGCAGGTGAGTTCGAT----GAATGTGTAGGG----------GGC----------GA-----TCCCAA---GAGTTA----TG--CATAT--TG-TGGCCATTTCAGAGTCTGGTTGGAGGCGATATTCGAAGGCGTTGGTGTCTCAATGGGCAGCCT
droSim2	3l:11389059-11389217 +	dsi_20598	CTTCCTATGCGAGCATTGTGGCACCGCCAGGCACCGATGCTACCATGCAGGTGAGTTCGAT----GATTG--TAGGG----------AGT----------GA-----GTCCAA---GAGTTA----AG--CTTAT--TG-TGGCCATTTCAGAGTCTGGTTGGAGGCGATATTCGAAGGCGTTGGTGTCTCAATGGGAAGCCT
droSec2	scaffold_0:3867518-3867676 +		CTTCCTATGCGAGCATTGTTGCACCGCCAGGCACCGATGCTACCATGCAGGTGAGTTCGAT----GATTG--TAGGG----------AGT----------GA-----TCCCAG---GAGTTT----AG--CTTAT--TG-TGGCCATTTCAGAGTCTGGTGGGAGGCGATATTCGAAGGCGTTGGTGTCTCAATGGGAAGCCT
droYak3	3L:11709846-11710005 +		CCTCCTATGCGAGCATTGTGGCACCGCCAGGAACGGATGCTACCATGCAGGTGAGCTTGAT----TATTG--TAGGA----------GTG----------AT-----ATCCCA---AAATTTA----TT--CATTT--CG-TGCCATTTCAGAGTCTGGTGGGAGGCGATATTCGAAGGCGTCGGTGTCTCAATGGGCAGCTT
droEre2	scaffold_4784:11663670-11663827 +		CTTCCTATGCGAGCATTGTGGCACCGCCAGGAACGGATGCTACCATGCAGGTGAGCTCGAT----GATTA--TGG-G----------AGG----------GA-----TCCCAA---AAGTTA----TT--CATTT--CG-TGCCATTTCAGAGTCTGGTTGGAGGCGATATTCGAAGGCGTCGGTGTCTCAATGGGCAGCCT
dp5	XR_group6:10012098-10012256 -		CCTCCTATGCCAGCATTGTTGCGCCACCGGGCACTGAGGGACCATGCAGGTACGTACAATCGATCATTG--TGGT-------CA------GAA---AT----------GG-----TTCTAA---**********-----CATCCC-ACTGCCTTGTACAGAGTCTGGTTGGTGGTATATTCGAGGGCGTTGGCGTCTCCATGGGAAGCTT
droPer2	scaffold_61:292552-292710 -		CCTCCTATGCCAGCATTGTTGCGCCACCGGGCACTGAGGCACCATGCAGGTATGTACAATCGATCATTG--TGGT-------CA------GAA---AT----------GG-----TTCTAA---**********-----CATCCC-ACTGCCTTGTACAGAGTCTGGTTGGTGGTATATTCGAGGGCGTTGGCGTCTCCATGGGAAGCCT
droWil2	scf2_1100000004762:2669819-2669982 -		CATCCTATGCCAGTATTGTGGCACCACCGGGCACAGAGGCCACCATGCAGGTGAGTACC----G----------GAGTGATTCAGCCTATCGAAATG---**********-----GTATC-------GTTTACA-TTG---**********-----AAT-TC--TACACTACACAGAGTCTGGTTGGTCCATCTTTGAGGGCGTGGGCGTATCAATGGGCAGTCT
droVir3	scaffold_13049:23894860-23895017 +		CCTCCTATGCCAGCATCGTTGGACCGCCTGGCACCGAGGCCACTATGCAGGTGAGAGATTC----T-CTG--ATCC----------T--------T----------TA-----ACACAA---GTGTTC----AT--ATTCTCA--TCCATCATTTCCAGAGTCTTGTGGGCGCCATTTTCGAGGGTGTCGGCGTCTCAATAGGCAGCCA
droMoj3	scaffold_6680:18523266-18523426 +		CTTCCTACGCCAGCATCGTCGGTCCGCCAGGCACGAGGGCTACCATGCAGGTAAACGCAATG----CGCAG--AGCGA----------A--ACGATG---**********-----GCAAT-------GATCATA-CTGAA---AAG-------**********-----TT-TTCTTCTTACAGAGTCTTGTGGGTGGCATCTTCGAGGGCATTGGCGTCTCCATGGGCAGCCA
droGri2	scaffold_15110:13774600-13774765 -		CCTCCTATGCCAGCATCGTGGCACCACCGGGCACCGAGGCCACCATGCAGGTAA-CAGCAGCAGCAGTTG--TA----TGATTCA------GAC---**********-----**-----ATGCAG---TGCTCC----AT--ATTTTT-GTTGCTACTTGCAGAGTCTGGTGGGTGCCATCTTTGAGGGCGTTGGCGTCTCCATGGGCAGCCA

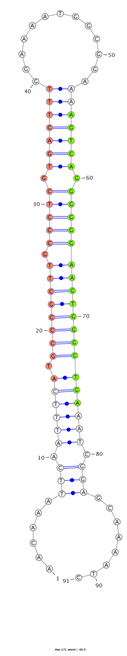
Generated: 09/08/2015 at 07:05 PM

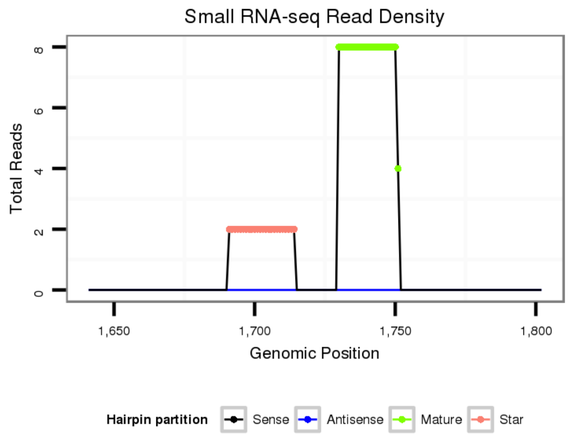
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	1
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

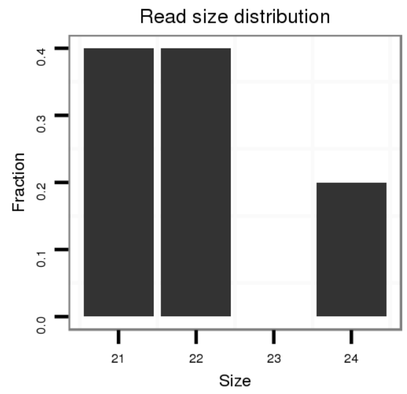
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_121	**scaffold_13322:1691-1752 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

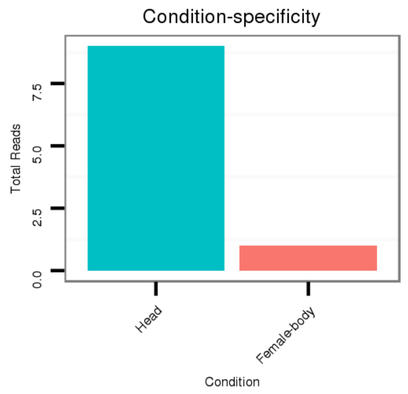
Legend: mature star mismatch in alignment mismatch in read

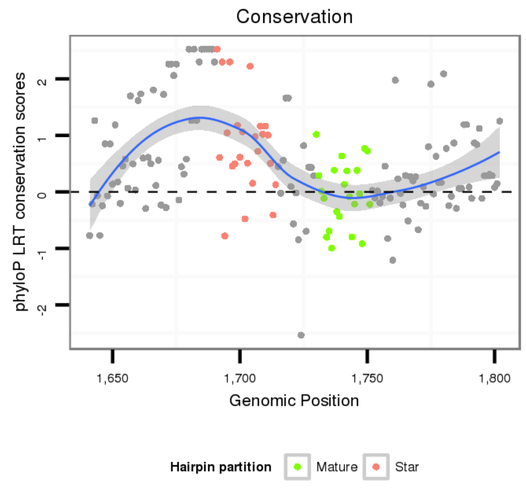
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

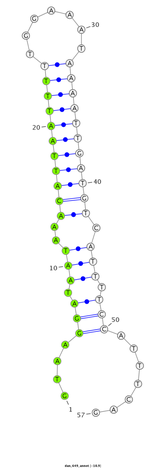
hide 3p reads | show mid mismatch reads

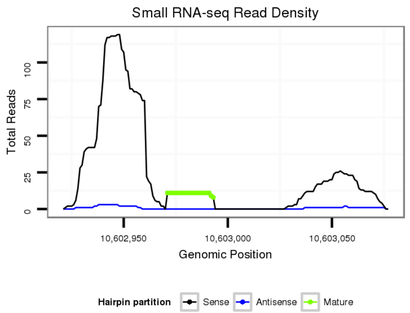
| | | | | | | | V106 | V055 | | | | M044 | | | | | | |

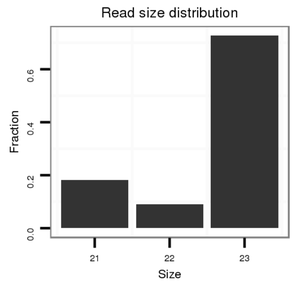
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_649	**scaffold_12916:10602971-10603027 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Comell Mirror)]

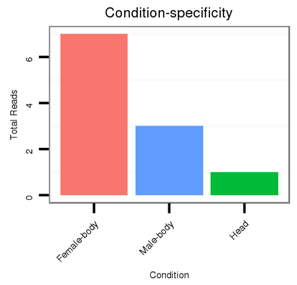
Legend: mature star mismatch in alignment mismatch in read

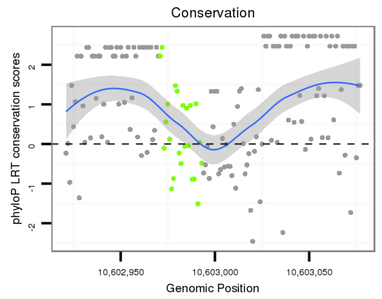
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dana\GF15554-in]; CDS [Dana\GF15554-cds]; CDS [Dana\GF15554-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTCTGGGCGCCTATGGAGCCGTTAAGGAGAGTGTGATGGTGATCAACCTGGTAAGGATAAATAAACATTAATTTTTGGAAATAAAATTGATGTCATTTTCCATTTCAGTATGGTGTTTGCCTGTTCCTGGTCTTCATCCTGGAGGTGTCCGCAGCTAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	M044 female body	M058 embryo	V039 embryo	V106 head	V055 head
**********....(((.(((..((((((((((((.......))))))))))).)))..))).....**********											
..................GTTAAGGAGAGTGTGATGGT.....	20	0	1	17.00	17	16	0	0	0	1	0
................GCCGTTAAGGAGAGTGTGATGGT.....	23	0	1	16.00	16	14	0	0	1	0	1
..................CGTTAAGGAGAGTGTGATGGT.....	21	0	1	13.00	13	9	1	1	1	1	0
....GTAAGGATAATAAACATTAATTT.....	23	0	1	8.00	8	2	6	0	0	0	0
......CGCCTATGGAGCCGTTAAGGAGAGAGT.....	25	0	1	5.00	5	2	2	1	0	0	0
........GCCTATGGAGCCGTTAAGGA.....	20	0	1	5.00	5	2	0	0	1	1	1
.......GCCTATGGAGCCGTTAAGGAGA.....	22	0	1	5.00	5	4	0	0	1	0	0
.......GCCTATGGAGCCGTTAAGGAGAGT.....	24	0	1	4.00	4	3	0	0	1	0	0
................AGCCGTTAAGGAGAGTGTGATGGT.....	24	0	1	4.00	4	3	0	1	0	0	0
.......CGCCTATGGAGCCGTTAAGGA.....	21	0	1	3.00	3	1	1	0	1	0	0
..................GTTAAGGAGAGTGTGATGGTGAT.....	23	0	1	3.00	3	2	0	0	0	1	0
......GCGCCTATGGAGCCGTTAAGGAGA.....	24	0	1	3.00	3	2	0	0	0	1	0
................GCCGTTAAGGAGAGTGTGATGGTGATC.....	27	0	1	2.00	2	2	0	0	0	0	0
....GTAAGGATAATAAACATTAAT.....	21	0	1	2.00	2	1	1	0	0	0	0
....TGCCTGTTCCTGGTCTTCATCCTG.....	24	0	1	2.00	2	0	2	0	0	0	0
..................TTAAGGAGAGTGTGATGGT.....	19	0	1	2.00	2	2	0	0	0	0	0
....GTTTGCCTGTTCCTGGTCTTCATCCTGGA.....	29	0	1	2.00	2	0	2	0	0	0	0
................AGCCGTTAAGGAGAGTGTGATGGTGAT.....	27	0	1	2.00	2	2	0	0	0	0	0
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....CTTCATCCTGGAGGTGTCCGCAGCT..	25	0	1	2.00	2	1	1	0	0	0	0
................GCCGTTAAGGAGAGTGTGATG.....	21	0	1	2.00	2	1	0	0	0	1	0
.........CTATGGAGCCGTTAAGGAGA.....	20	0	1	2.00	2	2	0	0	0	0	0
..................CGTTAAGGAGAGTGTGATGGTGAT.....	24	0	1	2.00	2	2	0	0	0	0	0
....CTGGTCTTCATCCTGGAGGTGTCCGC.....	26	0	1	1.00	1	0	1	0	0	0	0
.........CTATGGAGCCGTTAAGGAGAGTGT.....	24	0	1	1.00	1	0	0	0	1	0	0
....TTCCTGGTCTTCATCCTGGAGGTGTCC.....	27	0	1	1.00	1	0	1	0	0	0	0
....CATCCTGGAGGTGTCCGCAG.....	20	0	1	1.00	1	0	1	0	0	0	0
.........CTATGGAGCCGTTAAGGA.....	18	0	1	1.00	1	0	1	0	0	0	0
..................CGTTAAGGAGAGTGTGATGGTGATCAAC.....	28	0	1	1.00	1	0	1	0	0	0	0
....GTTCCTGGTCTTCATCCTGGA.....	21	0	1	1.00	1	0	1	0	0	0	0
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....GTTCCTGGTCTTCATCCTGGAGGT.....	24	0	1	1.00	1	1	0	0	0	0	0
....GCCTGTTCCTGGTCTTCATCCTGGA.....	25	0	1	1.00	1	0	1	0	0	0	0
....CATCCTGGAGGTGTCCGCAGC.....	21	0	1	1.00	1	0	1	0	0	0	0
.........CTATGGAGCCGTTAAGGAGAG.....	21	0	1	1.00	1	1	0	0	0	0	0
....CTTCATCCTGGAGGTGTCCGCAGC.....	24	0	1	1.00	1	0	1	0	0	0	0
.....GGCGCCTATGGAGCCGTTAAGGA.....	23	0	1	1.00	1	0	0	1	0	0	0
....GTAAGGATAATAAACATTAATT.....	22	0	1	1.00	1	0	0	0	0	1	0
................GCCGTTAAGGAGAGTGTGATGGTG.....	24	0	1	1.00	1	0	1	0	0	0	0
....CATCCTGGAGGTGTCCGCA.....	19	0	1	1.00	1	0	1	0	0	0	0
....CTTCATCCTGGAGGTGTCCGCA.....	22	0	1	1.00	1	0	1	0	0	0	0
....TTCCTGGTCTTCATCCTGGA.....	20	0	1	1.00	1	0	1	0	0	0	0
....TTGCCTGTTCCTGGTCTTCATCCTG.....	25	0	1	1.00	1	0	1	0	0	0	0
.........TTAAGGAGAGTGTGATGGTGAT.....	22	0	1	1.00	1	1	0	0	0	0	0
.........TATGGAGCCGTTAAGGAGA.....	19	0	1	1.00	1	0	0	0	0	1	0
..................GAGAGTGTGATGGTGATCAAC.....	21	0	1	1.00	1	0	0	1	0	0	0
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....GTCTTCATCCTGGAGGTGTCCG.....	22	0	1	1.00	1	0	0	0	0	1	0
..................AAGGAGAGTGTGATGGTGATCAACCT.....	26	0	1	1.00	1	0	0	1	0	0	0
..CTGGGCGCCTATGGAGCCGTTAAGGAGA.....	28	0	1	1.00	1	1	0	0	0	0	0
....TTGCCTGTTCCTGGTCTTCA.....	20	0	1	1.00	1	0	1	0	0	0	0
..................GTTAAGGAGAGTGTGATGGTG.....	21	0	1	1.00	1	0	1	0	0	0	0
..................GTTAAGGAGAGTGTGATGGTGATC.....	24	0	1	1.00	1	1	0	0	0	0	0
....GTTTGCCTGTTCCTGGTCTT.....	20	0	1	1.00	1	0	1	0	0	0	0
..................GTTAAGGAGAGTGTGATGT.....	19	1	1	1.00	1	1	0	0	0	0	0
....TTCATCCTGGAGGTGTCCGC.....	20	0	1	1.00	1	1	0	0	0	0	0
.........CTATGGAGCCGTTAAGGAG.....	19	0	1	1.00	1	1	0	0	0	0	0
.........CTATGGAGCCGTTAAGGAGAGTGTGA.....	26	0	1	1.00	1	1	0	0	0	0	0
....ATGGTGTTTGCCTGTTCCTGGT.....	22	0	1	1.00	1	0	1	0	0	0	0
..................GTTAAGGAGAGTGTGATGGTGATCAAC.....	27	0	1	1.00	1	1	0	0	0	0	0
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....TATGGTGTTTGCCTGTTCCTGGTCTT.....	26	0	1	1.00	1	0	1	0	0	0	0
....GTTTGCCTGTTCCTGGTCTTC.....	21	0	1	1.00	1	0	1	0	0	0	0
..................GTTAAGGAGAGTGTGATG.....	18	0	1	1.00	1	0	1	0	0	0	0
.TCTGGGCGCCTATGGAGC.....	18	0	1	1.00	1	0	1	0	0	0	0
..................ATGGAGCCGTTAAGGAGAGTGT.....	22	0	1	1.00	1	1	0	0	0	0	0
..................CGTTAAGGAGAGTGTGATGGTG.....	22	0	1	1.00	1	0	1	0	0	0	0
.........TATGGAGCCGTTAAGGAGAGTGTGATG.....	27	0	1	1.00	1	0	1	0	0	0	0
..................TTAAGGAGAGTGTGATGGTGA.....	21	0	1	1.00	1	1	0	0	0	0	0
..................GCCGTTAAGGAGAGTGTGAT.....	20	0	1	1.00	1	1	0	0	0	0	0
....GTTCCTGGTCTTCATCCTGG.....	20	0	1	1.00	1	0	1	0	0	0	0
.....CCTATGGAGCCGTTAAGGAGAGT.....	23	0	1	1.00	1	1	0	0	0	0	0
.........CCTATGGAGCCGTTAAGGAG.....	20	0	1	1.00	1	1	0	0	0	0	0
..................CGTTAAGGAGAGTGTGATGGTGA.....	23	0	1	1.00	1	0	0	1	0	0	0
..................TTAAGGAGAGTGTGATGGTGATCAACCT.....	28	0	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

