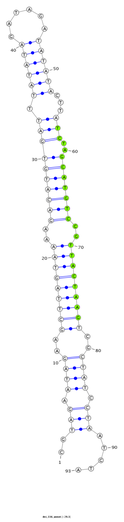
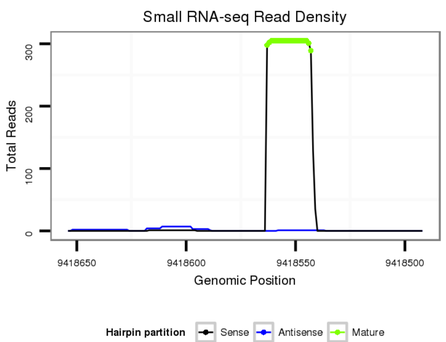
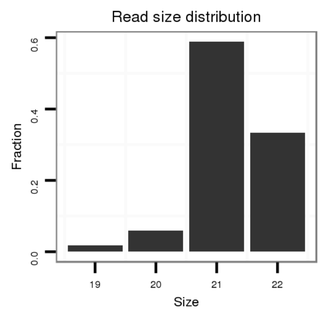
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_336	**scaffold_12970:9418542-9418604 -**	**confident-exception**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

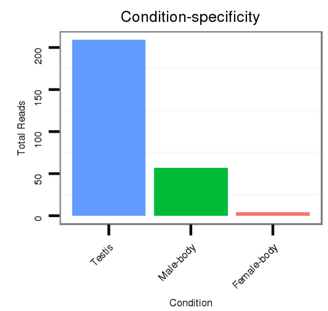
Legend: mature star mismatch in alignment mismatch in read

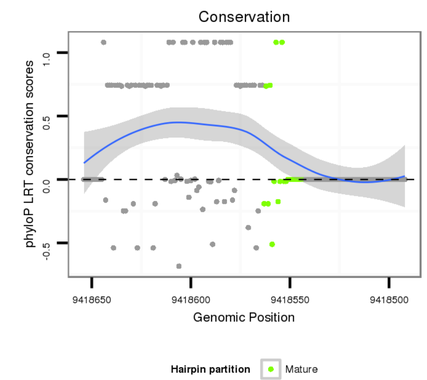
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TATTCTATCTAGATACATAGTAAGAGACATAGATACGTAGAATAGAAGCTTAGTAAAAGACATGTGATTTATATAGATAGATATATACTTATCTAGCATGTCCGTTACTAAGTCGCTATCCTAATCTACATCTTTCTCTTCTATATAGTATAAATTTATGTAG	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060679 140x9_testes_total	V116 male body	M027 male body	SRR060657 140_testes_total	SRR060681 Argx9_testes_total	M047 female body	SRR2096014 Ovary_Strain_160_oxidized	M028 head	SRR060678 9x140_testes_total	SRR2096013 Ovary_Strain_9_oxidized
**********..(((.((((..((((((((..((((((((((.(((((.....))))))...)))).))))))))..))))))))..))))).))).....**********															
.....TCTAGCATGTCCGTTACTAAG.....	21	0	1	157.00	157	115	17	13	8	3	1	0	0	0	0
.....TCTAGCATGTCCGTTACTAAGT.....	22	0	1	90.00	90	56	21	3	2	6	2	0	0	0	0
.....TCTAGCATGTCCGTTACTAAGTC.....	23	0	1	35.00	35	21	11	3	0	0	0	0	0	0	0
.....TCTAGCATGTCCGTTACTAA.....	20	0	1	12.00	12	11	1	0	0	0	0	0	0	0	0
.....TCTAGCATGTCCGTTACTAAGTA.....	23	1	1	9.00	9	9	0	0	0	0	0	0	0	0	0
.....TCTAGCATGTCCGTTACTA.....	19	0	1	4.00	4	4	0	0	0	0	0	0	0	0	0
.....TCTAGCATGTCCGTTACTAA.....	21	1	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....TCTAGCATGTCCGTTACTAAGTT.....	23	1	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....TAGCATGTCCGTTACTAAGT.....	20	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TCTAGCATGTCCGTTACTAAGTTC.....	24	2	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TCTAGCATGTCCGTTACTAAGA.....	22	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....CTAGCATGTCCGTTACTAAG.....	20	0	1	2.00	2	1	1	0	0	0	0	0	0	0	0
.....TCTAGCATGTCCGTTACTAAGTAA.....	24	2	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....CTAGCATGTCCGTTACTAAGT.....	21	0	1	2.00	2	1	1	0	0	0	0	0	0	0	0
.....CTAGCATGTCCGTTACTAAGTAA.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TCTAGCATGTCCGTTACTAAAA.....	22	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TCTAGCATGTCCGTTACTAAGTCT.....	24	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....TAGCATGTCCGTTACTAAG.....	19	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0
.....TAGCATGTCCGTTACTAAGTTC.....	22	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....CTAGCATGTCCGTTACTAAGTTC.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....CTAGCATGTCCGTTACTAAGTCT.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TAGAATAGAAGCTTAGTAAAAG.....	22	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0

Anti-sense strand reads

ATAAGATAGATCTATGTATCATTCTCTGTATCTATGCATCTTATCTTCGAATCATTTTCTGTACACTAAATATATCTATCTATATATGAATAGATCGTACAGGCAATGATTCAGCGATAGGATTAGATGTAGAAAGAGAAGATATATCATATTTAAATACATC	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060677 Argx9_ovaries_total	SRR060679 140x9_testes_total	SRR060675 140x9_ovaries_total	SRR060681 Argx9_testes_total	SRR060685 9xArg_0-2h_embryos_total	SRR060686 Argx9_0-2h_embryos_total	SRR2096059 Ovary_Min_164	SRR060667 160_females_carcasses_total	SRR2096057 Ovary_Min_50	M027 male body	M047 female body	SRR060673 9_ovaries_total	SRR2096014 Ovary_Strain_160_oxidized
**********..(((.((((..((((((((..((((((((((.(((((.....))))))...)))).))))))))..))))))))..))))).))).....**********																		
.....CATCTTATCTTCGAATCATTT.....	21	0	1	4.00	4	3	0	1	0	0	0	0	0	0	0	0	0	0
..AAGATAGATCTATGTATCATTCTCTG.....	26	0	1	2.00	2	0	2	0	0	0	0	0	0	0	0	0	0	0
.....TCTTCGAATCATTTTCTGTACA.....	22	0	1	2.00	2	1	0	0	0	1	0	0	0	0	0	0	0	0
.....GTACAGGCAATGATTCAGCGAT.....	22	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0
.....AATTCGAATCATTTTCTGTACACT.....	24	2	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0
.....TCTTCGAATCATTTTCTGTACAC.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12970:9418492-9418654 -	dvi_336	TATTCTATCTAGATACATAGTAAGAGACATAGATACGTAGAATAGAAGCTTAGTAAAAGACAT-GTGATTTATATAGATAGATATATACTTATCTA--GCATGTCCGTTACTAAGTCGCTATCCTAATCTACATCTTTCTCTTCTATATAGTATAAATTTATGTAG
droWil2	scf2_1100000004513:5874368-5874413 +		----------AT----------AAAAGTTTAAAAAGGACAT-ACAATTTATATAG----------TAATATATT----------
droBia1	scf7180000302428:2447109-2447203 -		----------AGATAGATAGATAGAAAGATAGATAGTAGAT-TAGATTAGCTAGATTGATAGATAGCTAGATAGATAGATAGATAGATACGTTTCAGGTCG----------

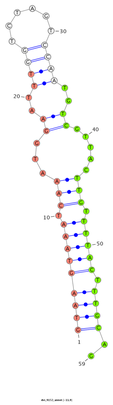
Generated: 09/08/2015 3:03:24 PM

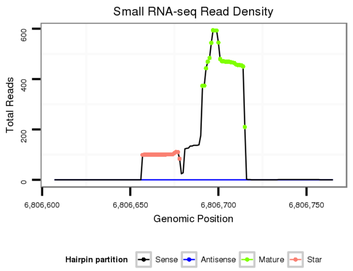
MAPQ	**241**
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

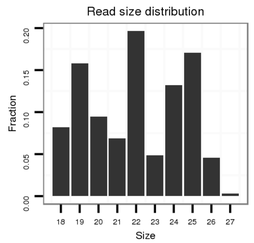
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_9152	**scaffold_12928:6806657-6806715 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

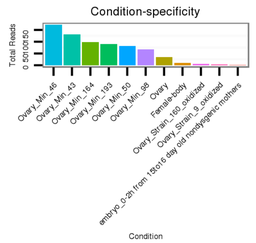
Legend: mature star mismatch in alignment mismatch in read

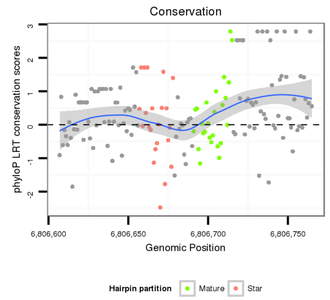
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dvir\GJ17026-in]; CDS [Dvir\GJ17026-cds]; CDS [Dvir\GJ17026-cds]; utr5 [utr5_plus_13918]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GACTGCTGGCAGCGGAGGTATTGGCAATGATTTATCCAATACCGTTAACAGTAAGTAAATCAAATGGAATTTGGTCTAGTCCAATGTCGTTACTTGTTTTACTTTGCAGGAGGTCCAAAGCAAATTGTTATGGGCGACGACAACAATATTGTCAAGCTG		Read size	# Mismatch	Hit Count	Total Norm	Total	SRR2096056 Ovary_Min_46	SRR2096055 Ovary_Min_43	SRR2096059 Ovary_Min_164	SRR2096060 Ovary_Min_193	SRR2096057 Ovary_Min_50	SRR2096058 Ovary_Min_98	SRR060677 Argx9_ovaries_total	SRR060676 9xArg_ovaries_total	M047 female body	SRR2096014 Ovary_Strain_160_oxidized	SRR2096013 Ovary_Strain_9_oxidized	GSM1528803 follicle cells	SRR060656 9x160_ovaries_total	SRR060673 9_ovaries_total	SRR060674 9x140_ovaries_total	SRR060675 140x9_ovaries_total	SRR060688 160_ovaries_total	SRR2096081 embryo_0-2h from 15to16 day old nondysgenic mothers	SRR060663 160_0-2h_embryos_total	SRR060672 9x160_females_carcasses_total
....TGTCGTTACTTGTTTTACTTTGCAG....		25	0	1	102.00	102	23	31	10	15	8	1	5	3	2	1	3	0	0	0	0	0	0	0	0	0
....TGTCGTTACTTGTTTTACTTTGCA....		24	0	1	90.00	90	17	16	16	11	7	14	1	4	2	2	0	0	0	0	0	0	0	0	0	0
....GTAAGTAAATCAAATGGAATTT....		22	0	1	64.00	64	9	9	9	4	12	5	6	5	4	0	0	0	0	1	0	0	0	0	0	0
....TTACTTGTTTTACTTTGCA....		19	0	1	48.00	48	10	8	1	13	4	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TCTAGTCCAATGTCGTTAC....		19	0	1	47.00	47	18	6	7	7	4	4	1	0	4	0	0	0	0	0	0	0	0	0	0	0
....TCGTTACTTGTTTTACTTTGCA....		22	0	1	44.00	44	5	14	8	9	2	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TCTAGTCCAATGTCGTTACT....		20	0	1	42.00	42	14	4	9	3	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TACTTGTTTTACTTTGCA....		18	0	1	40.00	40	10	10	6	5	4	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TCGTTACTTGTTTTACTTTGCAG....		23	0	1	29.00	29	5	10	3	0	1	8	0	0	1	0	1	0	0	0	0	0	0	0	0	0
....GTAAGTAAATCAAATGGAATT....		21	0	1	26.00	26	6	4	7	3	0	4	1	0	1	0	0	0	0	0	0	0	0	0	0	0
....ATGTCGTTACTTGTTTTACTTTGCAG....		26	0	1	23.00	23	3	3	5	5	4	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0
....CGTTACTTGTTTTACTTTGCAG....		22	0	1	23.00	23	6	2	6	1	5	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0
....TTACTTGTTTTACTTTGCAG....		20	0	1	12.00	12	4	3	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TACTTGTTTTACTTTGCAG....		19	0	1	10.00	10	3	4	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
....CGTTACTTGTTTTACTTTGCAG....		23	1	1	9.00	9	6	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....ATGTCGTTACTTGTTTTACTTTGCA....		25	0	1	9.00	9	3	0	2	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GTTACTTGTTTTACTTTGCAG....		21	0	1	8.00	8	4	1	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GTTACTTGTTTTACTTTGCAG....		22	1	1	6.00	6	2	0	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TCTAGTCCAATGTCGTTACTT....		21	0	1	6.00	6	3	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GTAAGTAAATCAAATGGAATTTGGTC....		26	0	1	5.00	5	0	0	2	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GGTCTAGTCCAATGTCGTTACT....		22	0	1	5.00	5	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TTTGGTCTAGTCCAATGTCGTTACT....		25	0	1	5.00	5	4	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TAGTCCAATGTCGTTACT....		18	0	1	5.00	5	3	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GTTACTTGTTTTACTTTGCA....		20	0	1	5.00	5	1	0	1	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GTCTAGTCCAATGTCGTTACT....		21	0	1	4.00	4	3	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....ATTTGGTCTAGTCCAATG....		18	0	1	4.00	4	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....AGTCCAATGTCGTTACTT....		18	0	1	3.00	3	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....ATGTCGTTACTTGTTTTACT....		20	0	1	3.00	3	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGTCGTTACTTGTTTTACTTTGC....		23	0	1	3.00	3	0	0	0	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0
....TGTCGTTACTTGTTTTACTTTGCAG....		26	1	1	3.00	3	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GTAAGTAAATCAAATGGAATT....		20	0	1	3.00	3	0	0	1	1	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0
....AATGTCGTTACTTGTTTTACTTTGCA....		26	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....CGTTACTTGTTTTACTTTGCA....		21	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....CTAGTCCAATGTCGTTACT....		19	0	1	2.00	2	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....CGTTACTTGTTTTACTTTGCAG....		23	1	1	2.00	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GTTACTTGTTTTACTTTGC....		19	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGTCGTTACTTGTTTTACTTTGCAG....		26	1	1	2.00	2	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TCCAATGTCGTTACTTGT....		18	0	1	2.00	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....AGTCCAATGTCGTTACTTGTTTTAC....		25	0	1	2.00	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGTCGTTACTTGTTTTACTTTG....		22	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
....TGTCGTTACTTGTTTTACT....		19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....ATGTCGTTACTTGTTTTA....		18	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TTGGTCTAGTCCAATGTCGTT....		21	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....ATTTGGTCTAGTCCAATGTCGTTACT....		26	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TTACTTGTTTTACTTTGCAG....		21	1	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGTCGTTACTTGTTTTACTTCAGGAG....		25	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....ATGTCGTTACTTGTTTTACTTTGCAGG....		27	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GTCGTTACTTGTTTTACTTTGCAG....		24	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
....TTATGGGCGACGACAACAATATTG....		24	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
....TAAGTAAATCAAATGGAATTT....		21	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
....AATGTCGTTACTTGTTTT....		18	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
....TGGAATTTGGTCTAGTCC....		18	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
....AGTCCAATGTCGTTACTTGTTTTACT....		26	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....AGTCCAATGTCGTTACTTGTTTTACTT....		27	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGTCGTTACTTGTTTTACTTTGCAG....		25	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GTCTAGTCCAATGTCGTTAC....		20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TAGTCCAATGTCGTTACTTGTTTTACT....		27	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....AGTCCAATGTCGTTACTTGTTTT....		23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
....GTTACTTGTTTTACTTTGCAG....		22	1	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
....TCCAATGTCGTTACTTGTTTTACTT....		25	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
....TTGGTCTAGTCCAATGTCGTTACT....		24	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

CTGACGACCGTCGCCTCCATAACCGTTACTAAATAGGTTATGGCAATTGTCATTCATTTAGTTTACCTTAAACCAGATCAGGTTACAGCAATGAACAAAATGAAACGTCCTCCAGGTTTCGTTTAACAATACCCGCTGCTGTTGTTATAACAGTTCGAC		Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060684 140x9_0-2h_embryos_total	V053 head	V047 embryo	SRR060667 160_females_carcasses_total

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12928:6806607-6806765 +	Dvi_9152	GACTGCTG-GCAGCGGAGGT----------ATTGGCAATGATTTATCCAATACCGTTAACAGTAAGTAAATCAA----------ATGGAA------TTTGGT-----CT--------AGTCCAATG-TCGTTAC----------TTGTTTTACTTTGCAGGAGGTCCAAAGCAAATTGTTATGGGCGACGACAACAATATTGTCAAGCTG
droMoj3	scaffold_6328:2472350-2472503 +		GACTGCGA-G-ZAA------T----------G-G-G-AAATGAGTGTCCAAGACCGTGAACGGTAAGTGAAGMGG----------GMGAATT----T----TAAGCT---------ACCGCCAGCGAAGCAC----------TGACCGCGTTTGCAGAGGTCGTCGAAGCAAATTGTGATGGTTATGGTATGATGATGAAGCTG
droGri2	scaffold_14853:3752825-3752980 -		GAGCGCCTC--------T----------TTGGCAATGAGTTGTCCGAGACCTTAACAAGTGAGTAAAGCGA----------ATGCAAA----------CT---------CCC------T--CTGCTTGCACCAACTACATCAACTACAGACTTATTTGAGAGGTCCGAAGCAAGTGTTATGGGCGACGAAACAACGGTGAAGCTG
droWil2	scf2_1100000004963:2287649-2287815 -		AACAATTG-GTAGCGGCGATCTGGCACACAGATGGGCAATGAGTAACGTTAATGATGAATGAAGTATGGAATC----T----AATGG---------GATCAATGTCGTTACTTTGCAGGAGGTCCTCGTCAAATGGTTGTGGGCGACAACAACGGGATGTGTAATGTA
dp5	XL_group3a:2355881-2355936 -		-------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------TTGCAGGTGCACCGGATATCATTGTAGGCAACAACAACGTATGTATGAAGCTC
droPer2	scaffold_11:2323754-2323809 +		-------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------TTGCAGGTGCACCGGATATCATTGTAGGCAACAACAACGTATGTATGAAGCTC
droAna3	scaffold_13117:5491757-5491832 -		ATATGTGTC---------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------ATTGCTATGCGCAGCTGGTCCGAAGATGATTAGCTGGGAATTACAACAAGGGCACCGCTTTG
droBip1	scf7180000039592 9:29573-29628 +		-------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------TACAGCCGGTCCGAAATGTAATTGATTGGAATTACAACAAGGGCACCGCTTTG
droKik1	scf7180000030261 0:1968583-1968718 -		GATGTATTGT--------T----------T----------AATTGGCAATGGTGTGGGG----------TTGGGT-----T----------T--------AGT------T--C---TTGGAGTTTTTAATTGATTTGTTTATTGTTGCAGTGCGGTCCGAAGCATTATTGGGCACATAATAGAGATTGTGGCGCTG
droFic1	scf7180000045390 1:353842-353917 -		GTGTGTGTG-T--------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------CTTTTCCGTTGCAGAGGCACCGAAGCGTGTTATGGCGATATAAACCGTATGTGAAGCTG
droEle1	scf7180000049051 1:93270-93335 +		-------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------TTATTTATTGCAGAGGTCCGAAGACCGTTGTTATTGGCGACATAATACCGTATGTGAAGCTG
droRho1	scf7180000077934:585776-585832 -		-------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------TTTGCAGAGGTCCGAAGACCGTGTTATTGGCGACATAATACCGTATGTGAAGCTG
droBia1	scf7180000301623:95730-95786 -		-------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------TTTGCAGAGGTCCGAAGACTCGTTTATTGGCGACATAATCCGTATGTGAAGCTG
droTak1	scf7180000415864:77867-77932 +		-------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------TTCCGAACTTTGCAGAGGTCCGAAGACCGCGTTTATTGGCGACATAATCCGCGATGTGAAGCTG
droEug1	scf7180000409076:90349-90405 +		-------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------TTTGCAGAGGTCCGAAGACTCGTTTATTGGCGACATAATCCGTATTGTGAAGCTG
dm3	chrX:4116379-4116512 +		GAC-----T----------T----------T----------T----------T----------TGAGCGAACAGTAAGTGTAATGGTTAAACAAGTGCGTAATTGGAACCGCCTAAT--T--------GAATACGT-T-------T----------TTGCGACTCGTTGCAGAGGTCCGAAGACTCGTTTATTGGCGACATAATCCGTATTGTCAAGCTG
droSim2	c:3815260-3815391 +	dsi_25613	GAC-----T----------T----------T----------T----------T----------TGAGCGAACAGTAAGTGTAATGGTTAAACAAGTGCGTAATTGGAACACGCCTAACCT--------T----CGT-T-------T----------TTGCGACTCGTTGCAGAGGTCCGAAGACTCGTTTATTGGCGACATAATCCGCATTGTCAAGCTG
droSec2	scaffold_4:2615279-2615380 -		GACAAGG-T----------T----------T----------T----------T----------T----------T----------T----------TGCGTAATTGGAACATCCTAATCT--------T----CGT-T-------T----------TTGCGACTCGTTGCAGAGGTCCGAAGACTCGTTTATTGGCGACATAATCCGTATTGTCAAGCTG
droYak3	Ki4320784-4320915 -		GAC-----T----------T----------T----------T----------T----------TGAGCGAACAGTAAGTGTAATGGTTTTGTAGTCCGCTTT----T----AAACTCATTTAATGAATACGT-T-------A-TGCGACTCGTTGCAGAGGTCCGAAGACTCGTTTATTGGCGACATAATCCGCATTGTCAAGCTG
droEre2	scaffold_4690:1485679-1485740 +		-------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------T----------TGCGACTCGTTGCAGAGGTCCGAAGACTCGTTTATTGGCGACATAATCCGTATTGTCAAGCTG

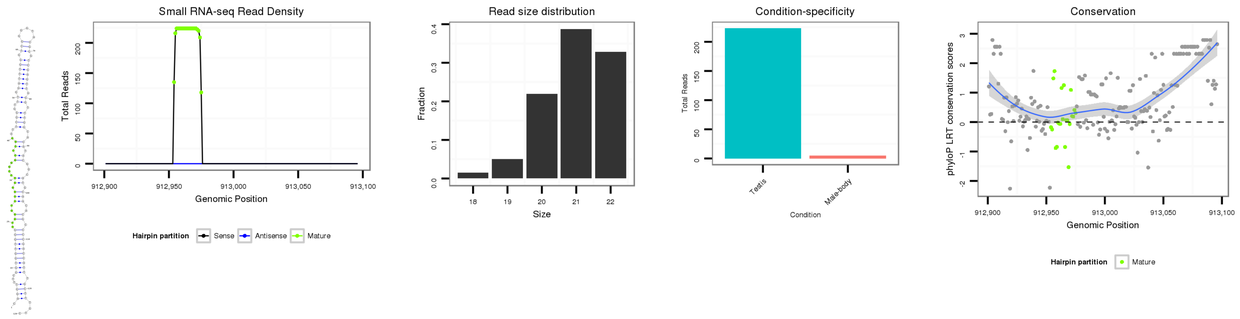
Generated: 09/08/2015 at 07:07 PM

	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.stem	1
crit.pairing	1
crit.top3	0
crit.tpisp3	0
crit.uri	1
crit.back	1
rescue.total	1
rescue.known	0
rescue.novel	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_188	**scaffold_13042:912951-913046 +**	**confident-exception**	**Testes-restricted**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [DviriGJ15837-in]

Repeatable elements

Name	Class	Family	Strand
(TTCGGG)n	Simple_repeat	Simple_repeat	+

mature	star
1: scaffold_12963:10501278-10501299 + 2: dvi_188 scaffold_13042:912954-912975 +	

Sense Strand Reads

hide 3p reads show mid mismatch reads

CGCACATTTTGTGCGACCAAGGGGGGAATCTAATGCAGGTTTCGGTGGTTGGGTTCGGTTTGGGTTTGGGTTTGGATTCGGTTTGGATTTGGGTCGGGTACGGGTCGAGTTGGGTTTGGGCACATACGGCATGCAACACGCCCCGACCATTTGCTTTGTCACCCTCTTGACTTAATGAGGCCTTTTTGTGCTCTT	Read aise	# Mismatch	Hit Count	Total Norm	Total	SRR060678 9x140_testes_total	SRR060655 9x160_testes_total	SRR060659 Argentina_testes_total	SRR060681 Argx9_testes_total	SRR060657 140_testes_total	SRR060679 140x9_testes_total	SRR060670 9_testes_total	SRR060680 9xArg_testes_total	SRR060689 160x9_testes_total	SRR060683 160_testes_total	V116 V047 male body	SRR060663 160_0-2h_embryos_total	SRR060662 9x160_0-2h_embryos_total	SRR060682 9x140_0-2h_embryos_total	SRR060664 9_males_carcasses_total	SRR060686 Argx9_0-2h_embryos_total	SRR2096057 Ovary_Min_50	SRR060684 140x9_0-2h_embryos_total	SRR1106722 embryo_10-12h	SRR1106716 embryo_4-6h	SRR1106728 larvae	M061 embryo
********************************.((((....((((((((((..((..((((.((.....((..((.....((((..((.(((((((.((((.....)))..))))))).))..))))..))..))...)))..))..))))))))))).))))....********************************																										
..... TTCGGTTTGGGTTTGGGTTTGG	22	0	2	75.00	150	17	13	39	14	33	6	3	7	7	4	7	0	0	0	0	0	0	0	0	0	0
..... TTCGGTTTGGGTTTGGGTTTG	21	0	2	51.50	103	20	21	3	18	3	13	8	8	2	5	2	0	0	0	0	0	0	0	0	0	0
..... TCGGTTTGGGTTTGGGTTTG	20	0	2	38.00	76	24	12	4	9	1	8	5	7	4	2	0	0	0	0	0	0	0	0	0	0	0
..... TCGGTTTGGGTTTGGGTTTGG	21	0	2	37.00	74	17	6	12	6	8	10	11	2	1	1	0	0	0	0	0	0	0	0	0	0	0
..... CGGTTTGGGTTTGGGTTTGG	20	0	2	6.50	13	4	2	1	0	2	1	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0
..... TCGGTTTGGGTTTGGGTTT	19	0	3	6.00	18	5	8	0	1	1	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0
..... TTCGGTTTGGGTTTGGGTTT	20	0	3	5.67	17	4	6	0	2	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..... CGGTTTGGGTTTGGGTTTG	19	0	2	2.50	5	2	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
..... TTCGGTTTGGGTTTGGGTT	19	0	4	2.50	10	0	1	0	5	0	0	0	2	1	1	0	0	0	0	0	0	0	0	0	0	0
..... TTCGGTTTGGGTTTGGGT	18	0	4	2.50	10	2	0	1	1	0	3	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
..... TTCGGTTTGGGTTTGGGTG	19	1	9	0.89	8	0	4	0	0	0	0	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0
..... TTCGGTTTGGGTTTGGGTTGG	22	1	4	0.75	3	1	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
..... TCGGTTTGGGTTTGGGTT	18	0	4	0.75	3	0	1	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
..... GGTTTGGGTTTGGGTTTGG	19	0	20	0.40	8	1	0	1	1	1	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
..... TTCGGTTTGGGTTTGGGTTG	22	1	3	0.33	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
..... TTCGGTTTGGGTTTGGGTTG	20	1	13	0.23	3	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
..... TTCGGTTTGGGTTTGGGTTA	21	1	5	0.20	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..... CGGTTTGGGTTTGGGTTTA	19	1	12	0.17	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..... GGTTTGGGTTTGGGTTTG	18	0	20	0.15	3	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
..... TCGGTTTGGGTTTGGGTTGA	21	1	7	0.14	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
..... TCGGTTTGGGTTTGGGTTT	20	1	10	0.10	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..... TTCGGTTTGGGTTTGGGTTGG	23	2	20	0.05	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

GCGTGTAAAACACGCTGGTTCCCCCCTTAGATTACGTCCAAAGCCACCAACCCAAGGCCAAACCCCAAACCTAAACCCAGCCCCATGCCCAGCTCAACCCAAACCGGTGTATGCCGTACGTTGTGCGGGGCTGGTAAACGAAACAGTGGGAGAACTGAATTACTCCGGAAAAACACGAGAA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060678 9x140_testes_total	SRR2096080 V053 embryo_0-2h from 15to16 day old mothers	head nondysgenic head	SRR2096055 Ovary_Min_43	SRR060655 9x160_testes_total	SRR060687 9_0-2h_embryos_total	SRR2096056 Ovary_Min_46	V047 embryo
********************************.((((....((((((((((..((..((((.((.....((..((.....((((..((.(((((((.((((.....)))..))))))).))..))))..))..))...)))..))..))))))))))).))))....********************************													

Show Alignment With Reads

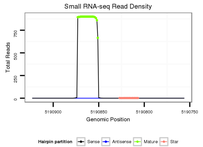
Re-alignment of all predicted orthologs

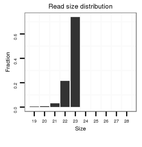
Species	Coordinate	ID	Alignment
droVir3	scaffold_13042:912901-913096 +	dvi_188	CGCACATTTTGTG---CG-ACCA--AG----------G-GGGGAATCTAATG----------CAGGTTTCG----------GTGGTTG-GGTTCGGT----------TGGGTTTGGGTTT------GATTCGGGTT----TGG----------ATTTGGGTCGGGGTACG----GGTCGAG-TTGGGTTTGGCACATAC----------GGCATGCAAC---ACG----------CCCCGACCATTTG----------CTTTGT-CACCCTCTTGACTTAATGAGGCCTTTTTGTGCTCTT
droMoj3	scaffold_6328:2905233-2905452 +		-TGCACATTTTGT---CAAGT-G--CACCGCGGGGCTTT----GG--------T-TTT-------G-------AGGGTGTTTCATTGGTTTGGGTGGTTGG-CAC-G-TA-------TC---GGCATGCA-ACCG-CG--CCTGCGTTATCCGCCCAGATCATTTGAATGTCTCCCCTCTT-T-TCT-TG-CTCGCTGTCTGTGTGTGTGTGTGTGTG-T-AC-T-CCCTTGTGACTTAATGAGGCCTTTTTGTGCTCTT
droGri2	scaffold_15081:2048793-2048977 +		-TGCACATTTTGTG---CTA----CG-ACA-------------CCCCAAA---G-GGGG-T-------GAGAGTATGG-----------GTGGTTG-CAT-G-TA------TGGGTTCTGTT-------T-------G----GGT-TG-TTGGGTT-TGCACATAC----------GGCATGCAAC-ACGC-CAAGC-----AAACG----------CCG-CACCATTTCCG----------TGTTGT-CACCCTCTTGACTTAATGAGGCCTTTTTGTGCTCTT
droMl12	scaf2_3100000004762:3816083-3816167 -		-ACCA-------T---T----T---T---GGAAAGG----------T-AAT-T-------T-------A-TTTTTT----------GTGTTG-CAT-G-TA-T---TGG----------T-------TGGCATTTT-------T-----T-----------------------T-------T-----T-----T-----

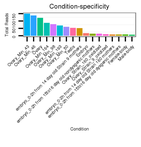
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_273	**scaffold_12855:5190806-5190873 -**	**confident-exception**	**Canonical miRNA**	**intergenic**
				[View on UCSC Genome Browser (Cornell Mirror)]

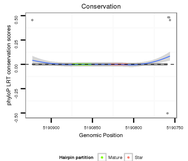
Legend: seed; flp; branch length error; mismatch error

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

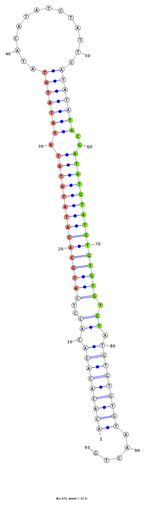
hide 3p reads | show mid mismatch reads

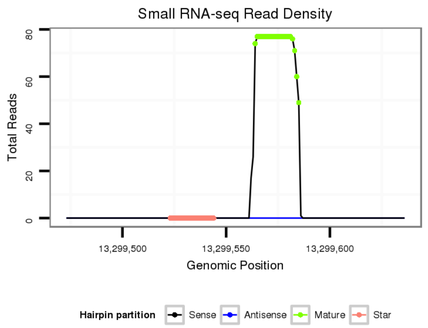
					SRR2096053	SRR2096056	SRR2096059	SRR2096058	SRR2096060	SRR2096057	SRR2096024 SRR2096038 webrys_D-webrys_D-day old 1-day old Strain 9 mothers	SRR2096036 webrys_D-webrys_D-day old 1-day old Strain 9 mothers	SRR2096014	SRR2096682 9x140_D-2h_embryos_total	SRR2096688	SRR2096673	SRR2096654	SRR2096677	SRR2096013	SRR2096676	SRR2096674	SRR2096681	M047 female	SRR2096678	SRR2096686	SRR2096679	SRR2096690 webrys_D-2h SRR2096684 day old 1-day old 140x9_D-mothers	V114 SRR2096655	SRR2096675	SRR2096687 webrys_D-day old mothers	SRR2096050 webrys_D-day old 14 mothers	SRR2096027	SRR2096670	SRR2096689	SRR2096041 SRR2096091 webrys_D-webrys_D-2h SRR2096085 day old 1-day old 140x9_D-mothers	SRR2096072 webrys_D-2h from day old mothers	SRR2096043	SRR2096079 webrys_D-2h from day old mothers	SRR2096058	SRR2096040	SRR2096083	SRR2096059	V053 M061	SRR2096047	SRR2096680	V047	SRR2096662	SRR2096041
GGTGAATTTTTAATTTTTATTTTTATAAAATCTACCGGTAATTTGTCTGTAAATATTTTTTATTTTTATTGCTTGTAAATTTTTTTCTTAAACTTC																																																
**********	(((((((