GAGACCCGCGGATACCTCGGCAATTCCTCTCACACTACCACTAGTTGGACCATTCCTATTATTTGTAATTAAAAACCTTTATTTTAACTACAGTAAAAGGTAAAGTCATACCACAAACGGACAAGGACCAGAAGTAGGACCTCCACAGGCGTCGATA	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	M058 embryo	V055 head	V106 head
**********....(((.(((..((((((((((.......))))))))))).)))..))).....**********									
....AGGACCTCCACAGGCGTCGA..	20	0	1	1.00	1	1	0	0	0
................CGGCAATTCCTCTCACACTAC.....	21	0	1	1.00	1	1	0	0	0
......CGCGGATACCTCGGCAATTCC.....	21	0	1	1.00	1	1	0	0	0
....ACGGACAAGGACCAGAAGTAG.....	21	0	1	1.00	1	1	0	0	0
..............CTCGGCAATTCCTCTCACACT.....	21	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

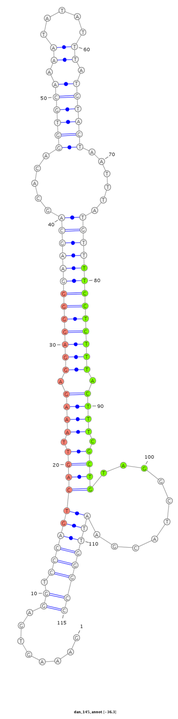
Re-alignment of all predicted orthologs

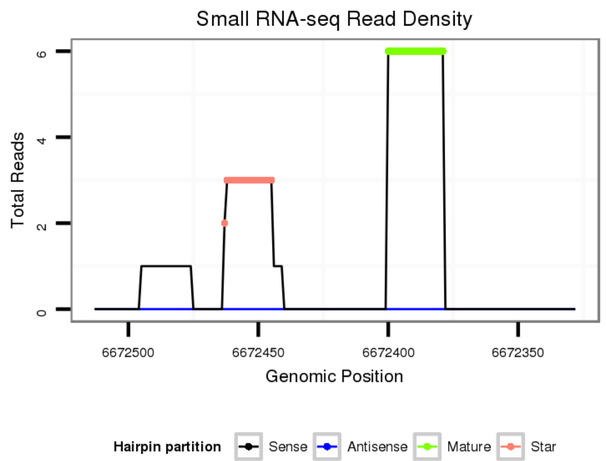
Species	Coordinate	ID	Alignment
droAna3	scaffold_12916:10602921-10603077 +	dan_649	CTCTGGGCGCCTATGGAGCCGTTAAGGAGAGTGTGATGGTGATCAACCTGGTAAGGATA--ATAAACATTAATTTTTGG----------AAAT---A----------AAA---------T----------TG-ATGTCA----T----TTTCCATTTCAGTATGGTGTTTGCCTGTTCCTGGTCTTCATCCTGGAGGTGTCCGCAGCTAT
droBip1	scaffold_71800003965 72:263284-263442 +		CTTTGGGCGCCTATGGAGCCGTTAAGGAGAGTGTGATGGTGATCAACCTGGTAAGGATA--ATAAGCATAGCGAAATGG----------ACAAAAAT---GGA----------------------

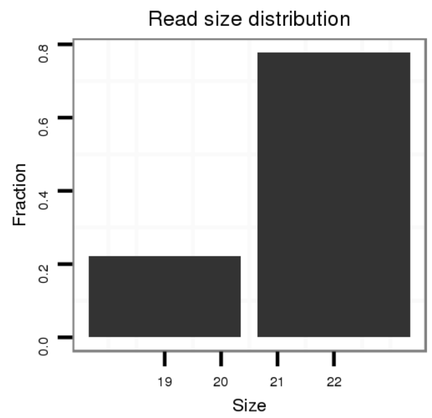
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_145	**scaffold_13337:6672378-6672463 -**	**candidate**	**Canonical miRNA**	**5pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

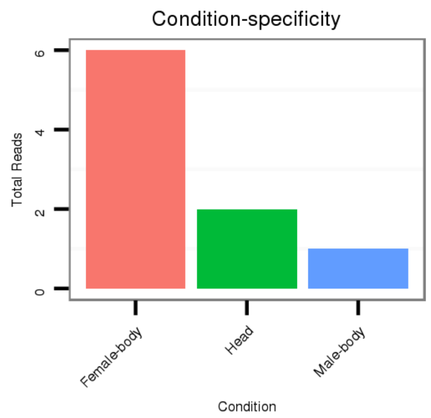
Legend: mature star **mismatch in alignment** mismatch in read

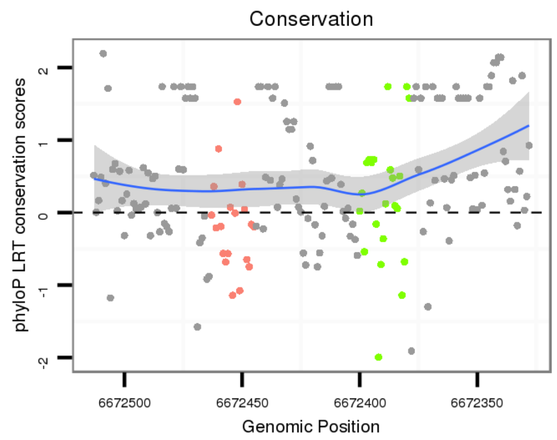
Predicted structure











Show Alternate Folds

Flybase annnotation

utr5 [utr5_plus_6306]; CDS [Dana\GF24443-cds]

No Repeatable elements found

Sense Strand Reads

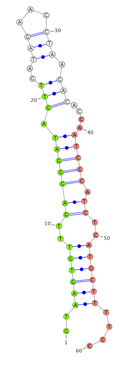
hide 3p reads | show mid mismatch reads

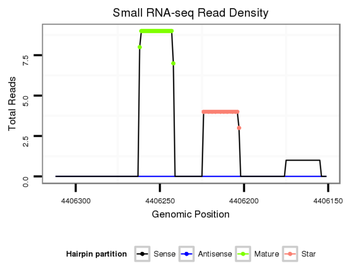
| | | |

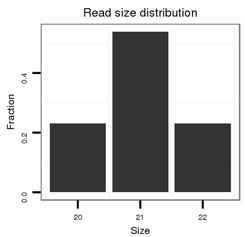
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_522	**scaffold_12916:4406201-4406262 -**	**candidate**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

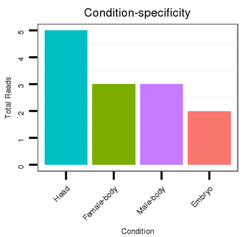
Legend: mature star mismatch in alignment mismatch in read

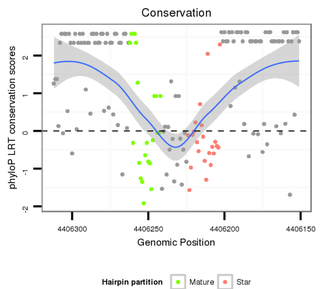
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana/GF14756-in]; CDS [Dana/GF14756-cds]; CDS [Dana/GF14756-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	M058 embryo	M044 female body	V055 head	V039 embryo
CAAGCAGATCACTGTCGAGTCGCGCATGTGCTTCGATGCCAAGCCAATCGGTAAGTGTTTGAGGGATAGTTGATAGAACCTAAGACACCAATCCCATCTCATGCTTTTCCAGAGGAATGCAAATCGAAACCAGCTGCCCTGAAGCCCGGCCAGACGGTGTTC											
********************************..(((((((..(((((((.(((..(((...)))..)))....)))))).)).)))))))....***											
.....GTAAGTGTTTGAGGGATAGTT.....	21	0	1	6.00	6	3	2	0	1	0	0
.....CAATCCCATCTCATGCTTTTCC.....	22	0	1	3.00	3	0	0	2	1	0	0
.....GTAAGTGTTTGAGGGATAGTT.....	20	0	1	2.00	2	0	1	0	0	1	0
.....GTAAGTGTTTGAGGGATAGTTA.....	22	1	1	1.00	1	0	1	0	0	0	0
.....GTAAGTGTTTGAGGGATAGTTA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....CCTGAACCCGGCCAGACGGT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CAATCCCATCTCATGCTTTTC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TAAGTGTTTGAGGGATAGTT.....	20	0	1	1.00	1	0	0	0	1	0	0

Anti-sense strand reads

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

Show Alignment With Reads

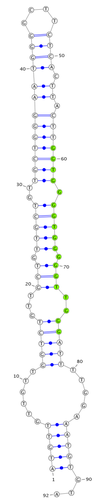
Re-alignment of all predicted orthologs

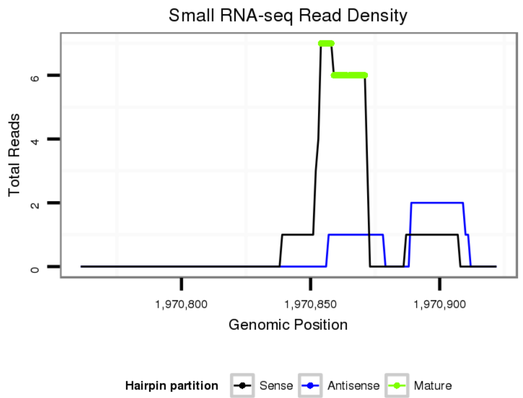
Species	Coordinate	ID	Alignment
droAna3	scaffold_12916:4406151-4406262_+	dan_522	CAAGCAGATCACTGTCGAGTCGCGCATGTGCTTCGATGCCAAGCCAATCGGTAAGTGTTTG----------A---GGGA----------TAGTTGATAGAAC-CTAAGACA---CAATCC----------C----------ATCTCATGCTTTTCCAGAGGAATGCAAATCGAAACCAGCTGCCCTGAAGCCCGGCCAGACGGTGTTC
droBip1	scf7180000396737:377657-377819_+		CAAGCAGATCACGTCGAGTCGCGCATGTGCTTCGATGCCAAGCCAATGGTAGTGTTTG----------A---AA-AT----------TAGTTGATAGAGTAAGTAGCAA---CAACGC----------C----------ATCTCGTGTTTCAGAGGAAGTGCAAATCGAACCAGCTGCCCTGAAGCCCGGCCAGACGGTGTTC
droKik1	scf7180000302472:1705959-1706028_-		C-CC----------T----------T---T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------TCGTTTATACCAGAGGAATGCAAATCGAACCAGCTGCCCTGAAGCCCGGCCAGACGGTGTTC
droFic1	scf7180000454115:913602-913804_+		CAAGCAGATCACGTCGAGTCGCGCATGTGCTTCGATGCCAAGCCAATGGTAAGTGCAC----------A---AA-A----------T----------T----------T----------T----------T----------T----------T----------T----------T----------TCATTTATGTTCATTAAACTTAATGTATAATATAATGTAATAATTTTATAATATTGTTATTATATTAATTTTATCAATCCTA---TT----------TCACAAGAGAGGAATGCAAATCGAACCAGCTGCCTTGAAGCCCGGCCAAACGGTGTTC
droLie1	scf7180000491046:2645736-2645794_+		CAAGCAGATCACGTCGAGTCGCGCATGTGCTTCGATGCCAAGCCAATGGTAAGTGTC----------A---AA-A----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T

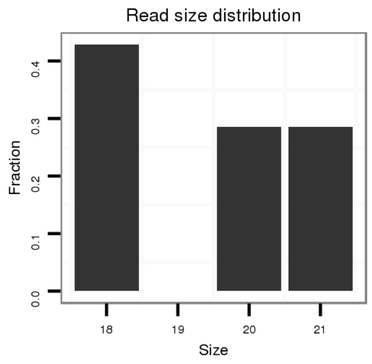
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_147	**scaffold_13117:1970811-1970872 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

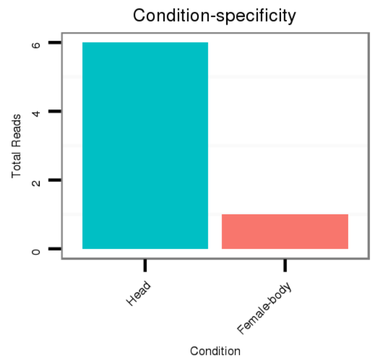
Legend: mature star mismatch in alignment mismatch in read

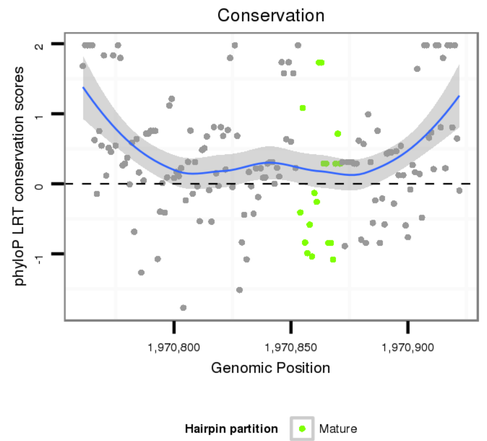
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTAAACGGAAAACTAACAAAGCAGGACCGTATGGGATGTTGTTGTTGGTCTGTTGCTGTTGCTGTTGCTGGGAATGGGGCTTCTCACTTACTTGGTGGGGTGGGGGTTGGGATTTTGGAAATGTGTACGGGGGCCCGGAATAGCCTTAGTCTAACTTATTGG	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	female body	V055 head	M058 embryo
**********(((((.....(((((...(((.(((((..(((((((((((((....)))))).))).)))))))..)))))..)))..))))).....))))))...**********										
.....GGTGGGGTGGGGGTTGGG.....	18	0	1	3.00	3	3	0	0	0	
.....TTGGTGGGGTGGGGGTTGGGA.....	21	0	1	2.00	2	2	0	0	0	
.....ACGGGGGCCCGGAATAGCCTT.....	21	0	1	1.00	1	1	0	0	0	
.....TGGTGGGGTGGGGGTTGGGA.....	20	0	1	1.00	1	1	0	0	0	
.....GCTTCTCACTTACTTGGTGG.....	20	0	1	1.00	1	0	1	0	0	