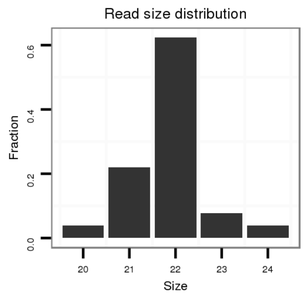
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_425	**scaffold_12875:13299523-13299586 +**	**candidate**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser [Cornell Mirror]]

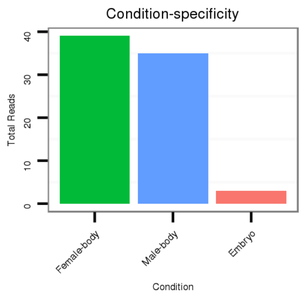
Legend: mature star **mismatch in alignment** mismatch in read

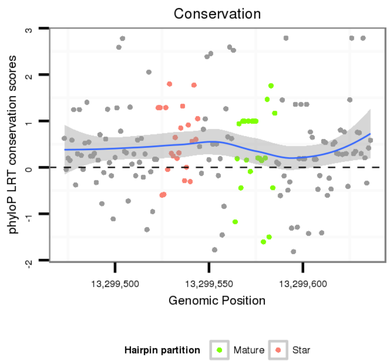
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dvir/GJ20351-in]

Repeatable elements

Name	Class	Family	Strand
(TA)n	Simple_repeat	Simple_repeat	+

mature **star**

1. scaffold_12420:3631-3652 +
2. scaffold_12472:450617-450638 -
3. dvi_425 scaffold_12875:13299523-13299544 +
4. scaffold_12928:835067-835088 +
5. scaffold_12928:7405196-7405217 +
6. scaffold_12932:310622-310643 -
7. scaffold_12963:1287557-1287578 -
8. scaffold_12963:1538799-1538820 +
9. scaffold_12963:18561490-18561511 +
10. scaffold_12970:1526842-1526863 +
11. scaffold_12970:3257035-3257056 +
12. scaffold_12970:7588673-7588694 -
13. scaffold_13042:1809099-1809120 -
14. scaffold_13047:13957885-13957906 +
15. scaffold_13047:18530090-18530111 -
16. scaffold_13049:85974-85995 -
17. scaffold_13049:3617869-3617890 +
18. scaffold_13049:19371287-19371308 +
19. scaffold_13049:20681317-20681338 -
20. scaffold_13049:22968551-22968572 +
21. scaffold_12928:3817654-3817675 -
22. scaffold_12928:7448411-7448432 -

Sense Strand Reads

hide 3p reads show mid mismatch reads

ACATTTTATAGCACATTCCAACTAGATATATATACACACACACACCTCATGCACATATATATATATATATATACATATCTATTCATATATACGATATGTATGTGCGTGTGTATGTGTGTGTAACTGCACATCGAGATAAAGAGAAAATCTATATAAATACT **********(((((((((.((..((((((((((((((((.(((((((.....)))))))..))))))))))))))))).)).)))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M047 V116 male body	M047 V116 female body	SRR060672 9x160_females_carcasses_total	SRR060667 160_females_carcasses_total	V047 embryo	SRR060666 160x9_0-2h_embryos_total	SRR060666 160_males_carcasses_total	SRR060659 Argentina_testes_total	SRR060679 160_0-2h_embryos_total	SRR060679 140x9_testes_total
.....TACGATATGTATGTGCGTGTGT.....	22	0	1	39.00	39	16	13	6	3	0	0	1	0	0	0
.....TATACGATATGTATGTGCGTGT.....	22	0	1	7.00	7	4	1	0	0	1	1	0	0	0	0
.....TACGATATGTATGTGCGTGTG.....	21	0	1	7.00	7	4	3	0	0	0	0	0	0	0	0
.....TATACGATATGTATGTGCGTG.....	21	0	1	4.00	4	1	2	0	0	1	0	0	0	0	0
.....ACGATATGTATGTGCGTGTGT.....	21	0	1	3.00	3	1	2	0	0	0	0	0	0	0	0
.....TATACGATATGTATGTGCGTGTGT.....	24	0	1	3.00	3	2	0	1	0	0	0	0	0	0	0
.....ATACGATATGTATGTGCGTGTGT.....	23	0	1	3.00	3	2	0	0	1	0	0	0	0	0	0
.....TACGATATGTATGTGCGTGTGTGA.....	22	1	1	3.00	3	3	0	0	0	0	0	0	0	0	0
.....ATACGATATGTATGTGCGTGT.....	21	0	1	3.00	3	0	3	0	0	0	0	0	0	0	0
.....ATACGATATGTATGTGCGTGTG.....	22	0	1	2.00	2	1	0	0	1	0	0	0	0	0	0
.....TATACGATATGTATGTGCGTGTG.....	23	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0
.....TACGATATGTATGTGCGTGTGTGT.....	23	1	1	1.00	1	0	0	0	1	0	0	0	0	0	0
.....ATACGATATGTATGTGCGTG.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....CGATATGTATGTGCGTGTGA.....	20	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0
.....ATACGATATGTATGTGCGTGTTAT.....	24	3	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TACGATATGTATGTGCGTGTGTA.....	23	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.....TATACGATATGTATGTGCGT.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0
.....TACGATATGTATGTGCGTGT.....	20	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0
.....ATGCACATATATATATATATAT.....	22	0	20	0.10	2	0	1	0	0	0	0	0	0	1	0
.....ATGTGCGTGTGTATGTGTG.....	19	0	19	0.05	1	0	0	0	0	0	0	0	1	0	0
.....TGTGCGTGTGTATGTGTGT.....	19	0	20	0.05	1	0	0	0	0	0	0	0	1	0	0

Anti-sense strand reads

TGTAAAATATCGTGTAAGGTTGATCTATATATATGTGTGTGTGTGGAGTACGTGTATATATATATATATATATGTATAGATAAGTATATATGCTATACATACACGCACACATACACACACATTGACGTGTAGCTCTATTTCTCTTTTTAGATATATTTATGA **********(((((((((.((..((((((((((((((((.(((((((.....)))))))..))))))))))))))))).)).)))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060684 140x9_0-2h_embryos_total	M027 male body	M047 female body
.....GTACGTGTATATATATATATAT.....	22	0	7	0.14	1	1	0	0
.....ACGTGTATATATATATATATA.....	21	0	20	0.05	1	0	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12875:13299473-13299636 +	dvi_425	ACATTTTATAGCACA--TTCCAACT-AGATATATAT-----ACACA----------C---ACACACACCTCATGCACATAT----------ATATA---TATATATATA--CAT----------ATCTATT-------CATATA----------TA--CGATATGTATGTGCGTGTG----TA----------T--GTGT---G-----TGT----------AACTGCACATCGAGAT--------AAAG-AGAAAAATCTATATAAAT-A-----CT
droMoj3	scaffold_6496:20592607-20592782 +		ACATTTTATAGCACA--TTCCAACT-AGATATATAT-----TTATA----------T---ATATATAGA--------TGCA------TACACATA----------TA-CA--------TATG--TATA----------ATATGTA-------CATATA----------T-T----------T---TATACATACATACATA--T---ATATA--TATACA--ATAAACAACAC----------AAATACTGCACATCGCAGCT-----ACAAG-AGAAAAATCTATATAAAT-ATA---GC
droGri2	scaffold_15245:7051816-7051983 -		ACATTTTATAGCACA--TTCCAACT-AGATATATAC-----ACAAA----------C---ACACACAC----------CA--CG--CA--------T--C----------CCC--------ACCACA------ACAACAACAGCAGCA--GCA----------T---CCCTA----------T--GTATT---G-----TGCAAATTTAAAAAACAGCAAAAAAGAAGAAAAACTGCACATCAAGAT------AGCAAG-AGAAAAATCTATATAAAT-G-----CT
droWil2	scf2_1100000004511:9322356-9322518 -		-CACTTCATTGCACT--TTTCGCAGCAGCATAATAAT-----ATATC----------AT-------TTATGTCCCT--------CTATCTATATA------TATATATATAAT----------ATA-----TG--------TATACATA----------CATATA----------T--CCATATATATGATGTGTGC----TC----------T--GTGT---T-----T----------T-----------GTATTTCTTCTAGACAGACCA-AAAAAAACTATATCAAA-T-----T
dp5	XL_groupla:6899574-6899716 +		----------T--TCCACCT-CGATATATAT-----CCATA---CC---AACAGGGC----------T-----T---GAAT----------ATATA---TATATATATA--TAT----------ATCTAAA-------TATATATACCAAAATGAT--------CATGCGT---------GTGCGTGTG----AA----------TCCG--T---GGCTC--CC----------GCTCCACTC-----C-A-CCCGAGAAAATCATATCACAT-T-----A
droPer2	scaffold_6:4221017-4221185 +		AAACCTCACCCAACT-ACTTATAACT-AAATGT-----T-----TTAGACGATGATATGCCCC----------T-----T--------TTATAAACAAG----------TA--CA--TATATATATATATA----------ACTATA-------CATATA----------C--C-CATATATATGTGTTTATA----TA----------T--TTATAATAAATA--T----------AATTTATATATACAAA--------A-AA-AACAAAGG-AAATGAAAA-G-----CT
droAna3	scaffold_13266:6249721-6249839 -		ACATTTTATAGCACA--TTCCAACT-AGCCTATAT-----ATATC----------T-----T----------TG--AA--TATCCTATA--TAT----------ATGCGTT-------TATATA----------GCAT----------T-----T----------ATA--T---AGACAGGGCA----------CATTCCAGT--------A-CA-AAAAAACTATATAAA-A-----CT
droBip1	scf7180000394792:64-215 -		ATCAATTTATTTTTATTTACTTATA-T-------TAT-----ACATT-TATATACATTTATATTTAG----------T-----T--------TTTATATACATATACATATACAT----------ATA--CA--TA--------T--TACATATACATATACATATA-------CATATA----------ACAT----A----------TACATA--TA-------CATATACATA--T---ACA----T----------CATATAT-----T-A-ATATCATATACATATCA-A-----T
droKik1	scf7180000301930:38624-38798 +		TT-----TATTATTTA---TATTTATTATCGCATACAG---TATATACATTAATATATTAATTATATATATATATATATTATCTATATA--------TATATA------TATATATA----------T--TA--------TATA--TATA----------ATATATA----------T-T----------T-----ATATATATATATATATATA---T----------ATATACGACG----------AATT-----CATCTATATATATATATACT-----CT
droFic1	scf7180000454066:500356-500478 +		ACATTTCATAGCACA--TTCCAACT-AGCCATATAT-----ATATA----------T-----T----AAG----------GTATG---TATATATGTA--TAT----------ATCTATG-------CATATA----------GCAT----------T-----T----------ATA--T---AGACGGAGCA----------CATTCCATT--------A-CG-AAAAAAATCTATATAAAT-G-----CT
droEle1	scf7180000491215:267703-267813 +		ACATTTCATAGCACA--TTCCAACT-AGCCATATAT-----ATATA----------T-----T----------T--------CATATATA--TAG----------ATCTATG-------CATATA----------GCAT----------T-----T----------ATA--T---AGACACGGCA----------CATTCCATT--------A-CG-AAAAAATCTATATAAAT-A-----CT
droRho1	scf7180000779957:118195-118295 +		ACATTTCATAGCACA--TTCCAACC-AGCCATATAT-----A----------T-----T----------T--------TAG----------ATCTATA-------CATATA----------GCAT----------T-----T----------ATA--T---AGACACCGCA----------CATTCCATT--------A-CG-AAAAAATCTATATAAAT-A-----CT
droBia1	scf7180000298095:86-257 -		ACGTTTTCTATACACA--CCCTCGTAT-ATATATATAT-----AAA-GATAAGACAAAGGCATA----------T-ACATACAGAGA------TACA----------TATAAATA----------T--ATATA---TACATATATA--TAT----------ATTTATTTATTTAAATATATATA----------TATATTT---------A-TTATTA----AA----------TATA--T---ATA----T----------CATTCATT-----T----T---TATTTATTTAAAT-ATATATA
droTak1	scf7180000416016:559690-559796 +		CA----------GA--TATAACT-ATATATATAT-----AAAA----------T-----T----------T--------TATATAGCATAACTACATATAGCGACTTTTTCC----------T-----T--------TAA--T----------T-----T----------G----------T-----T----------T--GTATT---T----TCT----------ATCTGCATATCGATAT----------T-----T-CTATTATTTATTATA-A----T
droEug1	scf7180000408961:339664-339819 +		ACCTTTTT-GTCA--A-------T-------AAA------CATA---AACCTAAAAGAATTATTACTAAATATATAT----CTTTACAT--------ATATATATA---TATATAAATATTGAGAAATATAAGA----------T-----T--------AAA--T----------T-----T----------G----------TG---TA----------T-----T----------TGTGCGATA----------AC-TATGATCTCTG----GCA-AAAAGCATCTATGAAAA-T-----CT
dm3	chr2R:8782857-8782989 -		ACATTTCATAGCACA--TTCCAACT-AGCCATATAT-----ACAAA----------C---ATATACA----------ATA--TA--CATATATATA--TAT----------ATCTGGG-------CATATA----------GCAC----A----------T-----TA----------CATA--T---AGATGCGGCG----------CATTCCATT--------T-CAAAAAAAATCTATATAAAT-G-----TT
droSim2	2r:9461582-9461719 -		ACATTTCATAGCACA--TTCCAACT-AGCCATATAT-----ACAAA----------C---ATATATATA----------TA--CA--TATATATATA--TAT----------ATCTGGG-------CATATA----------GCAC----A----------T-----T-------ACATACATA--T---AGACGCGGCG----------CATTCCATT--------T-CAAAAAAAATCTATATAAAT-G-----TT
droSec2	scaffold_1:6299018-6299153 -		ACATTTCATAGCACA--TTCCAACT-AGCCATATAT-----ACAAA----------C---ATATATATA----------GCA--CATATATATATATA--TAG----------ATCTGGG-------CATATA----------GCAC----A----------T-----AA----------CATA--T---AGACGCGGCG----------CATTCCATT--------T-CAAAAAAATCTATATAAAT-G-----TT
droYak3	2R:8188610-8188750 +		ACATTTCATAGCACA--TTCCAACT-AGCCATATAT-----ACCTA----------C---ATCTGGTTA------TATATA------CAAACA----------T-----TATATATACA--TAG----------ATCTGGG-------ATATATA----------GCAC----A----------T-----TA----------TATG--T---AGATACGGCG----------CATTCCATT--------A-CG-AAAAAAATCTATATAAAT-G-----TT
droEre2	scaffold_4845:17042295-17042425 +		ACATTTCATAGCACA--TTCCAACT-AGCCATATAT-----ACAAA----------C---ATATATATG----------T-----T----------ATATCG--CACATATATA--TAG----------ATCTGGG-------CATATA----------GCAC----A----------T-----T----------ATA--T---AGACGCGGCG----------CATTCCATT--------A-CG-AAAAAAATCTATATAAAT-G-----TT

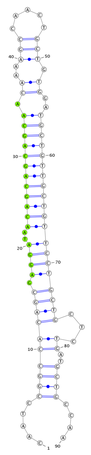
Generated: 09/08/2015 at 08:34 PM

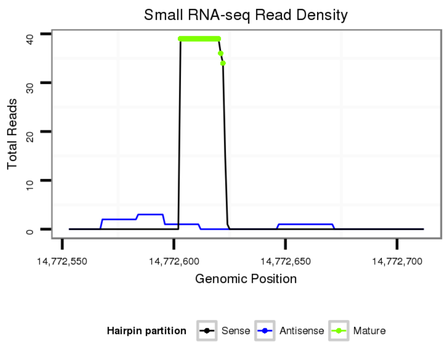
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

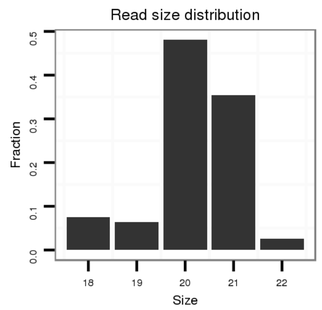
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_297	**scaffold_12963:14772603-14772662 +**	**candidate**	**Canonical miRNA**	**antisense_to_CDS**	[View on UCSC Genome Browser [Cornell Mirror]]

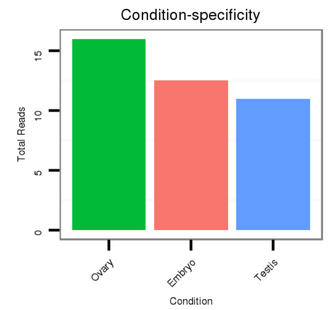
Legend: mature star mismatch in alignment mismatch in read

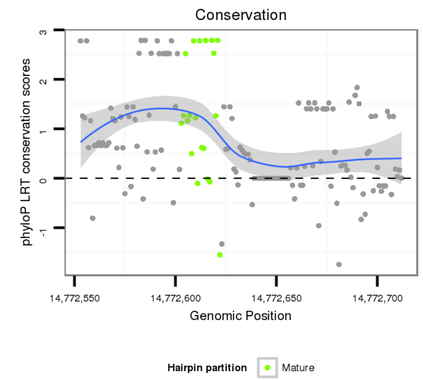
Predicted structure











Show Alternate Folds

Flybase annotation

Antisense to CDS [Dvir\GJ21312-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TGCTGGGGCTCAGCTTGGCGCCGTGCAGGCACTCGCAATCCGGCCACAGCGAGGATAACAGCAGCAGCAACAAAAGCCAACTGCTGTGGATGCTGTTGCTGTTCCTGCTGCTCTGATGCTGCCAACAGGATGCGGGCTGCGTGTGCCATAAATGGCGTTT	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060684 140x9_0-2h_embryos_total	SRR060675 140x9_ovaries_total	SRR060679 140x9_testes_total	SRR060657 140_testes_total	SRR060674 9x140_ovaries_total	SRR060658 140_ovaries_total	SRR060673 9_ovaries_total	SRR060678 9x140_testes_total	SRR060676 9xArg_ovaries_total	SRR2096081 embryo_0-2h from 15to16 day old nondysgenic mothers	SRR060689 160x9_testes_total	SRR2096014 Ovary_Strain_160_oxidized
**********.....((((((((((.((((..((((((((((.((..((((.....)))..))..))))))))))))))))))...))..))))....**********																	
.....GAGGATAACAGCAGCAGCAA.....	20	0	1	19.00	19	5	3	8	2	1	0	0	0	0	0	0	0
.....GAGGATAACAGCAGCAGCAAC.....	21	0	1	14.00	14	6	7	0	0	1	0	0	0	0	0	0	0
.....GAGGATAACAGCAGCAGCAAN.....	21	1	1	3.00	3	2	0	1	0	0	0	0	0	0	0	0	0
.....GAGGATAACAGCAGCAGCAACT.....	22	1	1	3.00	3	3	0	0	0	0	0	0	0	0	0	0	0
.....GAGGATAACAGCAGCAGC.....	18	0	2	3.00	6	1	4	0	0	0	1	0	0	0	0	0	0
.....GAGGATAACAGCAGCAGCA.....	19	0	2	2.50	5	0	3	1	1	0	0	0	0	0	0	0	0
.....GAGGATAACAGCAGCAACA.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....GAGGATAACAGCAGCAGCAAT.....	21	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0
.....GAGGATAACAGCAGCAGCAAG.....	21	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0
.....GAGGATAACAGCAGCAGCAACTGG.....	24	3	5	1.00	5	2	2	0	0	0	0	0	0	1	0	0	0
.....GAGGATAACAGCAGCAGCAACTG.....	23	2	4	0.75	3	0	1	0	2	0	0	0	0	0	0	0	0
.....GAGGATAACAGCAGCAGT.....	18	1	2	0.50	1	0	1	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

ACGACCCCGAGTCGAACCGCGGCACGTCCGTGAGCGTTAGGCCGGTGTCGCTCCTATTGTCGTCGTCGTTGTTTTCGGTTGACGACACCTACGACAACGACAAGGACGACGAGACTACGACGGTTGTCCTACGCCCGACGCACACGGTATTTACCGCAAA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR2096057 Ovary_Min_50	M047 female body	M061 embryo	V053 head	SRR060679 140x9_testes_total	SRR2096038 embryo_0-2h from 14 day old Strain 9 mothers	SRR060684 140x9_0-2h_embryos_total	SRR2096014 Ovary_Strain_160_oxidized	SRR060654 160x9_ovaries_total	SRR2096079 embryo_0-2h from 15to16 day old dysgenic mothers	SRR060669 160x9_females_carcasses_total	SRR060657 140_testes_total	V116 male body
**********.....((((((((((.((((..((((((((((.((..((((.....)))..))..))))))))))))))))))...))..))))....**********																		
.....ACCGCGGCACGTCCGTGAGCGTTAGGCC.....	28	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0	0	0
.....CAACGACAAGGACGACGAGACTACG.....	25	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0
.....GAGCGTTAGGCCGGTGTCGCTCCTATTG.....	28	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0
.....CCTATTGTCGTCGTCGTTGT.....	20	0	2	0.50	1	0	0	0	0	1	0	0	0	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12963:14772553-14772712 +	dvi_297	TGCTGGGGCTCAGCTTGGCGCCGTGCAGGCACTCGC---AATCCGGCCACAGCGAGGATAA---CAGCAGCAGCAACAAAAGCCAAC-TGCTGTGGATGCTGTTGCTGTTCCTGCTGCTCTGATGCTGCCAAC----------AGG----------A-----------TGCGGG----------CTGCGTGT----------GCCATAAATGGCGTTT
droMoj3	scaffold_6500:17713252-17713384 +		TGCTGGCGCTCAGCTTGGCGCATGCAGGCACTCGCAG--TCCGGCCAGAGGAGGACAA---CAGCAGCAGGAGCAGCAGCG-AC-----------GTGCTGCAGGATGCCAT---CTGTGCCGG----------GTC--G----------CTGTGTGT----------GCCATAAATGGCGTTT
droGri2	scaffold_15126:4590282-4590435 -		TGTGCGCGCTCAGCTTGGCGCATGTACATCTCGCAG--TCCGGCCAGAGCGAGGATAA---CAGCAGCAGGAGCGCGCAGCG-ACGTGCTG----------GCGCTAGTCTGATGACGCCAGC----------G---------AGGATG--G----------GTGCCTGTGTCAGCAG----------CTGCGAGT----------GCCATAAATGTGCGTT
droWil2	scf2_1100000004585:6818148-6818280 +		TGTTAC--------TTGCAGCCTGCAGGCACTGCGCAACAATCCGGCCAGTGAGGATAGCAACAAGAGGATTTCTATGTGC---TA----------GGCGTCAGCTGTGTGCGCCAAC----------AGGATT----------TGTGGATG--GCGT-------G--TATAGTTGAT--GT------
dp5	4_group5:393039-393269 -		TATTGC--------CGCGGCCGTGCAGGCAGTCGCAGCAGCATCCGGCCAGAGCCTCTGAG--GAAAGCAGGATAAGCAGTATGC---CT----------GGTGCAGCTGCGCGCCAAC----------G----------G--GAGTGCGAGGGTGTATGTG---GATGTGAGTGTCTTCTATTTTGGACTGGATCTGCTTCTCCTCCTCCTCGTT---TC---AACAGCTGACGCTTCTACTGAGTTGGTGAGATTG
droPer2	scaffold_12:201210-201319 +		----C--------TGCAGCGCAGTGGCAGTGGCA--**********----GCAGCAGCAATTGTTTAGGT----------GTTGGCGTTGGCGTTGT---CGTTGCAGC----------GACTGCC---GCCAG--------G---GATGACGCATTTGTGG------**********----------CCACCGAA----TTT
droAna3	scaffold_12916:8479139-8479307 -		TGTGC--------TGCTACCGTGCAGGCAGTCGCAGCAATGTGGCCACAGGCTGGTGAG---CAGCAAGAGGATTAGCAGTGTGC---TC----------GGCGTCAGCTGTGCGCCAGCAGCCTCCGGGTGTCCT---GCTTGTAT-------GATGGCTGGCTGTAT---GTCCGGGTTGTCCCGGATGAGAATGGGGATG------**********----------**********----------
droBip1	scf7180000396572:2918735-2918916 +		TGTTAC--------TGCAGCATGCAGGCAGTCGCAGCAATGTGGCCACAGGCTGGTGAG---CAGCAGCAGGATTAGCAGTGTGC---TC----------GGCGTCAGCTGTGCGCCAGCAGCCTCCGGGTGTCCT---GGGTGTCCTGCTGCATGATGGTTGGCTGTAT---GTCCGGGATGTCCCGGGTGTGTATGGGGATGTCTT------**********----------**********----------
droKik1	scf7180000302468:251335-251464 +		TGTGC--------TGCGCCATGCAGGCACTCGCAGCCCTCGGCCAGAGCCTGGTGAG---CAGCAGCAGGAGCAGCAGGAGGC----------TGGCCTCTGGGTGGCGA---GGAGGCTGA----------GTTGACTGGAGCCG--------G---GATAATGGGGT------**********----------**********----------GG
droFic1	scf7180000453815:257170-257361 -		TGTGC--------TGCGCCGTGTGCAGGCACTCGCAGCAATCCGGCCAGAGCCTGGTGAG---CGACAGCAGGAGGCGCAGGGTGC----------CCGCCTCCGGGTGTGCC---GGGTGTCCTGCCGCGTG---TCCCGCCGGGT---GTCCG--------G---GGTAATGGAGGTGTCTCCGCCGCGGG----------CTGGTGGCTCCTCCAGCTGTTGC---CGGTGACAGAGGTGAGG---
droEle1	scf7180000490970:120295-120424 -		TGTGC--------TGCGCGTGTGCAGGCACTCGCAGCCATCCGGCCACAGGCTGGTGAG---CAGCAAGAGGATGAGCAGGGTGC----------ATGCCTCCGGGTGTCCT---GGATGGGTC----------GTTGGATG---GTACG--------G---GATAATGGAGGTGTCT------**********----------**********----------
droRho1	scf7180000780014:69277-69404 -		TGTGC--------TGCGCGTGTGCAGGCACTCGCAGGTATCCGGCCACAGGCTGGTGAG---CAGCAGCAGGATGAGCAGGGTGC----------AGGCCTCCGGGTGTCCT---GGATGTCCC----------GTTGCATG---GTACG--------G---GATAATGGAGGTGTCT------**********----------**********----------
droBia1	scf7180000302422:2676536-2676677 -		TGTGC--------TGCGCCGTGCAGGCAGTCGCAGCAATCCGGCCACAGGCTGGTGAG---CAGCAGCAGGATTAGCAGGTGC----------AGGCCTCCGGGTGTCCT---GGGTGTCCTGCTGCATG---TGCGGCTGGAT---GTGCG--------G---GGTAATGGAGGTGTCT------**********----------**********----------
droTak1	scf7180000415104:26122-26289 -		TGTGC--------TGCCGCCGTGCAGCACTCGCAGCAATCCGGCCAGAGCCTGGTGAG---CAGCAGCAGGATTAGCAGGTGC----------CCTGGCTCCGGGTGTCCTCCTGGCTGTCCT----------GCTGGAT---GTCCT--------G---GATAATGGAGGTGTCTCCGCCGCGGG----------CTGAATGCTCCTCCAGCTGGCGG------**********---TG
droEug1	scf7180000409463:2216487-2216647 +		TGTGC--------TGCCGCCGTGCAGACATTCCAGCAATCCGGCCAGAGCCTGGTGAG---CAGCAGCAGGATTAGCAGGTGC----------AAGCTTCCGGGTGTCCT---GGATGTCCT----------GCTGGAT---GTCCG--------G---GATAATGGAGGTGCCTCCTCCGCGGG----------CTGGATGC---ACCAGCTGACGC------**********---T
dm3	chr2L:6897848-6897977 -		TGTGC--------TGCCGCCGTGCAGGCACTCGCAGCAATCCGGCCAGAGCCTGGTGAG---CAGCAGCAGGATGAGCAGGCAC----------ACGCCTCCGGGTGTCGG---GGTTGTACG----------GCTGATG---GTCCG--------G---GATAATGGAGGTGTCT------**********----------**********----------
droSim2	2L:6666216-6666375 -		TGTGC--------TGCCGCCGTGCAGGCACTCGCAGCAATCCGGCCAGAGCCTGGTGAG---CAGCAGCAGGATGAGCAGGGCAC----------ACGCCTCCGGGTGTCGG---GGTTGTACG----------GCTGATG---GTCCG--------G---GATAATGGAGGTGTCTCCTCCGCGGG----------CTGCGCGC---ACCAGCTGGCGC------**********----------
droSec2	scaffold_3:2431616-2431775 -		TGTGC--------TGCCGCCGTGCAGGCACTCGCAGCAATCCGGCCAGAGCCTGGTGAG---CAGCAGCAGGATGAGCAGGGCAC----------ACGCCTCCGGGTGTCGG---GGTTGTACG----------GCTGATG---GTCCG--------G---GATAATGGAGGTGTCTCCTCCGCGGG----------CTGCGCGC---ACCAGCTGGCGC------**********----------
droYak3	2L:6012198-6012327 +		TGTGC--------TGCCACCGTGCAGGCACTCGCAGCAATCCGGCCAGAGCCTGGTGAG---CAGGAGCAGGATGAGCAGGGCAC----------ACGCCTCCGGGTGTCCT---GGATGTCCT----------GCTGGCT---GTCCG--------G---GATAATGGAGGTGTCT------**********----------**********----------
droEre2	scaffold_4929:15811192-15811351 -		TGTGC--------TGCCACCGTGCAGGCACTCGCAGCAATCCGGCCAGAGCCTGGTGAG---CAGGAGCAGGATGAGCAGGGCAC----------ACGCCTCCGGGTGTCCT---GGATGTCCT----------GCTGGAT---GTCCG--------G---GATAATGGAGGTGTCTCCTCCGCGGG----------CTGGTGC---TCCAGCCGGCGC------**********----------

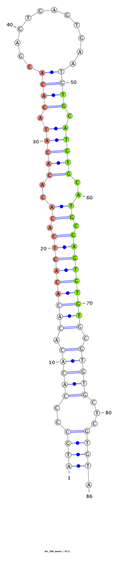
Generated: 09/08/2015 at 08:18 PM

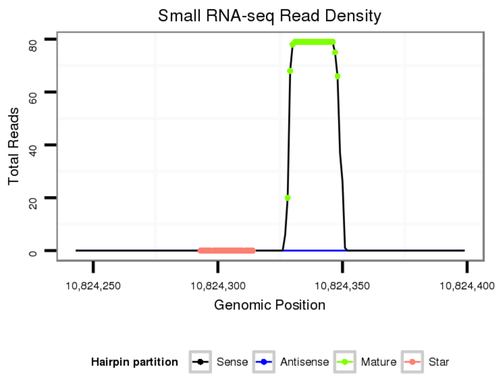
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

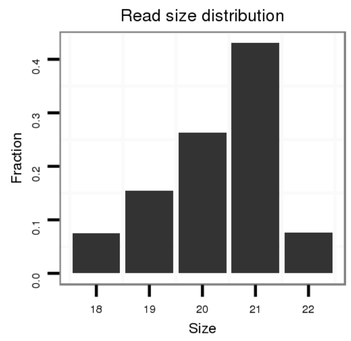
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_380	**scaffold_12875:10824293-10824349 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

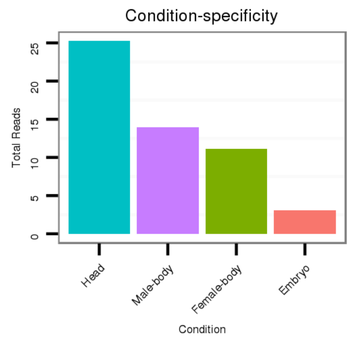
Legend: mature star mismatch in alignment mismatch in read

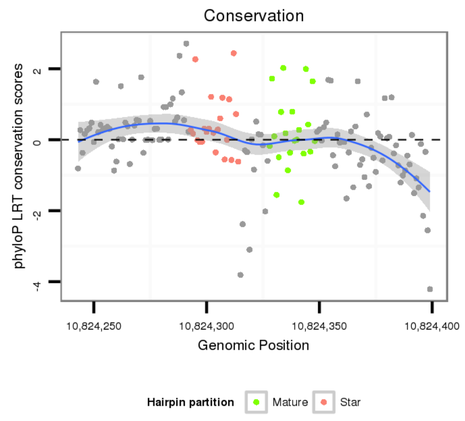
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
(CA)n	Simple_repeat	Simple_repeat	+

mature **star**

1. scaffold_12514:112425-112446 -
2. scaffold_12726:2475374-2475395 -
3. scaffold_12855:3803548-3803569 -
4. scaffold_12855:7095528-7095549 -
5. scaffold_12855:8570014-8570035 -
6. scaffold_12875:107516-107537 -
7. scaffold_12875:5133167-5133188 +
8. dvi_380 scaffold_12875:10824293-10824314 +
9. scaffold_12928:4867374-4867395 -
10. scaffold_12928:6913849-6913870 -
11. scaffold_12963:7371472-7371493 -
12. scaffold_12963:9364134-9364155 -
13. scaffold_12963:9849958-9849979 -
14. scaffold_12970:3538571-3538592 -
15. scaffold_12970:4996319-4996340 +
16. scaffold_13047:9913313-9913334 +
17. scaffold_13047:15829298-15829319 -
18. scaffold_13049:5761162-5761183 +
19. scaffold_13049:11766730-11766751 +
20. scaffold_13246:1799424-1799445 -
21. scaffold_12723:5226849-5226870 -
22. scaffold_12723:5311258-5311279 -
23. scaffold_12875:2115882-2115903 -
24. scaffold_12875:19982133-19982154 -
25. scaffold_12970:6737264-6737285 -

Sense Strand Reads

hide 3p reads show mid mismatch reads

GTTGCTTGTCTGCGCGTTCGCAGTTATTTTCGTTTATGCCCCACACACACACACACACACGAGTGAGTGAATGTGCATGTGCATGCGAGTGTGTGCGTGTGCTCGTGTATCTTAAAATCTGCTGAAAAGTTGCGCCAATCGAAGG **********	Read size	# Mismatch	Hit Count	Total Norm	Total	V053 head	V116 male body	M047 female body	V047 embryo	GSM1528803 follicle cells	M027 male body	SRR060656 9x160_ovaries_total	SRR060682 9x140_0-2h_embryos_total	SRR2096081 embryo_0-2h from 15to16 day old nondysgenic mothers	M061 embryo	SRR060658 140_ovaries_total	SRR060678 9x140_testes_total
.....GCATGTGCATGCGAGTGTGTGC.....	22	0	1	20.00	20	9	3	1	7	0	0	0	0	0	0	0	0
.....TGCATGTGCATGCGAGTGTGT.....	21	0	1	13.00	13	11	1	1	0	0	0	0	0	0	0	0	0
.....GCATGTGCATGCGAGTGTGTG.....	21	0	1	10.00	10	4	5	0	1	0	0	0	0	0	0	0	0
.....GCATGTGCATGCGAGTGTGT.....	20	0	1	10.00	10	3	4	1	1	0	1	0	0	0	0	0	0
.....GCATGTGCATGCGAGTGTG.....	19	0	1	6.00	6	1	1	4	0	0	0	0	0	0	0	0	0
.....CATGTGCATGCGAGTGTGTGC.....	21	0	1	5.00	5	3	1	1	0	0	0	0	0	0	0	0	0
.....GTGCATGTGCATGCGAGTGTGT.....	22	0	1	4.00	4	2	1	0	1	0	0	0	0	0	0	0	0
.....GCATGTGCATGCGAGTGT.....	18	0	1	2.00	2	0	0	2	0	0	0	0	0	0	0	0	0
.....CATGTGCATGCGAGTGTGT.....	19	0	1	2.00	2	1	0	1	0	0	0	0	0	0	0	0	0
.....GTGCATGTGCATGCGAGTGT.....	20	0	1	2.00	2	0	1	1	0	0	0	0	0	0	0	0	0
.....CATGTGCATGCGAGTGTG.....	18	0	1	2.00	2	1	0	1	0	0	0	0	0	0	0	0	0
.....CATGTGCATGCGAGTGTGTGCA.....	22	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0
.....GCATGTGCATGCGAGTGTGTT.....	21	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0
.....TGCATGTGCATGCGAGTGTGTG.....	22	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0
.....CATGTGCATGCGAGTGTGTG.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....TGCATGTGCATGCGAGTGTG.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....ATGTGCATGCGAGTGTGTGCG.....	21	0	2	1.00	2	0	2	0	0	0	0	0	0	0	0	0	0
.....GCATGTGCATGCGAGTGTGTTA.....	22	2	2	0.50	1	0	1	0	0	0	0	0	0	0	0	0	0
.....ATGTGCATGCGAGTGTGTGC.....	20	0	2	0.50	1	0	0	1	0	0	0	0	0	0	0	0	0
.....ATGTGCATGCGAGTGTGTG.....	19	0	4	0.25	1	1	0	0	0	0	0	0	0	0	0	0	0
.....ACACTCACACACATACACAC.....	22	0	20	0.10	2	0	0	1	0	0	0	0	0	1	0	0	0
.....CACACTCACACACATACA.....	20	0	20	0.05	1	0	0	1	0	0	0	0	0	0	0	0	0
.....ACACACTCACACACATACA.....	21	0	20	0.05	1	1	0	0	0	0	0	0	0	0	0	0	0
.....CACTCACACACATACACA.....	20	0	20	0.05	1	0	0	1	0	0	0	0	0	0	0	0	0
.....CACACACACTCACACACATA.....	22	0	20	0.05	1	0	0	0	0	0	0	0	0	0	0	0	1

Anti-sense strand reads

CAACGAACAGACGCGCAAGCGTCAATAAAAGCAAATACGGGGTGTGTGTGTGTATGTGTGCTCACTCACTTACACGTACACGTACGCTCACACACGCACACGAGCACATAGAATTTTAGACGACTTTTCAACGCGGTTAGCTTCC **********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060673 9_ovaries_total	V047 embryo	SRR060685 9xArg_0-2h_embryos_total
.....TACACGTACGCTCACACACGC.....	21	0	2	0.50	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12875:10824243-10824399 +	dvi_380	GTTGCTTG---TCTGCGCGTTCGCAGTTATTTT----------CGTTTATGCCC---------CA--CACA--CA----------CACAC--TCACACAC----AC--ATACACACGAGTG---------AGT---------GA----------ATGT-------GCATGTGCATGCGA----G--T--GT----------G----------TGCGT----GT--GC----------TCGTGTATCTTAAAA-TCT-------GCTGA---AAA----GTTGCGCCAATCGAAGG
droMoj3	scaffold_6496:16117763-16117930 -		GTTGCCTG---TCTGCGCGACGCAGCTATTTT----------CGTTTATGCCC---------CA--CACACATACTAAGAGGAGGTGTGTGT--GTGTGTTTATC----GC--GCGCGCGTTA---------AAT---------GA----------AAGCG---CATCTGATGTGC--TCTGTGT---G--GT----------G----------CCTGT----GT--------------------CCACATCTTTCAAAATTC-------GCTTA--TAAA----ATTTC------GACAA
droGri2	scaffold_15245:3930188-3930357 +		GTTGCTTTTAGTCT--GCCCTCGCAGTTATTTT----------CGTTTA----------AATACA--CA----------CAAAC--CCACAC----AC--AACACATCATCG--A-GCC---CGT---------GAGTGTGAGCAGATGTC---------AGTCTCATGTGTGTGCTGCTACTCG----------GTGT----GTGTATGTGTGTGCGAGTGTGT-GTGT-----TGTC-------------TTGTGGCACATCTCTC
droWil2	scf2_1100000004909:9902054-9902217 +		GTATTTAG---TTTTTGCATTTCTATTTATTTTGCTATATACAC----------ACACACA--CACA--CA----------CAC--ACACACACAT----AC--ATACACACCA---------CAAGCA-------AATAATTGTA----A--T--CACAATTTATTCATACTGAACTTTAATTTAG---GTCAAC----------A---A------AAAA-ACA-------AC-------AACAACAACAACAGAAGA
dp5	Unknown_singleton_1895:13118-13243 -		TTT-----C----------GGCCACA--CTC--A----------CTCACACACACACAC----AC--ATACACACGT--T--C-----ACT---------TATGCTGA---TGTCTGTGTGC--CTCGTG---T--CC----------G----------CCTGT----GT--GT----------GTGTATTTTTTGTGA-TCC-------CCC---TTGA---GCCCGTTTTCTTCCCC
droPer2	scaffold_15:1169878-1170007 +		TCTG--TA---TCTGCTGCTCCGCAGCACTCTC----------CATTTC----------CA--CACA--CA----------CACAG--ATACACTC----AC--ACATGCACGAGCAATGT--ATC---------TGCGACTG---T--CTGTGTCTGTCTGTGT-TGTG----------G----------TGTGT----GTGTAC----------A---TAC-------------ATCTT
droAna3	scaffold_13337:2671884-2671922 -		---------CA--CACA--CA----------CACAC--ACACACCC----AC--ACACACACGAATC---------AGT
droKik1	scf7180000302696:1098272-1098304 +		---------CA--CACA--CA----------CACAG--ACACACATC----AC--AGCCACATGA---------CAT
droFic1	scf7180000454106:1741986-1742112 -		---------CA--CACC--CA----------CACAC--ACACACAC----AC--ACACACACACATT---------ACT---------CATTGTGCGGTTGTCTGTG----ACTGCTG---T---T----------G----------CCGCT----GT--CT----------TTGTGATGTTAAAA-GTTATGAATTTT--A--TAGA----AATTGGCGTGCTAAAG
droEle1	scf7180000491006:57434-57507 +		ACA-----CACCACC------CACAA--A--CA----------CAC-----AAACAGACATAC----GCAGTC--G--C-----ACAGAGAACGCATTA----------AATT--------GTTATGCATA----------G----------CCGCT----GT--CT----------CCA
droRho1	scf7180000779872:341298-341360 +		---------CA--CACA--CA----------CACAC--ACACACAC----AC--ACACACATCAACC---------CGCCAAATA----C--GTCATATCATAA----------G----------GT----GT--CT----------CT----------CT
droBia1	scf7180000302041:138782-138892 +		TTA-----TTTT----------AGTTCAAACCTAACGAAGCATA--CCC--A----------TACACAAACACTCAC----AC--ACACACACCT--T---------AC----------AGCAGC---A--AC----------G----------ATACC----AT--CT----------ATACATAATGTAAGGCC----------CCAAACCAAAGC
droTak1	scf7180000415381:115420-115450 +		---------CA--CACA--CA----------CACAC--ACACACAC----AC--ACACACAG-----------G----------CAT----------G----------CCGCT----GT--CT----------CT----------CT
droEug1	scf7180000409553:231455-231560 +		ATA-----CA--CACA--CA----------CACAC--ACACACAC----AC--ACAGCAACC----AT--ACC---CAAAAAGC----CATCTGTGTGTGTGTTTCTG----------G----------TGTGT----GTGTAC----------T---TA------CGA-ACC----------AAGA--GAAACAA--ACCAAA
dm3	chr3L:21491700-21491750 +		---------CA--CACA--CA----------CACAC--ACACACAC----AC--ACACACAG-----------G----------CGT----------TCAATTTAAACGATTTT----------CGCGCATATGTATGCT----G--T--GT----------G----------TGTGT----GTGGCGAC----------A---TAA--ATTTCCA-TAT-------GCCAACCT--CATGCATATCCAC
droSec2	scaffold_10:2904436-2904491 -		---------CG--CACA--AA----------TCATA--AGCCCATA---GT--AAGCC-----------G----------TGTGTGTGTGTGTGTGT----------G----------TGTGT----GT--CT----------CT----------CT
droYak3	X:1815492-1815634 -		GTT-----CA--A--CA----------CACAC--TCATACAC----ATGCACACACTCGAGC-----A--CGT----------TCAATTTAAACGATTTT----------CGCGCATATGTATGCT----G--T--GT----------G----------TGTGT----GTGCGCAC----------A---TAA--ATTTCCA-TAT-------GCCAACCT--CATGCATATCCAC
droEre2	scaffold_4929:12583349-12583463 +		TTG-CTTG---T-GGCGCCAATCTTCCACTTC----------CGTTTA----------GACACA--CA----------CACAC--TTCACTT----CC--ACTCGCATCT----GT--ATC---------TGTGTGTGC--TGCGCGCATG----TGTCTGTGTCCGTG----------G----------TGTGTGTGTGT----------CT----------CT

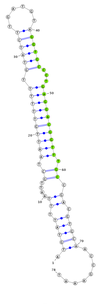
Generated: 09/08/2015 at 08:36 PM

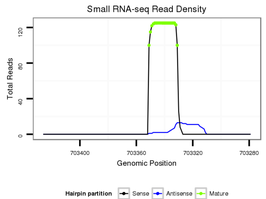
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

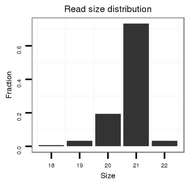
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_383	**scaffold_12967:703329-703376 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (GeneB Mirror)]

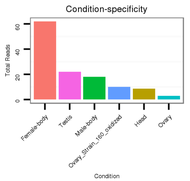
Legend: mature star mismatch in alignment mismatch in seed

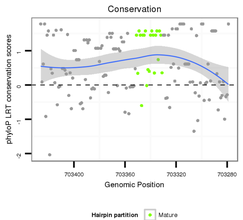
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
PENELOPE	LINE	Penelope	-

Sense Strand Reads

Hide 3p reads show mid mismatch reads

TGTATGTAAAATATTTAAATTTATGTTTTATCCTAATGTATTTTAATTGCTAATTGTTTTTGTATCTTGATGTA	Read # size	0 Mismatch	1 Hit Count	72.00 Norm	72 Total	M047 female body	V116 male body	SRR060672 9x160_females_carcasses_total	V053 head	SRR060667 160_females_carcasses_total	SRR2096014 Ovary_Strain_160_oxidized	SRR060683 160_testes_total	SRR060668 160x9_males_carcasses_total	SRR060689 160x9_testes_total	SRR060666 160_males_carcasses_total	SRR060679 140x9_testes_total	SRR060669 160x9_females_carcasses_total	SRR060657 160_testes_total	SRR060656 9x160_ovaries_total	SRR060688 160_ovaries_total	SRR060654 160x9_ovaries_total	SRR2096057 Ovary_Min_50	SRR060671 9x160_males_carcasses_total	SRR060678 9x140_testes_total	SRR2096079 embryo_0-2h from 15to16 day old dygenic mothers	SRR060658 140_ovaries_total	SRR060674 9x140_ovaries_total	SRR2096055 Ovary_Min_43	V047 embryo	SRR060659 Argentina_testes_total	SRR060676 9xArg_ovaries_total	SRR2096072 embryo_0-2h from 15to16 day old dygenic mothers	SRR060662 9x160_0-2h_embryos_total	M027 male body	SRR060675 140x9_ovaries_total
**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********
.....GGTGCCCTGAGGACGGTTTGC.....	21	0	1	72.00	72	15	7	6	7	5	8	5	4	3	3	2	2	3	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....GGTGCCCTGAGGACGGTTTGC.....	20	0	1	22.00	22	10	1	3	1	2	0	2	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGCCCTGAGGACGGTTTGCC.....	21	0	2	14.50	29	24	0	0	3	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGCCCTGAGGACGGTTTGCC.....	22	0	1	4.00	4	3	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCCCTGAGGACGGTTTGCCG.....	21	0	2	4.00	8	2	0	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GCCCTGAGGACGGTTTGCCGA.....	21	0	2	2.50	5	1	1	0	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GGTGCCCTGAGGACGGTTT.....	19	0	1	2.00	2	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CCCTGAGGACGGTTTGCCGA.....	20	0	2	1.50	3	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGCCCTGAGGACGGTTTGC.....	20	0	2	1.50	3	2	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCCCTGAGGACGGTTTGC.....	19	0	2	1.50	3	0	0	0	0	0	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCCCTGAGGACGGTTTGC.....	18	0	2	1.00	2	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCCCTGAGGACGGTTTGCCGA.....	22	0	2	1.00	2	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCCCTGAGGACGGTTTGCC[G].....	22	1	2	0.50	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GCCCTGAGGACGGTTTGCCGA[G].....	22	1	2	0.50	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGCCCTGAGGACGGTTTGCC.....	19	0	2	0.50	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCCCTGAGGACGGTTTGCC.....	20	0	2	0.50	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGCCCTGAGGACGGTTTGC[G].....	23	2	2	0.50	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AAATTAAAATAAAATTGT.....	18	0	6	0.17	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

ACATACATTTTATAAATTTAAATACAAAATAGGATTACATAAAATTAACGATTAACAAAAAACATAGAACATCA	Read # size	0 Mismatch	2 Hit Count	4.00 Norm	8 Total	M047 female body	V116 male body	SRR2096014 Ovary_Strain_160_oxidized	SRR2096055 Ovary_Min_43	M027 male body	SRR060689 160x9_testes_total	SRR2096057 Ovary_Min_50	SRR060688 160_ovaries_total	SRR2096050 embryo_0-2h from 14 day old mothers	SRR2096061 embryo_0-2h from 14 day old mothers	SRR060672 9x160_females_carcasses_total	V053 head	SRR060666 160_males_carcasses_total	SRR060683 160_testes_total	SRR060668 160x9_males_carcasses_total	M028 male	SRR060656 9x160_ovaries_total	SRR060680 9xArg_testes_total
**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********	**********
.....CGGCTGCACGTTGGCTTTATA.....	21	0	2	4.00	8	0	1	0	3	0	1	2	0	0	0	0	1	0	0	0	0	0	0
.....GGCTGCACGTTGGCTTTATAT.....	21	0	2	2.00	4	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
.....CGGGACTCCTGCCAAACGGCT.....	21	0	2	1.50	3	0	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	0	0
.....AACGGCTGCACGTTGGCTTTA.....	21	0	2	1.50	3	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0
.....CCACGGGACTCCTGCCAAACGGCTGCA.....	27	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....AAACGGCTGCACGTTGGCTTT.....	21	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
.....CAACGGCTGCACGTTGGCTT.....	21	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CCAACGGCTGCACGTTGGCTT.....	22	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....[G]CGGCTGCACGTTGGCTTTA.....	21	1	2	1.00	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ACGGCTGCACGTTGGCTTTAT.....	21	0	2	1.00	2	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
.....GGGACTCCTGCCAAACGGC.....	19	0	2	0.50	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AACGGCTGCACGTTGGCTT.....	20	0	2	0.50	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
.....AACGGCTGCACGTTGGCTT.....	19	0	2	0.50	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CACGGGACTCCTGCCAACGG.....	21	0	2	0.50	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ACGGCTGCACGTTGGCTTT.....	19	0	2	0.50	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....[G]CGGCTGCACGTTGGCTTTA.....	21	1	2	0.50	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....[GG]CGGCTGCACGTTGGCTTTA.....	21	2	3	0.33	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....[T]GGCTGCACGTTGGCTTTATAT.....	23	2	4	0.25	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....[T]CGCCAAACGGCTGCACGT.....	20	1	20	0.05	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Show Alignment With Reads

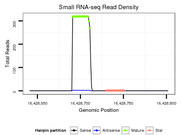
Re-alignment of all predicted orthologs

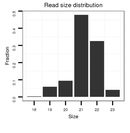
Species	Coordinate	ID	Alignment
droVir3	scaffold_13367:703278-703435:-	dvi_383	TGTATGTAAAATATTTAAAT-TTATGTTTTATCCTAATGTATTTTAATTGCTAATTGTTTTT---TG----------TAT----------CTTGATGTAGGTGCCCTGAGGACGGTTTGCCGACGTGCAACCGAAATATATTGGGGAAAAAA-TTAAA-ATAAAA-TTGTTCACT
droWil2	scaff_1300000024367:203027-203216:+		TGTATGT[G]-[G]-[A]AA[A]A-TT[G]-[T]-[T]-[T]AATGT[AACA]AATT[G]-[A]A[T]-[T]-[T]-- -- ----------CCTTG[TA]----------[G]-[A]CGTGCAACCGAAATATATG[G]-[AA]-[A]-[A]-[A]AAA-[A]-[G]-[TTG]
droAna3	scaffold_8720:4232-4306:+		[TA]A[A]-[T]-[T]-[T]AAT-TTA[T]TTA[T]TTA[T]AATGT[T]-[T]-[T]-

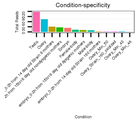
ID:	Coordinate:	Confidence:	Class:	Genome Locale:
dvi_270	**scaffold_13047:16428691-16428752 +**	**candidate**	**Canonical miRNA**	**intron**
				[View on UCSC Genome Browser (Central Mature)]

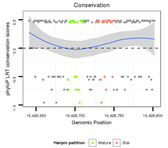
Legend: loop 5p 3p mismatch or bulge mismatch loop

Predicted structure









Show Alternate Folds

FlyBase annotation

mirc:[DroID]CR30141-aa

No Repeatable elements found

Sense Strand Reads

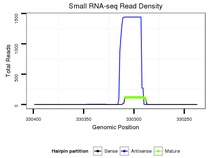
Hide 3p reads | show mid mismatch reads

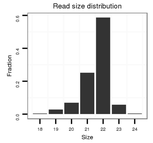
| | | | |

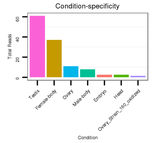
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_268	**scaffold_12963:330287-330349 -**	**confident-exception**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Cotsell Mouse)]

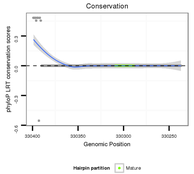
Legend: **mature** **star** **mismatch in alignment** **mismatch in loop**

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

mature	star
1. dvi_263 scaffold_12723:464093:464095:+ 2. dvi_268 scaffold_12963:330286:330309:-	

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTTGTTTTCCCAGACATCGGAACGGAATCGATAAGCCTCCTAACTAATTACAGCTGCACCAAGGTTTAATAAATCTGAAGATAATTA	Read # size	M.mismatch	Hit Count	Total Norm	Total	SRR040678 9x140_testes_total	SRR040679 female 140x9_testes_total	SRR040681 body	SRR040680 Arga9_testes_total	SRR040672 140x9_testes_total	SRR040669 9x140_females_carcasses_total	SRR040689 140x9_testes_total	SRR040667 140_females_carcasses_total	SRR040668 140x9_males_carcasses_total	SRR040676 9xkrg_ovaries_total	SRR040680 9xkrg_testes_total	SRR040669 140x9_females_carcasses_total	V116 SRR040666 140_males_carcasses_total	SRR040675 140x9_ovaries_total	SRR040677 Arga9_ovaries_total	SRR040671 9x140_males_carcasses_total	SRR040674 9x140_ovaries_total	SRR040686 Arga9_0-2h_embryos_total	SRR2096014 140x9_0-2h_embryos_total	Ovary_Strain_140_unstained	SRR040684	V053 SRR040655 9x140_testes_total	SRR040656 9x140_ovaries_total	SRR040657 140_testes_total	SRR040683 140_ovaries_total	SRR2096013 Ovary_Strain_9_unstained	SRR040685 9xkrg_0-2h_embryos_total	SRR2096072 embryo_0-2h from 15to16 day old gynogenic mothers	SRR040659 head	Argentina_testes_total	M028 SRR040660 Argentina_ovaries_total	SRR040661 140x9_0-2h_embryos_total	9_females_carcasses_total	SRR040670 9_testes_total	SRR040673 9_ovaries_total	SRR040688 140_testes_total	SRR040687 140_ovaries_total	SRR2096058 9_0-2h_embryos_total	Ovary_Mix_96
**********	((((.((.(.((((((.((((.((((.((((...((((...(((.....)))))))))))).))))).))))).))))).)))).)))))))))).)))))))))))	Hsa																																												
.....	.ATGCTGATGCTGCTCTATAATT.	22	0	2	65.00	130	28		22	10				2																																
.....	.ATGCTGATGCTGCTCTATAATT.	21	0	2	23.50	47	4		4	1		1		2																																
.....	.ATGCTGATGCTGCTCTATAAT.	22	1	2	10.00	20	4		4	3		3		1																																
.....	.TAATGCTGATGCTGCTCTATAA.	23	1	2	8.50	17	3		1	1		0		0		1																														
.....	.AATGCTGATGCTGCTCTATAAT.	22	0	2	6.50	13	1		1	0		0		0		0																														
.....	.AATGCTGATGCTGCTCTATAT.	21	0	2	4.50	9	1		1	2		1		0		0																														
.....	.ATGCTGATGCTGCTCTATAAT.	21	0	2	4.00	8	0		0	1		0		0		0																														
.....	.ATGCTGATGCTGCTCTATAAT.	23	1	2	3.50	7	1		0	2		1		0		1																														
.....	.ATGCTGATGCTGCTCTATAAT.	20	0	2	3.00	6	0		0	1		0		0		0																														
.....	.ATGCTGATGCTGCTCTATAAT.	23	1	2	2.50	5	0		1	3		0		0		0																														
.....	.TGCTGATGCTGCTCTATAA.	20	0	2	2.50	5	0		0	0		0		0		1																														
.....	.TGCTGATGCTGCTCTATAAT.	21	0	2	2.00	4	1		2	0		1		0		0																														
.....	.TAATGCTGATGCTGCTCTATA.	24	1	2	2.00	4	0		0	0		0		0		0																														
.....	.AATGCTGATGCTGCTCTATAA.	21	0	2	1.50	3	1		0	0		0		1		0																														
.....	.TAATGCTGATGCTGCTCTAT.	20	0	2	1.50	3	0		0	0		0		0		0																														
.....	.AATGCTGATGCTGCTCTAT.	19	0	2	1.50	3	0		3	0		0		0		0																														
.....	.ATGCTGATGCTGCTCTATA.	19	0	2	1.50	3	0		0	0		0		0		0																														
..... ACTGAATTACAGGGTGCACCAG..	24	2	1	1.00	1	0		0	0		0		0		0																														
.....	.TGCTGATGCTGCTCTATATAA.	22	0	2	1.00	2	0		0	0		0		0		0																														
.....	.TGCTGATGCTGCTCTATAAT.	20	0	2	1.00	2	0		0	0		0		0		0																														
.....	.TAATGCTGATGCTGCTCTAA.	22	0	2	1.00	2	0		0	1		0		0		0																														
.....	.TAATGCTGATGCTGCTCTA.	19	0	2	1.00	2	0		0	0		0		0		0																														
.....	.ATGCTGATGCTGCTCTATAA.	21	1	2	0.50	1	0		0	0		0		0		1																														
.....	.AATGCTGATGCTGCTCTATAA.	22	2	2	0.50	1	0		0	0		0		0		1																														
.....	.AATGCTGATGCTGCTCTATAA.	23	2	2	0.50	1	0		0	0		0		0		1																														
.....	.ATGCTGATGCTGCTCTATAAT.	24	2	2	0.50	1	0		0	0		0		1		0																														
....CGTAAGCTCCTAACTAA..	18	0	2	0.50	1	0		0	0		0		0		0																														
.....	.ATGCTGATGCTGCTCTA.	19	1	2	0.50	1	0		1	0		0		0		0																														
.....	.AATGCTGATGCTGCTCTATAAT.	23	0	2	0.50	1	0		0	0		0		0		0																														
.....	.ATGCTGATGCTGCTCTATAA.	22	1	2	0.50	1	0		0	1		0		0		0																														
.....	.AATGCTGATGCTGCTCTATAT.	24	2	2	0.50	1	0		0	0		0		0		0																														
.....	.ATGCTGATGCTGCTCTA.	20	0	2	0.50	1	0		1	0		0		0		0																														
.....	.TGCTGATGCTGCTCTA.	19	0	2	0.50	1	0		0	0		0		0		0																														
.....	.TAATGCTGATGCTGCTCTAA.	22	2	2	0.50	1	0		0	0		0		0		0																														
.....	.TTAATGCTTGATGCTGCTCTATAAT.	24	0	2	0.50	1	0		0	0		0		0		0																														

Anti-sense strand reads

AAACAAAACGGTCTGTATTAACCTTGCCTTAGCTATTCGAGGATTGATTAATGTCCGAGCGTGGTTCCAAATTATTTACACTTCTATTAA	Read # size	M.mismatch	Hit Count	Total Norm	Total	SRR040678 9x140_testes_total	SRR040681 Arga9_testes_total	SRR040679 140x9_testes_total	SRR040670 9_testes_total	SRR040680 9xkrg_testes_total	SRR040669 140x9_testes_total	SRR040683 140_testes_total	SRR040655 9x140_testes_total	V116 SRR040657 male 140_testes_total	SRR040659 Argentina_testes_total	M047 Female body	M027 SRR040674 male 9x140_ovaries_total	SRR040656 9x140_ovaries_total	SRR040676 9xkrg_ovaries_total	SRR040677 Arga9_ovaries_total	SRR040688 140_ovaries_total	SRR2096013 Ovary_Strain_9_unstained	SRR040658 140_ovaries_total	SRR040671 9x140_males_carcasses_total	SRR040682 9x140_0-2h_embryos_total	SRR040684 140x9_0-2h_embryos_total	SRR2096059 Ovary_Mix_164	V047 SRR040666 embryo 140_males_carcasses_total	SRR040672 9x140_females_carcasses_total	SRR040673 9_ovaries_total	SRR040675 140x9_ovaries_total	SRR040685 9xkrg_0-2h_embryos_total	SRR040686 Arga9_0-2h_embryos_total	SRR1104728 larvae	SRR2096056	SRR2096081 embryo_0-2h from 15to16 day old nondysgenic mothers
**********	((((.((.(.((((((.((((.((((.((((...((((...(((.....)))))))))))).))))).))))).))))).)))).)))))))))).)))))))))))	Hsa																																			
.....	.TTAATTGCGAACTACGACAGAT.	24	1	2	781.50	1563	551		348	348		5	123	80	36	18	3	0	0	0	0	0		0	0	0	0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGAT.	23	1	2	572.00	1144	371		293	290		3	86	40	47	5		7	0		0	0		1	0		0	0		0	0	0	0	0	0	0	
.....	.TAATTGCGAACTACGACAGAT.	24	2	2	247.00	494	164		113	103		2	42	18	39	4		7	0		2	0		1	0		0	0		0	0	0	0	0	0	0	
.....	.TAATTGCGAACTACGACAGAT.	21	0	2	203.50	407	90		99	109		0	32	19	20	2		5	19		8	0		2	0		0	0		0	0	0	0	0	0	0	
.....	.ATTGCGAACTACGACAGATAT.	22	0	2	182.00	364	116		99	77		0	23	17	14	3		12	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.ATTGCGAACTACGACAGAT.	23	0	2	90.50	181	53		47	44		1	15	5	11	0		2	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.ATTGCGAACTACGACAGATAT.	21	0	2	62.50	125	32		24	22		0	13	15	7	4		4	1		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TAATTGCGAACTACGACAGAT.	22	1	2	61.50	123	39		16	26		2	7	8	15	3		2	0		1	3		0	0		0	0		0	0	0	0	0	0	0	
.....	.ATTGCGAACTACGACAGAT.	19	1	2	55.00	110	82		18	24		0	7	4	11	1		0	2		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TAATTGCGAACTACGACAGAT.	24	2	2	40.00	80	24		19	20		0	7	2	6	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TAATTGCGAACTACGACAGATAT.	23	1	2	39.50	79	30		20	16		0	3	3	5	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.AATTGCGAACTACGACAGAT.	20	0	2	28.50	57	21		16	15		0	2	0	3	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TAATTGCGAACTACGACAGAT.	24	1	2	26.50	53	17		8	9		0	2	0	2	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TAATTGCGAACTACGACAGAT.	25	3	2	25.50	30	10		11	4		0	5	2	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TAATTGCGAACTACGACAGAT.	23	2	2	14.50	29	11		6	8		0	2	0	3	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TAATTGCGAACTACGACAGAT.	23	1	2	14.50	29	8		8	10		1	2	0	3	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TAATTGCGAACTACGACAGATAT.	23	0	2	12.50	25	7		3	3		0	1	0	2	0		1	1		1	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGTAT.	20	2	2	10.50	21	6		2	1		0	3	5	3	0		1	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGAT.	25	2	2	5.00	10	2		3	1		0	1	0	3	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGAT.	22	1	2	5.00	10	2		2	2		0	1	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGAT.	25	3	2	3.50	7	2		2	2		0	1	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TAATTGCGAACTACGACAGAT.	23	1	2	3.00	6	0		1	1		0	0	0	1	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TAATTGCGAACTACGACAGATAT.	24	2	2	2.50	5	0		1	2		0	0	1	1	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
....CTCCACCGTCGTTCCAAATT..	20	0	1	2.00	2	0		0	0		0	0	1	0	1	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.AATTGCGAACTACGACAGAT.	22	2	2	2.00	4	2		0	1		0	0	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TACGACAGCGAGATAT.	19	0	2	2.00	4	2		1	1		0	0	0	1	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGATAT.	24	1	2	2.00	4	2		1	1		0	0	0	1	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGAT.	23	2	2	1.50	3	2		1	0		0	0	0	1	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGAT.	24	3	2	1.50	3	2		1	0		0	0	0	1	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGAT.	24	2	2	1.50	3	1		2	0		0	0	0	1	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGAT.	21	1	2	1.50	3	2		1	0		0	0	0	1	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTACGACAGCGAGATAT.	18	0	2	1.50	3	0		0	1		0	0	2	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
....CTCCACCGTCGTTCCAAATT..	18	0	1	1.00	1	0		0	0		0	0	0	0	0	0		0	1		0	0		0	0		0	0		0	0	0	0	0	0	0	
..... ATGTCCGACGTCGTTCCAAATT...	22	0	1	1.00	1	0		0	0		0	0	0	0	0	0		0	1		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGAT.	25	3	2	1.00	2	0		0	0		0	0	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.AATTGCGAACTACGACAGATA.	21	0	2	1.00	2	0		1	1		0	0	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.ACGAACTACGACAGATAT.	18	0	2	1.00	2	0		1	1		0	0	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.AATTGCGAACTACGACAGATAT.	23	0	2	1.00	2	0		0	0		0	1	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGAT.	20	0	2	1.00	2	0		0	0		0	1	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGAT.	20	1	2	0.50	1	0		0	0		0	0	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAG..	21	1	2	0.50	1	1		0	0		0	0	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
..... TTTCTTTAATTACGACTA..	19	0	2	0.50	1	0		1	0		0	0	0	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACGACAGAT.	22	1	2	0.50	1	0		0	0		0	0	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGA.	23	1	2	0.50	1	1		0	0		0	0	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGAT.	24	3	2	0.50	1	0		0	0		0	0	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGA.	21	1	2	0.50	1	0		0	0		0	0	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGAT.	26	3	2	0.50	1	0		0	0		0	0	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
..... TTTCTTTAATTACGACTAT..	20	0	2	0.50	1	0		0	0		0	0	1	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTACGACAGCGAGATAT.	21	1	2	0.50	1	0		0	0		0	0	1	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGA.	23	1	2	0.50	1	0		0	0		0	0	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	
.....	.TTAATTGCGAACTACGACAGAT.	24	2	2	0.50	1	1		0	0		0	0	0	0	0		0	0		0	0		0	0		0	0		0	0	0	0	0	0	0	