Anti-sense strand reads

CATTTGCCTTTTGATTGTTTCGTCCTGGCATACCCTACAACAACAACCAGACAACGACAACGACAACGACCCTTACCCCGAAGAGTGAATGAACCACCCCACCCCCAACCCTAAAACCTTTACACATGCCCCCGGGCCTTATCGGAATCAGATTGAATAACC	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	V039 embryo	V055 head
**********(((((.....(((((...(((.(((((..(((((((((((((....)))))).))).)))))))..)))))..)))..))))).....))))))...**********									
.....CCCCCGGGCCTTATCGGAATC.....	21	0	1	1.00	1	1	0	0	
.....CCCCACCCCCAACCCTAAAACC.....	22	0	1	1.00	1	1	0	0	
.....CCCCCGGGCCTTATCGGAATCAG.....	23	0	1	1.00	1	1	0	0	

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13117:1970761-1970922 +	dan_147	GTAAAC-----GGAAAACTAACAAAG-----CAGG---A----------CCGTATGGGATGTTGT----------TG--TT----------GGTCTGTTGCTGTTGCTGTTGCTGGGAATGG----------GGCTTCTCACTTACTTG------GTG----------GGGTGGGGGTTGGGATTTTGGAAATGTGTACGGGGGCCCGGA--ATAGC---------CTTA--GTCTAACTTATTGG
droBipl	scf7180000396425:96361-96523 -		GTAAAC-----TAAAAACTAACAAAGAC---CAGG---A----------CCGTATAGCCTGTTGT----------TG--TT----------GGTTCGTTGCTGTTGCTGTTGCGCGTTCCTGG----------GGCTTCTACTTACTTG------GCG----------GGGTGGGGCACGGGGAATTTGGAAATGTATATGCAGGGCCTGGA--CTAGC---------CTTA--GTCTAACTTATTAA
droKik1	scf7180000302469:1015477-1015645 +		GTAAAC-----TA-------AGG---GATCATGTCAGA-GCAA----------TATAAATTAA----------CGTAATTGTGTTGTTGTCGTTGTCTGGC---T---TGTTGTTGTGCTGTTGTCTAGGTGGCTGGA----------TC----TCACTTACGTA------GAAGTT-TTATTGTCAACGG----------GGGGTGG----------G----------GGTGGA-ATTAGC---------CGTAGTGTCTAACTTATTGG
droFic1	scf7180000454072:1744286-1744436 +		GTAAAC-----GAGAGCGTGACA---GATGGTGCCGTCCACAA----------TTTAATCCAT----------CGCCTTT---------T---T---GTTGTT-----GTTGCGCTCATTGTTGTGCGGTAAGC----------AG----TTACTTACTTA------GTAGAT-AAACTGAGTTGGA----------GTAACGC----------GGAA-------A---------AGAGC---------GCTA--TTTTAACCTATTGG
droEle1	scf7180000491024:10060-10210 -		GTAAAC-----GAGAGCGTGACAGATTT---CCCC---C----------AATTC-C----------CGCCTTT---------T---T---GTTGTTGTTGT------TTGCTGCGTTGCTTGATGAGT----------AC----TTACTTACTTA------GAAGTT-TTATTAGGAAGGG----------GTCGGGTTACGC----------GAAT-------GGGGCCTGGT-TCCGC---------TCTA--GTCTATCTTATTGG
droRho1	scf7180000776645:13111-13273 +		GTAAAC-----GAGAGCGTGACA---GATGGTGTCGGCCGTAA----------TTTAATTCAG----------CGCCTTC---------T---T---GTGGTTGTTGT------TTGTTGCGTTGTTCAGTGAAT----------AC----TTACTTACTTT------AGTT-TTATTGGGATGGG----------GTAACGC----------GAAT-------GGGGTGTGGT-CTCAGC---------GTTA--GTCTAACTTATTGG
droBia1	scf7180000301760:3948780-3948942 -		GTAAAC-----GAGAGCGTGACA---GATGGTGTCGGCCAAAA----------TTCAATTCGG----------CGCC---------T---T----------TCTGTCGCTTGTTGTTGTCCGGTGAGTAGTA------AT-CA---CACAG----TTACTTACGTTTACTTGGCAGATTTTTGT----------GGGGTGG----------GGAG-------GGGGCCTGGA-CCTA--------AGTTA--GACTAACTTATTGG
droTak1	scf7180000415704:958130-958292 -		GTAAAC-----GAGAGCGTGACA---GATGGTGTCGACCATAAACTATAATTTAATTTTAATTCAG----------CGCCTTC---------T---T---GTTGA-----TGTTGTTGTTGTGCTGTCCAGTGAGTAGTG------AGTTA------GTACTTACGTTTAATTG-ACAGA-TTCTTTT----------T--------AGATCTTA--------AGTTA--GACTAACTTATTGG
droEug1	scf7180000408994:69847-70011 -		GTAAAC-----GAGAGCGTGACAGA---TCAGTCTGCCATAA----------TCTAATTCGG----------CGCCTTC---------T---T---G-------AATGTTGTTGTTAAGCCGTGAGTAGTT-------AC-------TAC----TTACTTACTTTTGTAG-AAGTT-TTATTGGG----------TTGGGGTAACGC----------GGAAG-----TGAAACAGTG-TTTAAC---------GTTA--GTCTAACTTATTGG
dm3	chrX:1360872-1361063 -		GTAAAC-----GAGACGCTGAGCGAGCAGATGGTCCG----------CCCGTCGC----------CC--CTCCATC---T---TCTGTTGTTGTGCTGCCGGTGAGTGGTTGTGT------TA---GTTAC----TTACTTGCTTACGTAG-ACGT-TCCG---GACGGGGTAGAGGGGTCCAGAC-GCCGC----------GAAA-------GGGGCCTGGGTTCAGCTTGGGATTAGCTA--GTCTAACTTAATGT
droSim2	x:1240878-1241069 -		GTAAAC-----GAGACGCTGAGCGAGCAGATGGTCCG----------CCCGTCGC----------CC--CTCCATC---A---TCTGTTGTTGTGCTGCCGGTGAGTGGTCAGT------TA---GTTAG----TTACTTGCTTACGCAG-TGCGT-TCCA---GACGGGGTAGATGGGTCCAGAC-GCCGC----------GGAA-------GGGGCCTGGGTCTAGCTTGGGATTAGCTA--GTCTAACTTAATGT
droSec2	scaffold_10:1187854-1188041 -		GTAAAC-----GAGACGCTGAGCGAGCAGATGGTCCG----------CCCGTCGC----------CC--CTCCATC---A---TCTGTTGTTGTGCTGCCGGTGAGTGGTG------AG------TTAC----TTACATGCTTACGTAG-TGCGT-TCCA---GACGGGGTAGATGGGTCCAGAC-GCCGC----------GGAA-------GGGGCCTGGGTTCAGCTTGGGATTAGCTA--GTTAACTTAATGT
droYak3	X:1265744-1265933 -		GTAAAC-----GAGACGCTGACAGAGATGATCAGCCG----------CCCGTCGCCCC----------CTTCCTCTATC---T---TCTGTTGTTGTGCTGCCGGTAAGTGGTGAGTGGTGAG-TA---GTTAG----TTACTTGCTTTTGTGG-ACGT-TTAGG----------GGGTCCAGAT-GCGC----------GAAA-------GGGGCCTGGGTAGTAGCTAGGACGTAGCTA--GTCTAACTAATGT
droEre2	scaffold_4644:1350524-1350712 -		GTAAAC-----GAGACGCTGACAGAGCAGATGGTACCG----------CCCGTCACCCC----------CC--CTCCATC---G---ACATTTCTGTTGTTGTGCTGCCGGTGAGTGGGGAGTAGGGAG-TA---TTTAG----TTACTTGCTTTTGTGG-ACGT-TTAGG----------GGGTCCAGGCACGC----------GAAA-------GGGGCCTGGGTATTAGCTAGGGCTTAGCTA--GTCTAACCTAATGT
dp5	XL_group1a:4656971-4657148 +		GTAAACCTAGAAGATCGTGACAGG---TAA---T----------CCGTATTCTCGTCGT---CGT----------CT--TC--GTTGTTT---TTGTGTGTTCTGTTGCTGTTTTGCGATTTTTT------AATATCTACAA-A----T-------TTTTGCTT-ACCGT-TTATTGTCGTGGA--GGA--------GGGGTGG------C---------GGATGGAGGCCTAGTATCTAGC---------CCTA--GTCTAACTTATTGA
droPer2	scaffold_11:1245825-1246003 +		GTAAAACTTAGAAGATCGTGACAGG-TAATCGGTATTC----------CCCGTCGTCGT----------CC--TC--GTTGTTT---TTGTGTGTTCTGTTGCTGTTTTCGATTTTTT------AATATCTACAA-A----T-------TTTTGCTT-ACCGT-TTATTGTCGTGGA----------GGACGGC----------GGGGCGCGA-TAAGCCTAGTATCTAGC---------CCTA--GTCTAACTTATTGA

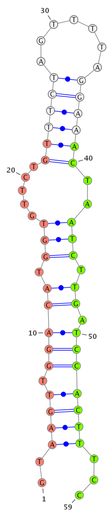
Generated: 09/08/2015 at 07:55 PM

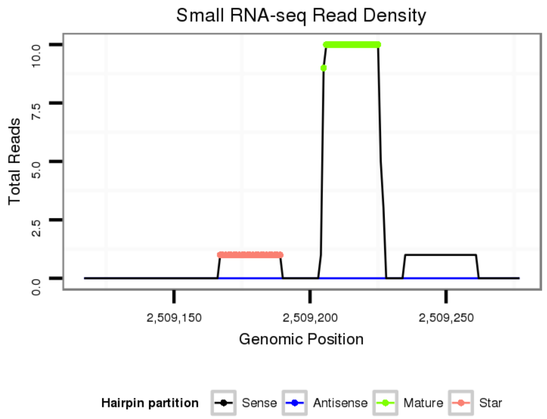
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

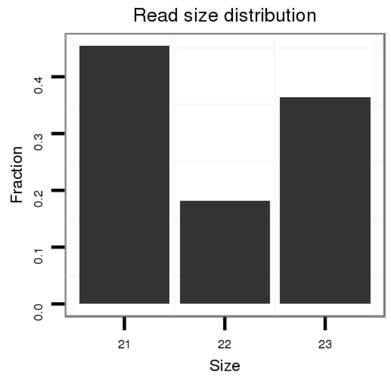
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_835	**scaffold_12929:2509167-2509227 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

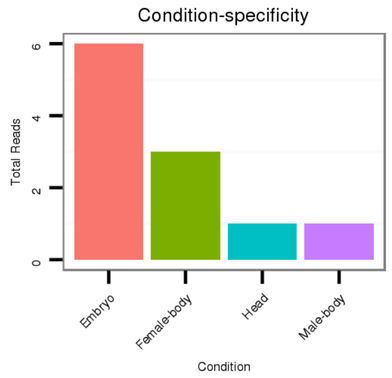
Legend: mature star mismatch in alignment mismatch in read

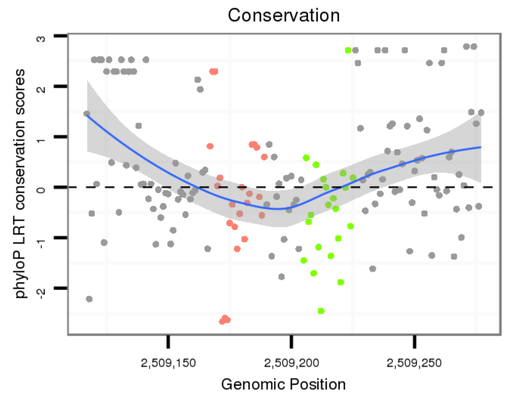
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF22232-in]; CDS [Dana\GF22232-cds]; CDS [Dana\GF22232-cds]; utr3 [utr3_minus_9640]; utr3 [utr3_minus_9639]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGATCATACAGGCGTGCCAGGACAACAACCGGAGGCAGCAAGGAATGCCGGTAAGTTGGACATGGTGTTCTGTTTCTAGTTTTAGGAAACTAATCTTGATCCACTTTCCAGTTCAAGTTAGATGCCACCACGAGTGAGCCGGGCCAGCATATGCATATGGT	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	M044 female body	V105 male body	V106 head	V055 head
**********..(((((.((((((.(((.....((((((.......)))))).))).)).)))))))).....**********										
.....ACTAATCTTGATCCACTTTCC.....	21	0	1	5.00	5	5	0	0	0	0
.....ACTAATCTTGATCCACTTTCCAG.....	23	0	1	2.00	2	1	1	0	0	0
.....GTAAGTTGGACATGGTGTTCTGT.....	23	0	1	1.00	1	0	0	1	0	0
.....AACTAATCTTGATCCACTTTCCA.....	23	0	1	1.00	1	0	1	0	0	0
.....CTAATCTTGATCCACTTTCCAG.....	22	0	1	1.00	1	0	1	0	0	0
.....ACTAATCTTGATCCACTTTCCA.....	22	0	1	1.00	1	0	0	0	1	0
.....TAGATGCCACCACGAGTGAGCCGGGCC.....	27	0	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

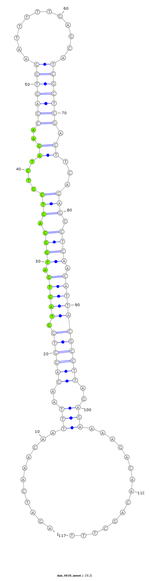
Re-alignment of all predicted orthologs

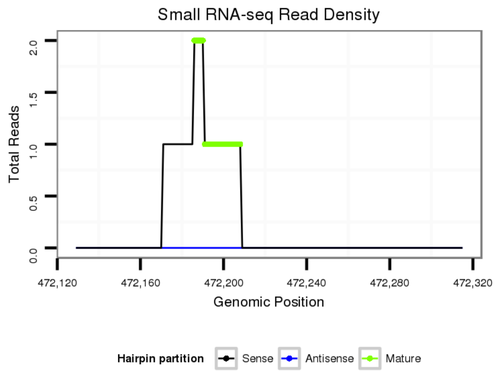
Species	Coordinate	ID	Alignment
droAna3	scaffold_12929:2509117-2509277 +	dan_835	TGATCATACAGGCGTGCCAGGACAACAAC----------CGGAGGCAGCAAGGAATGCCGGTAA------GTTGG--------ACATGGT----------GTTCTGTTTCTAGTTTT----------AGGA----------AA------CT---AATC----------TTGATCCA------CTTTCCAGTTCAAGTTAGATGCCACCACGAGTGAGCCGGGCCAGCATATGCATATGGT
droBip1	scf7180000396434:498758-498915 +		TGATAATCCAGGCGTGCCAGGACAATAAT----------CGAAGACAGCAAGGATGCCGGTAAGTTGGATGTGT-TTCT---------------------------------AAC-----CAT-----TATCTCTGAAACT---TACCT----------GT-GACCA------TAATTAGTTCAAGTTAGATGCCACCACGAGTGAACCGGGCCAGGCAAGCATATGGT
droKik1	scf7180000302344:791755-791954 -		TATTCATCCAGGCCTGCCAGACGGAGCCTGACAAGAAGCTGGAGCAGGATCAGCATGGATTGCCAGTAA------GACAG--------CA--------AACAACAGGAGTTCTTCTCTACATCTACGA---G----------AG------C---CTAATTTTTGTTCTGTTT--GTTT-TCCCTTTTGCTCCGTGCAGTACGCCTTAGATGCCACCACACGTCGCCGGGCCAGCATTTGCACATGTT
droFic1	scf7180000454072:2434140-2434319 +		TGATCATTCAGGCGTGCCAGGAGGAGGCCCCAAAAAAGGAGAGGGAGAGTCCTCAGGATTGCCCGTAA------GTTGT--------TTTC---GATCAATAGTCGGCTTA----------AAAG---TGTATTGTA----------TC------TC---CATT----------GGA-TTCTT------ATTTTCAGTTTAAGATCGATGTTATCACCCAGTCACCGGCCAGCACGTGAATATGGT
droEle1	scf7180000491001:752813-752990 +		TGATCATTCAGGCCTGCCAGGAGGAAGCTCCCGAGGAGGGAGACCAGAGTCAGCAGGGATTGCCAGTAA------GCGT--------------------------ATTTTTAGGGATTTAATTAGGCAATC--------AC------A---TTTATTAT---------TTGAT-CCCCT------ATTTTCAGTTTAAAATCGATGTAGACCACCCAGTCGCCTGCGCAACATCTTTATATGGT
droRho1	scf7180000779976:585099-585316 +		TGATCATTCAGGCCTGCCAGGAGGAGGCTCCCAACAAGGGAGAGCGATAATGAGCAGCATTGCCGGTAA------GCATT--CT----TTTT---TAGGATTAGTCAGTTTT----------AAAA---GCTCTAATATTGATTACA-ACCCATA----TTGTC--GAGTCTATTCA---TTTTCTTAT---------TTTA--TTTC------TTTTTCAGTTCAAGCATCATGTAACCAGACAGTCACCTGGCAACACGTTAATATGGT
droBia1	scf7180000302069:135242-135436 +		TAGTCATCCAGGCTTGCCAGGAGGAGGTCATCAATGAAGACAAGCCAAATCAAGGGGCCTTGCCGGTACGTAT-TTAT----ACC---CGTTACTGGTAGAGTAA----------A-AGGGTA---CACTAGATTC----------GTC----AGATC---------TTAT---------TGTAT-TCTTC------ATTTTCAGTTTAAAATCGATGTAGACCACGCAGTCGCCAGGTCAACATCTTATATGGT
droTak1	scf7180000415704:833375-833464 +		TCATCATCCAGGCCTGCCAGGAGGAGGCGCTCCGGGAGGGCGAGGAAAACAG---------CGAGTAG------GCCTG---------AT----------ATTCA---TC-AGGGTT----------GC------AGATC---------TTAT---------TGTAT-TCTTC------ATTTTCAGTTTAAAATCGATGTAGACCACGCAGTCGCCAGGTCAACATCTTATATGGT
droEug1	scf7180000408973:15523-15584 +		T------------------------------