Show Alignment With Reads

Re-alignment of all predicted orthologs

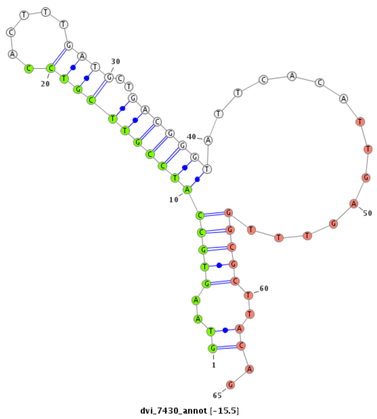
Species	Coordinate	ID	Alignment
dmel(r5)	chr2L:8 12963:330287-330349:-	dvi_268	TTTGTTTTCCCAGACATAACCGGAACGGAATCGATAAGCCTCTAACTAATTACAGCTGCACCAAGGTTTAATAAATCTGAAGATAATTA-ACCTTGATGCTCCTTATATTCCCATCCTCACTTGTTATTCCTTTATTACTCATAAC
dsim(r5)	chr2L:8 10453720-10453789:-		TTTGTTTTCCCAGACATAACCGGAACGGAATCGATAAGCCTCTAACTAATTACAGCTGCACCAAGGTTTAATAAATCTGAAGATAATTA-ACCTTGATGCTCCTTATATTCCCATCCTCACTTGTTATTCCTTTATTACTCATAAC

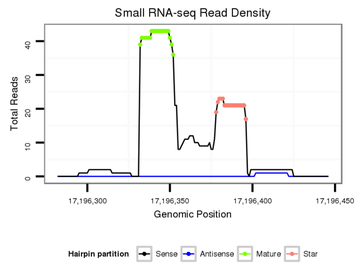
Generated 09/08/2015 at 09:40 PM

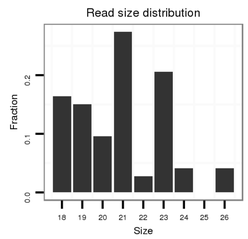
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_7430	**scaffold_12875:17196332-17196396 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

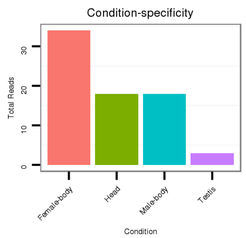
Legend: mature star mismatch in alignment mismatch in read

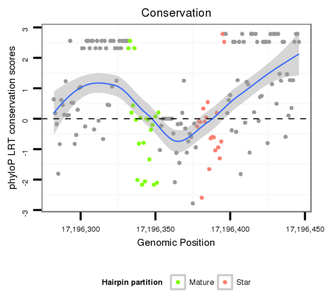
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DvirGJ22261-in]; CDS [DvirGJ22261-cds]; CDS [DvirGJ22261-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGGTGTCCAGCTGCCGCGCGGCATGTTCGACGTCTCCAACGTGCGTGATAAGTAAGTGCCATCCGTTCGTCCACTTTGATGCTGACGGGTATTCACATTGAGTTTGGCGCTTACAGATGATGCGCCGTCGGCCTTCTCGATGCCGCATTTCTATGGCAGCAGCTAC						M028	SRR060667	SRR060672	SRR060668	SRR060669	M027	SRR060671	SRR060665	SRR060664	SRR2096057	M047 female body	SRR060679	V053 head	SRR060680	SRR060681	SRR2096058	SRR2096059	SRR2096060	V116 male	SRR060682 9x140_0-2h_embryos_total
**********	((..((((((((((((((.....)))).)))))))).....)))))..))..**********	Read # size	Mismatch	Hit Count	Total Norm	Total	head 160_females_carcasses_total	9x160_females_carcasses_total	160x9_males_carcasses_total	160x9_females_carcasses_total	male 9x160_males_carcasses_total	9_females_carcasses_total	9_males_carcasses_total	Ovary_Min_50	body	140x9_testes_total	head	9xArg_testes_total	Argx9_testes_total	Ovary_Min_98	Ovary_Min_164	Ovary_Min_193	body	2h_embryos_total
....GTAAGTGCCATCCGTTCGTCC....		21	0	1	17.00	17	3 4	2	2	3	3 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GTAAGTGCCATCCGTTCGTCCAC....		23	0	1	13.00	13	8 2	0	0	0	2 0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
....TTGAGTTTGGCGCTTACAG....		19	0	1	6.00	6	0 2	2	1	0	0 0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGAGTTTGGCGCTTACAG....		18	0	1	4.00	4	0 0	1	0	0	0 2	0	0	0	0	1	0	0	0	0	0	0	0	0	0
....TTGAGTTTGGCGCTTACA....		18	0	1	3.00	3	0 1	0	0	0	0 1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
....GTAAGTGCCATCCGTTCG....		18	0	1	3.00	3	0 0	3	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....ATTGAGTTTGGCGCTTACAG....		20	0	1	3.00	3	0 1	0	0	0	0 0	1	0	0	0	0	0	1	0	0	0	0	0	0	0
....GTAAGTGCCATCCGTTCGTC....		20	0	1	3.00	3	0 1	0	0	1	0 0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
....TAAGTGCCATCCGTTCGTCCAC....		22	0	1	2.00	2	2 0	0	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....CATTGAGTTTGGCGCTTACAG....		21	0	1	2.00	2	0 0	0	1	0	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GATGCCGTCGGCCTTCTCGATGCC....		26	0	1	2.00	2	0 0	0	0	0	0 0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
....TGAGTTTGGCGCTTACAG....		18	1	1	2.00	2	0 0	2	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....CCATCCGTTCGTCCACTTTGATGCTG....		26	0	1	2.00	2	2 0	0	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GTAAGTGCCATCCGTTCGT....		19	0	1	2.00	2	0 0	0	1	0	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TTTGATGCTGACGGGTATTCACA....		23	0	1	1.00	1	0 0	0	0	0	0 0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
....GTAAGTGCCATCCGTTCGTCCACT....		24	0	1	1.00	1	0 0	0	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GAGTTTGGCGCTTACAGA....		18	0	1	1.00	1	0 0	0	0	0	0 0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
....ACTTTGATGCTGACGGGTATTCACAT....		26	0	1	1.00	1	0 1	0	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GATGCTGACGGGTATTCA....		18	0	1	1.00	1	0 0	0	1	0	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....ATTGAGTTTGGCGCTTACA....		19	0	1	1.00	1	0 1	0	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....ATTGAGTTTGGCGCTTACAGT....		21	1	1	1.00	1	0 0	0	0	0	0 0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
....GTTATCACATTGAGTTTGGCGCTTACAG....		28	1	1	1.00	1	0 0	0	0	1	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TCCACTTTGATGCTGACG....		18	0	1	1.00	1	0 0	0	0	0	0 0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
....TGATGCTGACGGGTATTCA....		19	0	1	1.00	1	0 0	0	1	0	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....ATGCTGACGGGTATTCACATTGAG....		24	0	1	1.00	1	0 0	0	0	0	0 0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
....CTGACGGGTATTCACATTGAG....		21	0	1	1.00	1	0 0	0	0	0	0 0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
....TTGAGTTTGGCGCTTACAGT....		20	1	1	1.00	1	0 0	0	1	0	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....CCGCGCGGCATGTTCGACGT....		20	0	1	1.00	1	0 1	0	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TTGATGCTGACGGGTATTC....		19	0	1	1.00	1	0 0	0	0	1	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GTAAGTGCCATCCGTTCGT....		20	1	1	1.00	1	0 0	0	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
....ACTTTGATGCTGACGGGTATTCAC....		24	0	1	1.00	1	0 0	1	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....CACATTGAGTTTGGCGCTTACAG....		23	0	1	1.00	1	0 0	1	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TTTGATGCTGACGGGTATTC....		20	0	1	1.00	1	0 0	0	0	1	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

ACCACAGGTCGACGGCGGCCGTACAAGCTGCAGAGGTTCACGCACTATTCATTCACGGTAGGCAAGCAGGTGAAACTACGACTGCCCATAAGTGTAACTCAAACCGCGAATGTGTACTACGCGGCCAGCCGGAAGAGCTACGGCGTAAAGATACCGTCGTCGATG						M047 female body	SRR060681 Argx9_testes_total	SRR060687 V053 9_0-2h_embryos_total	SRR060682 9x140_0-2h_embryos_total	SRR2096060 Ovary_Min_193	M028 head	SRR060686 Argx9_0-2h_embryos_total	SRR2096013 Ovary_Strain_9_oxidized	GSM1528803 follicle cells	SRR2096057 Ovary_Min_50	SRR2096058 Ovary_Min_98
**********	((..((((((((((((((.....)))).)))))))).....)))))..))..**********	Read # size	Mismatch	Hit Count	Total Norm	Total										
....CGCGGCAGCCGGAAGAGCTA....		20	0	1	1.00	1	1 0	0	0	0	0	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12875:17196282-17196446 +	dvi_7430	TGGTGTCCAGCTGCCGCGCGGCATGTTCGACGTCTCCAACGTGCGTGATAAGTAAGTGCCAT----------CCGTTCG----------TCCACTTTGATGC------TGACG----------GGTATTC----------ACAATTGAGTT----------TGGCGCTTACAGATGATGCGCCGTCGGCCTTCTCGATGCCGCATTTCTATGGCAGCAGCTAC
droMoj3	scaffold_6496:10809963-10810144 -		CGCGCGTAAGCTGCCGCGCGGCATGTTCGAGGTCTCCAAGTCGTGTGATAAGTAAGTGCTCC--AGTCACCTAG-------A----------GGC-----A-T-----TCGC-AGAGCA--TTCATCTCTCAATCATCTCTCTCTCTATCAATCTCGCTAAGATGATGCGCCGTCGGCCTTCTCGATGCCCATTTCTATGGCGCAGCTAC
droGri2	scaffold_15245:16715902-16716090 +		TAATGTCCCATTGCATGCAGGCATGTTCGAGTGTCGATGTGTGATAAGTCAGTCA-GCCACAATCAAACTTCGTATTTGTTCTACAA---------ATCATGATTTACTTCTTCTT-------TTTTTTTATTTTTCTTTTT----------TG--CAAGTAAGATAGCGCCGTCGGCCTTCTCGATGCCCATTTCTATGGCGCAGCTAC
droWil2	scaf2_1100000004512:1512136-1512193 -		CT--ACTAAGATGATGCGCCGTCGTCTTCTCTCAGCCCATTTCTATGGCAGTGACTAC
dp5	5:197136:1971528 -		CGCCATCCAATGCCACAAACGCATGTTCGACGTCTCCAAGTCGTGATAAGTAAGTCG-AC--GGCGCATTCCCTCAGAAA-----C----------AT-----ATTTTTGAATTATTTCTCACGCTTTGTGCATCGCGTGAAGATGATGCGCCGTCGGCCTTCTCGAGCCCATGTTCTATGGCAGCAGCTAC
droPer2	scaffold_21244471-2144638 -		CGCCATCCAATGCCACAAACGCATGTTCGACGTCTCCAAGTCGTGATAAGTAAGTCG-AC--GGCGCATTCCCTCAGAAA-----C----------AT-----ATTTTTGAATTATTTCTCACGCTTTGTGCATCGCGTGAAGATGATGCGCCGTCGGCCTTCTCGAGCCCATGTTCTATGGCAGCAGCTAC
droAna3	scaffold_13266:12153759-12153930 -		G-CCTACCAGCTGCCGTGACGGCATGTTCGACGTCTCGAAGTCGTGATAAGTCAGTCG-TCCAGCGTATGAGGTTTTTCTTTGCTCAGTTA---------TTACGG-TACG-----------C--CG-TTGTGT-----------TCGCTGCGCAGAGCGCGATGCGCGCGTCGGCCTTCTCGATGCCGCATTTCTAGGCAGCAGCTAC
droBip1	scaffold_1800000396547:326185-326343 +		CCTCTACCAGCTGCCAGACGGCATGTTCGACGTCTCCAAGTCGTGATAAGTCAGTCG-CCCAAGATT--TCACGTTTTCCT-------C-------C---GTA-----C-T-G-----G---ACGGCG--TTC----------------------------AATCCGCTTGAGAGCGATGCGCGCGTCGGCCTTCTCGATGCCGCATTTCTAGGCAGCAGCTAC
droKik1	scaffold_1800000302366:1003797-1003956 -		G-CGTAAAGCTGCCAGACGGCATGTTCGACGTCTCCAAGTCGTGATAAGTAGTCG-TCC----------------------------------CG-GATA--------TC-CA-------CGTAGCGATA---TATA--A-C-----CTGA---C-CGC-GTC----------------------------ATCGCGAGAGCGATGCGCGCGTCGGCCTTCTCGATGCCGCATTCTAGGCGCAGCTAC
droPic1	scaffold_1800000453858:635057-635224 +		CGCCATCCAATGCCGCCGGCATGTTCGACGTCTCCAAGTCGTGATAAGTCCTAT-GA--GCACGC-----C-----C----------CTATCCCTCGATAGCCGGCT-----A-A-----CC-GAGTGAGT-T-----TGT--CTCCCCAAGAGCGCGCGTCGGCCTTCTCGATGCCGCATTCTAGGCGGCAGCGCTAC
droEle1	scaffold_8000004491107:322888-323069 +		CGCCATCCAATGCCGCCGGCATGTTCGACGTCTCCAAGTCGTGATAAGTAGTCGA-TC----------------------------------GTGACTTCGCCG-----C-----C----------TTAACCATCGT--ACGGCAAAGTACATA----------CAAGTAGTAACCC---CACTAATAA----------TGACGTTCCCGAAGCGATGCGCGCGTCGGCCTTCTCGATGCCGCATTCTAGGCGGCAGCGCTAC
droRho1	scaffold_1800000762736:52435-52628 -		CGCCATCCAATGCCGCCACGCATGTTCGACGTCTCCAAGTCGTGATAAGTACTAG-TA----------------------------------GTGGCCTCTCG-----C-----C----------CTAAACATGGCTCATAGGCAAGGGCCTTATTCTAG-T----------AAGTAGTAATC---CCG-A-A--T---C----------TGCGTCGCCGAAGAGCGATGCGCGCGTCGGCCTTCTCGATGCCGCATTCTAGGCGAGCAGCTAC
droBia1	scaffold_1800000317541:5833145-5833309 -		CGCCATCCAATGCCTACGCGGCATGTTCGACGTCTCCAAGTCGTGATAAGTAGTCGCT-CTT-GGTT----------------------------------A----------GAA-GTGCCCAAATAG-----CATA----------TGGTAACC---CAG-A-A--T-C----------TGAAATCTCCGAAGAGCGATGCGCGCGTCGGCCTTCTCGATGCCGCATTCTAGGCAGCAGCTAC
droTak1	scaffold_1800000415805:355482-355638 +		CGCCATCCAATGCCACGCGGCATGTTCGACGTCTCCAGTCGTGATAAGTAGTCT-T-----------------------------------AAA-ATC--------CAACA---------A----------TAA-----TATA----------A-AATAATC---CAATAA--T---C----------TGTCAACCCGAAGAGCGATGCGCGCGTCGGCCTTCTCGATGCCGCATTCTAGGCAGCAGCTAC
droEug1	scaffold_8000004094464:1461897-1462091 +		CGCAATTAAGCTGCACGCGGCATGTTCGACGTCTCCAGTCGTGATAAGTAGCTCT-GA--AACCAAACTTTTT----------GT--C----------AGCCAAATAA-----C----------CCACCTTGAATTGGTAGCTCGTTGATGTTGTAACC---CAG-A-A--T-C----------TGCTTTTCCGAAGAGCGATGCGCGCGTCGGCCTTCTCGATGCCGCATTCTAGGCGAGCAGCTAC
dm3	chr2R:20861589-20861754 -		CGGTGTCCAGCTGCCGCGGCATGTTCGACGTCTCCAGTCGTGATAAGTAGCGC-TC----------------------------AGTGCC----------AAGA---------GAC----------GGTTC-TAA-------C----------GTA-----A-A-----TCGA-AGAGCA--TTC----------TA--CCCCAAGAGCGCGCGTCGGCCTTCTCGATGCCCATTCTAGGCAGCAGCTAC
droSim2	2r:21324688-21324855 -	dsi_27640	CGGTGTCCAGCTGCCGCGGCATGTTCGACGTCTCCAGTCGTGATAAGTAGCGC-TC----------------------------AGTGCC----------AAGA---------GAC----------GGTTC-TTA-------C----------GTA-----A-A-----TCGA-AGAGCA--TTC----------TAGCCCCAAGAGCGCGCGTCGGCCTTCTCGATGCCCATTCTAGGCAGCAGCTAC
droSec2	scaffold_23:718535-718702 -		CGTGTCCAGCTGCCGCGGCATGTTCGACGTCTCCAGTCGTGATAAGTAGCGC-TC----------------------------GCTGCC----------AAGA---------GAC----------GGTTC-TTA-------C----------GTA-----A-A-----TCGA-AGAGCA--TTC----------ACCCCAAGAGCGCGCGTCGGCCTTCTCGATGCCCATTCTAGGCAGCAGCTAC
droYak2	2R:20825381-20825543 -		CGCCATCCAATGCCGCCGGCATGTTCGACGTCTCCAGTCGTGATAAGTAGTCGCT-C----------------------A-GCCA----------AACA---------GCA----------CCGCA-GGTTC-TAA-------C----------AGA-A-T-C----------TGCCGCCAAGAAGCGATGCGCGCGTCGGCCTTCTCGATGCCCATTCTAGGCAGCAGCTAC
droEre2	scaffold_4845:2223414-2223575 -		CGCCATCCAATGCCGCCGGCATGTTCGACGTCTCCAGTCGTGATAAGTAGCGC-TC----------------------------GCTGCA----------TAG---------TAACC----------GGAGAC-TA----------A-A-----TC--CAACAC---A----------TGCATCGCCAAGAAGCGATGCGCGCGTCGGCCTTCTCGATGCCCATTCTAGGCAGCAGCTAC

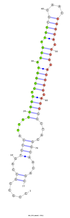
Generated: 09/08/2015 at 07:09 PM

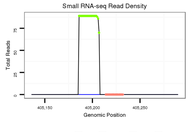
	PASS/FAIL
crit.star	1
crit.loop	1
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.score	0
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

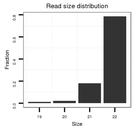
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_154	**scaffold_12928:405186-405240 +**	**candidate**	**Canonical miRNA**	**CDS**	View on UCSC Genome Browser (Cornell Mirror)

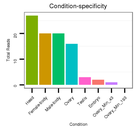
Legend: [illegible] [illegible] [illegible]

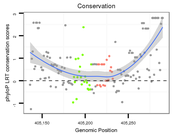
Predicted structure











Show Alternate Fields

FlyBase annotation

CDS [FlyFGCN:CDS-cds]

No Repeatible elements found

number	color
1	scaffold_12875:0:5613-0:5639(-)
2	scaffold_12875:27842:0:27842(+)
3	scaffold_12875:0:5613-0:5639(-)
4	scaffold_12875:0:5613-0:5639(-)
5	dvi_154 scaffold_12928:405186-405232 (+)
6	scaffold_12928:405186-405232 (+)
7	scaffold_12928:0:5613-0:5639(-)
8	scaffold_12928:0:5709-0:5726(-)
9	scaffold_12928:0:5709-0:5726(-)
10	scaffold_12963:0:5613-0:5613(?)
11	scaffold_12970:0:5613-0:5613(?)
12	scaffold_12970:0:5613-0:5613(?)
13	scaffold_12970:0:5613-0:5613(?)
14	scaffold_12970:99:7806-99:7824
15	scaffold_13012:0:5613-0:5613(?)
16	scaffold_13017:0:5613-0:5613(?)
17	scaffold_13017:0:5613-0:5613(?)

Sense Strand Reads

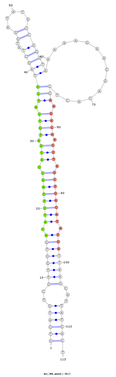
hide 3p reads show mid-mismatch reads

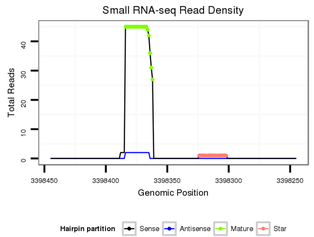
| | | |

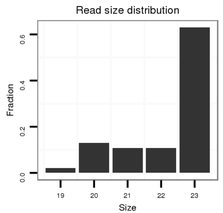
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_286	**scaffold_12928:3398295-3398395 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

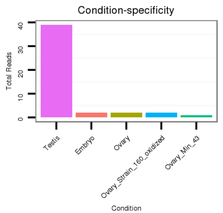
Legend: mature star mismatch in alignment mismatch in read

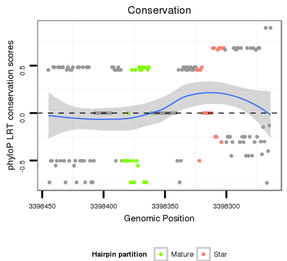
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CACCACAAGTTGCTCATTGATGAAGTCAGCGATGTAAGAAGCTTACGTGATGTCCTTGGTGACATGTCAGCGATGATGTCATCGTAGCTATGGATATGCCGGCTAAAAGAACGACACTCGAAGACAACGTAGCTGACATATCATTAAGCATTATCACTGCTTACTTAAGTACACCTAAACCAATCCATGCTTATTTGCTT	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060681 Argx9_testes_total	SRR060679 140x9_testes_total	SRR060678 9x140_testes_total	SRR2096058 Ovary_Min_98	SRR2096060 Ovary_Min_193	SRR060677 Argx9_ovaries_total	SRR060680 Ä 9xArg_testes_total	SRR2096014 Ovary_Strain_160_oxidized	SRR060659 Argentina_testes_total	SRR060686 Argx9_0-2h_embryos_total	SRR2096055 Ovary_Min_43	SRR060654 160x9_ovaries_total	SRR060656 9x160_ovaries_total	SRR060670 9_testes_total	SRR060674 9x140_ovaries_total	SRR1106730 embryo_16-30h	SRR2096038 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096056 Ovary_Min_46	SRR2096057 Ovary_Min_50	V116 male body	SRR060663 160_0-2h_embryos_total	V053 female head	M047 female body	SRR2096080 embryo_0-2h from 15to16 day old nondygenic mothers
ACATGTCAGCGATGATGTCATCG	23	0	1	27.00	27	11	7	3	0	0	0	0	0	2	1	1	1	0	0	1	0	0	0	0	0	0	0	0	0
ACATGTCAGCGATGTGTCA	20	0	1	6.00	6	3	2	0	0	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0
ACATGTCAGCGATGTGTCAT	21	0	1	5.00	5	1	1	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ACATGTCAGCGATGATGTCATC	22	0	1	4.00	4	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ACATGTCAGCGATGTGTCATCG	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ACATGTCAGCGATGTGTC	19	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GGTGACATGTCAGCGATGATGT	22	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GGTGACATGTCAGCGATGATGTC	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAGACAACGTAGCTGACATATCA	23	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

GTGGTGTTCAACGAGTAACTACTTCAGTCGCTACATTCTTCGAATGCACTACAGGAACCACTGTACAGTCGCTACTACAGTAGCATCGATACCTATACGGCCGATTTTTCTTGCTGTGAGCTTCTGTTGCATCGACTGTATAGTAATTCGTAATAGTGACGAATGAATTCATGTGGATTTGGTTAGGTACGAATAAACGAA	Read size	# Mismatch	Hit Count	Total Norm	Total	M028 head	SRR2096013 Ovary_Strain_9_oxidized	SRR060666 160_males_carcasses_total	V053 head	M047 female body	SRR060658 140_ovaries_total	V116 male body	SRR060668 160x9_males_carcasses_total	SRR2096014 Ovary_Strain_160_oxidized	SRR060681 Argx9_testes_total	SRR060687 9_0-2h_embryos_total
TGTACAGTCGCTACTACAGT	20	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0
GTACAGTCGCTACTACAGT	20	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
TGTTGCATCGACTGTATAGTAA	23	1	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0
GTACAGTCGCTACTACAGT	20	1	2	0.50	1	1	0	0	0	0	0	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12928:3398253-3398434 -	dvi_286	GCTCA----------TTGATGAAGTCAGCGATGTAAGAAGCTT--ACGTGATGTCCTTGGTGACATGTCAGCGATGATGTCATCGTAGCTATGGATATGCCGGCTAAAAGAACGACACTCGAAGACAACGTAGCTGACATATCATTAAGCATTATCACTGCTTACTTAAGTACACCTAAACCAATCCATGCTT
droMoj3	scaffold_6308:3305292-3305435 -		ACGTATGCCAAAAGTTTTATTATTGTTAAAATAAAATATAAATAAA-AAATTATAGCATAGCGAAAGCAAGCAAATCGTTTGA----------ATGCTAGCAGCAG-AG-GG-AA-AGC-G-G-A----------G-GGAAGACAACGTAGCTGA----------CATGCTGTT
droWil2	scaffold_13000:4047621-5586013 -		----A----------GA-GAATAAT-TTCAAATTACTTGAAGCAA-G-G-G-GATCCATGCTGT

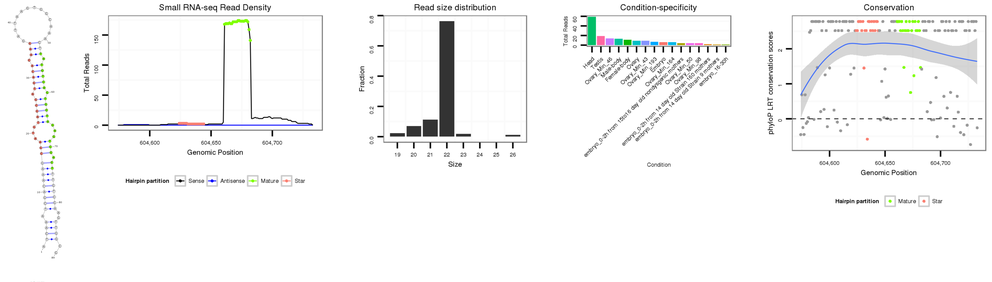
Generated: 08/05/2015 at 08:28 PM

score	160.3
crit.exp	0
crit.loop	0
crit.mor	0
crit.loc	0
crit.pairing	1
crit.top3	1
crit.loop3	1
crit.5bulge	1
crit.5stem	1
rescue.total	1
rescue.dominant	1
rescue.recessive	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_381	**scaffold_13052:604624-604683 +**	**confident-exception**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: sense 5p mismatch in alignment mismatch in loop

Predicted structure



Show Alternate Folds

Flybase annotation

CDS [Dvir(GI12217-cds);:un3 (un3_plus_7397); intron [Dvir(GI12217-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAAAAACACGTACAAATTCCACGCAAAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATCTT	Read #	Hit	Total	M028 head	V053 head	SRR2096056 male	SRR2096055 male	V116 male	SRR2096040 male	SRR060672 9x160_females_carcasses_total	M027 male	SRR060679 140x9_testes_total	M047 female	SRR2096059 body	SRR060681 Arge9_testes_total	SRR2096057 Ovary_Min_50	M061 embryo	SRR060674 9x140_ovaries_total	SRR060676 9xArq_ovaries_total	SRR2096014 Ovary_Strain_160_oxidized	SRR2096058 Ovary_Min_98	V047 embryo	SRR060654 160x9_ovaries_total	SRR060655 9x160_testes_total	SRR060656 9x160_ovaries_total	SRR060675 140x9_ovaries_total	SRR060677 Arge9_ovaries_total	SRR060678 9x140_testes_total	SRR2096080 embryo_0-2h from 15to16 day old mothers	SRR2096081 embryo_0-2h from 15to16 day old nondygenic mothers	SRR060670 nondygenic 9_testes_total	SRR060689 160x9_testes_total	SRR2096013 Ovary_Strain_9_oxidized	SRR060663 160_0-2h_embryos_total	SRR060684 2h_embryos_total	SRR060686 Arge9_0-2h_embryos_total	SRR2096024 embryo_14-30h	SRR2096050 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096061 embryo_0-2h from 14 day old Strain 160 mothers	SRR060665 9_females_carcasses_total
**********	size	Mismatch	Count	Norm	Total							body																											
.....TATGTCAGTGCTAGAGTCGACT.....	22	0	1	129.00	129	32	12	10	9	5	4	6		3	4	1	3	5	4	1	1	0	0	4	2	3	2	1	0	0	3	3	1	1	1	0	0	0	1	1	1	1	0
.....TATGTCAGTGCTAGAGTCGAC.....	21	0	1	18.00	18	4	0	4	0	0	0	0		1	1	0	2	0	0	0	1	0	0	0	1	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0
.....TATGTCAGTGCTAGAGTCGA.....	20	0	1	12.00	12	5	4	0	0	2	0	0		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATGTCAGTGCTAGAGTCGA[G].....	22	1	1	5.00	5	3	0	0	0	0	0	0		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTATGTCAGTGCTAGAGTCGACT.....	23	0	1	3.00	3	0	0	0	0	1	1	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATGTCAGTGCTAGAGTCG.....	19	0	1	3.00	3	1	1	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
.....AAGGTAGCCTCATTGGCTCGATCTT.	25	0	1	2.00	2	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTGTCGAAGTTGGCGCGTTACGATG.....	25	0	1	2.00	2	0	0	0	2	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGCTAGAGTCGACTTTGT.....	19	0	1	2.00	2	0	0	0	0	2	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGGCGCGTTACGATGAAGGTAGCCTCA.....	27	0	1	2.00	2	0	0	0	0	0	0	0		0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TAGAGTCGACTTTGTCGAAGTTGGCGC.....	27	0	1	1.00	1	0	0	0	0	0	0	0		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TAGAGTCGACTTTGTCGAAGTTGGCG.....	26	0	1	1.00	1	0	0	0	0	0	0	0		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCAGTCGACTTTGTCGAAG.....	27	0	1	1.00	1	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CGGAGTTGGCGCGTTACGATGAAGGT.....	26	0	1	1.00	1	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATGTCAGTGCTAGAGTCGA.....	19	0	1	1.00	1	0	0	0	0	0	0	0		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CGAATGTAGCGATGACACAAG.....	21	0	1	1.00	1	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TAAGTGGCAAACTTATGTCAGTGCTA.....	24	0	1	1.00	1	0	0	0	0	0	0	0		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATGTCAGTGCTAGAGTCGA[G].....	24	1	1	1.00	1	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTCGAAGTTGGCGCGTTACGATG.....	23	0	1	1.00	1	0	0	0	0	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ACAAGGATTAATGTGCAAACTTATGT.....	26	0	1	1.00	1	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGCTAGAGTCGACTTTGTC.....	20	0	1	1.00	1	0	0	0	1	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATGTCAGTGCTAGAGTCGA[G].....	22	1	1	1.00	1	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCGACAAGCGAATGTAGCGATGAC.....	25	0	1	1.00	1	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTGTCGAAGTTGGCGCG.....	20	0	1	1.00	1	0	0	1	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATGTCAGTGCTAGAGTCGA[G].....	22	1	1	1.00	1	0	0	0	0	0	0	0		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GAAGTTGGCGCGTTACGATG.....	23	0	1	1.00	1	0	0	0	0	0	0	0		0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTGTCGAAGTTGGCGCG.....	20	0	1	1.00	1	0	0	1	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATGTCAGTGCTAGAGTCGA[G].....	22	1	1	1.00	1	0	0	0	0	0	0	0		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATC.....	29	0	1	1.00	1	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TACGATGAAGGTAGCCTCATTGGCTCGATCTT.	29	0	1	1.00	1	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GCGTTACGATGAAGGTAGC.....	19	0	1	1.00	1	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CGAGTTTGTCGAAGTTGGCGC.....	21	0	1	1.00	1	0	0	0	0	0	0	0		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCGAAGTTGGCGCGTTACGATGAAGGT.....	27	0	1	1.00	1	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATCAAATCGACAAAGCGAATGT.....	22	0	1	1.00	1	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATGTCAGTGCTAGAGTCG.....	20	1	1	1.00	1	1	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

TTTTTTTGTCATGTTTAAGGTGCGTTTTAGCTACTAGTTTAGCTGTTTGCTTACATCGCTACTGTGTTCCTAATTCACCGTTTGATCACGTCACGATCTCAGCTGAACACGCTTCAACCGCGCAATGCTACTTCCATCGGAGTAACCGAGCTAAGAA				M027	SRR060664		V053	V116	SRR2096040	SRR060666	SRR060669	SRR060667
**********	Read # size	Hit Mismatch	Total Count	Total Norm	male body	9_males_carcasses_total	head	male body	Ovary_Min_193	160_males_carcasses_total	140x9_females_carcasses_total	160_females_carcasses_total
.....TTGTCATGTTTAAGGTGCGTT.....	21	0	1	1.00	1	0	1	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species Coordinate	ID	Alignment
droYer1 scaffold_14552:604536-604592 +	dvi_381	AAAAAACAGTACAAATTCCACGCAAAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATCTT
droMo33 scaffold_6438:166636-166695 -		----------AAAAACAGTACAAATTCCACGCAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAGGGTAGCCTCATTGGCTCGATCTT
droGri2 scaffold_14522:273139-273249 -		----------AAAAACAGTACAAATTCCACGCAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATCTT
droWil2 Chr2_LSU00000049835:553332-553442 +		ATTTTTTTTTTTTTCAATACAAATTCCACGCAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAGGGTAGCCTCATTGGCTCGATCTT
droFer2 scaffold_5148518:683238.0 -		----------AAAAACAGTACAAATTCCACGCAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATCTT
droKan3 scaffold_13689:435681 -		----------AAAAACAGTACAAATTCCACGCAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATCTT
droBip2 scaffold_8500:351458:3183-3241 +		----------AAAAACAGTACAAATTCCACGCAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATCTT
droFIX1 scaffold_8500:300954:8351-8452 +		----------AAAAACAGTACAAATTCCACGCAAAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATCTT
droFlc1 scaffold_5343:16548-16646 +		----------AAACAGTACAAATTCCACGCAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATCTT
droIle1 scaffold_8500:490694:17783-17836 +		----------AAAAACAGTACAAATTCCACGCAAAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATCTT
droRho1 scaffold_8500:37367:52245-52318 +		A----------AAAAACAGTACAAATTCCACGCAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATCTT
droSil4 scaffold_8500:351512:8768-8921 +		A----------AAAAACAGTACAAATTCCACGCAAAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATCTT
droTak3 scaffold_8500:416631:13022-13155 -		A----------AAAAACAGTACAAATTCCACGCAAAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATCTT
droEug1 scaffold_8500:489841:8183-8241 +		----------AAAAACAGTACAAATTCCACGCAAAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATCTT
Sh3 chr1:2268732:2268924 +		----------AAAAACAGTACAAATTCCACGCAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATCTT
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droYak3 Chr3:1285398:1322993.0 -		----------AAAAACAGTACAAATTCCACGCAAAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATCTT
droZer2 scaffold_8500:416631:8683-8741 +		----------AAAAACAGTACAAATTCCACGCAAATCGATGATCAAATCGACAACAGAAGTTAAGTGGCAAACTTATGTCAGTGCTAGAGTCGACTTTGTCGAAGTTGGCGCGTTACGATGAAGGTAGCCTCATTGGCTCGATCTT

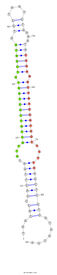
Generated: 09/08/2015 at 08:29 PM

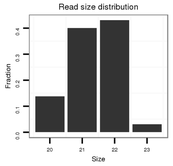
	PASS/FAIL
critLeaf	0
critBest	0
critAnnot	0
critTaxF	0
critTaxG	0
critParsim	0
critSynt	0
critTopol	0
critMaxA	0
critLikelihoodA	0
critLikelihoodB	0
rescueMaxA	0
rescueLikelihoodA	0
rescueLikelihoodB	0
rescueKnown	0
rescueConfident	0
rescueCandidate	0

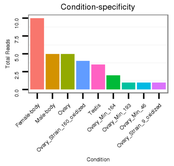
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_429	**scaffold_13049:22743190-22743250 +**	**confident-exception**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (Comp8 Mmu+)]

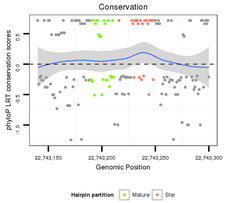
Legend: sense siRNA mismatch to alignment mismatch to miR

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ACACTTTTTATTGTCATAATACAAAAATTTTGTCATACACACGGAGTTAATATTACATGGTAGTGCACTGAATTAATCTAAAATATCGAAACTATCGATAGTTTTTTAGCTCGTGATAATGATCAACGTTTCGTGATCGATTATCACACTTTCACTT	Read #	Hit	Total	Mismatch Count	Total Norm	M047 Female body	V116 Male body	SRR2096056 male	SRR2096040 Ovary_Min_46	SRR2096059 Ovary_Min_193	SRR060678 Ovary_Min_164	SRR060656 9x140_testes_total	SRR060677 9x160_ovaries_total	V053 Argx9_ovaries_total	SRR060655 head	SRR060673 9x160_testes_total	SRR060680 9_ovaries_total	SRR2096014 9xArg_testes_total	SRR060672 Ovary_Strain_160_oxidised	SRR060679 9x160_females_carcasesex_total	SRR060689 140x9_testes_total	SRR060659 160x9_testes_total	SRR060674 Argentina_testes_total	SRR2096057 9x160_ovaries_total	M027 Ovary_Min_50	SRR060670 male_9_testes_total	SRR060676 body	SRR060681 9xArg_ovaries_total	SRR060683 Argx9_testes_total	SRR2096013 160_testes_total	SRR2096055 Ovary_Strain_3_oxidised	SRR060654 Ovary_Min_43	SRR060682 160x9_ovaries_total	SRR060684 9x140_0-2h_embryos_total	SRR060686 140x9_0-2h_embryos_total	SRR2096038 Argx9_0-2h_embryos_total	SRR2096058 Strain 9 mothers	SRR2096072 embryo_0-2h from 15to16 day old Ovary_Min_50 mothers	SRR060668 olt Argenic mothers	160x9_males_carcasesex_total	VD47 embryo	GSM1528803 follicle cells	SRR1106729 mixed whole adult body
**********	size	Mismatch	Count	Total	Norm	body	male	4	Ovary_Min_46	Ovary_Min_193	Ovary_Min_164	9x140_testes_total	9x160_ovaries_total	Argx9_ovaries_total	head	9x160_testes_total	9_ovaries_total	9xArg_testes_total	Ovary_Strain_160_oxidised	9x160_females_carcasesex_total	140x9_testes_total	160x9_testes_total	Argentina_testes_total	9x160_ovaries_total	Ovary_Min_50	male_9_testes_total	body	9xArg_ovaries_total	Argx9_testes_total	160_testes_total	Ovary_Strain_3_oxidised	Ovary_Min_43	160x9_ovaries_total	9x140_0-2h_embryos_total	140x9_0-2h_embryos_total	Argx9_0-2h_embryos_total	Strain 9 mothers	Ovary_Min_50 mothers	Argenic mothers	160x9_males_carcasesex_total	embryo	follicle cells	mixed whole adult body
.....TATTACTATCGGTGATATCGAT.....	22	0	1	13.00	13	5	4	8	0	3	1	3	2	3	2	2	0	1	0	1	4	2	1	0	3	0	1	2	2	1	0	0	0	1	0	0	1	1	0	0	0	0	0	0
.....TATTACTATCGGTGATATCGAT.....	21	0	1	16.00	16	2	5	0	0	1	0	0	0	0	1	1	0	1	1	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
.....TATTACTATCGGTGATATCGATA.....	23	0	1	14.00	14	2	2	0	0	2	0	0	0	0	3	1	0	0	1	1	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATTACTATCGGTGATATCGATA.....	22	0	1	13.00	13	7	2	0	0	1	0	0	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
.....ATTACTATCGGTGATATCGAT.....	21	0	1	12.00	12	0	3	1	1	1	1	2	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATTACTATCGGTGATATCGL.....	20	0	1	9.00	9	2	0	0	0	0	0	0	0	0	1	0	0	0	0	2	0	0	2	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATTACTATCGGTGATATCGA.....	20	0	1	4.00	4	1	0	0	0	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATATTACTATCGGTGATATCGAT.....	24	1	1	2.00	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATTACTATCGGTGATATCGAT.....	23	1	1	2.00	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
.....TCGAAACTATCGATAGTTTTT.....	22	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATTACTATCGGTGATATCGA.....	20	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCGAAACTATCGATAGTTTTT.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATTACTATCGGTGATATCGATA.....	23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATTACTATCGGTGATATCGA.....	22	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCGAAACTATCGATAGTTTTT.....	20	0	2	0.50	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

TGTGAAAATAACAGTATTATGTCTTTTAAACAGTATTGTGGCTCATTAATATAATGATGATGCCATGCATCTATCACATTAGATTTTATAGCTTGATAGCTATCAAAAAT	Read #	Hit	Total	Mismatch Count	Total Norm	SRR060679 140x9_testes_total	SRR060681 Argx9_testes_total	SRR060659 Argentina_testes_total	SRR060655 9x160_testes_total	M047 female body	SRR060660 Argentina_ovaries_total	SRR2096059 Ovary_Min_164	GSM1528803 follicle cells	SRR060686 Argx9_0-2h_embryos_total
**********	size	Mismatch	Count	Total	Norm									
.....AGCTTTGATAGCTATCAAAA.....	20	0	2	1.50	3	1	1	0	0	0	1	0	0	0
.....TGATAGCCATCATAGCTAT.....	19	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TAGCTTTGATAGCTATCAAAAATCG.....	26	0	1	1.00	1	0	0	1	0	0	0	0	0	0
.....TGATAGCCATCATAGCTATTA.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....ATAGCTTTGATAGCTATCAAAA.....	22	0	2	0.50	1	0	0	0	1	0	0	0	0	0
.....AGCTTTGATAGCTATCAA.....	18	0	4	0.25	1	0	0	0	1	0	0	0	0	0

Show Alignment With Reads

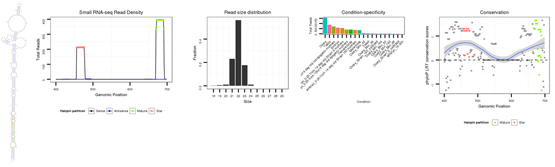
Re-alignment of predicted orthologs

Species	Coordinate	ID	Alignment
dvi(+)	scaffold_13049:22743140-22743240:+	dvi_429	ACACTTTTTATTGTCATAATA----------CAAAAATTTTGTCATACACACGGAGTTAATATTACATGGTAGTGCACTGAATTAATCTAAAATATCGAAACTATCGATAGTTTTTTAGCTCGTGATAATG+ATTCAACGTTTCGTG----ATCGATTATATCACTTTCACTT
drosMel(3)	scaffold_6540:17463174-17463234:-	dmel_3191	G--AC-TTTATT-G-TGGA-G-TAG--------AGC-G-TGCA-G-CAA-G-TA-G-CG-TATCG-AT-TCGATCAG-G-G-G-AAA-G-GCAAATCGGATAGCTCT-G-AGCTCGTGA-G-TAA-G-CGA-GATAGCTCT-G-TTCACTT
drosSim(12)	scaffold_15110:2785573-2785633:-		-G-TTTGAC-TG-------TACTTAAGTTAG-AAAAAGGC-G-TAAG-G-G-TTTAAT-G-G-G-TACG-GATGCGAGCTCGT-TCTCATCGGAGCTCGTCATCGGAGCTCGTCATCGGAGCTCG

ID	Coordinate	Confidence	Class	Genome Locus
dvi_23834	**scaffold_794:450-692 +**	**Candidate**	**Unknown**	**intergenic**

Legend: DICER 21 PAIRED 21 PAIRED 22

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
SINE_2/3_Marco/SQ	Unknown	SINE	+

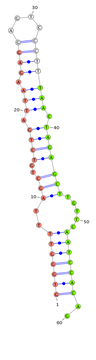
Genome

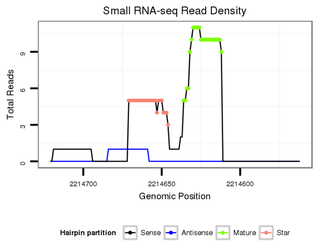
Chr	Chr Size
1	dm_23834_scaffold_794:0-9,491
2	scaffold_1000:1,010,012-1,010,056
3	scaffold_1000:1,010,012-1,010,056
4	scaffold_794:450-692
5	scaffold_1000:1,010,012-1,010,056
6	scaffold_1000:1,010,012-1,010,056
7	scaffold_1000:1,010,012-1,010,056
8	scaffold_1000:1,010,012-1,010,056
9	scaffold_1000:1,010,012-1,010,056
10	scaffold_1000:1,010,012-1,010,056
11	scaffold_1000:1,010,012-1,010,056
12	scaffold_1000:1,010,012-1,010,056

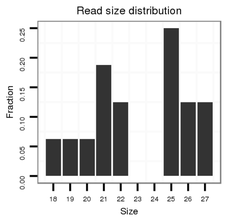
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_15239	**scaffold_13047:2214612-2214671 -**	**candidate**	**Mirtron**	**antisense_to_intron**	[View on UCSC Genome Browser [Cornell Mirror]]

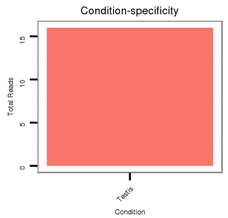
Legend: mature star mismatch in alignment mismatch in read

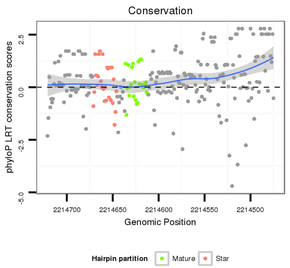
Predicted structure











Show Alternate Folds

Flybase annotation

Antisense to intron [DvirGI23748-in]; intron [DvirGI23477-in]; CDS [DvirGI23477-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TATGCCCAAGTGGATAAATTCGCGTTTGTTCACATCCGGCGACTGTGAAAGTGGGTTTTAGCTGTCTGATTAAGAGCGAGTCCCTTTAACTAGAGCTTGTTCAATCCACAGAAACCAGTGAGGAATGCTGTTGCGAGCGACCCGAACACTTGCAGCCGAAT						SRR060681	SRR060659	SRR060678	SRR060679	SRR060655	SRR060680	SRR060683	SRR060689	SRR060671	SRR2096058	GSM1528803	M047	SRR060684	M027	SRR060667	SRR2096081	SRR060686	M061	SRR2096059	V053	V116
**********	Read # size	Mismatch	Hit Count	Total Norm	Total	Argx9_testes_total	Argentina_testes_total	9x140_testes_total	140x9_testes_total	9x160_testes_total	9 Argx9_testes_total	160_testes_total	160x9_testes_total	9x160_males_carcasses_total	Ovary_Min_98	follicle cells	female body	140x9_0-2h_embryos_total	male body	160_females_carcasses_total	embryo_0-2h from 15to16 day old nondysgenic mothers	Argx9_0-2h_embryos_total	embryo Ovary_Min_164	head	male body
.....	25	0	1	3.00	3	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	21	0	1	3.00	3	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	26	0	1	2.00	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	22	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	25	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	27	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
.....	25	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	22	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	19	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

ATACGGGTTCACCTATTTAAGCGCAAACAAGTGTAGGCCGCTGACACTTTCACCCAAAATCGACAGACTAATTCTCCTCAGGGAATTGATCTCGAACAAGTTAGGTGTCTTTGGTCACTCCTTACGACAACGCTCGCTGGGCTTGTGAACGTCGGCTTA						M047	M061	V053	M028	SRR060669	SRR060672	SRR060684	SRR060686	SRR060658	SRR2096014	SRR060665	V047	V116	GSM1528803	SRR2096058	SRR060663	SRR060666	SRR060667	SRR060668	SRR060682	SRR060687	SRR2096055	M027	SRR060678	SRR2096026
**********	Read # size	Mismatch	Hit Count	Total Norm	Total	female body	embryo	head	head	160x9_females_carcasses_total	9x160_females_carcasses_total	140x9_0-2h_embryos_total	Argx9_0-2h_embryos_total	140_ovaries_total	Ovary_Strain_160_oxidized	9_females_carcasses_total	embryo	follicle body	cells	Ovary_Min_98	160_0-2h_embryos_total	160_males_carcasses_total	160_females_carcasses_total	160x9_males_carcasses_total	9x140_0-2h_embryos_total	9_0-2h_embryos_total	Ovary_Min_43	male	9x140_testes_total	embryo_0-2h from 14 day old Strain 9 mothers
.....CCGCTGACACTTTCACCCAAAATCGA.....	26	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Show Alignment With Reads

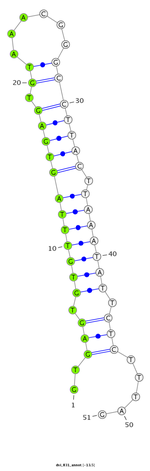
Re-alignment of all predicted orthologs

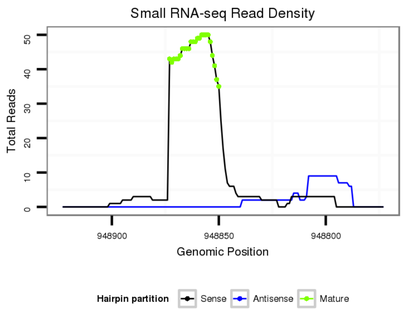
Species	Coordinate	ID	Alignment
droVir3	scaffold_13047:2214481-2214727 -	dvi_15239	AGTCTCTATGCCCAAGTGGATAAATTCGCGTTTGTTCACATCCGGCGACTTTGAAAGTGGGTT--------TTAGCTGTC-----T-GATTAA----------GAGGAGCCCCTTAACTAGAGCTTG-TTCAA----------CCACAGAAACCAGTGAGGAATGCTGTTGCGAGCGACCCGAACACTTGCAGCCG---AATTGTGAATCGATTGGGATTCGGTGCATCCACCGGGTCAACCCTATAAGCCCGTGATACACACTACTGGTATCCAGATCCG
droMoj3	scaffold_6540:22692106-22692329 +		AGTAAAATGCCCGAGTGGATGAATTCGCGTTTGTTGTCTC--TTCG---CGAAGTGCGAT----GTGCG--------------C-CAGTTCC----------TGGGATCTCGTTTAAGCGAGCTTG-CTTCGA----------TGCACAGATGTAGGAGGATGCTGTTGGAGGAG----------G---GG---CCGTGTGATCGATTGGGATTCTTACGATCCACCGGTCGCCTATGAGCCCGCGTGATCACACTACTGGTATCCGATCCG
droGri12	scaffold_14926:9042675-9042922 -		GA-----AACCCAAGTGGATGAATTCGCGTTTGTTCATCGCGGACCGAAAGGTAAAAAGGTTTGCGGCTTGCGGG-C-AGCTA--------AGGCTGCGCAGTGGTTTTTCTTCAAAA----------TGCACAGATGCAGGAGTATGCGAATGAGCGACGCTGTGTTGCAGCCG---AATAGGAAATCATTGGGATGAACTGCCTCCACCGGTCGCCTATGAGCCCGCGTGATCACACTACTGGTATCCGATCCG
droWil2	scf2_1100000004902:6927402-6927641 -		----------
dp5	12253412-2753484 -		G----------G-----G-----G-----

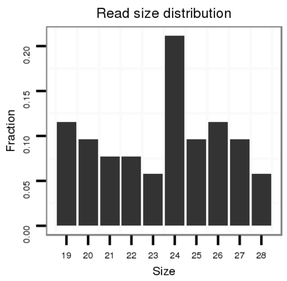
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_831	**scaffold_10324:948823-948873 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

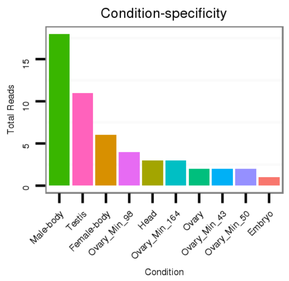
Legend: mature star mismatch in alignment mismatch in read

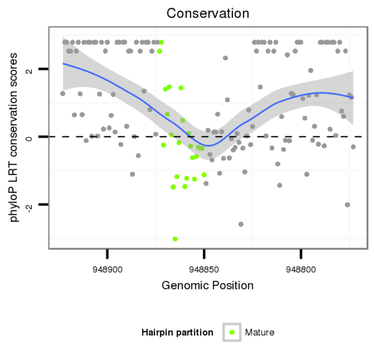
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dvir\GJ14969-in]; CDS [Dvir\GJ14969-cds]; CDS [Dvir\GJ14969-cds]; utr3 [utr3_plus_2491]; utr3 [utr3_plus_2492]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CAAGGAGCAGCTGAAGAAGCTGCAAAAGAAATACGGCTTAGAGAATGAAAGTGAGTGTGTTTAGTGAGTGTAAACGGGCCTTACTTAAATATTCTCTTTAGAATTCGTGGAGGTGAGCGTCAATCCGAATCCAAATTATAATGATCGCAGT	Read size	# Mismatch	Hit Count	Total Norm	Total	V116 male body	SRR2096055 Ovary_Min_43	M047 female body	SRR060678 9x140_testes_total	SRR2096058 Ovary_Min_98	SRR2096059 Ovary_Min_164	M028 head	SRR060679 140x9_testes_total	SRR060680 Ä 9xArg_testes_total	SRR060660 Argentina_ovaries_total	SRR060681 Argx9_testes_total	SRR2096057 Ovary_Min_50	M061 embryo	SRR060670 9_testes_total	SRR060675 140x9_ovaries_total	SRR060677 Argx9_ovaries_total	V047 embryo	SRR2096026 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096072 embryo_0-2h from 15to16 day old dysgenic mothers	SRR2096080 embryo_0-2h from 15to16 day old nondysgenic mothers	M027 male body
..(((.(((((((((((.(((.....)))))))).))))))).))).....GTGAGTGTGTTTAGTGAGTGTAAA	24	0	1	11.00	11	3	0	0	2	2	0	1	0	0	0	1	2	0	0	0	0	0	0	0	0	0
GTGAGTGTGTTTAGTGAGTGTAAACG	26	0	1	6.00	6	2	0	0	0	0	0	0	1	1	0	0	0	0	1	1	0	0	0	0	0	0
GTGAGTGTGTTTAGTGAGTGTAAAC	25	0	1	5.00	5	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
GTGAGTGTGTTTAGTGAGTGTA	22	0	1	4.00	4	2	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GTGAGTGTGTTTAGTGAGTG	20	0	1	4.00	4	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GTGAGTGTGTTTAGTGAGTGTAAACGG	27	0	1	4.00	4	1	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
GTGAGTGTGTTTAGTGAGTGTAA	23	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GTGAGTGTGTTTAGTGAGTGT	21	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TTAGTGAGTGTAAACGGGCCT	21	0	1	2.00	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GTGTTTAGTGAGTGTAAAC	19	0	1	2.00	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TGGAGGTGAGCGTCAATCCGA	21	0	1	2.00	2	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
GTGAGTGTGTTTAGTGAGT	19	0	1	2.00	2	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TACGGCTTAGAGAATGAAAAA	21	2	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GAGTGTGTTTAGTGAGTGT	19	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
CAAAAGAAATACGGCTTAGA	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AAATACGGCTTAGAGAATGAAA	22	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GAGTGTAAACGGGCCTTACTTAAATATT	28	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CGGGCCTTACTTAAATATTCTCTTTAG	27	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ACGGGCCTTACTTAAATATTCTCTTTAG	28	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CGGCTTAGAGAATGAAAG	18	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TGTGTTTAGTGAGTGTAAAC	20	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GTGAGTGTGTTTAGTGAGTGTAAACGGG	28	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CGTGGAGGTGAGCGTCAATCCGA	23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
GTGAGTGTAAACGGGCCTT	19	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

GTTCCTCGTCGACTTCTTCGACGTTTTCTTTATGCCGAATCTCTTACTTTCACTCACACAAATCACTCACATTTGCCCGGAATGAATTTATAAGAGAAATCTTAAGCACCTCCACTCGCAGTTAGGCTTAGGTTTAATATTACTAGCGTCA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR2096014 Ovary_Strain_160_oxidized	SRR060658 140_ovaries_total	SRR2096060 Ovary_Min_193	SRR060656 9x160_ovaries_total	SRR2096056 Ovary_Min_46	SRR060668 160x9_males_carcasses_total	SRR060675 140x9_ovaries_total	SRR060679 140x9_testes_total	SRR2096055 Ovary_Min_43	SRR2096058 Ovary_Min_98	SRR060666 160_males_carcasses_total
..(((.(((((((((((.(((.....)))))))).))))))).))).....TCGCAGTTAGGCTTAGGTTTA	21	0	1	6.00	6	0	1	3	1	0	0	0	1	0	0	0
AATTTATAAGAGAAATCTTAAGCACCT	27	0	1	2.00	2	0	0	0	0	1	0	0	0	0	1	0
CCTCCACTCGCAGTTAGGCTT	21	0	1	2.00	2	0	2	0	0	0	0	0	0	0	0	0
CTCGCAGTTAGGCTTAGGTT	20	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_10324:948773-948923 -	dvi_831	CAAGGAGCAGCTGAAGAAGCTGCAAAAGAAATACGGCTTAGAGAATGAAAGTGAGTGTGTTTAGT---------GAGTGTAA----------ACGGGCC----------T----------TACTTAAAT----AT---TCTCTTTAGAATTCGTGGAGGTGAGCGTCAATCCGA-----AT---CCAAATTATAATGATCGCAGT
droMoj3	scaffold_6496:2821490-2821658 -		CAAGGAGCAGCTGAAGAAGCTGCAAAAGAAGTACGGCTTGGAGAATGAAAGTGAGTTCGT---GGGTGT---------A-----TACAT-------TGATGCGCA---------AGGATAATGATG--------TA-------T---TTATT--------ATTATTAATATTATTGAGAATTGTGGAGGAGGAGCGCAATCCGA-----AT---CCAAATTAGAATGATCGCAGT
droGri2	scaffold_15245:8628407-8628568 -		CAAGGAGCAGCTGAAGAACTGCAAAAGAAATACGGCTTGGAGAATGAAAGTGAGTAAA----AGTTGA--ATGA------C------TTAAG-------CATGAGTTT-------ACTTATCGTTTCTCG-GATTCACTTAGAATTGTGGAGGCTAGCGCGAATGTGA-----AT---CACAGTATAAAGATCGTAGT
droWil2	scaf2_1100000004513:2303058-2303224 +		CAAGGACAACTGAAGAAGCTGCAAAAGAAATAGGCTTGAAAATGAAAGTGTGTACCCTATA--------------GA----GAAAACTTGATCAGGAGTA---TATGAACA-------ACTTT----------T----------GATTT----------T-CTCTCTGTGTAGAATTCGTTGATATCGAGCGCAATGGCCAACAGA--ATTTGAATTATAATGATCGTGCC
dp5	3:466051-466244 +		CAAGGAGCAGCTGAAGAAGCTGCAAAAGAAGTACGGCTTGGAGAATGAGATGAGTAGTA----GC--------CGTCGTCAACGTAACTACTTCGACGTGTGTTTCTTACCAGGAACGCATTTCCTT------TATCCTCTTATCGGTTATAGAATTGTTGAAGCTAGTGGCAATGGACAGCAGA--AACCAAATAGAATGATCGTGCG
droPer2	scaffold_2:652928-653121 +		CAAGGAGCAGCTGAAGAAGCTGCAAAAGAAGTACGGCTTGGAGAATGAGATGAGTAGTA----GC--------CGTCGTCAACGTAACTACTTCGACGTGTGTTTCTTACCAGGAACGCATTTCCTT------TATCCTCTTATCGGTTATAGAATTGTTGAAGCTAGTGGCAATGGACAGCAGA--AACCAAATAGAATGATCGTGCG
droAna3	scaffold_13266:2239129-2239296 -		CAAGGACAGCTGAAGAACTGCAGCGCAAGTAGGCTTGGAGAATGAAAGTGAGTACTATTAA--------------GATATGGGAATTGTAATGGATACTAT------TATC-------ATGTCTCTTTGAAATTGTGGAGTGGCGTTGCCAATGGTCAGTCCA--ACTTGAATTAGAATGACTAGGT
droBip1	scf7180000396759:1283473-1283640 -		CAAGGACAGCTGAAGAACTGCAGCGCAAGTAGGCTTGGAGAATGGAGTGAGTACTATTA--------------GACTTAGAAATTTTAATGAAAACTAA------TATC-------ATGTTTAAA-----TT---AACTTGTAGAATTGTGGAGTGCTGTTGCCAATGGTCAGTCCA--ACTTGAATTATAAGGATAGAGGT
droKik1	scf7180000302386:633496-633657 -		CAAGGAGCAGCTGAAAAAGCTGCAAAGGAAATAAGGACTGGAGAATGAGATGAGCAAGC----------------------TTT-------GGCTTAAAAACCCTTACC----------GGCTTGGCT-----ATTTCGCCTTTAGAATTGTTGAATCCAGTTGCAATGGTCAGTCGG--CCCCCAACTAGAAGATAGGGT
droFic1	scf7180000453342:812185-812350 -		CAAGGAGCAGCTGAAAAAGCTGCAGGGAAGTAGGCTTAGAAAATGAGATGAGTAGCA----T----CGTTGCCATAA--------------------------------ACTGAATATTT----ATGTAT--------T----------TAGTTAGAA----ATTCACACATTGAGAATTGTGGAGTGCCAGCAGCAATGGTCC-----AA---TGAATTAGAATGATCGCCT
droEle1	scf7180000491214:3957854-3958017 +		CAAGGAGCAGCTGAAGAAGCTGCAGGCAAATAGGGCTTGGAGAATGAGATGAGTCTCCT----------TCCTTAACTT-------------------CATAGATC-------ATGTTCTCAACTATTTACGTATTGAGAATTGTGGAGACCAGTGGCAATGGTC-----AGCCTTGAAGTAGAAGGATCCGGCC
droRho1	scf7180000776849:731377-731540 -		TAAGGAGCAGCTGAAGAAGCTGCAGGGAAATAGGGCTTAGAAATGAGATGAGTTTCCT----------TGTTTGATACAA----------------------CTTAGA--TCA-------ACTTTGCAATTATTTACTATTGAGAATTGTGGAGACCGGTGGCAATGGTC-----AGGGCTAAAGTAGAATGAGCGGCT
droBia1	scf7180000302143:311836-311992 -		CAAGGAGCAGCTGAAGAAGCTGCAGGGAAATAGGGCTTGGAGAATGAGATGAGTACACTATAAC--------------------------------CATCCTTTAGTGCAATGATTTCTAAGTTGTT---------T----------T--------TTTATTAGTTGGAGAACTGGCGCAATGGCAATGGTC-----AG---TGAATTAGAATGCGGCGCC
droTak1	scf7180000415878:906543-906704 -		CAAGGAGCAGCTGAAAAAGCTGCAGGGAAATAGGGCTTGGAGAATGAGATGAAAATAGCTTAGGTGTGTC----------------------------------GGATC------TA-------T---TTATTCCTCTGAAAGTGAACTATCCCATCGAATTTGTGAGATTGTTGAGTCTGTTGCCAATGGTC-----AG---TGAATTAGAATGATCGGCGCC
droEug1	scf7180000409462:37995-38154 -		CAAGGAGCAGCTGAAAAAGCTGCAAAGGAAGTAGGACTAGAAAAGGAAAGTGAGTACGTTTCAA--------------------------------GGATC------ACGTCATTCCTCTCCAACTTGCAATCTTATTCGAAGTTTTAGAATTGTTGAGCCT---GCAATGGTC-----AG---TGAATTAGAATGATCGTGGT
dm3	chr2R:11110438-11110596 +		CAAGGAGCAGCTGAAAAAGCTGCAGGGCAAATAGGGACTAGAAAAGGAAAGTGAAAAAACAA----GACAAC--------------T-----TATAC-------TCTCACTTT-------ACCTTGCAATCCTTAATTCACCTTTAGAATTCGTGGTAGTAGCGCAATGGCGCA-----AG---TGAATTAGAATGATCGTGCC
droSim2	2r:11781059-11781217 +		CAAGGAGCAGCTGAAAAAGCTGCAGGGCAAATAGGGACTGGAAAAGGAAAGTGAAAAAACAA----GACAAC--------------C-----TCTAC-------TCTCACTTT-------ACCTTGCAATCCTTAATTCACCTTTAGAATTCGTGGTAGTAGCGCAATGGCGCA-----AG---TGAATTAGAATGATCGGCC
droSec2	scaffold_1:8603829-8603987 +		CAAGGAGCAGCTGAAAAAGCTGCAGGGCAAATAGGGACTGGAAAAGGAAAGTGAAAAAACAA----GACAAC--------------C-----TCTAC-------TCTCACTTT-------ACCTTGCAATCCCTATTCACCTTTAGATTCGTGGTAGTAGCGCAATGGCGCA-----AG---TGAATTAGAATGATCGGGCC
droYak3	2R:11032001-11032167 +		CAAGGAGCAGCTGAAGAAGCTGCAGGGCAAATAGGCCTTGGAGAATGAAAGTGAAAAACAA----GACTAT--------------C-----TCTAC-------TC-------CCATCACATCTCTTTATCTTGCAATCCTTAATTAACTTTTAGAATTCGTGGTAGTACTGCGCGCAATGGCGCA-----AG---TGAATTAGAATGATCGGCC
droEre2	scaffold_4845:14757092-14757256 -		CAAGGAGCAGCTGAAGAAGCTGCAGGGCAAATACGGCTTGGAGAATGAAAGTGAAAAACAA----GACTAC--------------C-----ACTAC-------TCTTCACTTACAATC-------ACCTTGCAATCCTTACTTAACTTTAGAATTCGTGGCACTGCGCGCAATGGCGCA-----AG---TGAATTAGAATGATCGGCC