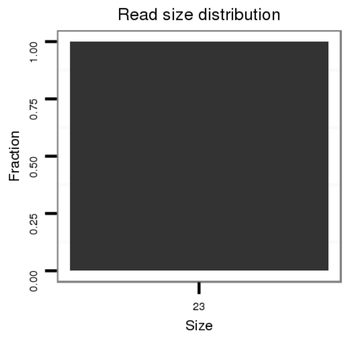
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_4039	**scaffold_13334:472179-472265 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

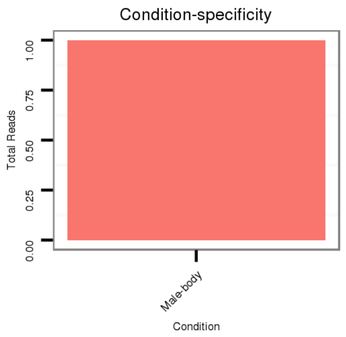
Legend: mature star mismatch in alignment mismatch in read

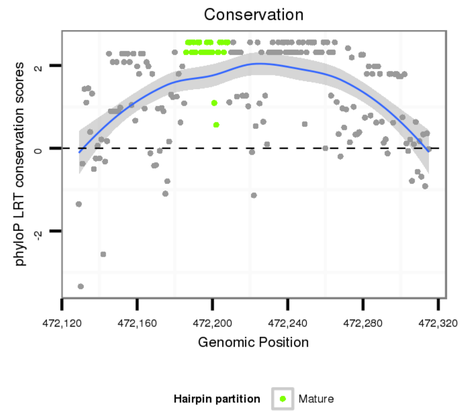
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF21808-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

							V105	M058	V039
TTAAATAGGTTATGGAAGCGGGAACTTGTTCTGAAAGATCAAACAATTTAAGAGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTTTGAGCATCGCTCGACTTCAGAGCCTCAACATTACGCCTTAGAGAAAAGACAACAGCTTTAGATCAATGCCAACCCGCTTAGGAAGTGCGAGCCT	Read size	# Mismatch	Hit Count	Total Norm	Total	male body	embryo	embryo
************************************.....(((..(((((((.(((((.(((((.(((.....((..(((((((.............)))))))..))...))).)))))..)))))))))))..)))..************************************									
.....ACAATTTAAGAGGTGGTAGT.....	20	0	1	1.00	1	1	0	0
.....GTAGTGATGGGACTCGTCTAGAA.....	23	0	1	1.00	1	1	0	0

Anti-sense strand reads

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

Show Alignment With Reads

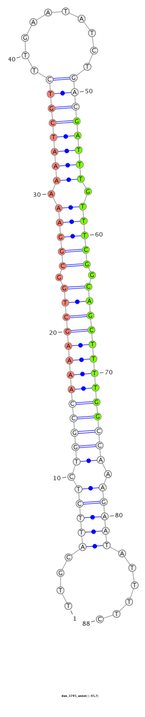
Re-alignment of all predicted orthologs

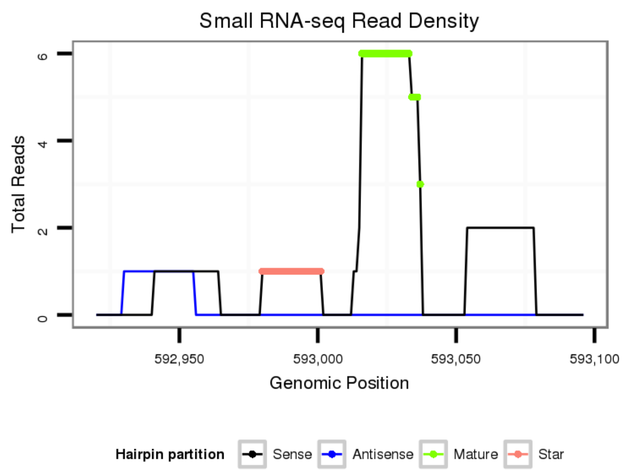
Species	Coordinate	ID	Alignment
droAna3	scaffold_13334:472129-472315 +	dan_4039	TTAAA----------TAGGTTAT-GGAAGC--GGGAACTTGTTCTGAAAGATCA-AA--CAATTTAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTTT-GAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCCTTAGAGAAAAGACAAC-AGCTT--TAGATCAATGCCAA---CCCGCTTAGGA----AGTGC-G---AG----------CCT
droBip1	scf7180000396431:1081232-1081416 -		TGAAA----------TA--GAT---A----TAGAA-ATATATAGC--GGGAACTTGTTCTGAAAGATCC-AA--CA-GTGAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTTG-AAGCATTGCTCG-ACTTCAGAGCCTCAACATTACGCCT-AGAGAACCAGACAAC-AGCTTTTAGATCAATGAACA---CCCGCTTGGGC-A---A-----------
droKik1	scf7180000302698:307803-308017 -		AAAAATAACTAT----------CCAAAAGCCCAGGAAAGACAAGACACAT----------AG-ATAAGC--GGGAACTTGTTCTGAAAGACC-AATACAAATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTA-AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCCT-AGAGAACC-GACAAC-AATTT--TAGATCAATGCCAC---CCCGCTTAGGA-----GTTGTAAGAGA----------
droFic1	scf7180000454073:1442983-1443189 +		TGAAATAA--TA----------TT--CA-AATTAGAAAGT-TCAAGC--GGGAACTTGTTCTGAAAGACAAA--G---ATTAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTC-AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCCT-AGAGAACCGACAAC-AGCTT--TAGATCAATGCCAC---CCCGCTTAGGA-----AGCCA-G---TAG--TACGAACTGGGATCT
droEle1	scf7180000491044:215049-215255 +		TTA------------TAAA----AGGAAAG-------CT--GAT---AA-AATTAGAAAAT-AAAAGC--GGGAACTTGTTCTGAAAGACC-TA----AAAGTAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTC-AAGCATTGCTCG-ACTTCAGAGCCTCAACATTACGCCT-AGCGAACC-GACAAC-AGCTT--TAGATCAATGCCAC---CCCGCTTAGGA-----AGCCA-G---AAT--TGCAG-------ACT
droRho1	scf7180000779510:38393-38578 +		AA---TAGGAACT-GTAAGC--GGGAACTTGTTCTGAAAGACC-TA----AAATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGCATTTA-AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCCT-AGAGAACC-GACAAC-AGCTT--TAGATCAATGCCAC---CCCGCTTAGGA-----AGCCA-G---TAT--TGCGA----A--CAG
droBia1	scf7180000302041:563673-563852 +		CAAA----------TAGGCACT-GTAAGC--GGGAACTTGTTCTGAAAGACC-CA----AAGTAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTC-AAGCCGCTCG-ACTTCAGAGCCTCAACATTACGCCT-AGAGAACC-GACAAC-AGCTT--TAGATCAATGCCAC---CCCGCTTAGGC-----AGCAG-G---CAC----------CG
droTak1	scf7180000414393:30817-31015 -		TTAA----------GACACTT--GCT---A----TAGGAACT-GTAAGC--GGGAACTTGTTCTGAAAGACA-AA----CCTTAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTC-AAGCGTCGCTCG-ACTTCAGAGCCTCAACATTACGCCT-AGAGAACC-GACAAC-AGCTT--TAGATCAATGCCAC---CCCGCTTAGGA-----AGCCA-A--TATATTGCCC-------ACT
droEug1	scf7180000408958:35924-36118 -		TTGA----------TAGGAATT-TTAAGC--GGGAACTTGTTCTGAAAGACC-AA--AAATAAAAGAGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTC-AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCCT-AGAGAACC-GACAAC-AGCTT--TAGATCAATGCCAC---CCCGCTTAGGAGAATAATCCA-G--TT---TAA-----GGACCT
dm3	chrX:13553573-13553737 +	dme_424	A---

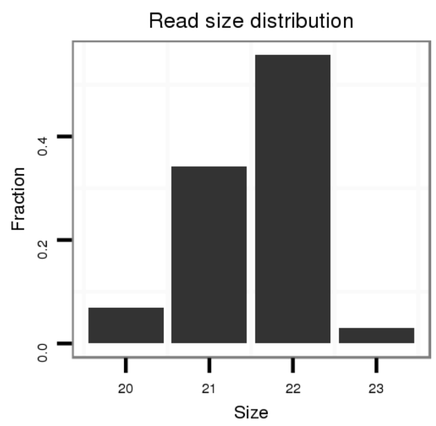
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_3795	**scaffold_13045:592970-593046 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

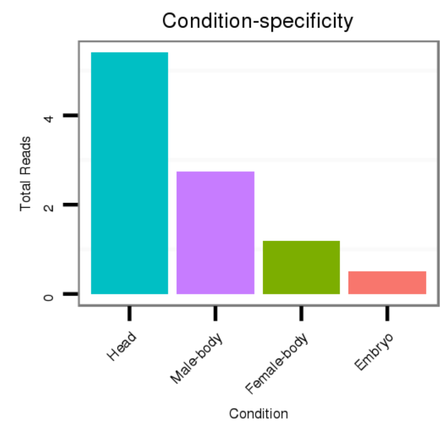
Legend: mature star mismatch in alignment mismatch in read

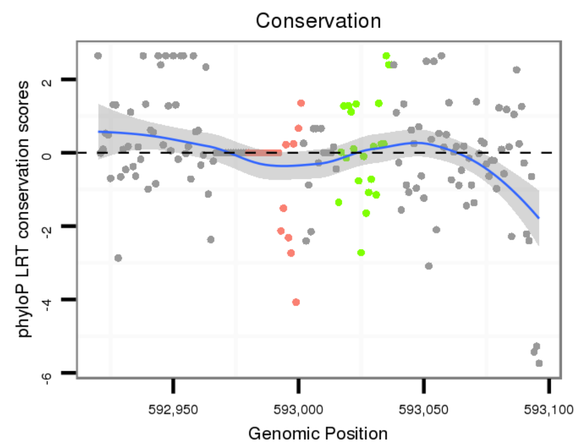
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dan_3795 scaffold_13045:593016-593037 + 2. dan_3802 scaffold_13045:602971-602992 +	1. scaffold_899:654-675 + 2. scaffold_8290:8413-8434 + 3. scaffold_9924:588-609 + 4. scaffold_12064:3340-3361 - 5. scaffold_12422:35251-35272 + 6. dan_3795 scaffold_13045:592980-593001 + 7. dan_3802 scaffold_13045:602935-602956 + 8. scaffold_13111:602790-602811 + 9. scaffold_13228:1056004-1056025 + 10. scaffold_13230:2093882-2093903 + 11. scaffold_13250:455828-455849 -

Sense Strand Reads

hide 3p reads show mid mismatch reads

TATTCATACACCAGGCACACGTCATCTTTCAAAATACGTGTGCCCTTGCATTCTCTGGCCAAAAGCTGGCGGAAAAAATCGTCTTGAATATCTGACGATTTGTTTCGGCAGCTTTTGGCCAAAGAATATTTTCGTCCAAGAACATCAGCCAAGTACGGCGACAAAAAAAAATAACCA **********....(((((.(((((((((((((((.(((((.(((((((((.........)))))))))))))))))))))))))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	V106 head	V105 male body	M044 female body	V055 head	V039 embryo
.....GATTTGTTTCGGCAGCTTTTGG.....	22	0	2	3.00	6	0	4	2	0	0	0
.....TCCAAGAACATCAGCCAAGTACGGC.....	25	0	5	2.60	13	13	0	0	0	0	0
.....TCATCTTTCAAAATACGTGTGCCC.....	24	0	20	1.60	32	32	0	0	0	0	0
.....GACGATTTGTTTCGGCAGCTT.....	21	0	2	1.50	3	0	0	1	2	0	0
.....GATTTGTTTCGGCAGCTTTTG.....	21	0	2	1.50	3	0	2	1	0	0	0
.....AAAAGCTGGCGGAAAAAATCGT.....	22	0	11	1.09	12	0	6	5	1	0	0
.....CGATTTGTTTCGGCAGCTTTTG.....	22	0	2	1.00	2	0	2	0	0	0	0
.....TTGTTTCGGCAGCTTTTGGC.....	20	0	2	0.50	1	1	0	0	0	0	0
.....ATCTTTCAAAATACGTGTGCCCTTGC.....	26	0	20	0.45	9	9	0	0	0	0	0
.....AAAAGCTGGCGGAAAAAATCGTC.....	23	0	10	0.30	3	0	1	2	0	0	0
.....AAAAGCTGGCGGAAAAAATCG.....	21	0	11	0.27	3	0	3	0	0	0	0
.....AAGAACATCAGCCAAGTACGGCG.....	23	0	5	0.20	1	0	0	0	0	0	1
.....AAGCTGGCGGAAAAAATCGTC.....	22	0	10	0.20	2	0	1	0	1	0	0
.....AGCTGGCGGAAAAAATCGTCTT.....	22	0	10	0.20	2	0	0	0	0	2	0
.....AAAGCTGGCGGAAAAAATCG.....	20	0	11	0.18	2	0	0	1	0	1	0
.....TCGTCCAAGAACATCAGCCAAGTACGG.....	27	0	20	0.15	3	3	0	0	0	0	0
.....TTTCGTCCAAGAACATCAGCC.....	21	0	20	0.15	3	0	0	0	3	0	0
.....CGTCATCTTTCAAAATACGTGTGCCC.....	26	0	20	0.15	3	3	0	0	0	0	0
.....AAGCTGGCGGAAAAAATCGTC.....	21	0	10	0.10	1	0	1	0	0	0	0
.....TCGTCCAAGAACATCAGCCAAGT.....	23	0	20	0.10	2	2	0	0	0	0	0
TATTCATACACCAGGCACACGTCATC.....	26	0	20	0.10	2	2	0	0	0	0	0
.....TTCGTCCAAGAACATCAGCCAAGTACGG.....	28	0	20	0.05	1	1	0	0	0	0	0
...TCATACACCAGGCACACGTCATCTTTC.....	27	0	20	0.05	1	0	0	0	1	0	0
.....CTTTCAAAATACGTGTGCCCT.....	21	0	20	0.05	1	1	0	0	0	0	0
.....CGTCCAAGAACATCAGCCAAGTACGG.....	26	0	20	0.05	1	0	0	0	0	0	1
.....AATATTTTCGTCCAAGAACATCAGCC.....	26	0	20	0.05	1	0	1	0	0	0	0