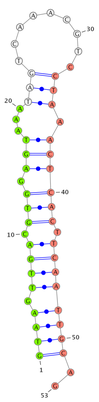
Generated: 09/08/2015 at 07:10 PM

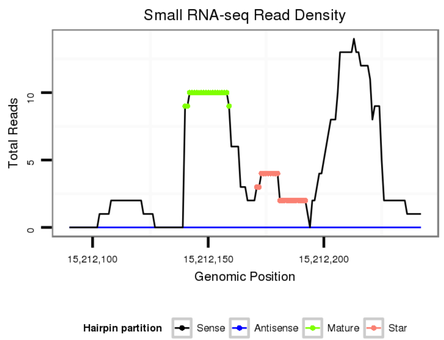
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.ptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

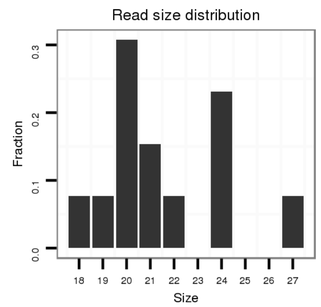
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_17006	**scaffold_13047:15212140-15212192 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

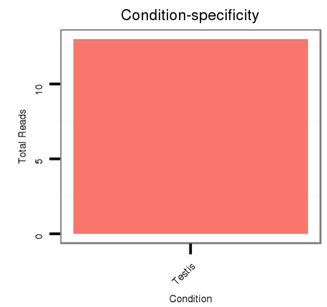
Legend: mature star mismatch in alignment mismatch in read

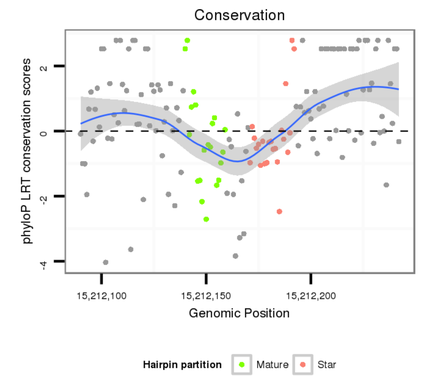
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dvir\GJ24477-in]; CDS [Dvir\GJ24477-cds]; CDS [Dvir\GJ24477-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CCGAGGAGGGGGTTTTCAATACACCATGGGCCCCATGACAAAAATTATTGGTAAGTTGACGTGGAGTAAATAGTCAAACGTCCTAAACTCACTTCAATTGCAGACAAAAGAGTTGGTCCCGGTCCCGGCGCACACGATGTTCATAATAAGCCA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060659 Argentina_testes_total	SRR060678 9x140_testes_total	M027 male body	SRR060679 140x9_testes_total	SRR060681 Argx9_testes_total	V116 male body	SRR060655 9x160_testes_total	SRR060657 140_testes_total	SRR060670 9_testes_total	SRR060683 160_testes_total	SRR060689 160x9_testes_total	SRR1106729 mixed whole adult body	SRR2096081 embryo_0-2h from 15to16 day old nondysgenic mothers	SRR060668 160x9_males_carcasses_total	V047 embryo
**********((((.(((((.(((.(((...(((.....)))).)))))).)))))))..**********																				
.....GTAAGTTGACGTGGAGTAAA.....	20	0	1	4.00	4	0	0	0	0	0	0	2	1	1	0	0	0	0	0	0
.....CCCGGTCCCGGCGCACACG.....	19	0	1	3.00	3	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGTTGACGTGGAGTAAATAGT.....	24	0	1	3.00	3	0	0	0	1	1	0	0	0	0	0	1	0	0	0	0
.....TCCCGGTCCCGGCGCACAC.....	19	0	1	2.00	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TAGTCAAACGTCCTAAACTCA.....	21	0	1	2.00	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
.....CACGATGTTCATAATAAGCCA	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0
.....GTAAGTTGACGTGGAGTAA.....	19	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
.....CCCGGCGCACACGATGTTCATAA.....	23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
.....AGTTGGTCCCGGTCCCGGCG.....	20	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
.....AAGATTGGTCCCGGTCCC.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGGTCCCGGTCCCGGCGC.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AAAAGAGTTGGTCCCGGTCCCGGCGC.....	26	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....TTTCAATACACCATGGGCC.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AAAAGAGTTGGTCCCGGTC.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTGGTCCCGGTCCCGGCGC.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTTGGTCCCGGTCCCGGCGCACAC.....	24	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCCCGGTCCCGGCGCACACGATGG.....	24	1	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....GTAAGTTGACGTGGAGTAAATAGTCAA.....	27	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
.....AAGTTGACGTGGAGTAAA.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TAAACTCACTTCAATTGCAGA.....	21	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
.....AGAGTTGGTCCCGGTCCCGGCGCACAC.....	27	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
.....CCTAAACTCACTTCAATTGCAG.....	22	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
.....ATACACCATGGGCCCCATG.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

GGCTCCTCCCCCAAAAGTTATGTGGTACCCGGGGTACTGTTTTTAATAACCATTCAACTGCACCTCATTTATCAGTTTGCAGGATTTGAGTGAAGTTAACGTCTGTTTTCTCAACCAGGGCCAGGGCCGCGTGTGCTACAAGTATTATTCGGT	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR2096080 embryo_0-2h from 15to16 day old nondysgenic mothers	V053 head	SRR2096081 embryo_0-2h from 15to16 day old nondysgenic mothers	SRR2096072 embryo_0-2h from 15to16 day old dysgenic mothers	SRR1106729 mixed whole adult body
**********((((.(((((.(((.(((...(((.....)))).)))))).)))))))..**********										

Show Alignment With Reads

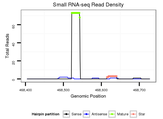
Re-alignment of all predicted orthologs

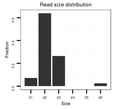
Species	Coordinate	ID	Alignment
droVir3	scaffold_13047:15212090-15212242 +	dvi_17006	CCGAGGAGGGGGTTTTCAATACACCATGGGCCCCATGACAAAAATTATTGGTAAGTTGAC--GTGGAG----------TAAATTCCCTAAACTCACTTCAATTGCAGACAAAAGAGTTGGTCCCGGTCCCGGCGCACACGATGTTCATAATAAGCCA
droMoj3	scaffold_6540:18690209-18690369 +		CGCGGGCAGGGGCGCCGACTACACTATGGGCCCCATGAGCAAAAATAATAGGTAGGTTGCAA-TCCGACTCGCCCCC

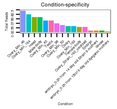
ID	Coordinate	Confidence	Class	Genome Locale	
dv1_24292	**scaffold_13042:468454-468678 +**	**Candidate**	**Unknown**	**Intergenic**	View on UCSC Genome Browser (GenomeBrowser)

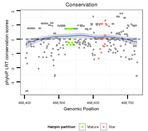
Legend: **Mature** **Star** **Mature/Star** **Alternative**

Predicted structure









Show Alternate Folds

Flybase annotation

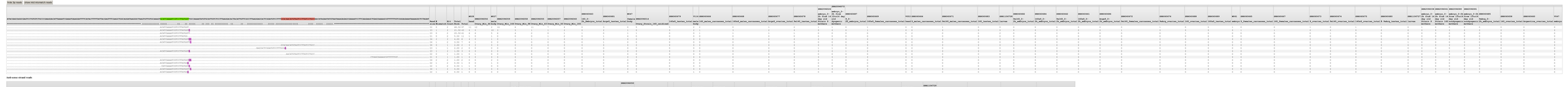
Intergenic

No Repeatable element found

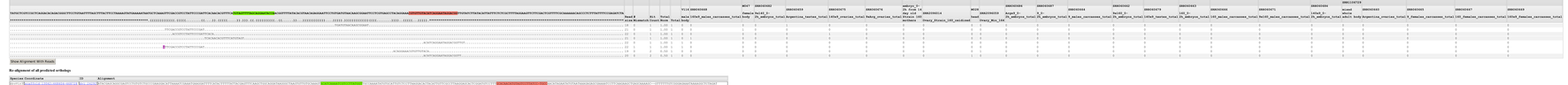
Feature	Gene
5_ALGN: scaffold_ACCCCMOOO:CMOOO:-	
3_ALGN: scaffold_CMOOO:CMOOO:MOFD:-	

Locus Sorted Reads

Note by reads | show mid mismatch reads

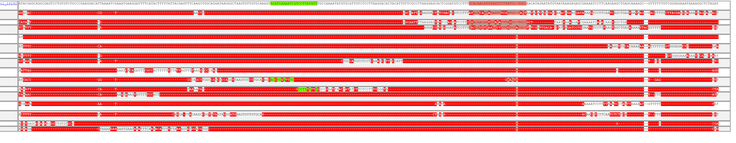


Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

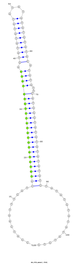


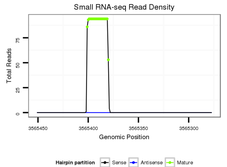
Generated 08/26/2019 at 01:07 PM

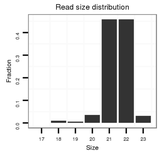
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_456	**scaffold_13042:3565327-3565401 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser] [Cosmiff-Mirez]

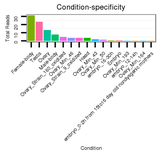
Legend: Sense 5p 3p mismatch in alignment mismatch in loop

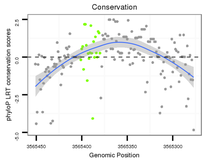
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
Copia-22_DW-0-1-int	LTR	Copia	+
17.6kb	Simple_repeat	Simple_repeat	+

name	star
1. dvi_240 scaffold_12970:3041393-3041418 -	
2. dvi_368 scaffold_12970:3818363-3818384 -	
3. dvi_456 scaffold_13042:3565380-3565401 -	

Sense Strand Reads

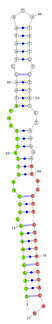
hide 3p reads show mid mismatch reads

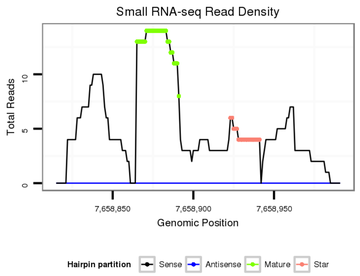
| AGTATGCACACGCTGGCGTGTTTCTACACAACTATTTCATCATATAT

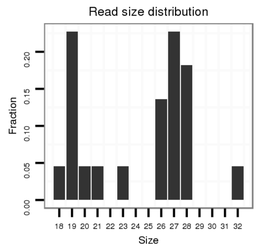
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_5665	**scaffold_12875:7658865-7658941 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

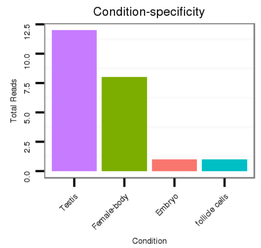
Legend: mature star mismatch in alignment mismatch in read

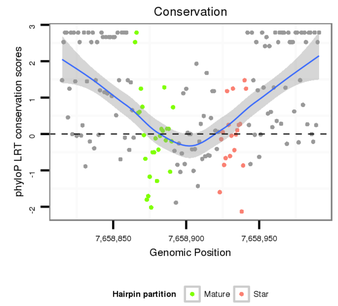
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dvir\GJ21619-in]; CDS [Dvir\GJ21619-cds]; CDS [Dvir\GJ21619-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M047 female body	SRR060678 9x140_testes_total	SRR060679 140x9_testes_total	SRR2096056 Ovary_Min_46	SRR060665 9_females_carcasses_total	SRR060670 9_testes_total	SRR060680 Ä 9xArg_testes_total	SRR2096057 Ovary_Min_50	GSM1528803 follicle cells	M061 embryo	SRR060666 160_males_carcasses_total	SRR060668 160x9_males_carcasses_total	SRR060669 160x9_females_carcasses_total	SRR060681 Argx9_testes_total	SRR060682 9x140_0-2h_embryos_total	SRR2096055 Ovary_Min_43	SRR060660 Argentina_ovaries_total	V116 male body
ACAAACAGAAATCATTAAAGCTGTGCGATCTCTATAAGAACTATTTTACGGTAGGTAAAGCGGCAAATTATTTCACATAAGCTAATAATATATTGTCTTATCTAAAAAATACGTTCTTTACTTACAGAGCATACGTCTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTCTTAGT																						
((((((((((.(((..(((.(((...((((((.((((((...)))))).))))))..))))..))))..))))))))))))..																							
.....GTAGGTAAAGCGGCAAATTATTTCACA.....	27	0	1	4.00	4	0	3	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
.....ATACGTTCTTTACTTACAG.....	19	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAGGTAAAGCGGCAAATTATTTCAC.....	26	0	1	3.00	3	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
.....TGTGCGATCTCTATAAGAACTATTT.....	25	0	1	2.00	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GAAATCATTAAAGCTGTGCGATC.....	23	0	1	2.00	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0
.....ATTAAAGCTGTGCGATCTCT.....	20	0	1	2.00	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GCATACGTCTGGAGCGCGAT.....	20	0	1	2.00	2	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....TAATATATTGTCTTATCTAAAAAATACG.....	28	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
.....ATACGTTCTTTACTTACAG.....	20	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CATACGTCTGGAGCGCGAT.....	19	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AAAGCTGTGCGATCTCTATAAGAACTAT.....	28	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CTCTATAAGAACTATTTTACGCGC.....	24	3	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GAAATCATTAAAGCTGTGCGAT.....	22	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TAATAATATATTGTCTTATCTAAAAAAT.....	28	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAGGTAAAGCGGCAAATTATTTCACAT.....	28	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAGGTAAAGCGGCAAATTATTTCACATAAGC.....	32	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
.....GCGATGATAAGCTGGGCATTAATA.....	24	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....GTAGGTAAAGCGGCAAATTAT.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GAAATCATTAAAGCTGTGCGATCT.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATATTGTCTTATCTAAAAA.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATTTCACATAAGCTAATAATATATTG.....	27	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GATGATAAGCTGGGCATTAATAGCT.....	25	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
.....AATACGTTCTTTACTTACAGG.....	21	2	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AAAGCGGCAAATTATTTCACATAAGCTA.....	28	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAGGTAAAGCGGCAAATT.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATACGTCTGGAGCGCGAT.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGGAGCGCGATGATAAGCTGG.....	21	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
.....AATACGTTCTTTACTTACAG.....	20	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AATACGTTCTTTACTTACAGG.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCGATCTCTATAAGAAC.....	18	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....GTAGGTAAAGCGGCAAAT.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAGGTAAAGCGGCAAATTATTT.....	23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0

Anti-sense strand reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M047 female body	SRR060672 9x160_females_carcasses_total	V047	M027 male body	SRR2096079 embryo_0-2h from 15to16 day old dysgenic mothers	SRR1106729 mixed whole adult body
TGTTTGTCTTTAGTAATTTCGACACGCTAGAGATATTCTTGATAAAATGCCATCCATTTCGCCGTTTAATAAAGTGTATTCGATTATTATATAACAGAATAGATTTTTTATGCAAGAAATGAATGTCTCGTATGCAGACCTCGCGCTACTATTCGACCCGTAATTATCGAAGAATCA										
((((((((((.(((..(((.(((...((((((.((((((...)))))).))))))..))))..))))..))))))))))))..											
.....TAATAATATATTGTCTTATCTAAAAAAT.....	28	0	1	1.00	1	0	0	0	0	0	0
.....AATACGTTCTTTACTTACAG.....	20	0	1	1.00	1	0	0	0	0	0	0
.....AATACGTTCTTTACTTACAGG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....ATACGTCTGGAGCGCGAT.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TGGAGCGCGATGATAAGCTGG.....	21	0	1	1.00	1	0	0	0	0	0	0
.....AATACGTTCTTTACTTACAG.....	20	0	1	1.00	1	0	0	0	0	0	0
.....AATACGTTCTTTACTTACAGG.....	21	1	1	1.00	1	1	0	0	0	0	0
.....TGCGATCTCTATAAGAAC.....	18	0	1	1.00	1	0	0	0	1	0	0
.....GTAGGTAAAGCGGCAAAT.....	18	0	1	1.00	1	1	0	0	0	0	0
.....GTAGGTAAAGCGGCAAATTATTT.....	23	0	1	1.00	1	0	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12875:7658815-7658991, +	dvi_5665	ACAAACAGAAATCATTAAAGCTGTGCGATCTCTATAAGAACTATTTTACGGTAGGTAA------AG-CG--GC-AA----------A----------TTATTTCACATAA-GCT--------AATAATATATTGTCTTATC-------TAAAAAATA----------CGT----------TCTT--TACTTACAGAGCATACGTCTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTCTTAGT
droMoj3	scaffold_6496:19686830-19686994, +		ACAAGCAGAAATCTTAAAGCTGTGCGATCTCTATAAGAACTATTTTACGGTAGGCAA------TATCTACTCCC---TTAACTGTTAAC--AGTA--CG----A-----T--CAAG-------G----------TATA--T--TTCTTATAGAGCATACGTCTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTC-TGTT
droGri2	scaffold_15245:1183250-1183435, +		ACAAACAGAAATCTTAAAGCTGTGCGATCTCTATAAGAAATATTTTACGATAGTAATAA------AG-CT-GC-AA----------C----------------------A---A-----CT--T----------AGT------TGTCACA-CA-------TAATTCCGGTATGAAAAACTCACCAGTTCTTCTT----------TCTTC-CA-TCTTTCCGTAGAGCATTCGTTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTCTTTGTT
droWil2	scf2_1100000004822:883908-884092, -		ACAAACAGAAATCTCCTGAATTTGTGCGATCTCTATAAGAATATTTTACGATAGTTTAGTATATTGT------CC-A--T---TTC----------ACCTTC-------AA-------T-------T---------T---------AGTATCGAATTGAAATCAATCATTTCTTTGTGATTTCT---------T-TATCGAATATATATTGAGAGCATACGATTGGATCGCGTGATGATAAGCTGGGCATTAATAGCTTTCTAGT
dp5	1:1691265-16591438, +		ACAAGCAGAAATCATTTAAATTTGTGCGATCTCTATAAGAACTATTTTACGTAGTAATTGC------AG-A--TTTC----------T---T----------T----T-----TCCGT---------AGTA--GTTGTCTTA-------TAATTTCCGATA-------TCCCCCCGT----------TCTTTGCTTCTGCAGAGCATACGCTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTCTTGGTT
droPer2	scaffold_4:170337-170507, -		ACAAGCAGAAATCATTTAAATTTGTGCGATCTCTATAAGAACTATTTTACGTAGTAATTGC------AG-A--T---T----------T----------T----------AG-----TCC---------GTA--GTTGTCTTA-------TAATTTCCGTA-------TCCCCCCGT----------TCTTTGCTTCTGCAGAGCATACGCTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTCTTGGTT
droAna3	scaffold_13266:13608239-13608397, -		ACAAGCAGAAATCCCTAAGCTGTGCGATCTCTATAAGAATATTTTCCTTTGATTTTGGGCA-A--T---CAA----------AAATCT-------AA----------A-AT--ATTTA--------AGTA--TT-----A-----T---TAAT-------G----------TA----------A-------ATT--TATTTACAGAGTATCGATGGATGATTCGATGATAAGCTGGGCATTAATAGCTTCTTTGTT
droBip1	scaffold_7180000396759:2527923-2528079, +		ACAAGCAGAAATCCCTAAAGCTGTGCGATCTCTATAAGAATATTTTCCTTTGATA-CTT-------A-A--T---AAC----------AAATCT-------AA-----T-A-----T---------RAT--ATATA-TTAA--TAA----------A----------TA----------A-------ATTTCAATTTTTAAGAGCATTCGCTGGAGCGCGATGATAAATTGGGCATTAATAGCTTCTTGGTT
droKik1	scf7180000302476:3219222-3219388, -		ACAAGCAGAAATCCCTAAGCTTGCGCATCTCTATAAGAATATTTTAGTTTAGTTGATTTT-----GA-A--T---TAG----------AAAC----------TTATTGATTGTGTA--------AATA----------A----------TA----------T-TATTGAATAATTACGAGAGCATTCGCTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTCTTGGTT
droFic1	scf7180000453948:2436529-2436690, -		ACAAGCAGAAAATCCCTAAGCTGTGCGATCTCTATAAGAATATTTTAGTTTAGTTGATTTT-----GCA-T---T---TAG----------AAAC----------TTATTGATTGTGTA--------AATA----------A----------TA----------T-TATTGGCCCAATTTTGTGAGCATTCGCTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTCTTGGTT
droEle1	scf7180000491214:1333067-1333224, -		ACAAGCAGAAAATCCCTAAGCTGTGCGATCTCTATAAGAATATTTTAGTTTAGTTGATTTT-----CC-CTATTAT----------A-A--T----------T----A-----AAA---------AGTA--ATTTA-------CTA----------A----------TA----------T-TATTCCCCAATTTTGTGAGCATTCGCTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTCTTGGTT
droRho1	scf7180000780084:323366-323527, -		ACAAGCAGAAATCCCTAAGCTGTGCGATCTCTATAAGAATATTTTAGTTTAGTTGATTTT-----G-T-TAAT-AC--T----------T----------T----------A-ATTTAG--TGT---------AGTA--ATTTA-------CTA----------A----------TA----------T-TACTCCGCTTATTTCTGTAGAGCATTCGCTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTCTTGGTT
droBia1	scf7180000301754:5244251-5244409, +		ACAAGCAGAAATCCCTAAGCTGTGCGATCTCTATAAGAATATTTTAGTTTAGTTGATTTT-----AAATTTT-TAAA----------T----------T----------T-----G-T---------CTA--AGTATCTAAT-------G----TA----------A----------TA----------T-TATAATTGTAGAGCATTCGCTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTCTTGGTT
droTak1	scf7180000415345:30840-31003, +		ACAAGCAGAAATCCCTAAGCTGTGCGATCTCTATAAGAATATTTTAGTTTAGTTGATTTT-----AG-AA--T--T----------T----------T----------A-ATTTGGG-CGCGATA--------AGTA--ATTTA-TGTTA--TATT----T--------A----------TA----------T-TATTTGTAGCTTTTCGAGAGCATTCGCTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTCTTGGTT
droEug1	scf7180000409672:2115077-2115238, -		GCAAGCAGAAATCCACTGCATTCTCCCT--------GCATAATCCCTTTTGCTTGCGAGTGAGTTATCC--TCCTTTAAACTATTATA-A--T----------T----------T----A-----TAAAGCAATTGAAATATTTA--TATTCCCT-----T-TTAG-------A----------T----------T----T------CGT-CATACTCCATCCA----TAAATGATAAAGCTGGGCATCGCAGCTTCTTAGT
dm3	chr2R:12993659-12993820, +		ACAAGCAGAAATCCCTAAGCTTGCGCATCTCTATAAGAATATTTTAGTTTAGTTGATTTT-----AG-TCTA-TCAA--TT----------A-T----------T----------T----A-----CGT-T-CGTTT--------CATTA----------T----------T----------T-ATATATAATGCAGTTTTGAGAGCATTCGCTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTCTTGGTT
droSim2	2r:13664172-13664332, +		ACAAGCAGAAATCCCTAAGCTGTGCGATCTCTATAAGAATATTTTAGTTTAGTTGATTTT-----AG-TCTA-TCAA--TT----------A-T----------T----------T----A-----CGT-T-CGTTT--------CTTTA----------T----------T----------T-ATATATAATTAACGTTTTGAGAGCATTCGCTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTCTTGGTT
droSec2	scaffold_1:10504093-10504266, +		ACAAGCAGAAATCCCTAAGCTGTGCGATCTCTATAAGAATATTTTAGTTTAGTTGATTTT-----AG-TCTA-TCAA--TT----------A-T----------T----------T----A-----CGT-T-CGTTT--------CTTTC-----C----------T----------T----------T-TTTACAAAGTAATATATA-ATTCACTTTACAGAGCATTCGCTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTCTTGGTT
droYak3	2R:18472761-18472918, +		ACAAGCAGAAATCCCTAAGCTGTGCGATCTCTATAAGAACTATTTTAGTTTAGTTGATTTT-----AG-TCTC-TCAA----------T----------T----------T----A-----CGT-T-CGTTT--------CTTTA-----A----------T----------T----------T-AATAATTGTAATTTCTTTGAGAGCATTCGCTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTCTTGGTT
droEre2	scaffold_4845:12848719-12848884, -		ACAAGCAGAAATCCCTAAGCTGTGCGATCTCTATAAGAATATTTTAGTTTAGTTGATTTT-----AG-TCCGCTCTC----------T----------T----------T----A-----CGT-T-CGTTT--------CATTC-----A----------T----------T----------T-TATA-ATTCAATTTTCTAGAGCATTCGCTGGAGCGCGATGATAAGCTGGGCATTAATAGCTTCTTGGTT

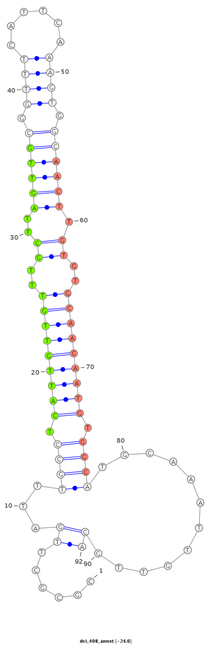
Generated: 09/08/2015 at 07:12 PM

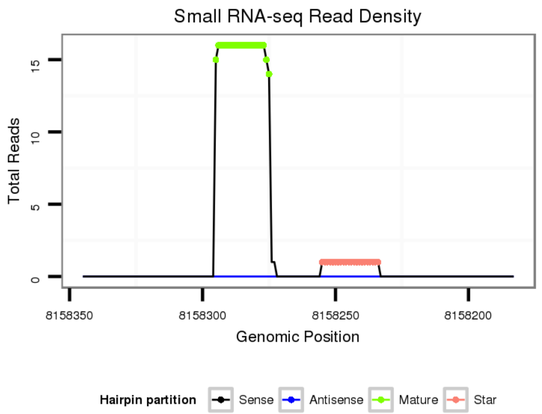
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.mar	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.gtop3	1
crit.un	1
crit.back	0
rescue.total	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

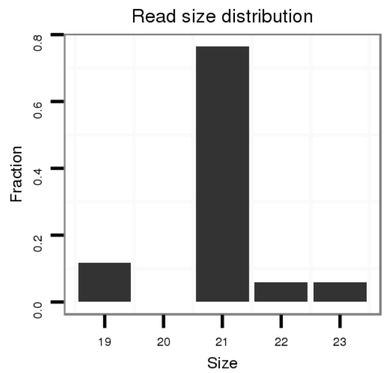
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_408	**scaffold_13049:8158233-8158295 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

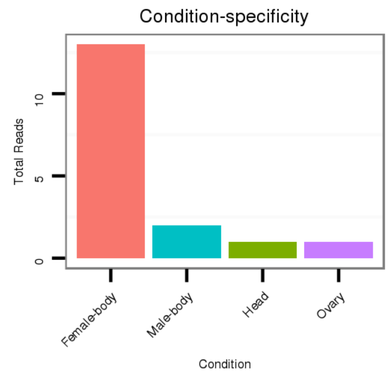
Legend: mature star mismatch in alignment mismatch in read

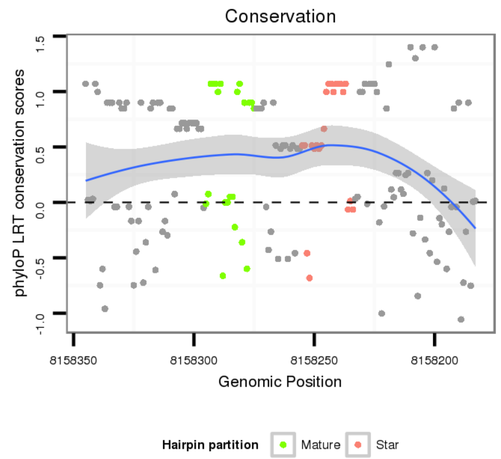
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTCATGCCGTTTAGTGCACGCGCATTGCATTTGGACGCGCTTGATTTGCCTCATTGTTGTTTGCTTAGTTGCGGTTTCATTCAAAGTGGCAACTTGTGTGCAACAATGTGGCATGCAAATTGTTGCAAATTGTCAACGAGACAAGACCAGCCAGAACTCACGC **********.....((...((((.(((((((((..((..((((((.((((.....)))).)))))).))..)))))))).)))).....))**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M047 female body	SRR060667 160_females_carcasses_total	SRR060668 160x9_males_carcasses_total	SRR060669 160x9_females_carcasses_total	SRR060688 160_ovaries_total	V053 head	V116 male body	SRR060686 Argx9_0-2h_embryos_total	V047 embryo
.....TCATTGTTGTTTGCTTAGTTG.....	21	0	1	13.00	13	6	3	1	1	0	1	1	0	0
.....AACTTGTGTGCAACAATGTGGC.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....CATTGTTGTTTGCTTAGTT.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TCATTGTTGTTTGCTTAGT.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....TCATTGTTGTTTGCTTAGTTGCG.....	23	0	1	1.00	1	0	0	0	0	1	0	0	0	0

Anti-sense strand reads

AAGTACGGCAAATCACGTGCGCGTAACGTAAACCTGCGCGAACTAAACGGAGTAACAACAAACGAATCAACGCCAAAGTAAGTTTCACCGTTGAACACACGTTGTTACACCGTACGTTTAACAACGTTTAACAGTTGCTCTGTTCTGGTCGGTCTTGAGTGCG **********.....((...((((.(((((((((..((..((((((.((((.....)))).)))))).))..)))))))).)))).....))**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V053 head	GSM1528803 follicle cells	SRR060663 160_0-2h_embryos_total	SRR060668 160x9_males_carcasses_total

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_13049:8158183-8158345 -	dvi_408	TTCATGCCGTTTAG---TGCACGC-GCATTGCATTTGGACG----------CGCTTGATTTGC--CTCATTGTTGTTTGCTTAGTTGCGGTTTCATTCAAAGTGGCAACTT----------GT-GTGCAACAATGTG--GCA--TGCAAATTGTTGCAAATTGTCAACGAGACAAGACCAGCCA------GAACTCACGC
droMoj3	scaffold_6680:11820152-11820240 -		TGCATG--------------------------CGCTTGATTTGCGGCTCATTGTG--CCGCT----------GCAACAATGTG--GCAAGCGCAAATTGTGCAAATTGTCAACGAGACAAGAATA----------TGC
droGri2	scaffold_15110:7186156-7186344 -		TTCATGGATTTAG---TGCAGAGTTTACAGCAGTTGAGCGTGTTTTTGTGGCGCTTGATTTGC--GGCATTGTG--TTACTAATTTGCGGTTGCATACAATGTAGCAATGTAGCAATGCAGCAATGTAGTGCAACAATGTGCAGCA--TGCACATTGCG-----TTGTCAA-GCAAAACCAAGCAACCCCAAGAACCCA-TC
droWil2	scf2_1100000004822:3412332-3412471 +		TTACTGGACTTTGACGTTGCATGC-GCAAACATTTGGACG----------T----------GGCTTATTGTA--TTACTAATTTGCGGTCGGA----------GGC--TGCAAATTGCCACGACGCCGGTGAAGGGAAGGGACGGAGGGGGGATGGATAGAAGA
droEle1	scf7180000490993:419643-419666 -		--AAATTCGCAATGTAACAAGAGTAG-----------

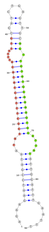
Generated: 03/04/2015 at 08:37 PM

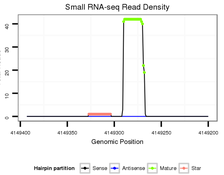
PASS/FAIL	
crit.star	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

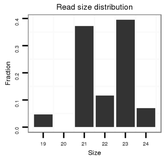
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_13110	**scaffold_12970:4149250-4149343 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

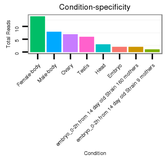
Legend: **mature** **star** **sub-match in a dg-seq** **mismatch in trim**

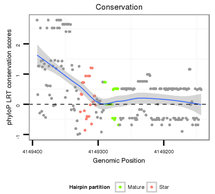
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dvir(GI:8945-in]

No Repeatmile elements found

Sense Strand Reads

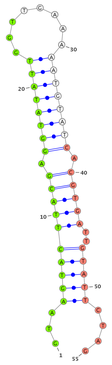
hide 3p reads show mid mismatch reads

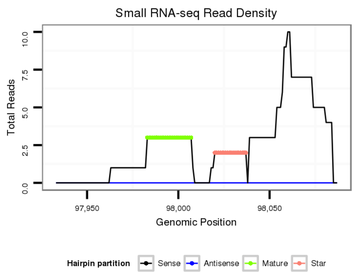
| | | |

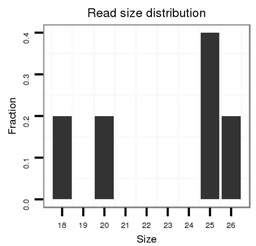
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_2275	**scaffold_12822:97983-98037 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

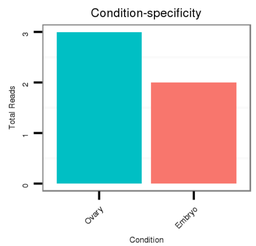
Legend: mature star **mismatch in alignment** mismatch in read

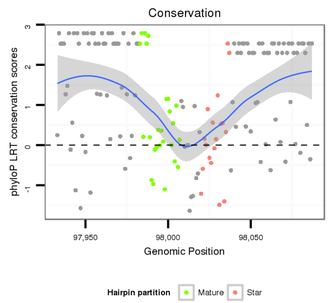
Predicted structure











Show Alternate Folds

Flybase annotation

intron [DvirGJ14370-in]; CDS [DvirGJ14370-cds]; CDS [DvirGJ14370-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CTGGGCTATTTTACATTGTCCATGCCCTGGATGTGGGGGATAGCTCTGGGGTAAGTACTTACGAGGTATATTGGTTGAAAAATGTATCACGTGATTGTATTCTAGCCTGGTCATCACAGCAGTCTCACCCAATGTTGTCGTCACAGTCATGCTTA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR2096014 Ovary_Strain_160_oxidized	SRR2096057 Ovary_Min_50	M047 female body	SRR060676 9xArg_ovaries_total	SRR060684 140x9_0-2h_embryos_total	SRR060679 140x9_testes_total	SRR2096056 Ovary_Min_46	SRR060673 9_ovaries_total	SRR2096055 Ovary_Min_43	SRR2096059 Ovary_Min_164	SRR2096060 Ovary_Min_193	V116 male body	V053 head	GSM1528803 follicle cells	V047 embryo	SRR2096013 Ovary_Strain_9_oxidized	SRR2096080 embryo_0-2h from 15to16 day old nondysgenic mothers	SRR060683 160_testes_total	SRR060659 Argentina_testes_total	SRR060664 9_males_carcasses_total	SRR060681 Argx9_testes_total	SRR2096050 embryo_0-2h from 14 day old Strain 160 mothers	SRR2096081 embryo_0-2h from 15to16 day old nondysgenic mothers
CTGTCATCACAGCAGTCTCACC	23	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CACCCAATGTTGTCGTCACAGTCATGC	27	0	1	3.00	3	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GTAAGTACTTACGAGGTATATTGGT	25	0	1	2.00	2	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GTCTCACCCAATGTTGTCGT	20	0	1	2.00	2	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CCCAATGTTGTCGTCACAGTC	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
GTAAGTACTTACGAGGTATATTGGT	26	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CACGTGATTGTATTCTAG	18	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
TCACCCAATGTTGTCGTCACAGTCATGC	28	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATGTGGGGGATAGCTCTGGG	20	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
TATCACGTGATTGTATTCTAG	22	1	1	1.00	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
ATCACGTGATTGTATTCTAG	20	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

GACCGGATAAAATGTAACAGGTACGGGACCTACACCCCCTATCGAGACCCATTCATGAATGCTCCATATAACCAACTTTTACATAGTGCACTAACATAAGATGGGACCAGTAGTGTCGTCAGAGTGGGTTACAACAGCAGTGTCAGTACGAAT	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060670 9_testes_total	SRR060655 9x160_testes_total	M047 female body	SRR060666 160_males_carcasses_total	V047 embryo	SRR060667 160_females_carcasses_total	SRR2096056 Ovary_Min_46

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12822:97933-98087 +	dvi_2275	CTGGCCTATTTTACATTGTCCATGCCCTGGATGTGGGGGATAGCTCTGGGGTAAGTAC---TT--------A----------CGAGGTATATTGGTTGAAAAATGT----------ATCAC-----G-TGATTG------T-AT----TCTAGCCTGGTCATCACAGCAGTCTCACCCAATGTTGTCGTCACAGTCATGCTTA
droMoj3	scaffold_6540:32787775-32787972 +		CTGGCCTATTTACATTGTCCATGCCCTGGATGTGGGGCTAGCTCTGGGGTAAGTAC---AACATGAACAG--CAAACTGAACTGAAGATGACAGACAAATATATTTGTACATATGTA----------T-TATGT-ATTTATGT----------GGGT-----------T-TGTTA------T-G----TCTAGCTGGTCATCACGCGTCTCGCGAATGTGTTGTCACAGTCATGCTGA
droGri2	scaffold_15074:3616104-3616271 -		TTGGCCTATTTTACATTGTCATGCCCTGGATGTGGGGATAGCTCTGGGGTAAGTTTGAA-GA--GTTAGTGTG----------CGATATGAAA----------TTAATCA--------G--------ATCGTTGTG-----G-----T-----T-----T-G-CACACTAAGCTGGTCATTACAGCGTCTCGCCCAATGTGTTGTCACGTCATGCTAA
droWil2	scf2_1100000004902:1221229-1221402 +		TTGGCTATTTTACATTGTCATGCCCTGGATGTGGGGATAGCTCTGGGGTAAGTCG--AGTA--GCAAT----------GAG-TATATAAAATATTTCTAAAGAG----------AAATTTNTGGTT----T-FAATCT----T-CG----TTAGCCTTGTCATCACAGCGTTCTCGCAATGTTGTTGTCGTCATGCTGA
dp5	2:6069864-6070036 +	dpa_391	CTGGCCTATCCTTACCTGTCATGCCCTGGATGTGGGGATATACTTGGGGTAGTGT--G-GG--GGGCT---C----------GCTA-----TCAATTTCCGTT-CCGAA-------T-CCCCCCACAGAGTTGGTCATCACGCGATCTCGCGAATGTGTTGTCACGTCATGCTTA
droPer2	scaffold_19:1808813-1808984 +		CTGGCCTATCCTTACCTGTCATGCCCTGGATGTGGGGATATACTTGGGGTAGTGT---G-GG--GCT-G----------T-GCC-GCT-G-T----GGATC----------GCTA-----TCAATTTCCGTT-CCGAA-------ACCCCCCACAGAGTTGGTCATCACGCGATCTCGCGAATGTGTTGTCACGTCATGCTTA
droAna3	scaffold_13340:12508245-12508299 +		TTGGCCTATCCTTACCTGTCATGCCCTGGATGTGGGGATAGCTCTGGGGTAAGCGA---T--------T----------GCTA-----TCAATTTCCGTT-CCGAA-------T-CCCCCCACAGAGTTGGTCATCACGCGATCTCGCGAATGTGTTGTCACGTCATGCTGA
droBip1	scf7180000396691:1398079-1398149 +		TTGGCCTATCCTTACCTGTCATGCCCTGGATGTGGGGATAGCTCTGGGGTAAGTCGA---T--------T----------GCTA-----TCAATTTCCGTT-CCGAA-------T-CCCCCCACAGAGTTGGTCATCACGCGATCTCGCGAATGTGTTGTCACGTCATGCTGA
droKik1	scf7180000302388:444019-444172 -		CTGGCCTATCCTTACCTGTCATGCCCTGGATGTGGGGATAGCTCTGGGGTAGTGA---AG-----ATA----------TATAT-------T-AGCATGCAGCT----------GCTA-----TCAATTTCCGTT-CCGAA-------T-CCCCCCACAGAGTTGGTCATCACGCGATCTCGCGAATGTGTTGTCACGTCATGCTGA
droPic1	scf7180000453906:1053355-1053535 +		CTGGCCTATCCTTACCTGTCATGCCCTGGATGTGGGGATAGCTCTGGGGTAGTGGGTTGA-TG--GTTA----------T-GAATACTCGATATCGGCACGCCTTAATGGCAACGGCTT------GT----GCTA-----TCAATTTCCGTT-CCGAA-------T-CCCCCCACAGAGTTGGTCATCACGCGATCTCGCGAATGTGTTGTCACGTCATGCTGA
droEle1	scf7180000490453:61602-61768 -		CTGGCCTATCCTTACCTGTCATGCCCTGGATGTGGGGATAGCTCTGGGGTAGTGGG---T-----TCA----------T-GAATACTCGGGCATCGGGGCGCCTATTGA------AT------GTGCTGTTTGT-----T-----T----AGAA-------T-CCCCCCACAGAGTTGGTCATCACGCGATCTCGCGAATGTGTTGTCACGTCATGCTGA
droRho1	scf7180000780164:119877-120038 +		CTGGCCTATCCTTACCTGTCATGCCCTGGATGTGGGGATAGCTCTGGGGTAGTGG---T-----GTA----------T-GAATACTCGCGATCGGGGCGCTATTGG-------GCTA-------T-----T-----T-GTTCAA-------T-CCCCCCACAGAGTTGGTCATCACGCGATCTCGCGAATGTGTTGTCACGTCATGCTGA
droBia1	scf7180000302402:4888771-4888944 +		CTGGCCTATCCTTACCTGTCATGCCCTGGATGTGGGGATAGCTCTGGGGTAGTGT---G-----GCTA----------T-GAATACTCGGGTATCGGATACGCTTAATGG----------TCCCGGGGGCCCCCGGGCGGAA-------T-CCCCCCACAGAGTTGGTCATCACGCGATCTCGCGAATGTGTTGTCACGTCATGCTGA
droTak1	scf7180000415400:76340-76520 +		CTGGCCTATCCTTACCTGTCATGCCCTGGATGTGGGGATAGCTCTGGGGTAGTGG---G-GA--GCTA----------T-GAATACTCGCGTATACCGATGTCCTAATGG--------GCTA-----TTGGGGCCCCCGCGCGCA-------T-CCCCCCACAGAGTTGGTCATCACGCGATCTCGCGAATGTGTTGTCACGTCATGCTGA
droEug1	scf7180000409768:972627-972808 -		CTGGCCTATCCTTACATTGTCATGCCCTGGATGTGGGGATAGCTCTGGGGTAGTGG---T-G---GTTA----------T-GAATACTCGATATCGATGCCTAATGG----------TCCTGTCGGGTT---CGGGCGAATGTTATGCTGCCCCAATGTTGTCGTCACGTCATGCTGA
dm3	chr3R:18812158-18812334 -		CTGGCCTATCCTTACATTGTCATGCCCTGGATGTGGGGATAGCTCTGGGGTAAGTTA---A-GA--GCTA----------T-GAATACTCGATATCGAATCGCCATAATGG----------GTACTGTGATGTT---G-GCGTA-------T-CCCCCCACAGAGTTGGTCATCACGCGATCTCACCCAATGTGTTGTCACGTCATGCTGA
droSim2	3r:18352689-18352865 -		CTGGCCTATCCTTACCTGTCATGCCCTGGATGTGGGGATAGCTCTGGGGTAAGTTA---A-GA--GCTA----------T-GAATACTCGATATCGAATCGCCATAATGG----------GTACTGTGATGTT---G-GCGTA-------T-CCCCCCACAGAGTTGGTCATCACGCGATCTCACCCAATGTGTTGTCACGTCATGCTGA
droSec2	scaffold_0:19176128-19176304		CTGGCCTATCCTTACCTGTCATGCCCTGGATGTGGGGATAGCTCTGGGGTAAGTTA---A-GA--GCTA----------T-GAATACTCGATATCGAATCGCCATATTGG----------GTACTGTGATGTT---G-GCGTA-------T-CCCCCCACAGAGTTGGTCATCACGCGATCTCACCCAATGTGTTGTCACGTCATGCTGA
droYak3	3R:19672229-19672406 -		CTGGCCTATCCTTACATTGTCATGCCCTGGATGTGGGGATAGCTCTGGGGTAAGTTA---A-GA--GCTA----------T-GAATACTCGATATCGAATGTCCTAATGG----------CTGCTGTGATGTT---CGCGCAA-------T-CCCCCCACAGAGTTGGTCATCACGCGATCTCGCGAATGTGTTGTCACGTCATGCTGA
droEre2	scaffold_4820:9256656-9256839 +		CTGGCCTATCCTTACATTGTCATGCCCTGGATGTGGGGATAGCTCTGGGGTAAGTCA---A-GA--GCTA----------T-GAACACTCGATATCCGGATCGCCTAATGG----------ATTAATGGTACTGTGATGTT---G-GCGCAA-------T-CCCCCCACAGAGTTGGTCATCACGCGATCTCGCCCAACGTGTTGTCACGTCATGCTGA

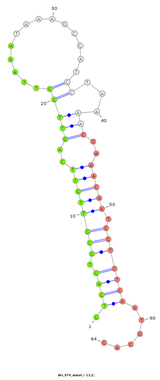
Generated: 09/08/2015 at 07:11 PM

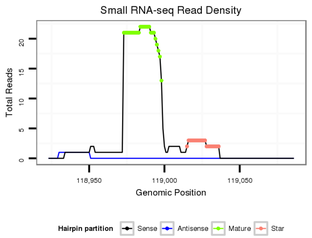
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.ltop3	1
crit.stem	0
crit.back	0
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

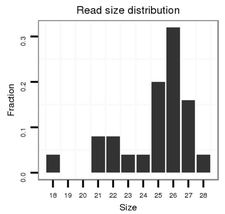
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_974	**scaffold_12472:118973-119036 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

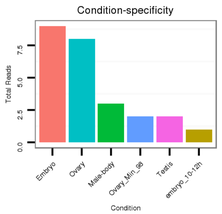
Legend: mature star mismatch in alignment mismatch in read

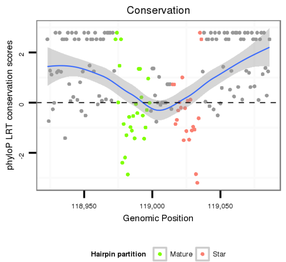
Predicted structure











Show Alternate Folds

Flybase annotation

intron [DviriGJ18529-in]; CDS [DviriGJ18529-cds]; CDS [DviriGJ18529-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CCAGCCTGCTGGGACATCTGGATGACTTTGATGCCACGCGCGCATATACTG	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060662 9x160_0-2h_embryos_total	SRR060658 140_ovaries_total	SRR060676 9xArg_ovaries_total	SRR060682 9x140_0-2h_embryos_total	SRR060677 Arg9_ovaries_total	SRR2096056 Ovary_Min_46	SRR2096058 Ovary_Min_98	V116 male body	SRR2096060 Ovary_Min_193	M047 female body	SRR060655 9x160_testes_total	SRR060661 160x9_0-2h_embryos_total	SRR060663 160_0-2h_embryos_total	SRR060667 160_females_carcasses_total	SRR060672 9x160_females_carcasses_total	SRR060678 9x140_testes_total	SRR060684 140x9_0-2h_embryos_total	SRR1106721 embryo_10-12h	SRR2096013 Ovary_Strain_9_oxidized	SRR060666 160_males_carcasses_total	SRR060679 140x9_testes_total	SRR060687 2h_embryos_total	SRR2096055 9_0-Ovary_Min_43	V053 head
**********	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
.....GTGAGTGCGTTGTTCAGTTGGTTAAA.....	26	0	1	8.00	8	0	3	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGCGTTGTTCAGTTGGTTAA.....	25	0	1	4.00	4	1	0	0	0	2	0	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
.....GTGAGTGCGTTGTTCAGTTGGTTAAAT.....	27	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GAAACAATCGTCTCAATGCAG.....	22	1	1	2.00	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGCGTTGTTCAGTTGGTT.....	23	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GATCAGTGAGAGCAGCGTTG.....	19	1	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
.....GGACATCTGGATGACTTTGA.....	20	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
.....CGAAACAATCGTCTCAATGCAG.....	22	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGCGTTGTTCAGTTGGT.....	22	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AAACGAAACAATCGTCTCAATGCAG.....	26	1	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTTCAGTTGGTTAAATAAAGGGATCCT.....	27	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGCGTTGTTCAGTTGGTTAAATA.....	28	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGCGTTGTTCAGTTGG.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGCGTTGTTCAGT.....	18	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GCGACCCTAAAACGAAACAATCGTC.....	25	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGCGTTGTTCAGTTGGTTA.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GAAACAATCGTCTCAATGCAG.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
.....TGATGCCACGCGCGATATACTG.....	22	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGCGTTGTTCAGTTG.....	18	2	7	0.29	2	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

GGTCGGACGACCCTGTAGACCTACTGAAACTACGGTGCGCGCTATATGAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M047 female body	SRR060666 160_males_carcasses_total	SRR060685 9xArg_0-2h_embryos_total	V047 embryo	SRR1106729 mixed whole adult body
**********	*	*	*	*	*	*	*	*	*	*
.....CGACCCTGTAGACCTACTGAA.....	21	0	1	1.00	1	1	0	0	0	0

Show Alignment With Reads

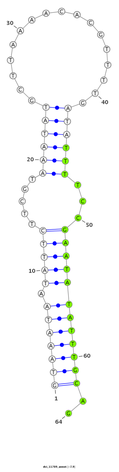
Re-alignment of all predicted orthologs

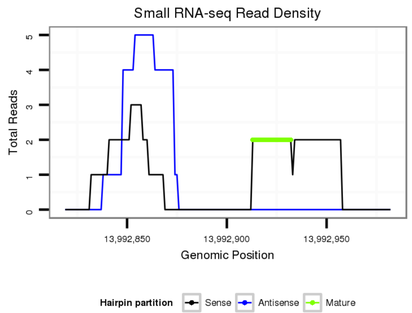
Species	Coordinate	ID	Alignment
droVir3	scaffold_12472:118923-119086,+	dvi_974	CCAGCCTGCTGGGACATCTGGATGACTTTGATGCCACGCGCGCATATACTGTGAGTGCGT---------T--------------------DTT-------------CAGTTGGTTA------AA----------TAAAGCGATCCTAAAACGAA----ACA-----A---TCGTCT-----C--AATGGAGGACCCATCATCGAACATGTCGGTGATCAGTGAGAGCAGCGTTGATTATCG
droMoj3	scaffold_6308:1430622-1450780,-		CCAGCTTCGCTGGGCCATCTGGATGATTTTGATGCCACGCGCGCATATACTGTGAGTTAA--------T-----------------CTAGTGA-ATGCTTAGTAG-----------------CAGTTA-----AC----------TAATC---TCTCAATCAAA---CTCCATCTTGGAGGTTCCTCTCTCGCATGTCGGTGATCAGTGAGAGCAGCGTTGATTATCG
droGri2	scaffold_15203:2034606-2034734,-		CCAGCTTCGCTGGGCCATCTTGATGACTTGATGCCACGCGCGCATACTGTGAGTTTAAAATAGGAGGAACAAAAAGGAAAAGCAGCAGCATCTG-----------------CAGTTA-CTG-------AA----------TAAA---TAATCAATC-------------------------------TATTTGGGTTTCC--TTATGCGAGGTCCATCATCGAGTGTCGGTGATCAGCGAGCAGCGTTGATTATCG
droWil2	scaf2_1100000024909:1940173-1940334,-		CCAGCCTTCGGGCCATCTGATGATTTGATGCCACGCATATACTGCTGAGTAACTGCTGGGCTAGACATC-------------A-----------------A---A-------AA-------------CTCAATT--CCGCATA-------------AT------GC----------CTTAATTC--CAATAA---TATATGCAATCCCTCCCTATGCTGTCATGTCGGTGATCAGTGATATGCTCTCGTCGATGTCGTGATCAGTGAGAGCAGCGTTGATTCTCG
dpo5	DL_groups:2023966-2024133,+		CCTCATTGCTGGGACATCTGATGATTTGATGCCACGCATATACTGTGTGAGTGCGT---------AA---TAAC-------------------------------CCTTCAAAAGAACCTTCTATATTAATTGAATTCTTGAATTTTAATTCTCCC

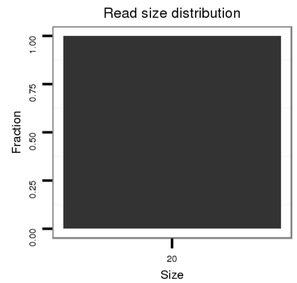
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_11709	**scaffold_12963:13992869-13992932 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

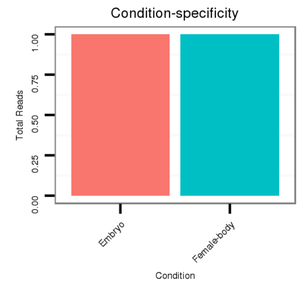
Legend: mature star mismatch in alignment mismatch in read

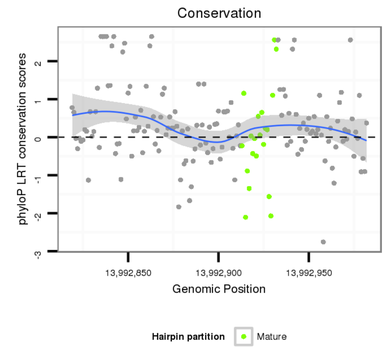
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dvir\GJ17515-in]; CDS [Dvir\GJ17515-eds]; CDS [Dvir\GJ17515-eds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CCAGGCACCAATATTTAAAAAAAGAAGCTGATCAACGGATGCTGCAAAGTGGTAAATAATATTCTTCGTAAATATGCTTAAAACACGTTTTGATATTTTCCGAATATATTTGCAGAAAACATTGACGTTGGCAGCGGAGCATTCGCGGCAAATAGTGGCACCATT	Read size	# Mismatch	Hit Count	Total Norm	Total	M047 female body	M061 embryo	SRR060656 9x160_ovaries_total	SRR060663 160_0-2h_embryos_total	SRR060669 160x9_females_carcasses_total	V047 embryo	V116 male body	SRR060655 9x160_testes_total	SRR060661 160x9_0-2h_embryos_total	SRR060681 Argx9_testes_total	SRR060685 9xArg_0-2h_embryos_total	SRR1106717 embryo_6-8h	SRR2096014 Ovary_Strain_160_oxidized	V053 head	SRR2096055 Ovary_Min_43	SRR060689 160x9_testes_total	SRR060677 Argx9_ovaries_total
((((((((.(((((.....((((((.....))))))...)))))))))))..																						
....................TTTTCCGAATATATTTGCAGA....	21	1	1	12.00	12	3	0	2	0	0	2	2	1	1	0	0	0	0	1	0	0	0
....................TTTTCCGAATATATTTGCAGA....	20	0	1	2.00	2	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
.....TTTAAAAAAGAAGCTGATCAACGGAT....	26	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
....................TTTCCGAATATATTTGCAGA....	20	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..............ACGGATGCTGCAAAGTG....	17	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
....................ATTTTCCGAATATATTTGCAGA....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....................AAACATTGACGTTGGCAGCGGAGC....	24	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
....................TTTTCCGAATATATTTGCAGA....	21	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..............CAACGGATGCTGCAAAGTGA....	20	1	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GAAGCTGATCAACGGATGCT....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....................AAAACATTGACGTTGGCAGCGGAGC....	25	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
....................TTTTCCGAATATATTTGCAGTCA....	23	3	3	0.67	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0

Anti-sense strand reads

GGTCCGTGGTTATAAATTTTTTCTTCGACTAGTTGCCTACGACGTTTCACCATTTATTATAAGAAGCATTTATACGAATTTTGTGCAAAACTATAAAAGGCTTATATAAACGTCTTTTGTAACTGCAACCGTCGCCTCGTAAGCGCCGTTTATCACCGTGGTAA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR2096014 Ovary_Strain_160_oxidized	GSM1528803 follicle cells	SRR060688 160_ovaries_total	SRR060676 9xArg_ovaries_total	SRR060685 9xArg_0-2h_embryos_total	SRR2096080 embryo_0-2h from 15to16 day old nondysgenic mothers	SRR2096081 embryo_0-2h from 15to16 day old nondysgenic mothers	SRR060684 140x9_0-2h_embryos_total	SRR2096026 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096079 embryo_0-2h from 15to16 day old dysgenic mothers	V053 head
((((((((.(((((.....((((((.....))))))...)))))))))))..																
..............TAGTTGCCTACGACGTTTCACCATTT....	26	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0	0
..............TTTCTTCGACTAGTTGCCTACGACGT....	26	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0
..............CCTACGACGTTTCACCATTTAT....	22	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0

Show Alignment With Reads

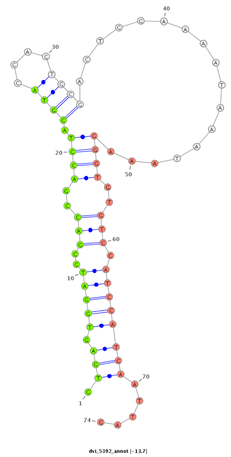
Re-alignment of all predicted orthologs

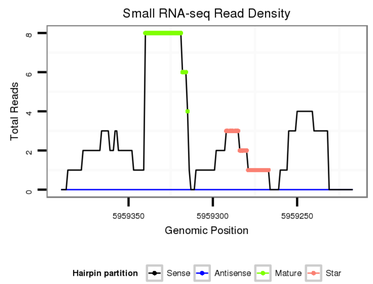
Species	Coordinate	ID	Alignment
droVir3	scaffold_12963:13992819-13992982 +	dvi_11709	CCAGGCACCAATATTTAAAAAAAGAAGCTGATCAACGGATGCTGCAAAGTGGTAAATAATATTCTTCG-----T-----AAATATG-----CT-TAAAACACGTT------TTG----------ATATTT--TCCGAATATATTTGCAGAAAACATTGACGTTGGCAGCGGAGCATT-------CGCGGCAAATAGTGGCACCATT---
droMoj3	scaffold_6500:29516605-29516778 +		GCAGGCGCCGATGTTTAAAAAAAGAAGCGGATCAACGCAATAACGCAAAGTGGTAAACGTCT----TGG----G-----G-------TAATCT-CGTAGA------TAAATTAAACATTAATCTTATAGTTATTGTGCGTC-TACTGCGTGTTTCAGAAAACATGAGGTTGGCGGAGCGCG-------GGCGGCAAATAGTGGCACCATT---
droGri2	scaffold_15126:1849156-1849325 -		GCAGGCCCCATGTTTAAAAAAAGAAGCGGATCAACGCGGTGATGCAAGCGCGGTATATATTCCGATATA----G---TATA----TATATT-TGCGA------AAACATATACTT--------GA-ATATATTTCGCGTCACGCAGATGCATGGATGCGGGTGCGGAGGGGC---TTTTGTGGCGTGCAGTGGCACGCGAT---
droWil2	scf2_1100000004961:1571032-1571102 +		GCAGGCACCAATGTTGAAAAAAGAAAGGATCAGCGATATATGCAATGCAAGGTGGAAATTAT---AT-------G-----G-----G-----

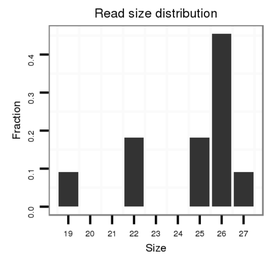
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_5392	**scaffold_12875:5959267-5959340 -**	**candidate**	**Mirtron**	**antisense_to_intron**	[View on UCSC Genome Browser (Cornell Mirror)]

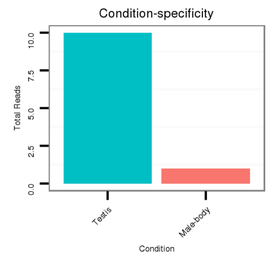
Legend: mature star mismatch in alignment mismatch in read

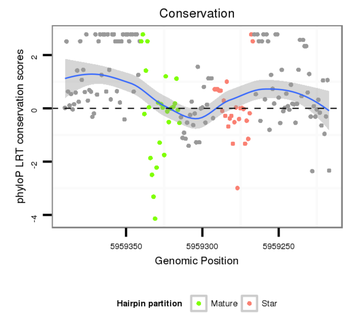
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [DvirGJ21512-in]; intron [DvirGJ20831-in]; CDS [DvirGJ20831-cds]; CDS [DvirGJ20831-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CGCTACGAAGGATCAAGGCTTGGTCATCAAAATGGCACAAAAGAACAAGGGTGAGTGGATCCGACCGACCTACGTACCACTGCGACTGGAAAATAAATAAAGGGTGTGTCCATCCATCAATTAGAAACGCAAACCGTTAAGATAGGTGGTGGCAATTGGTTTGCAGTGCCCCCA **********.(((.(((((..(((..((((.((((....)))).....)))))..))))..))))))))).....**********		Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060678 9x140_testes_total	SRR060670 9_testes_total	SRR060679 140x9_testes_total	SRR060680 9xArg_testes_total	SRR060689 160x9_testes_total	SRR2096057 Ovary_Min_50	SRR060684 140x9_0-2h_embryos_total	SRR060682 9x140_0-2h_embryos_total	SRR060674 9x140_ovaries_total	SRR060681 Argx9_testes_total	V116 male body	SRR060660 Argentina_ovaries_total	SRR2096055 Ovary_Min_43	SRR060659 Argentina_testes_total	SRR2096050 embryo_0-2h from 14 day old Strain 160 mothers	M047 female body	M027 male body	SRR060662 9x160_0-2h_embryos_total	SRR2096080 embryo_0-2h from 15to16 day old nondysgenic mothers	V047 embryo
.....GTGAGTGGATCCGACCGACCTACGTA.....		26	0	1	3.00	3	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGGATCCGACCGACCTA.....		22	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTTAAGATAGGTGGTGGCAATTGG.....		24	0	1	2.00	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGGATCCGACCGACCTACGT.....		25	0	1	2.00	2	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
.....ATAAATAAAGGGTGTGTCC.....		19	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GATAGGTGGTGGCAATTGG.....		19	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCGACTGGAAAATAAATAAAGGGTG.....		26	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGGCACAAAAGAACAAGG.....		18	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AAAGGGTGTGTCCATCCATCAATTAG.....		26	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGGATCCGACCGACCTACGTAC.....		27	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....CATCAAAATGGCACAAAAG.....		19	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AAACCGTTAAGATAGGTGGT.....		20	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...ACGAAGGATCAAGGCTTGGTCATCA.....		25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CAAGGCTTGGTCATCAAAATG.....		21	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