Anti-sense strand reads

ATAAGTATGTGGTCCGTGTGCAGTAGAAAGTTTTATGCACACGGGAACGTAAGAGACCGGTTTTCGACCGCCTTTTTTAGCAGAACTTATAGACTGCTAAACAAAGCCGTCGAAAACCGGTTTCTTATAAAAGCAGGTTCTTGTAGTCGGTTCATGCCGCTGTTTTTTTTTATTGGT **********....(((((.(((((((((((((((.(((((.(((((((((.........)))))))))))))))))))))))))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	V039 embryo	M044 female body	V055 head	V106 head	V105 male body
.....GGTCCGTGTGCAGTAGAAAGTTTTAT.....	26	0	20	1.90	38	0	38	0	0	0	0
.....AAAGCAGGTTCTTGTAGTCGGTTCAT.....	26	0	20	0.95	19	19	0	0	0	0	0
.....GGTTTCTTATAAAAGCAGGTTCTTGT.....	26	0	5	0.40	2	0	0	2	0	0	0
.....CAGGTTCTTGTAGTCGGTTCATGCCGC.....	27	0	5	0.40	2	2	0	0	0	0	0
.....CAGGTTCTTGTAGTCGGTTCATG.....	23	0	20	0.30	6	6	0	0	0	0	0
.....GCAGGTTCTTGTAGTCGGTTCAT.....	23	0	20	0.25	5	0	0	5	0	0	0
.....GGTTCTTGTAGTCGGTTCATGCCGC.....	25	0	5	0.20	1	1	0	0	0	0	0
.....CGGTTTCTTATAAAAGCAGGTTCTTGTA.....	28	0	5	0.20	1	0	0	1	0	0	0
.....CCGGTTTCTTATAAAAGCAGGTTCT.....	25	0	5	0.20	1	1	0	0	0	0	0
.....CAGGTTCTTGTAGTCGGTTCATGCCG.....	26	0	5	0.20	1	1	0	0	0	0	0
.....CGGTTTCTTATAAAAGCAGGTTCT.....	24	0	5	0.20	1	1	0	0	0	0	0
.....AGGTTCTTGTAGTCGGTTCATGCCGC.....	26	0	5	0.20	1	1	0	0	0	0	0
.....CCCGTGTGCAGTAGAAAGTTTTATGCA.....	27	1	20	0.15	3	3	0	0	0	0	0
.....AAAGCAGGTTCTTGTAGTCGGTTCATG.....	27	0	20	0.10	2	2	0	0	0	0	0
....GTATGTGGTCCGTGTGCAG.....	19	0	20	0.10	2	0	0	0	0	2	0
......ATGTGGTCCGTGTGCAGTAGAAAG.....	24	0	20	0.05	1	0	0	0	0	0	1
.....TGGTCCGTGTGCAGTAGAAAGT.....	22	0	20	0.05	1	0	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13045:592920-593096 +	dan_3795	TATTCA-TACACCAGGCACACGTCATCTTTCAAAATACGTGTGCCCTTGCATTCTCTGGCCAAAAGCTGGCGGAAAAAATCGTCTTGAATATCTGACGATTTGTTTCGGCAGCTTTTGGCCAAAGAATATTTTC---GTCCAAGAACATCAGCCAAGTACGGCGACAA-A----AAAAA----------ATAACCA
droBip1	scf7180000392260:130-271 +		TATAATAATACACGGCGCACGTGTCTTTCAAGATCGTGTGCCCAC----------GCTGATGTTCAAG--------ACGATTTGTTCTCCCAGATTTTGGCCAGAGAATCTTTTC---GTCCAAGAACATCAGCCTAGTT-CCGTAAAG-A----AAAAA----------GTTAAAA
droKik1	scf7180000298305:578-714 -		TTTTCT-TACCCCAGGAACATTTGCTCTTTCAAGATAAATGTTCCTGA----------CGAAGTGTTTGGC--------AGTCTATGCTCTGCGGAAACCTGGCCAGAGTATGTGGTT---GTCAAAGAGTTTGAA---------GGTAGGA-A-AAAGAAAA----------AGGGGCC
droFic1	scf7180000453132:11376-11508 -		TTTTCA-TACGGTAGGAACATTTCATCTTTCAAGATAAGTGTTCCTGA----------CGAACTTTTAAC--------ACCATATGCTCGAGGCGATTTTGGCCAGCAAAATGGTGC---GTTAAGAGTTCGTA---------GCGAAAA-T----AAAA----------AGAAAG
droEle1	scf7180000491101:4237-4376 -		TTTTCT-TAGGGTAGGGACATTTAATCTTTCAAGATTACTAGGG--TA----------CGAAATCTATGCT--------GTCATTTGCTCTGGTGACTTTTGGCCGGAAAATATTGTGC---GTAAAGATTCGATAAGA-TAAAGGTAAGA-T----AAAAA----------AGAAGCG
droRho1	scf7180000763948:4634-4767 +		TTTTCT-TATGGTAGAGACATTTCATCTTTCAAGATAACTGGCCCTTA----------CAAGCTTTTGAA--------GCCATATGCTCGGGGGACTGTTGGCCGGATAATATGGTT---GTAAAGAATCGAGG---------GGTAAGA-T----AAAGA----------AGAAGGG
droBia1	scf7180000302021:52198-52342 -		TTTTCA-TATGGTCGTAGGATATCATCTTTTAAAATATTGTCTCCGCCC----------TGACATTTTTTAT--------GTTTTACTTTCCGAAAGCTTTTGGCTTAATGATGGTTTAGTAATTATAAGAATTTGTCCCAAATA-AACCGAGA-A----CAAAA----------AACAGGC
droTak1	scf7180000414730:6479-6620 -		TTTTCG-TACGCCCGCAGGATATGCTCTTTTAAAATATTGTCTCCGCC----------TGATGTGTTTAAT--------GTACTACTTTCTGAAAGCTTTTGGCTTAATGATGATTTGGTAATGTAAAGAATTTGTT---------CCCAATAAACCAAGAACA----------AATAACA
droEug1	scf7180000409639:53618-53763 +		TATTCC-TACGCTAGGAACATGCCATCTTTCAAGATCCGTGTTCCTCC----------GATGAGTTTTGAC--------GACATCTGTTCGACCAATTTCTGGCCGGAACATATTTTC---GTTCAAGAACATCAG---------CTTAAAA-A----TAAAAAGAAGAAAAAAAGTGGCCA
dm3	chr3RHet:2456914-2457056 -		TATTCT-TACTGTAGACACATTTCATCTTTCAAGATAACTGTCCCAAA----------TAAAATATTTCGAAGA----TATGTATGTTCTGGTGATTTTTGGCCGGATAGTATGGTGC---GTAAAGAGTTCAAA---------GGTAAGA-T----TTAAAATAGG-------AAAACG
droSim2	node_23530:425-564 -		TTCTCT-TACGGTAGGGACATATCATCTTTCAAGATAACTTTCGCAAA----------CGAGCTGTTTTCG--------ACCATATGTTCGCGGTGATTTTTGGCCGGATAGTATGGTGC---GTAAAGAGCTAA-GGT-AAAA-AGGTAAGA-T----CAAAA----------ATAAGAA
droSec2	scaffold_49:151673-151816 -		TTCTCT-TACGGTAGGGACATATCATCTTTCAAGATAACTGTCCCAAA----------CGAGCTCTTTTCG--------ACCATATGTTCGCGGTGATTTTTGGCCGGATAGTATGATGC---GTAAAGAGTTTGAA---------GGTAAGA-T----CAAAAATAAGAAAA-A-GGTGACC
droYak3	v2_chr2L_random_010:58199-58339 -		TTTTCT-TATGGTAGGGACATGCTCATCTTTCAAGATAACTGTCCCAAA----------TGAGCTATTCTCA--------ACCATATGTTCTGGTGATTTTTGGCCGAAAAGTATGATT---GTGAAAGATTTGAA---------GGTAAGAAT----TAAAATATAGGA------TAAAAAG
droEre2	scaffold_4784:23045698-23045831 -		TTTTCT-TAGGATAGGGACATTTAATCTTTAAGATAACTGTCCCTAA----------TAAGCAACTTCCA--------ACCATATGTTTTGGTAATTTTTGGCCGGATAGTATGGTAA---GTGAAAGGGTTCGAA---------GGCAAGA-T----CAAAA----------ATAGCAA
dp5	Unknown_group_274:2540-2672 +		TTCTCT-TATGAGAGGGAGATATCTTGCTTCAAAATAAGTGTCTCCCC----------AACTCACTTTGAC--------ACCATTTGCTTCGCCAAATTTTGGCCAGAGCATGTGGTGC---GTGAAGAAGTTCAAG---------GGTAAGA-A----CAAAA----------ATAGGCC
droPer2	scaffold_165:46685-46815 -		TTTTCT-TATGCCAGGGAGAGATATCTTGCTTCAAGATAAGTGTCTCCCC----------AACTCTTTTGAC--------ACCATTTGCTCTGCCAAATTTTGGCCAGAGCATTTGGTGC---GTGAAGAAGTTCAAG---------GGTAAGA-A----CAAAA----------AT---ATAG
droWil2	scf2_1100000004965:614973-615113 -		TTTTCT-TATTTCCGGGACATTTCGTCTTTAAAATATGTGTTTCTGC----------CAATATCTTCGAT--------ACCATATGTCGAAGAAGATTTTTGGCCTTAAACATATAATA---TTTAAGTAA-TATAAGTATA-TACTGTAAAAA-A----CAAAA----------ATGGCCA
droVir3	scaffold_12936:148274-148405 +		TCGCCTATGGAACATATATATTGCATGCTTTATAATAATTGTTCCGCCC----------AGAAATATTTACT--------AACATTTGTTTATAAGAGTCTTGGCCGGAATACTTAATA---GTCAAAGAATATAAG---------GGCAAAA-A----------GA----------TTAATTG
droGri2	scaffold_15126:8188956-8189069 +		TT--A-TATATAAGAGCAATTTCGCTCTTGTAAAATAAGTGTTCCGTC----------TGAAGTATTTGC--------ACAAGTTGTTGTGCCACTTCTGGCCGAAAGCAATAG---------AGGAGTATAC----------------------AA----------ATAAAAA

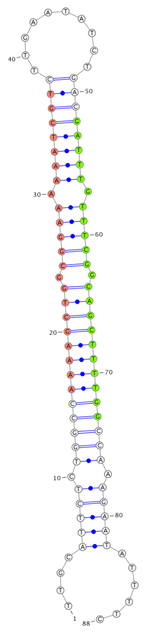
Generated: 09/08/2015 at 08:03 PM

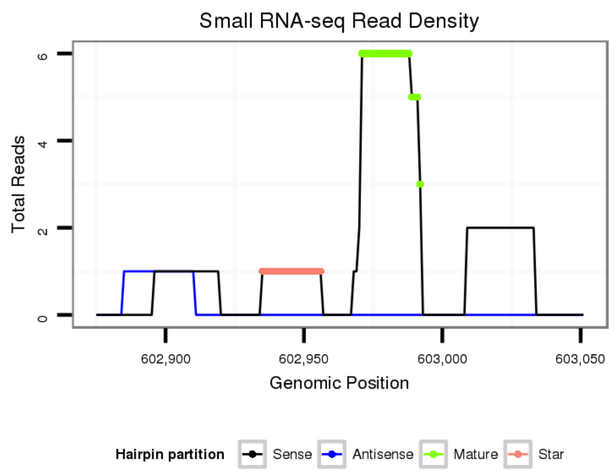
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

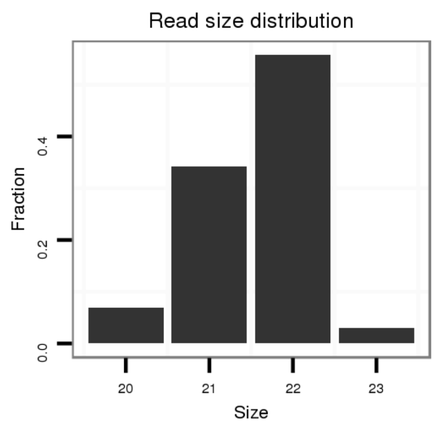
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_3802	**scaffold_13045:602925-603001 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

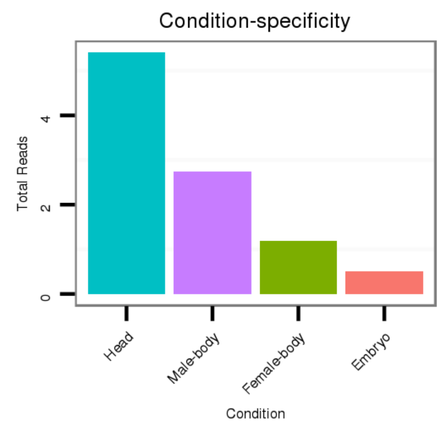
Legend: mature star mismatch in alignment mismatch in read

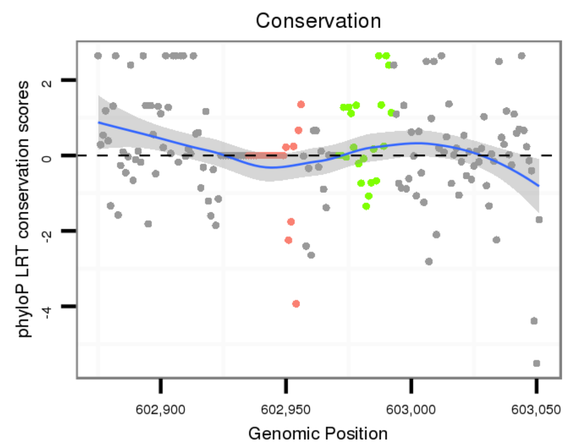
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dan_3795 scaffold_13045:593016-593037 + 2. dan_3802 scaffold_13045:602971-602992 +	1. scaffold_899:654-675 + 2. scaffold_8290:8413-8434 + 3. scaffold_9924:588-609 + 4. scaffold_12064:3340-3361 - 5. scaffold_12422:35251-35272 + 6. dan_3795 scaffold_13045:592980-593001 + 7. dan_3802 scaffold_13045:602935-602956 + 8. scaffold_13111:602790-602811 + 9. scaffold_13228:1056004-1056025 + 10. scaffold_13230:2093882-2093903 + 11. scaffold_13250:455828-455849 -

Sense Strand Reads

hide 3p reads show mid mismatch reads

TATTCATACACCAGGCACACGTCATCTTTCAAAATACGTGTGCCCTTGCATTCTCTGGCCAAAAGCTGGCGGAAAAAATCGTCTTGAATATCTGACGATTTGTTTCGGCAGCTTTTGGCCAAAGAATATTTTCGTCCAAGAACATCAGCCAAGTACGGCGACAAAAAAAAATAACCA **********....(((((.(((((((((((((((.(((((.(((((((((.........)))))))))))))))))))))))))))))))).)))))......**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	V106 head	V105 male body	M044 female body	V055 head	V039 embryo
.....GATTTGTTTCGGCAGCTTTTGG.....	22	0	2	3.00	6	0	4	2	0	0	0
.....TCCAAGAACATCAGCCAAGTACGGC.....	25	0	5	2.60	13	13	0	0	0	0	0
.....TCATCTTTCAAAATACGTGTGCCC.....	24	0	20	1.60	32	32	0	0	0	0	0
.....GATTTGTTTCGGCAGCTTTTG.....	21	0	2	1.50	3	0	2	1	0	0	0
.....GACGATTTGTTTCGGCAGCTT.....	21	0	2	1.50	3	0	0	1	2	0	0
.....AAAAGCTGGCGGAAAAAATCGT.....	22	0	11	1.09	12	0	6	5	1	0	0
.....CGATTTGTTTCGGCAGCTTTTG.....	22	0	2	1.00	2	0	2	0	0	0	0
.....TTGTTTCGGCAGCTTTTGGC.....	20	0	2	0.50	1	1	0	0	0	0	0
.....ATCTTTCAAAATACGTGTGCCCTTGC.....	26	0	20	0.45	9	9	0	0	0	0	0
.....AAAAGCTGGCGGAAAAAATCGTC.....	23	0	10	0.30	3	0	1	2	0	0	0
.....AAAAGCTGGCGGAAAAAATCG.....	21	0	11	0.27	3	0	3	0	0	0	0
.....TCGTCCAAGAACATCAGCCAAGTACGG.....	27	0	20	0.15	3	3	0	0	0	0	0
.....CGTCATCTTTCAAAATACGTGTGCCC.....	26	0	20	0.15	3	3	0	0	0	0	0
.....AAGCTGGCGGAAAAAATCGTC.....	21	0	10	0.10	1	0	1	0	0	0	0
TATTCATACACCAGGCACACGTCATC.....	26	0	20	0.10	2	2	0	0	0	0	0
.....TCGTCCAAGAACATCAGCCAAGT.....	23	0	20	0.10	2	2	0	0	0	0	0
.....TTCGTCCAAGAACATCAGCCAAGTACGG.....	28	0	20	0.05	1	1	0	0	0	0	0
.....AATATTTTCGTCCAAGAACATCAGCC.....	26	0	20	0.05	1	0	1	0	0	0	0
.....CGTCCAAGAACATCAGCCAAGTACGG.....	26	0	20	0.05	1	0	0	0	0	0	1
...TCATACACCAGGCACACGTCATCTTTC.....	27	0	20	0.05	1	0	0	0	1	0	0
.....AAAATACGTGTGCCCTTGCA.....	20	0	20	0.05	1	0	0	0	1	0	0
.....CTTTCAAAATACGTGTGCCCT.....	21	0	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

ATAAGTATGTGGTCCGTGTGCAGTAGAAAGTTTTATGCACACGGGAACGTAAGAGACCGGTTTTCGACCGCCTTTTTTAGCAGAACTTATAGACTGCTAAACAAAGCCGTCGAAAACCGGTTTCTTATAAAAGCAGGTTCTTGTAGTCGGTTCATGCCGCTGTTTTTTTTTATTGGT **********....(((((.(((((((((((((((.(((((.(((((((((.........)))))))))))))))))))))))))))))))).)))))......**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	V039 embryo	M044 female body	V055 head	V106 head	V105 male body
.....GGTCCGTGTGCAGTAGAAAGTTTTAT.....	26	0	20	1.90	38	0	38	0	0	0	0
.....AAAGCAGGTTCTTGTAGTCGGTTCAT.....	26	0	20	0.95	19	19	0	0	0	0	0
.....CAGGTTCTTGTAGTCGGTTCATGCCGC.....	27	0	5	0.40	2	2	0	0	0	0	0
.....GGTTTCTTATAAAAGCAGGTTCTTGT.....	26	0	5	0.40	2	0	0	2	0	0	0
.....CAGGTTCTTGTAGTCGGTTCATG.....	23	0	20	0.30	6	6	0	0	0	0	0
.....GCAGGTTCTTGTAGTCGGTTCAT.....	23	0	20	0.25	5	0	0	5	0	0	0
.....CGGTTTCTTATAAAAGCAGGTTCT.....	24	0	5	0.20	1	1	0	0	0	0	0
.....GGTTCTTGTAGTCGGTTCATGCCGC.....	25	0	5	0.20	1	1	0	0	0	0	0
.....AGGTTCTTGTAGTCGGTTCATGCCGC.....	26	0	5	0.20	1	1	0	0	0	0	0
.....CGGTTTCTTATAAAAGCAGGTTCTTGTA.....	28	0	5	0.20	1	0	0	1	0	0	0
.....CCGGTTTCTTATAAAAGCAGGTTCT.....	25	0	5	0.20	1	1	0	0	0	0	0
.....CAGGTTCTTGTAGTCGGTTCATGCCG.....	26	0	5	0.20	1	1	0	0	0	0	0
.....CCCGTGTGCAGTAGAAAGTTTTATGCA.....	27	1	20	0.15	3	3	0	0	0	0	0
....GTATGTGGTCCGTGTGCAG.....	19	0	20	0.10	2	0	0	0	0	2	0
.....AAAGCAGGTTCTTGTAGTCGGTTCATG.....	27	0	20	0.10	2	2	0	0	0	0	0
......ATGTGGTCCGTGTGCAGTAGAAAG.....	24	0	20	0.05	1	0	0	0	0	0	1
.....TGGTCCGTGTGCAGTAGAAAGT.....	22	0	20	0.05	1	0	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13045:602875-603051 +	dan_3802	TATTCATACACCAGGCACACGTCATCTTTCAAAATACGTGTGCCCTTGCATTCTCTGGCCAAAAGCTGGCGGAAAAAATCGTCTTGAATATC-TGACGATTTGTTTCGGCAGCTTTTGGCCAAAGAATATTTTCG---TCCAAGAACATCAGCCAAGTACGGCGA----------CAAAAAAAAATA---------ACCA
droBip1	scf7180000392260:130-271 +		TATAATAATACACGGCGCACGTCTTCTTTCAAGATTCGTGTGCCCACGC----------TGATGTTCAAG---ACG-A-----TTTGTTCTCCCAGTTTTTGGCCAGAGAATCTTTTCG---TCCAAGAACATCAGCCTAGT-TCCGTA----------AAGAAAAAGTT---------AAAA
droKik1	scf7180000300067:249-387 +		TTTTCATACCCAGAGACATCTCATCTTTCAAGATAAGTGTCTCCCTCG----------ATCTTTTTGAC---ACA-A-----TTTGTTCTGGTGACTTCTGGCCTCAGCAGCGTGTAG---TCAAGAGTACGAG---------GTAA----------AAATAAAGAAAAAACA-----AACCA
droFic1	scf7180000453132:11376-11508 -		TTTTCATACCCTAGGACATTTCATCTTTCAAGATAAGTGTTCCTGACG----------AACTTTTAAC---ACC-A-----TATGCTCGAGGCGATTTTGGCCAGCAAAATGGTGG---TTAAGAGTTCGTA---------GCGA----------AAATAAAAAAGA---------AAG
droEle1	scf7180000491101:4237-4376 -		TTTTCTTAGGCTAGGGACATTTATCTTTCAACATTACTAGGGT--ACG----------AAATGTATGCT---GTC-A-----TTTGCTCTGGTGACTTTTGGCCGGAAAATATTGTGG---TAAAAGATTCGAT-AAGATAAAGCTA----------AGATAAAAAAGA---------AGCG
droRho1	scf7180000763948:4634-4767 +		TTTTCTTATGCTAGAGACATTTCATCTTTCAAGATAACTGGCCGTTACA----------AGCTTTTTGAA---GCC-A-----TATGCTCGGGGGACTGTTGGCCGGATAATATCGTTG---TAAAAGAATCGAG---------GGTA----------AGATAAAGAAGA---------AGGG
droBia1	scf7180000297828:12980-13123 -		TTTTCATACCCTTGTAGGATATCGTCTTTTAAAATATTTGCTCCGCCTG----------ATCTTTTTAA--TGTT-T-----TACTTTCTGAAAGCTTTTGGCTTAATGATGATTTAGTAATTAAAGAATTTGTT---------CCAA---ATAAACCC-AGAA--CAAATA---------AGAA
droTak1	scf7180000414730:6479-6620 -		TTTTCGTAGCCCGCAGGATATCGTCTTTTAAAATATTTGCTCCGCCTG----------ATGTGTTTAAT---GTA-C-----TACTTTCTGAAAGCTTTTGGCTTAATGATGATTTGGTAATGAAAGAATTTGTT---------CCCA---ATAAACCA-AGAA--CAAAT-----------AACA
droEug1	scf7180000409639:53618-53763 +		TATTCCTACCCTAGGAACATGCCATCTTTCAAGATCCGTGTTCCTCCGA----------TGAGTTTTGAC---GAC-A-----TCTGTTCGACCAATTCTGGCCCGGAACATATTTTCG---TTCAAGAACATCAG---------CTTAAAAATAAAAAGAAGAAAAAAAGTC---------GCCA
dm3	chr3RHet:2456914-2457056 -		TATTCTTAGTCTAGAGACATTTCATCTTTCAAGATAACTGTTCCAAATA----------AAATATTTTCGAACATATG-----TATGTTCTGGTGATTTTTGGCCGGATAGTATGGTGG---TAAAAGATTCAAA---------GGTA----------AGATTTAAAATAGGAA-----AAACG
droSim2	node_23530:425-564 -		TTCTCTTAGCCTAGGGACATATCATCTTTCAAGATAACTTTCGCAAACG----------AGCTCTTTTCG---ACC-A-----TATGTTCGGGTGATTTTTGGCCGGATAGTATGGTGG---TAAAAGAGCTA-AGGTAA-A-AAGGTA----------AGATCAAAAATA---------AGAA
droSec2	scaffold_49:151673-151816 -		TTCTCTTAGCCTAGGGACATATCATCTTTCAAGATAACTGTTCCCAAACG----------AGCTCTTTTCG---ACC-A-----TATGTTCGGGTGATTTTTGGCCGGATAGTATGATGG---TAAAAGATTTGAA---------GGTA----------AGATCAAAAATAAGAAAAAGGTGACC
droYak3	v2_chr2L_random_010:58199-58339 -		TTTTCTTATGCTAGGGACATCTCATCTTTCAAGATAACTGTCCCAAATG----------AGCTATTCTCA---ACC-A-----TATGTTCTGGTGATTTTTGGCCGAAAAGTATGATTG---TGAAAGATTTGAA---------GGTA---AGA------AATTAAAAATAGGATA----AAAAG
droEre2	scaffold_4784:23045698-23045831 -		TTTTCTTAGGATAGGGACATTTATCTTTTAAGATAACTGTTCCTAATA----------AGCAACTTCCA---ACC-A-----TATGTTTTGGTAATTTTTGGCCGGATAGTATGGTAG---TGAAAGGGTTCGA---------GGCA----------AGATCAAAAATA---------GCAA
dp5	Unknown_group_274:2540-2672 +		TTCTCTTATGACAGGGAGATATCTTCGTTCAAAATAAGTGTTCTCCCAAA----------CTCAGTTTGAC---ACC-A-----TTTGCT-TGCCAAATTTTGGCCAGAGCATGTGGTGG---TGAAGAAGTTCAAG---------GGTA----------TGAAGAAAAATA---------GGCC
droPer2	scaffold_165:46683-46815 -		TTTTCTTATGCCAGGGAGAGAATCTTCGTTCAAGATAAGTGTTCTCCCCAA----------CTCTTTTGAC---ACC-A-----TTTGCTCTGCCAAATTTTGGCCAGAGCATTTGGTGG---TGAAGAAGTTCAAG---------GGTA----------AGAAGAAAAATA---------G-GC
droWil2	scf2_1100000004965:614973-615113 -		TTTTCTTATTCTCGGGACATTTCGTCTGTTTAAAATTAGTGTTTCTGCCA----------ATATCTTCGAT---ACT-A-----TATGTCGAAGAAGATTTTTGGCCCTAAACATATTAATAT---TTATGTA-TATAAGTATA-TACTGTAA----------AAAAGAAAAATC---------GCCA
droVir3	scaffold_12958:3521294-3521424 -		TTTT-TTATTAAAGGCTATTTCACACTTTAAAATAAGTGTTCGCGCGG----------AAATATTCATT---GAC-A-----TTTGTTCTAAGGAGTTTTGACCAGAACACCTAATAG---TGAAAGAATTATAAG---------GCCA----------AAAACAAAAATC---------GG
droGri2	scaffold_15126:8188956-8189069 +		TT--AATAATAAAGAGCAATTTCCTCTTTGTAAAATAAGTGTTCCCTCTG----------AAGTATTTTGC---ACA-A-----GTTGTTGTCCACTTTCTGGCCGAAAGCAATA----------GAGGAGTTATA----------------------------CAAATA---------AAAA

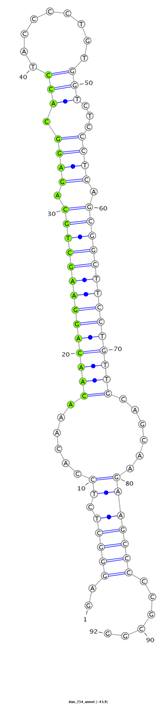
Generated: 09/08/2015 at 08:03 PM

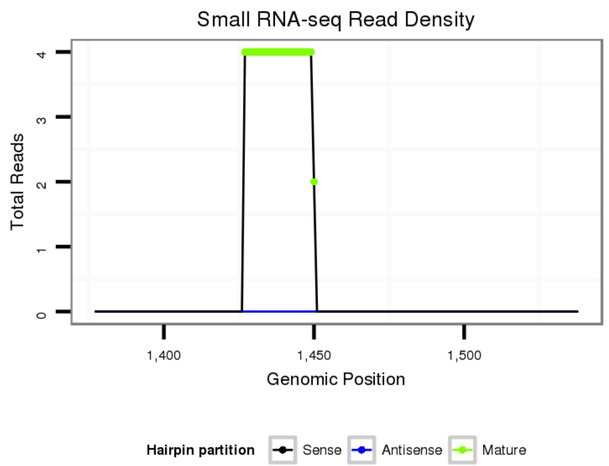
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

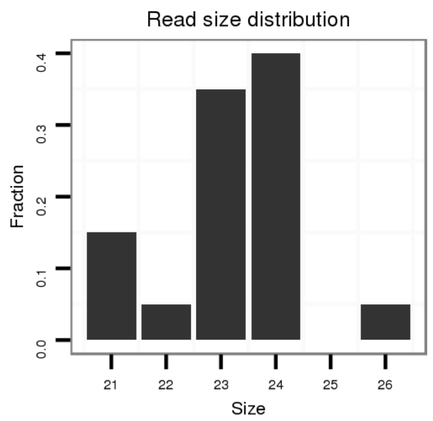
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_254	**scaffold_11565:1427-1488 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

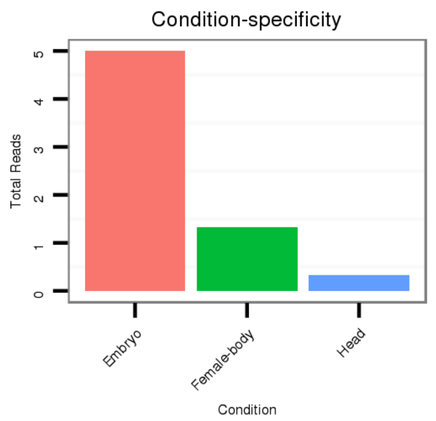
Legend: mature star mismatch in alignment mismatch in read

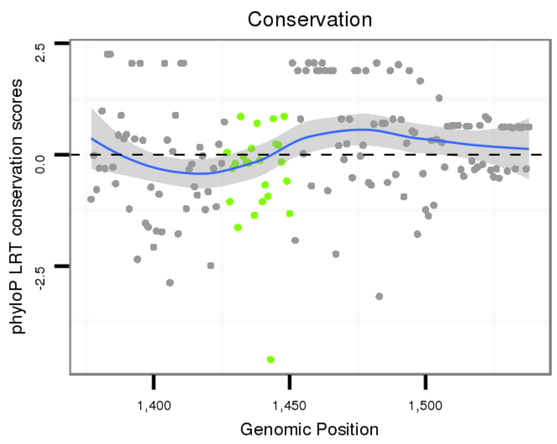
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. dan_254 scaffold_11565:1427-1450 + 2. scaffold_12672:4263-4286 + 3. scaffold_13163:63127-63150 -	

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CAGGAGATGCACAACGCTGCCTTTATCGCTACTCCGAGGGCTCTCCACAAACAACAGGAAGCTGCAGAGGCACCTACCCCTGTGGTCTCCCTCAGCGGCTTCCTGTTGCAGCAAGAAGCCCCCGCGGAGACGGAAAAGGCCATATTGAGCGATATCTAGAGA **********..(((((.((.....(((((((((((((((.((((.(((.........)))...)))))..)))))))))))))).....)))))))*****..***********	Read size	# Mismatch	Hit Count	Total Norm	Total	M058 embryo	M044 female body	V055 head	V106 head	V105 male body
ACAACAGGAAGCTGCAGAGGCACC	24	0	3	2.67	8	7	1	0	0	0
ACAACAGGAAGCTGCAGAGGCAC	23	0	3	2.33	7	7	0	0	0	0
ACAGGAAGCTGCAGAGGCACC	21	0	3	0.67	2	0	2	0	0	0
ACAACAGGAAGCTGCAGAGGCA	22	0	3	0.33	1	0	0	0	1	0
ACAACAGGAAGCTGCAGAGGCACCTA	26	0	3	0.33	1	0	1	0	0	0
ACAACAGGAAGCTGCAGAGGC	21	0	3	0.33	1	1	0	0	0	0
CAGGAGATGCACAACGCTGCC	21	0	8	0.13	1	0	0	0	1	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_11565:1377-1538 +	dan_254	CAGGAGATGCACAACGCTGCCTTTATCGCTACTCCGAGGGCTCTC-----CACAAACAACAGGAAGCTGCAGAGGCACCTACCCCTGTGGTCTCCCTCAGCGGCTTCC--TGTTGCAGCAAGAAG-CCCCCGCGGAGA--C------GGAAAAGGCCATATTGAGCGATATCTAGAGA
droBip1	scf7180000391804:29522-29654 -		CAAGAGATGCACAACGCTGCCTTAATTGCAACTCCTAGGGCTCCA-----GCCAACAATAGGAAGATGCAAGGCATTTACACCTGTGGTCTCCTGAAGTGGCTGCACTCCTCAATGAGAAGAAGAGGACGCAGAAGGA-A------
droFic1	scf7180000453140:5762-5913 -		CAAGAGATGCACAACGCCGCCGCTTATGGCACTCCAAGAGTCTTA-----CACCACTTTTGGCCAGATCACAGGAAGTTGCATCTGTGGTCGCCGGAAATTGCTGCACTTGTCGCAGAAAAACGAAGACTGAGAAGAA-A------
droEle1	scf7180000491104:840674-840805 -		CAGCAGATGTGCAACGCGGCTACACATGCATGCCGAGAATTCC-----ACCACACCTAAACCAGCCACTAAGGATCTGCATCTCTGGTCTCCTGACGTTGCTGCACTGGTTGCAGAAAAGAGGCGGCTACGAAGA--A------
droRho1	scf7180000774462:2142-2178 +		AGGAAAATACATTTAGCAGCACGTATCGGCACTCCAA---
droTak1	scf7180000413608:271-402 -		CAGCAGATGTGCAACGCTGCTACACATGCATGCCGAGAATCCC-----ACCACACCTAAACCTGCCACTAAGGATCTGCATCTCTGGTCTCCTGATGTTGCTGCACTGGTTGCAGAAAAGAGGCGGCTACGAAGA--A------
droEug1	scf7180000408968:24246-24378 +		CATGAAATTCACAATGTTGCCGAGAGAGGCCTTCCTAGGTTTCTG-----CACCACGGCCAGACCGCACCAAAGGAGCTTACACCTCTGGTCCCCAAAAGTGGCTGCTCTGGTGCGCAGAGAAACGCGACTCCGTAGAG-A------
dm3	chrU:2686542-2686673 -		GATGAGATGTACAATGCTGCTGAGTTTGCAATCCTCCTCCTTCA-----ACG-ACCCCAAAACTGCTGGTACGAGACCTTCACCTCTGGTCTCCAGAAATTGCGGCCTTCGTAGCGGAAAAAGCGCCCTGAGGAGA--A------
droSim2	node_58775:75-205 -		GAGGAGATGCACAATGCTGCTGAGTTTGTCAATCCTGCTCCTCCA-----ACG-ACCCCGAGAACTGCTGGTGACGAGACCTTCACCTCTGGTCTCCAGAAATTGCGACGTTCGTAGCGGAAA-AAGCGCCTCATGGAGA--A------
droSec2	scaffold_79:58958-59116 +		AAGGAGATGCACATGTGCCGCTGAGTTTGCAACCCTCCTCCCGCT-----ACG-ACCCCGAGAACTGCCCGAAGAGACTTCGCACCTGTGGTCCCCAGAAATGCGTCGCCATCGTGGCCGCAAAAAAGCGCCCCAAAAGAGATCGCGCAGGAAATTGCTTCACTGAG----------
droYak3	chrXh:100146-100274 -		GAGGAGATGCACAATGCGGCTAAGTTCGCCAACCCTCCTCCTCCA-----ACT-ACCCTGAGAACAGCTGAGCGAGTTCTTCGACCTTTGGTCTCCAGAAATTGCGGCCTTCGTGGCGGAGAAGAGCGCCCTCAGA---A------
droEre2	scaffold_4837:3289-3418 -		GAGGAGATGAACAACGTGCTCGAGTTCGCCAATCCTCCTCCTCCTCA-----ACT-ACCCCGAGAACAGCTAAACGAGTTCTTCGACCTCTGGTCTCCGGA-ATTGCGAGCGCCTTCGTGGCGGAA-AGAGCGCCCTCCGACGA--A------
droWil2	scf2_1100000004968:2914347-2914471 +		GCGAGCATACACCAGGCTGCCGTCTATGGAACACCTCCGCTAGGAGCTCGTCGAGTAACAGCGTCCCTCATAGAGACATCGACCTCTGGTCACCCGATGTAGCTGCATTGGTAGCAGAGAAGAG-A---------A------
droVir3	scaffold_10471:62881-62918 +		CAGGAAATTTACAATGCTGCAGTCATAGCTACCCGAG---
droMoj3	scaffold_6362:15066-15189 +		ATTGAAATTCACAACGCCGTTTCTCAGGTCACTCCGCCGTCTAGA-----TCC-CATAAAAGAGTGCCTCATAGGGACATCGACCTCTGGTCGCCAGAAGTAGCTGCTCTGGTCGCGAGAAAAGGCGCC---------A------

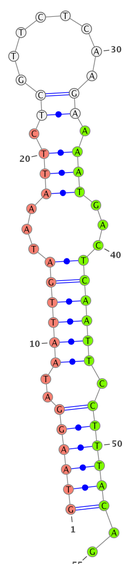
Generated: 09/08/2015 at 08:00 PM

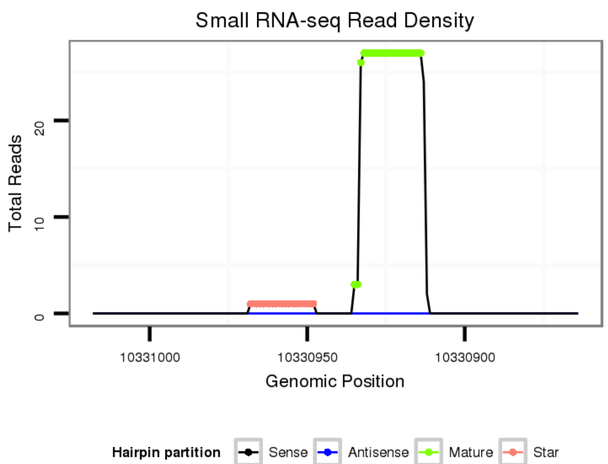
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

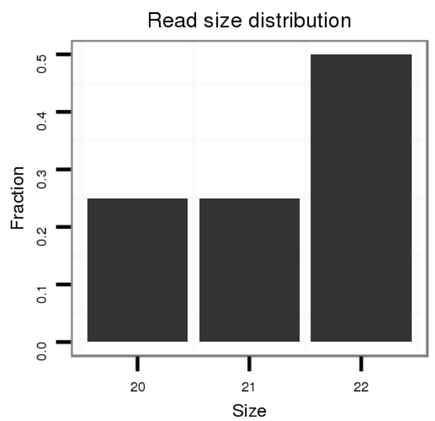
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_2546	**scaffold_13337:10330914-10330968 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

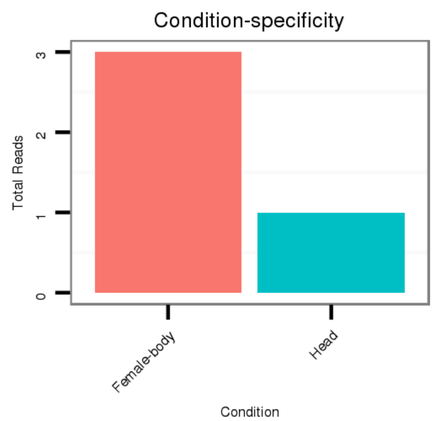
Legend: mature star mismatch in alignment mismatch in read

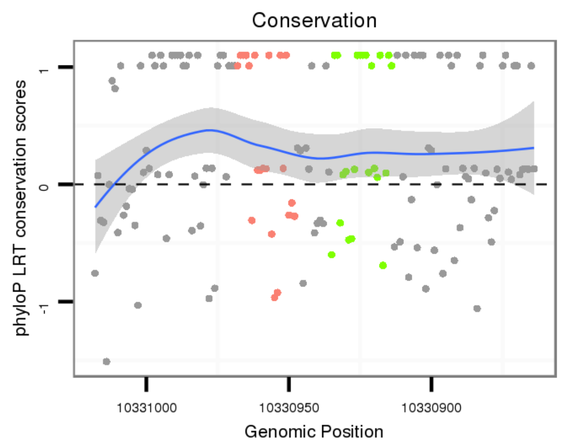
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF24177-in]; CDS [Dana\GF24177-cds]; utr5 [utr5_plus_8293]; CDS [Dana\GF24177-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GAACGGAGCCAGAGAAGCCAAGCACACAAATGGAGTTAGTTTGGAAGGCGGTAAGGATAATTGATAAATTCTCGTTCTCAAGAAAATGACTCAATTCCTTTACAGTTTCTGCTATTATGGGTGATCCTGTATCTGCACACAGCCAACGGCCTCGA	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	M044 female body	V105 male body	V055 head	V039 embryo
**********(((((..(((((..(((.((.....)).)))...)))))).)))))..**********										
.....ATGACTCAATTCCTTTACAGT.....	21	0	1	20.00	20	12	4	3	1	0
.....ATGACTCAATTCCTTTACAGTT.....	22	0	1	2.00	2	1	1	0	0	0
.....AAATGACTCAATTCCTTTACAG.....	22	0	1	2.00	2	0	2	0	0	0
.....TGACTCAATTCCTTTACAGT.....	20	0	1	1.00	1	0	1	0	0	0
.....AAATGACTCAATTCCTTTACAGT.....	23	0	1	1.00	1	0	1	0	0	0
.....GTAAGGATAATTGATAAATTC.....	21	0	1	1.00	1	1	0	0	0	0
.....ATGACTCAATTCCTTTACAG.....	20	0	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

CTTGCCTCGGTCTCTTCGGTTCGTGTGTTTACCTCAATCAAACCTTCCGCCATTCCTATTAACTATTTAAGAGCAAGAGTTCTTTTACTGAGTTAAGGAAATGTCAAAGACGATAATACCCACTAGGACATAGACGTGTGTCGGTTGCCGGAGCT	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_13337:10330864-10331018 -	dan_2546	GAACGGAGCCAGAGAAGCCAAGCAC-ACAAATGGAGTTAGTTTGGAAGGCGGTAAGGATAATTGATAAATTCTCGTTCTCAAGAAAATGACTCAATTCCTTTACAGTTTCTGCTATTATGGGTGATCCTGTATCTGCACACAGCCAACGGCCTCGA
droBip1	scf7180000396569:1039718-1039872 +		CTACGAAGTCCCAGAAGCCAAGCAC-ACAAATGGAGCTAGTTTGGAAAGCGGTAAGGATAATTGAAAATTCTCATTCCCAAGAAAATGACTCAATTCCTTTACAGTTTTGCTATTTTGGGTGATCCTGTATCTGCACACAGTCAAAGGCCTCGA
droFic1	scf7180000453839:1687838-1687982 +		CATTCGAGCCTCTATTGC-AAGCACACCAAATGGATTTCTTTCGAAAGCGGTAAGAATAAATTGAAA-------CCCTTTGGTAAATCTTTAATTCCTGTCCAGATATTCCTCTT---CCTGTTCGTATATCTTCAGCTAACCAGCGGATATGT
droRho1	scf7180000758913:1088-1233 +		GATTTGAGCCTCTAGAGT-AAGCACTACAAATGGATTTCCCGTGGAAAGCGGTAAGTACGCAATGTGAAAG------TCCTTTGGAAACTATCTAATTTCTGTACACATGTTGTTCTT---ACTCTTCTATGTATTTCCAGTGCACCAGCGGATATGT
droBia1	scf7180000302428:3814106-3814244 -		GAACG---CCT---TCGC-AAGCACTGAAAATGGATTTCCTGATGAAAGCGGTAAGAATAGATGATAAGA-------TCTTCGGGGAACTAACTAATTCCCCTGCAGCTTTTGTTTTTT---CCTTTTCCTAACCTACCACTGCACCAGCGGATATGT
droTak1	scf7180000414337:6981-7123 -		GAATCG--TCT---TTGC-TAGAACTACAAATGGATTTCCTATTGAAAGCGGTAAGAATAAATACGAAATAA----TCCGTTGGGAACTAATTAATTCCTGTGTAGCTTTTCTTTTT---CCTTTTCCTGTCCTTTCATTGCACCAGCGGATATGT

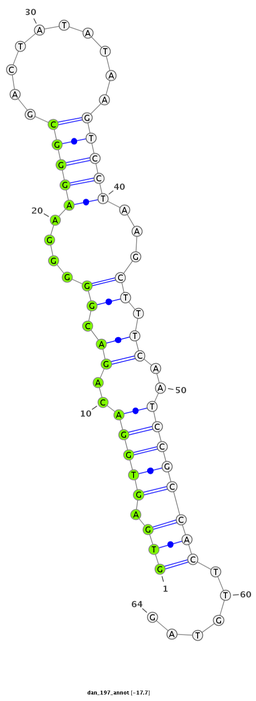
Generated: 09/08/2015 at 07:06 PM

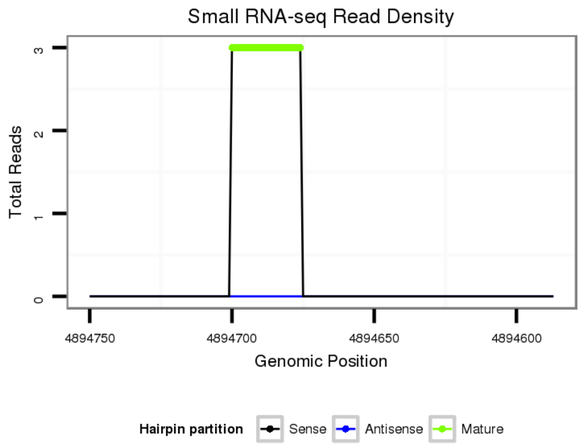
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

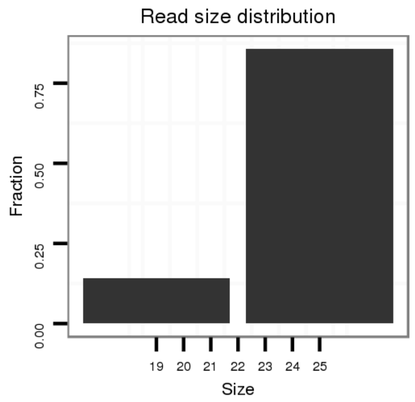
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_197	**scaffold_13266:4894637-4894700 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

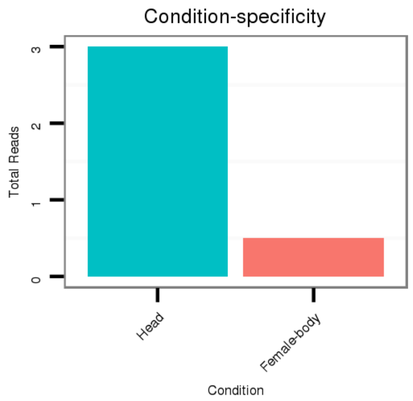
Legend: mature star mismatch in alignment mismatch in read

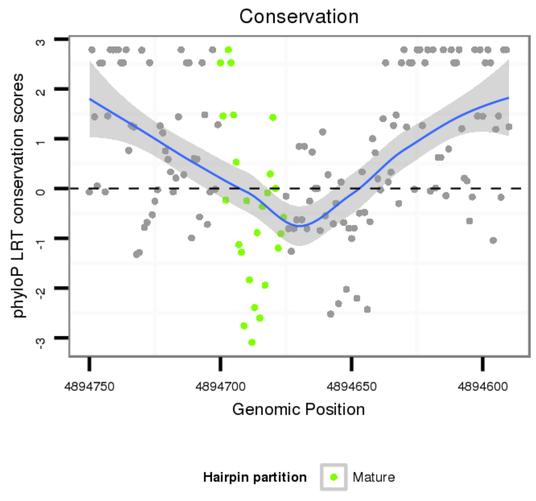
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF12114-in]; CDS [Dana\GF12114-cds]; CDS [Dana\GF12114-cds]

No Repeatable elements found

mature	star
1. scaffold_13266:4892144-4892168 - 2. dan_197 scaffold_13266:4894676-4894700 -	

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTTTCCCAAAATGGACGCTGTGGCCCAGGAGTTCTTCGGCCCGGTTCTGGGTGAGTGGACAGACGGGGGAAGGGCGACTATATAAGTCCTAAGCTTTCAATCCGCCACTTGTAGGTGAGGTTCCTAAGGTGAGGCAGCTGGAGAAGGAAACCTCAGTGATGCTC **********(((.((((((..((.((....((((((.....))))))...)).)..)))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V106 head	V105 male body	M044 female body	V055 head	M058 embryo
.....GTGAGTGGACAGACGGGGGAAGGGC.....	25	0	2	3.00	6	6	0	0	0	0
.....GGAGTTCTTCGGCCCGGTC.....	19	1	2	0.50	1	0	0	1	0	0
.....GTTCTTCGGCCCGGTTCTGG.....	20	0	2	0.50	1	0	0	0	0	1
.....CGGGGGAAGGGCGACTATA.....	19	0	2	0.50	1	0	0	1	0	0
.....TCTTCGGCCCGGTTCTGC.....	18	1	3	0.33	1	0	0	1	0	0

Anti-sense strand reads

AAAAGGGTTTTACCTGCGACACCGGGTCCTCAAGAAGCCGGGCCAAGACCCACTCACCTGTCTGCCCCCTTCCCGCTGATATATTCAGGATTCGAAAGTTAGGCGGTGAACATCCACTCCAAGGATTCCACTCCGTCGACCTCTTCCTTTGGAGTCACTACGAG **********(((.((((((..((.((....((((((.....))))))...)).)..)))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M044 female body	M058 embryo	V055 head	V039 embryo
.....GACCCACTCACCTGTCTGCCCCCTT.....	25	0	2	0.50	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_13266:4894590-4894750 -	dan_197	TTTTCCCAAAATGGACGCTGTGGCCCAGGAGTTCTTCGGCCCGGTTCTGGGTGAGTGGACAGA-----C-GGG--------G-G-AAGGGCGACTATATAAGTCCTAAGCTTT----------CAATCC---GCCA------CTTGTAGGTGAGGTTCCTAAGGTGAGGCAGCTGGAGAAGGAAACCTCAGTGATG
droBip1	scf7180000395751:699323-699480 -		TTTCCCTAAAATGGACGCACTGGCAGAGGAGTACTTTGGCCCGGTTCTGGGTGAGTGGTCAAG-----A-CGGCA-AGAGGA-G-------TAAGTGTT----TTG-A----------GCCCCA-CAATCT---CCCA------CTTTTAGGTGAGGTGCCGAAGGTGAGGCAGTTGGAGCGGAAACCTCAGTGATA
droKik1	scf7180000302682:154187-154336 +		CTTTCCCAAAATGGATGGCGGTGACAAGGAGTTCTTTGGTACCGTTCTGGGTTAGTTAATGAGAGAAC-TTCTCTATTTAA-A----------GTC-----A-----TTAATC---GTTT------CTTGCAGGTGAAGTGCCAAAGGTAAGGCACATGGAGCGGCAAATGTGTCTGATG
droFic1	scf7180000453811:175975-176131 +		CTTTCCCAAAATGGATGGCGTGACCAAGGAGCATTTTGGTAGCGTTTTGGGTGAGTTAATCTA-----A-CGGTTTGTT--GGT-AA-TTGA----------AG-----GC---TCGGCTA-AAACGA---TTGC------CTTCCAGATGAAGTGCCAAAGGTCAGGAACATGGAGACGCAAATGTCGTGATG
droEle1	scf7180000491232:281977-282127 +		TTTTCCCAAAATGGATGCTGTGGCCAAGGAGTTTTTGGCCCGCGTTTGGGTGAGTTGCAAAG-----T-TTGTTTATTAAT-G-----------AAC---AGAACTA-TAATAG---GTGA------ATTCTAGATGTGGTGCCAAAGGTCAGGCACATGGAGCGAGAAATGTCAGTGATG
droRho1	scf7180000775957:203-352 -		TTTTCCCAAAATGGATGGCAGTGACGCAGGAGTTCTTTGGTACCGTTCTGGGTAAGTTCCGAA-----A-ACCTA-GCTGGA-G-----------AAC---GCACCTA-AGATAA---GAAA------ATTCTAGATGAGGTGCCAAAGGTCAAGCACATGGAGCGGGAAATGTCGGTGATG
droBia1	scf7180000302143:1315604-1315755 +		TTTTCCAAAATGGATGGCGTAGCCAGGGAGTTTTTGGCCCTGCTTTGGGTAAGATGATGAG-----T-CTGTCT-TCTGG-G-G-----------GGAA-GCCACCTG-ACCTTT---GTGC------ATTTCAGCTGAGGTGCCAAAGGTCAAGCACATGGAACGCGAAATGTCGTGATG
droTak1	scf7180000410787:38306-38461 +		TTTCCCAAAATGGATGGCGTGGCCAATGAGTTTTTGGCCCGTTTTAGGTGAGTTAAGAACAAAGC-TTTCTTTTTTGT-G-----------AAG---CCACCTA-CCTCTG---GTGT------CTTCCAGCTGAGGTGCCAAAGGTCAAGCAGATGGAACGGGAAATGTCAGTGATG
droEug1	scf7180000409474:842360-842513 +		TTTTCCGAAAATGGATGGCATAGCCAGGGAGTTCTTTGGCCCGCGTAATGGGTTAGTTAAGACG-----A--ATCCTATTCTA-G-G-----------AACATTACACCTGTAGTTTA---GTGT------TTTCCAGCTGAGGTGCCAAAGGTTAGTCACATGGAGCGGGAAATGTCAGTGATG
dm3	chr2R:17103908-17104060 -		TTTTCCGAAAATGGATGGCGGTGGCCAGGGAGTTCTTTGGACCCGTACTGAGTGAGTTACGGTA-----A-TGGTTTATCTGA-G-G-----------AACA-TACACCTG-AGTAGA---GTGT------TTTCCAGCCGAGGTGCCCAAGGTCAAGCACATGGAGCGTCAAATGTCAGTGATG
droSim2	2r:17658891-17659043 -	dsi_27498	TTTTCCGAAAATGGATGGCGGTGGCCAGGGAGTTCTTTGGACCCGTACTGGGTGAGTTACGGTC-----A-TGGTTTATCTGA-G-G-----------AACA-TACACCTG-AGTAGA---GTGC------TTTCCAGCCGAGGTGCCCAAGGTCAAGCACATGGAGCGGGAAATGTCAGTGATG
droSec2	scaffold_9:430129-430281 -		TTTTCCGAAAATGGATGGCGGTGGCCAGGGAGTTCTTTGGACCCGTACTGGGTGAGTTACGGTC-----A-TGGTTTACCTGA-G-G-----------AACA-TACACCTG-AGTAGA---GTGC------TTTCCAGCCGAGGTGCCCAAGGTCAAGCCACATGGAGCGGGAAATGTCAGTGATG
droYak3	2R:12085893-12086043 +		TTTTCCGAAAATGGATGCGGTGACCAGGGAGTTCTTTGGACCTGTAATGGGTAAGTTGCAGTT-----A-TGGTTTGTCTGA-T-G-----------AGC---CCACTTG-AGAGCA---GTGT------CTTCTAGCCGAGGTGCCCAAGGTCAAGCACATGGAGCGGGAAATGTCAGTGATG
droEre2	scaffold_4845:11247279-11247430 -		TTTTCCCAAAATGGATGGCGGTGACCAGGGAGTTCTTTGGACCCGTGTTGGGTGAGTTGCGAGCG-----A-TCCTTT-TCTCT-G-G-----------AAAG-CCCACCTG-AGTGCA---GTGT------TTTCCAGCCGAGGTGCCCAAGGTAAGCACATGGAGCGGGAAATGTCAGTGATG
dp5	3:3573921-3574073 -		CTTCCCCAAAATGGATGCGGTAGCGAGGAGGAGTTCTTTGGCCCGGTCGTGGGTGAGTGGGGGTT-----C-CACGTGATG--A-GAAA----------TGGGAAACCAAT----------TCGTGT---GT-G------CTTGCAGGCGATGTCCCAAAGGTCAGGCAGATGGAGAGAGATGTTGTGTAATG
droPer2	scaffold_2:3762570-3762717 -		GTCA---CAAATGGATGGCGT-CGC-GAGGAGTCCGTCGGCCCGTTCTAGGGAGTGGGGGCG-----TCCAGT--ATACGA-GAAA----------TGGAAACCCAAT----------TTGTGT---GTGG------CTTGCAG-CGAGGTGCCCAAAGGTCAGGCAGATGGAGAGAGATGTTGTGTAATG
droWil2	scf2_1100000004514:115398-115559 +		TTTTCCCAAAATGGATGCCGTAACGCAGCAACACTTTGGCCCTGTCTTAGGTGAGTTGCCAAA-----T-TGGTTTG-GTGG-G-G-------TGTGTGTTG----------CCA-TGAAGTTA-ACTTTAGTTATTC------AGACGGCAAGGTGCCAAAGGTCAGACACATGGAGACGCAAATGTCGCCATG
droVir3	scaffold_12875:14275426-14275572 -		CTTTCCCAAAATGGATGCCATCAGGAGCTCTACTTCGGCCAGTCTTAGGTGAGTGCCGACA-----G-TTG----CT--GTA-AA-GAGA----------ATGCCCTC----------CT--ATTTGT---TTCA------CCGGAGCTGAGGTGCCCAAGGTCAGGCACATGGAGACGCAAATGTCAGTGATG
droMoj3	scaffold_6496:9722234-9722392 -		CTTTCCCAAAATGGACGCCATCACTGAGCGGTACTTTGGTCAAGTTTGGGTGAGTGCCAACC-----C-ATTC--CA--GTA-GA-CT----------TAACTCTCTGATTCC-----A-----CTGCCC---GTTT----GGCCCGCAGCTGAAGTGCCCAAGGTCAGGCACATGGAGACGCAAATGTCGCTCATG
droGri2	scaffold_2262:569-730 +		CTTTCCCAAAATGGATAACCTTGCGAAGCAGCACTTTGGAAATGTATTGGGTGAGTGCGACA-----C-TTTGCTATCCTT-G-G-----------AAAA-GGGTATTA-AATATATTTCATCCTTGCGGTTGCAGCTGATGTGCCCAAAGTCAGGCAAATGGAGAAAGCAAATGTCGGTAATG

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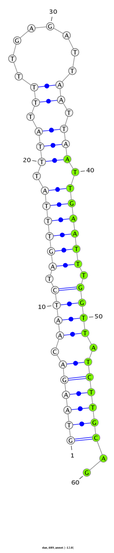
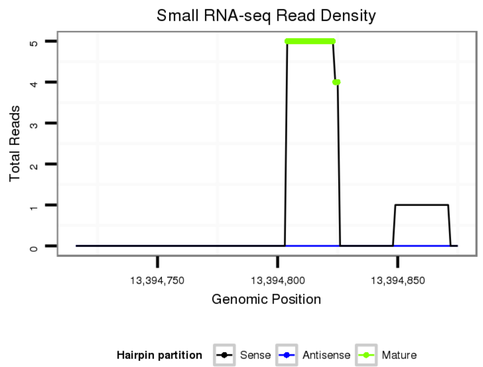
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

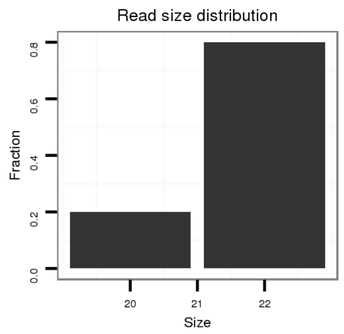
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dan_689	**scaffold_12916:13394766-13394825 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

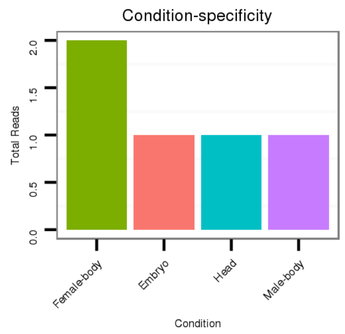
Legend: mature star mismatch in alignment mismatch in read

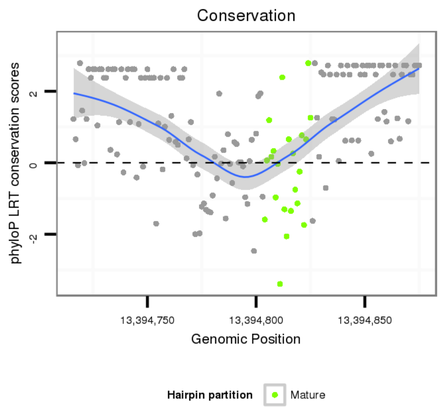
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dana\GF15687-in]; CDS [Dana\GF15687-cds]; CDS [Dana\GF15687-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GCCTACCAGAATATGCAGATACTCGAGTTCCGTGAGGGACCAGCCATACGGTAAGACAATCTAGTTTATTTATTTTTGAGATTAATTAATTGAATTTGGTTATCTTGCAGATGCGGCTCACCCAGCAGCTATGAGATTTGTAAACAACAGTCAACCGAAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V105 male body	M058 embryo	M044 female body	V055 head	V106 head	V039 embryo
**********(((((((.((((.(((((((.(((.((.........)).))))..)))))))..)))).)))))).)))))).**********((((((((((.((((((((((.....)))))))))).))))))))))											
.....ATTGAATTTGGTTATCTTGCAG.....	22	0	1	4.00	4	1	1	1	0	1	0
.....TTGAATTTGGTTATCTTGCAGT.....	22	1	1	4.00	4	4	0	0	0	0	0
.....AGATTTGTAAACAACAGTCAACC....	23	0	1	1.00	1	0	1	0	0	0	0
.....ATTGAATTTGGTTATCTTGCAGT.....	23	1	1	1.00	1	1	0	0	0	0	0
.....ATTGAATTTGGTTATCTTGCAGC.....	23	1	1	1.00	1	0	1	0	0	0	0
.....ATTGAATTTGGTTATCTTGC.....	20	0	1	1.00	1	0	0	1	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droAna3	scaffold_12916:13394716-13394875 +	dan_689	GCCTACCAGAATATGCAGATACTCGAGTTCCGTGAGGGACCAGCCATACGGTAAGAC----------AATC----------TAG----------TTTAT----TTATTTTG----------AGATTAATTAATTG----------A--ATTTGGTTA-TCTTGCAGATGCGGCTCACCCAGCAGCTATGAGATTTGTAAACAACAGTCAACCGAAT
droBip1	scf7180000396580:103302-103462 -		GCCTACCAGAATATGCAGATACTCGAGTTCCGAGAGGGCCAGCCATACGGTAGCAA----------AAC----------TTT---TA----------C----------AT----------AT-TTTATTGTCTT----ACAT-TTTATCATTCA--TG--CTTA-TCTTGCAGATGCGGCTCACCCAGCAGCTATGAGATTTGTAAACAACAGTCAACCGAAT
droKik1	scf7180000302679:1508229-1508391 +		GCCTACCAGAAGATGCAGATACTCGAGTTTCGGCGAGGGTCCGGCTATAAGGTGAGCGT----------GGGG----------GAA---TG----------C----------ATT---GTAA-T---GGATATTCTACTAT----------A----------AATTC---------GGATCTACTTT-ATGTTCAGCTGTGGATGCGCCCAGCAGCTATGAGATTTGCAAACAGCAGTCAACCGAAT
droFic1	scf7180000453924:1315189-1315357 -		GCCTACCAGAAGATGCAGATACTCGAGTTCCGCGAGGGACGCGCTATAGGGTGAGCAA----------ATGC----------TTA----------AGATG---TAATA---GAAT-----TGTTTAAC-----TTTATCTAATTAACTAA----TATTT----------A--A-----TAT-TGGTTCAGTTGTGGCTCGCCAAGCAGCTACGAGATCTGCAAACAGCAGTCAACCGAAT
droEle1	scf7180000491046:2037155-2037234 -		GCCTACCAGAAGATGCAGATACTCGAGTTCCGCGAGGGTCGCGCTATAGGGTGAGCGC----------AT--------------------