GCGATGCTTCCTAGTTCCGAACCAGTAGTTTTACCGTGTTTTCTTGTTCCCACTCACCTAGGCTGGCTGGATGCATGGTGACGCTGACCTTTTATTTATTTCCCACACAGGTAGGTAGTTAATCTTTGCGTTTGGCAATTCTATCCACCACCGTTAACCAAACGTCACGGGGGT **********.(((.(((((..(((..((((.((((....)))).....)))))..))))..))))))))).....**********		Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060684 140x9_0-2h_embryos_total	SRR060686 Argx9_0-2h_embryos_total	SRR060682 9x140_0-2h_embryos_total	SRR060667 160_females_carcasses_total	SRR2096055 Ovary_Min_43	V047 embryo	M027 male body	SRR060660 Argentina_ovaries_total	SRR060685 9xArg_0-2h_embryos_total	SRR2096014 Ovary_Strain_160_oxidized	V116 male body	M061 embryo	SRR060689 160x9_testes_total	SRR060662 9x160_0-2h_embryos_total	SRR2096013 Ovary_Strain_9_oxidized
.....TGCGACTGGAAAATAAATAAAGGGTG.....		26	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGGCACAAAAGAACAAGG.....		18	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
.....AAAGGGTGTGTCCATCCATCAATTAG.....		26	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGGATCCGACCGACCTACGTAC.....		27	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
.....CATCAAAATGGCACAAAAG.....		19	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
.....AAACCGTTAAGATAGGTGGT.....		20	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
...ACGAAGGATCAAGGCTTGGTCATCA.....		25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CAAGGCTTGGTCATCAAAATG.....		21	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12875:5959217-5959390 -	dvi_5392	CGCTACGAAGGATCAAGGCTTGGTCATCAAAATGGCACAAAAGAACAAGGGTGAGTGGATC----------CG---ACCGACCTACG---TA----------CCACTGCGACTGGAAAATAAATAAA-GGGTGTGT----------CCAT---C---CATCAATTAGAAACGCAA-----ACCGTTAAGATAGGTGG----------TG--------GCAATTGGTTTGCAGTGCCCCCA----------
droMoj3	scaffold_6496:24088048-24088243 +		CGCTAC-AAGGATCAAGGCTTGGTCATCAAAATGGCACAAAAGAACAAGGTGAGTGCCGAATACC----------CCACAGCC----------GGC--------T----------TGCTAAATAAAGAAAGGGTGTGTCCATACATCCATCCCATTT-ATATCCACCCACCCAT---C---CATCAATTAGAAACGCAA-----ACGTTAAATAGGTG----GCG-------A----------CAAATTGGTTTGCGTGCCC-C----------
droGri2	scaffold_15112:879863-880059 -		CGCTA-TTTCA-TCAAGGCATGGTCATCAAAATGGCACAAAAGAAGAAGGTGAGTTG-TGTGTGTT----------GTGTGGCCCAG-CCTAC---------A----T----CTTAATTCAT---T---AATTCATTAGAAACACAA-----ACG-GTAAACG-CGGTGG----------G---------A-AATTGC-AAGATCCAGCC-A----------
droWil2	scf_1100000004514:3616600-3616781 -		TGCGAC-CGAAGCAAGGCTGTGTCATCAAAATGGCACAAAAGAAGAAGGTAGAAGAGTC----------A----ACCGTTTTTATT-TGGTTGA----------T----------GGTTT---------GACTT---A---GTTCCTAGAAAACTCAA-----ACGATGAATTTGGCGAGGCTGTGGCATTGCCACACCACATCCAACTGGTTTGCACCTGTGCCA----------
dp5	1:14268448-14268630 -		C-----CAGGCTAAACAACTGTCATTGCATCACAAGAACAAGGTGAGCCTACAGGC--A----AGGACAGCAGTGGGTGCCCAG-CTCGC---------T----------TCACCCAC----------T---------T--GCCT----------CATCT-T--CCAATTCCAACACAGACGCAGCCTCCACCCGCAAGCCGTCCC----------CGA---------CAA-TGGTTGCCGCAGGTAGTAGCCTAT----------CCG
droPer2	scaffold_4:1047241-1047429 +		A-TGGACAGGCTAAACAACTGTCATTGCATCACAAGAACAAGGTGAGCCTACAGGC--A----AGGACAGCAGTGGGTGCCCAG-CTCGC---------T----------TCACCCAC----------T---------T--GCCT----------CATCT-T--CCAATTCCAACACAGACGCAGCCTCCACCCGCAAGCCGTCCC----------CGA---------CAA-TGGTTGCCGCAGGTAGTAGCCTAT----------CCG
droAna3	scaffold_13266:12917656-12917833 -	dan_1970	ATCGGCCAGGCTCAAGGCTTGGTCATCAAAATGGCCAAAAGAACAAGGTTCGTCCTCGAAATAGCTT----------T--CG---------A-------TTTCATTAAAAC----------T---------T--TGATT----------AACGTT-T--A---CGTTTCCAGAACTCAA-----ACGTTAAGATTGTGCCGGCGGAGGAATGGCTT---------CAATTGGTTAATTGAGTGGTG---TAT----------
droBip1	scf7180000396730:1004119-1004286 +		A-TCG-CCAGGCTCAAGGCTTGGTCATCAAAATGGCCAAAAGAACAAGGTGTAGAGCGCGGGTCAGGAT----------CG---CG---------T-------TTACATCTAAAC----------T---------A-TCAT---A---CCTTTCCAGAACTCAA-----ACGTTAAGATAGTGCCGGCGGAGGAATGGCTT---------CA----------
droKik1	scf7180000302476:1056500-1056651 -		A-TCG-CCAGGCTCAAGGCTTGGTCATCAAAATGGCCAAAAGAACAAGGTAAGTGCGTGG----------ATTCTCCA-TTAA---------G-T-------ATCTCTCG----------T---------T--GCCT----------GACCT---G---GCATCCGCAGACTCAA-----ACGTTAAGTTTGTGCCGGCGGAGGTCTGGCCA---------CA----------
droFic1	scf7180000453858:1080519-1080717 +		A-TCG-CCTCCAGCTCAAGGCTGGTCATCAAATGGCCAAAAGAACAAGGGTAGGCGCAGATC----------T--AG--------TT---G-----TTCCCCCCAATCTCCATCCCGTT-ATTCGAATCCAAAT---T-------C----------T---------T--GCAT----------GCATCCG---G---AATCCCCCAGACAGCA-----ACGTTAAACAGCGCCGCACTGGGG---------CAA-TGGTTACAACCCTGTGGG----------
droEle1	scf7180000491107:1459896-1460088 +		A-TCG-CCAGGCTCAAGGCTGGTCATCAAAATGGCCAAAAGAACAAGGTAAGTCTAGGG-TC----------TGTTGG------CA----TA-------+----------T---------AAC-------TACTTCAA----------T---------T--GCAT----------CTGTTGCCCAATCCGCA---C---AATCCCATAGAAACCAA-----ACGTTAAGTTTGTGCCGGTGGCGGACTAGCCA---------CAA-TGGTTT-CCCCTGTGG---TTTGGCGCC---------CCA
droRho1	scf7180000777217:542891-543086 -		A-TCG-CCAGGCTCAAAGTTTGGTCATCAAAATGGCCAAAAGAACAAGGTGAGCATTTGTTTTGGGGAGGAGTG----------A----TAG-------+----------T---------AGA----------T---------T----TACCT---------A-----G---TACAATTGTAA---AACAAATCCATAGAAACCAA-----ACGTTAAGTTGATGCCGGTGGCGGACTGGCCA---------CAA-TGGTTTGCCCTGTGG-GGCCTATGGGGCACCTC----------
droBia1	scf7180000301506:1067593-1067764 +		A-TCG-CCAGGCTCAACGCTTGGTCATCAAAATGGCCAAAAGAACAAGGTGAGTTAGGACC--A----------T----ACC---AGTGGC-TTTCCTC----------T-------CAAA----------T--GATT----------AATTTTCGAAAA---ACCCTCCCAGACAGCA-----ACGTTAAGTTGTGCCGGTGGCGCTCTGGCCA---------CAA-TGGTTTA-CCCC----C----------CA----------
droTak1	scf7180000415870:652185-652366 +		A-TCG-CCAGGCTCAACGCTTGGTCATCAAAATGGCCAAAAGAACAAGGGTGAGTTTGGGCT----------T----------C----TGTAAGGT-GAC-TTCCCAA----------T-------C----------T-------ATCACGAC---TTTAATTC-T--T-A-AGTCGAGAACAGCA-----ACGTTAAGTTGATGCCGGTGGCGGACTGGCCA---------CAA-TGGTTT-CCCCTGTGGTG----------
droEug1	scf7180000409209:522757-522933 +		A-TCG-CCAGGCTCAACAGCTTGGTCATCAAAATGGCCAAAAGAACAAGGTGAAGCTTTAATTCCCGGAA---AGT----------T----------T----------TCCCCTG----------T-------TAAAAGGG----------T-------AGCTTTAA---A---AATCCTCTAGAAACCAA-----ACGTTAAGTTGATGTCCGGTGGACTGGCTA---------CAA-TGGTTTAGCCCCGTGG-G----------
dm3	chr2R:5645187-5645369 -		TGCCG-CCAGGCTCAAGCTTGGTCATCAAAATGGCCAAAAGAACAAGGTGAGCCATAGC----------T--C----------AAG-G-------TGTTCTCGGAA----------GATTC-T-TAG-AAA----------T--GTATGT----------T-------CGT---A---AATCTTCTAGAACCAA-----ACGTTAAGTGTGCCCGGAGGCGGGCTGGTCA---------CAA-TGGTTTGCCCCGTGA-C----------
droSim2	scaffold_6422046:6423249 -		TGCCG-CCAGGCTCAAACGCTTGGTCATCAAAATGGCCAAAAGAACAAGGTGAGCCAAAGAGAAAAGAAAGAGAAGCAAGGTTGAGCCAAAGC----------T--C----------AAG-G-------TTTCTCGGAA----------GTCTC-T-TAG-AAA----------T--GTAAGC----------T-------CGT---A---AATCTTCTAGAACCAA-----ACGTTAAGTGTGCCCGGAGGCGGGCTGGTCA---------CAA-TGGGTTTGCCCCGTGA-C---------TTTGGGCCACCAGGGATTCCA
droYak3	ch:18271083-18271262 -		A-TCG-CCAGGCTCAACGCTTGGTCATCAAAATGGCCAAAAGAACAAGGTGAGCCAAAGAGAAAAGAAAGAGAAGCAAGGTTGAGCCAAAGC----------T--C----------AAG-G-------TGTCCTCTGGA----------GTTTC-T-TAG-AAA----------T--GTAAGC----------T-------CGT---A---AATCTTCTAGAACCAA-----ACGTTAAGTGTGCCCGGAGGCGGGCTGGTCA---------CAA-TGGTTTGCCCCGTGA-C----------
droEre2	scaffold_4929:8719273-8719445 +		A-TCG-CGTAGGCTCAAGGCTTGGTCATCAAAATGGCCAAAAGAACAAGGTGAGCCAACAAGC----------T--CTTAC---------G-GGCTCGG----------T-------TGTCGAAA----------T--GTAAGC----------T-------AA---G---C---AATCTTCCTAGAACCAA-----ACGTTAAGTGATGCCGGAGGCGGGATGGCCA---------CAA-TGGTTTA-CCCCGTGGA----------

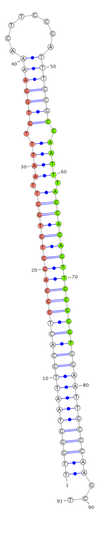
Generated: 09/08/2015 at 07:13 PM

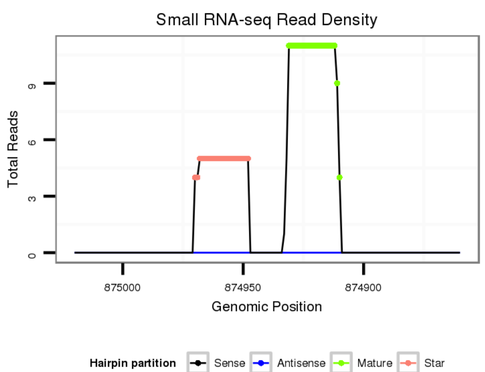
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.gmean	0
crit.dori	0
crit.back	0
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

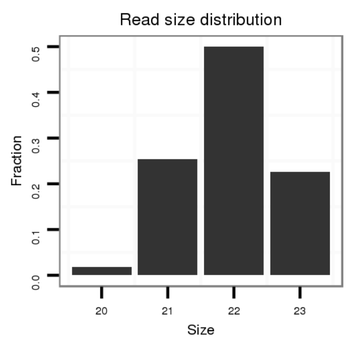
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_403	**scaffold_12928:874910-874970 -**	**candidate**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser [Cornell Mirror]]

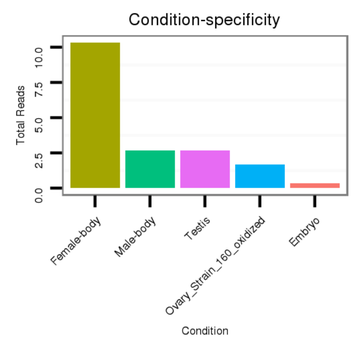
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annnotation

Antisense to intron [Dvir\GJ16751-in]

No Repeatable elements found

mature	star
1. scaffold_12875:1843124-1843145 + 2. dvi_403 scaffold_12928:874910-874931 - 3. scaffold_12958:1682328-1682349 -	

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTTATAGGAACCTAGTGCATATGTGATCCAGCGATTTGGGTAATTCCACTCGCAGCTGTGGTTAATTTGTGGAAAACTTCCGATTTCCGCCAATTTACCACAGTTGCGGGTGGAATTGCCCAAGCTCAACATTTTCCCTGAGCAAGGCCTGCGAATGCTCG **********(((((((((((((((((((((((((.((((.(((((((.....)))))))).)))).)))))))))))))))))))))))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M047 female body	V116 male body	SRR060683 160_testes_total	SRR2096014 Ovary_Strain_160_oxidized	M027 male body	SRR060689 160x9_testes_total	SRR060684 140x9_0-2h_embryos_total	SRR060672 9x160_females_carcasses_total	SRR060686 Argx9_0-2h_embryos_total	SRR1106714 embryo_2-4h	SRR2096056 Ovary_Min_46	V053 head	SRR060663 160_0-2h_embryos_total
.....CCAATTTACCACAGTTGCGGGT.....	22	0	3	4.33	13	5	2	2	3	0	0	1	0	0	0	0	0	0
.....CGCAGCTGTGGTTAATTTGTGGA.....	23	0	1	4.00	4	0	2	1	0	0	1	0	0	0	0	0	0	0
.....GCCAATTTACCACAGTTGCGGG.....	22	0	2	3.00	6	6	0	0	0	0	0	0	0	0	0	0	0	0
.....CCAATTTACCACAGTTGCGGG.....	21	0	3	2.00	6	4	0	0	2	0	0	0	0	0	0	0	0	0
.....GCCAATTTACCACAGTTGCGG.....	21	0	2	1.50	3	3	0	0	0	0	0	0	0	0	0	0	0	0
.....CGCCAATTTACCACAGTTGCGG.....	22	0	2	1.50	3	3	0	0	0	0	0	0	0	0	0	0	0	0
.....CAGCTGTGGTTAATTTGTGGA.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0
.....GCCAATTTACCACAGTTGCG.....	20	0	3	0.33	1	1	0	0	0	0	0	0	0	0	0	0	0	0
.....CCAATTTACCACAGTTGCGGGTT.....	23	1	3	0.33	1	1	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

AAATATCCTTGGATCACGTATACACTAGGTCGCTAAACCCATTAAGGTGAGCGTCGACACCAATTAAACACCTTTTGAAGGCTAAAGGCGGTTAAATGGTGTCAACGCCCACCTTAACGGGTTCGAGTTGTAAAAGGGACTGCGTTCCGGACGCTTACGAGC **********(((((((((((((((((((((((((.((((.(((((((.....)))))))).)))).)))))))))))))))))))))))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V053 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12928:874860-875020 -	dvi_403	TTTATAGGAACCTAGTGCATATGTGATCCAGCGATTTGGGTAATTCCACTCGCAGCTGTGGTTAATTTGTGGAAAACTTCCGATTTCCGCCAATTTACCACAGTTGCGGGTGGAATTGCCCAAGCTCAACATTTTCCCTGAGCAAGGCCTGCGAATGCTCG

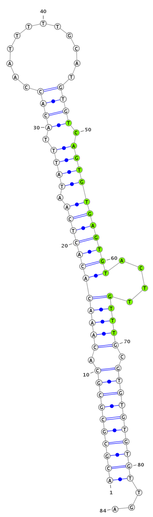
Generated: 02/04/2015 at 08:55 PM

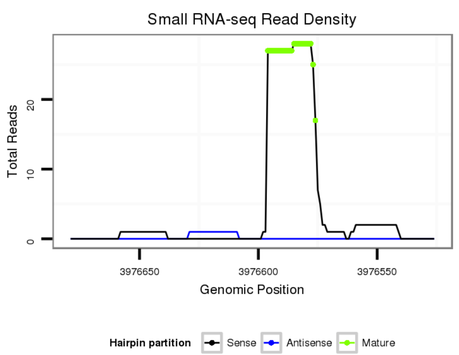
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

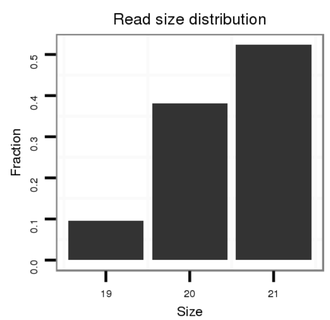
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_170	**scaffold_12855:3976576-3976629 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

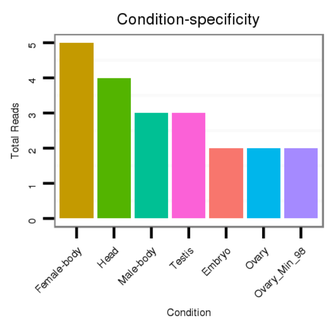
Legend: mature star mismatch in alignment mismatch in read

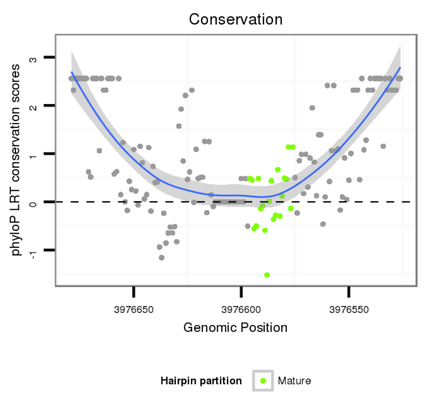
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ACATAAATAAATTGTGCAATAATGTTTGCCATACAACGCGCGCGCACAAACACACTCAATATTTACACCAATTTTTGCATGTGTCAGTGTGAGTGTACTTGTTTGCGTGTGTGTGTTGATTTTTACCCGATGCCGAATGACAATATACACGCAA **********((((((((((.(((((((((((.((((.((((.....)))).))))))))))....)))))).))))))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M047 female body	V116 male body	V053 head	M061 embryo	SRR060677 Argx9_ovaries_total	SRR060681 Argx9_testes_total	SRR060686 Argx9_0-2h_embryos_total	M028 head	SRR2096058 Ovary_Min_98	V047 embryo	M027 male body	SRR060656 9x160_ovaries_total	SRR060672 9x160_females_carcasses_total	SRR060676 9xArg_ovaries_total	SRR060685 9xArg_0-2h_embryos_total	SRR1106722 embryo_10-12h	SRR2096055 Ovary_Min_43
.....TCAGTGTGAGTGTACTTGTTT.....	21	0	1	10.00	10	1	1	1	1	2	3	1	0	0	0	0	0	0	0	0	0	0
.....TCAGTGTGAGTGTACTTGTT.....	20	0	1	8.00	8	3	1	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0
.....TCAGTGTGAGTGTACTTGTTTGC.....	23	0	1	3.00	3	0	1	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0
.....TCAGTGTGAGTGTACTTGTTTG.....	22	0	1	2.00	2	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
.....TCAGTGTGAGTGTACTTGT.....	19	0	1	2.00	2	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
.....TCAGTGTGAGTGTACTTGTTTTAAA.....	24	3	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
.....TCAGTGTGAGTGTACTTGTTTGT.....	23	1	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
.....ATGTTTGCCATACAACGCGC.....	20	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCAGTGTGAGTGTACTTGTTTA.....	22	1	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
.....TGTCAGTGTGAGTGTACTTGT.....	21	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCAGTGTGAGTGTACTTGTTTGCGT.....	25	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
.....ATTTTTACCCGATGCCGAATG.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
.....TTTTACCCGATGCCGAAT.....	18	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
.....GTACTTGTTTGCGTGTGTGTGT.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCAGTGTGAGTGTACTTGTG.....	20	1	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

TGTATTTATTTAACACGTTATTACAAACGGTATGTTGCGCGCGCGTGTTTGTGTGAGTTATAAATGTGGTTAAAAACGTACACAGTCACACTCACATGAACAAACGCACACACACAACTAAAAATGGGCTACGGCTTACTGTTATATGTGCGTT **********((((((((((.(((((((((((.((((.((((.....)))).))))))))))....)))))).))))))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060656 9x160_ovaries_total	V116 male body	V047 embryo
.....GTGTGAGTTATAAATGTGGTT.....	21	0	1	1.00	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12855:3976526-3976673 -	dvi_170	ACATAAATAA-ATTGTGCAATAATGTTTGCC-ATA-----CAACGC----GC-----GC-GC-ACAAACACAC----TC-AATATTTACACCAATTTTTGCATGTGTCAGT---GTGAG--T--GTA--CTTGTTT----GCGTGTGTGT--------------GT--T---G-A---TT-TTTAC----------CCGATGCCGAATGACAATATACACGCAA
droMoj3	scaffold_6540:8284322-8284453 -		ACATAAATTT-ATTTTGCAATAATATT-TTGC-ACA-----A-----TATACACATAT--T---------AAGGTAGA----CATACA----------T-TATGTAT---ACAAG--G--ATA--CAAATAT----GTGTGTGTTTGTT---------T--T---T--T---T--T----GCCTTTTGC----------CCGATGCCGATGACAATATACACGCAA
droGri2	scaffold_14906:6597375-6597503 -		ACATAAATTCATTGTGCAATATTTG-CCGT-A--------CAAG-----T---T--GCGGGC-GT-ACGAACACAGAGTCAGAATAATAAAGC----------T---T--CCCC-T-TACT--CAAACACAT--GTACTCAAGGG----------T--T---T--A---GTGTGTGTG----------TGTGTGCCAGTGACAATATACACGCAA
dp5	2:11330929-11331118 -		ACATAAATAAATTGTGCAATAATTT-CC-C-ATA-----CGAG-----T--TCGGCTTTG-AGTCGCACAGAGATAGAGATCATTTG----------T---T--TACG--T-ATT-GAAATAT----GCGTTTGTGTCTATTTG--------T--T---T--T---GTTTTGCCTTCTGCCGCTGCCCCTGCGGCTGCCAGCGATTGCCAGC-----GATTGCCTGCCTGCGTGCCGAGTGACAATATACACGCAA
droPer2	scaffold_0:9184920-9185115 +		ACATAAATAAATTGTGCAATAATTT-CC-C-ATA-----CGAG-----T--TCGGCTTTG-AGTCGCACAGAGATAGAGATCATTTG----------T---T--TACG--T-ATT-GAAATAT----GCGTTTGTGTCTATTTG--------T--T---T--T---GTTTTGCCTTCTGCCGCTGCCCCTGCGGCTGCCAGCGATTGCCTGCCCGCCTGCCGCCGCTGCCTGCGTGCCGAGTGACAATATACACGCAA
droAna3	scaffold_13340:9339749-9339876 -		ACATAAATAAATTGTGCAATAATCTT-CCGCC-ATA-----------T---T--T--T--------GAGATAGAGATAGAGATAGTAT----------TTTACCTT--CC----GGGTGTAT--GTGTGTGTGTGTCTATTTCGCC-----T--T---T--T---TTTTTTTT----------CGACCGCCTAGTGACAATATACACGCAA
droBipl	scf7180000396712:2960519-2960658 -		ACATAAATAAATTGTGCAATAATTT-CCGCC-ATA-----C-----T---T--T--T--T-----ACAGAGATAGAGATAGAGTAT----------TTTACCTT--CC----GGGATCT--GTGTGTGTGTGTCTATTTCGTATTTGTAT--T---T--T--TTTTTTTC----------GGACCGCCTAGTGACAATATACACGCAA
droKik1	scf7180000302634:808643-808787 +		ACATAAATAAATTGTGCAATTATTT-TGCC-ACA-----C-----T---T--GACAGGGGCGCGATA----GAG--AGACAGCACACA----------T---T--CTCTCC--T-T--------T----TCGTTTGTGTGTCTATTTCGTCTATATTCT--T---TCTATATTTTTTTCG----------CGCCCGCCTAGCGACAATATACACGCAA
droFic1	scf7180000453800:1301165-1301301 +		ACATAAATAAATTGTGCAATAATTT-CCGCC-ACA-----T-----T---T--T--T-------TAGAGGCAGAGATACACATT----------T---C-TCTCCCTT--TAAATAT----GCGTTTGTGTGTCTATTTCGTATATGTTGCGC---TCT---TTTTTTCG----------CGCCCGCCTAGTGACAATATACACGCAA
droEle1	scf7180000486474:134932-135047 +		ACATAAATAAATTGTGCAATAATTT-CCGCC-ACA-----T-----T---T--T--T-------CAGAGCCAGAGATACACATT----------T---C-TCTCTCTT--TAAATAT----GCGTTTGTGTGT----------T--T---T--TTTTTTCG----------CGCCCGCCTAGTGACAATATACACGCAA
droRho1	scf7180000778053:48582-48694 +		ACATAAATAAATTGTGCAATATTTT-CCGCC-GCA-----T-----T---T--T--T-------CAGAGCCAGAGATACACATT----------T---C-TCTCTCTT--TAAATAT----GCGTTTGTGTG----------T--T---T--TTTTTTCG----------CGCCCGCCTAGTGACAATATACACGCAA
droBia1	scf7180000299102:1117161-1117292 -		ACATAAATAAATTGTGCAATAATTT-CCGCCGTCTCCGCAGGAGACACA-----T---T--ACACGCACAGAGTCGAGATACATACA----------T---TTCT-CTTTT-GAAATGT----G--------T--T--T--T---TTTTTTCG----------CGCCCGCCTAGTGACAATATACACGCAA
droTak1	scf7180000415653:25722-25845 -		ACATAAATAAATTGTGCAATAATTT-CCGCC-ACA-----C-----T---T--T--GAACACACAGAGCCAGAGATACATACA----------T---TTCTCCCTTTT-GAAATAT----GTGTTTT---T--T--T--T---TTATTTCG----------CGCCCGCCTAGTGACAATATACACGCAA
droEug1	scf7180000409802:1190202-1190345 -		ACATAAATAAATTGTGCAATAATTT-TGCC-ACA-----C-----T---T--T--T-----AGACCGAAAAAT-CTTTACACATAAGTTAGAGATACATACA----------T---TTCT-CCCTGTAAAATAT----GCGTTTGTGTGTATGTT---------T-T---C-C---TTTTTTCG----------CGCCCGCCTAGTGACAATATACACGCAA
dm3	chr3R:8838122-8838234 +		ACATAAATAAATTGTGCAATAATTT-CCGCC-GCA-----C-----T---T--T--T----G-----A-----T---T--T--T----G-CACAGAGCCAGAGATACATACA----------T---CTCT-CTTT-GAAATTT----A---------T--T--T--A---TTTTTTCG----------CGCCCGCCTAGTGACAATATACACGCAA
droSim2	3r:12326873-12326986 -		ACATAAATAAATTGTGCAATAATTT-CCGCC-GCA-----C-----T---T--T--T----G-----A-----T---T--T--T----G-CACAGAGCCAGAGATACATACA----------T---CTCT-CTTT-GAAATTT----A---------T--T--TA--T--TTTTTTCG----------CGCCCGCCTAGTGACAATATACACGCAA
droSec2	scaffold_0:13158214-13158327 -		ACATAAATAAATTGTGCAATAATTT-CCGCC-GCA-----C-----T---T--T--T----G-----A-----T---T--T--T----G-CACAGAGCCAGAGATACATACA----------T---CTCT-CTTT-GAAATTT----A---------T--T--TA--T--TTTTTTCG----------CGCCCGCCTAGTGACAATATACACGCAA
droYak3	JRI13132528-13132641 +		ACATAAATAAATTGTGCAATTATTT-CCGCC-GCA-----C-----T---T--T--T----G-CACAGAGCTAGAGATACATACA----------T---T--C--T--CTTT-GAAATTT----A---------T--T--TATA-T--TTTTTTCG----------CGCCCGCCTAGTGACAATATACACGCAA
droEre2	scaffold_4770:12810432-12810543 -		ACATAAATAAATTGTGCAATTATTT-CCGCC-GCA-----C-----T---T--T--T----G-CACAGAGCTAGAGATACATACA----------T---TTCT-CTTT-GAAATTT----A---------T--T--T--T--TTTTTTCG----------CGCCCGCCTAGTGACAATATACACGCAA

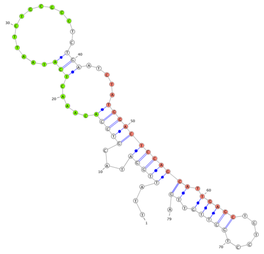
Generated: 09/08/2015 at 08:38 PM

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

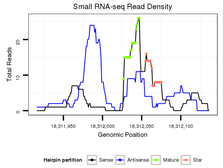
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_24641	**scaffold_13049:18311966-18312086 +**	**candidate**	**Canonical miRNA**	**antisense_to_CDS**	[View on UCSC Genome Browser (Cornell Mirror)]

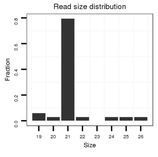
Legend: loop 5p mature 3p alignment mismatch in star

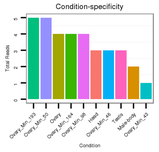
Predicted structure

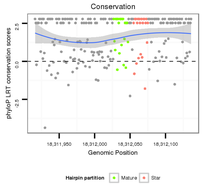


dvi_24641_annot [-14.5]









Show Alternate Folds

Flybase annotation

Antisense to CDS [Dn4Gf11562-cds]

No Repeatable elements found

Sense Strand Reads

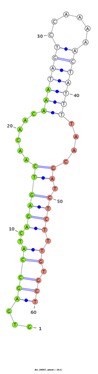
hide 3p reads show mid mismatch reads

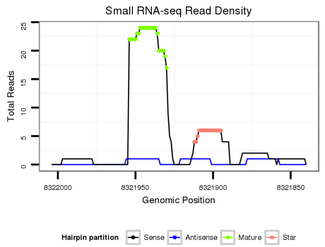
| Read # | Hit | Total | | |

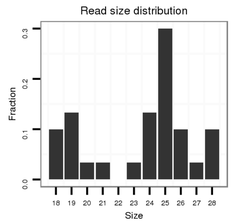
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_18967	**scaffold_13049:8321890-8321954 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

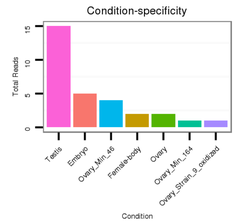
Legend: mature star mismatch in alignment mismatch in read

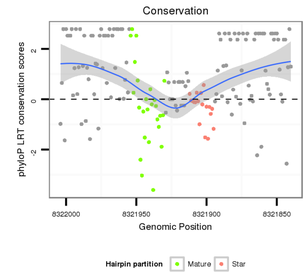
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DviriGJ12168-in]; CDS [DviriGJ12168-cds]; CDS [DviriGJ12168-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ACTCTGGCATGAGCTGCGCCAGGGCAAACTGCCCGAGGAGTTCATAAACA[TGAGCCA----TC---AGA---GT--CAAC----------AA----CA-AA]TAGTCCAAAAACTATTTTAACGATCTCTTTGTGCTTGCAGCAATCTCAGTGGAGCTGCAGCAGGTCATCAAGTGCATGATGTCGCCCGAA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060678 9x140_testes_total	SRR2096056 Ovary_Min_46	SRR060681 Argx9_testes_total	SRR060683 160_testes_total	SRR060686 Argx9_0-2h_embryos_total	M047 female body	SRR060676 9xArg_ovaries_total	SRR060679 140x9_testes_total	SRR060684 140x9_0-2h_embryos_total	M061 embryo	SRR060657 140_testes_total	SRR060659 Argentina_testes_total	SRR060680 9xArg_testes_total	SRR060682 9x140_0-2h_embryos_total	SRR2096013 Ovary_Strain_9_oxidized	SRR2096059 Ovary_Min_164	SRR2096081 embryo_0-2h from 15to16 day old mothers	M047 nondysgenic male body	M027 embryo	SRR2096014 Ovary_Strain_160_oxidized
...GTGAGCCATCAGAGTCAACAACAAA	25	0	1	8.00	8	4	0	1	0	0	0	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0
...GTGAGCCATCAGAGTCAAC	19	0	1	3.00	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
...GTGAGCCATCAGAGTCAACAACAAAT	26	0	1	3.00	3	0	0	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
...GTGAGCCATCAGAGTCAACAACAAATAG	28	0	1	3.00	3	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...TAACGATCTCTTTGTGCTTGCAG	18	0	1	2.00	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...GTGAGCCATCAGAGTCAACAACAA	24	0	1	2.00	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...GTGAGCCATCAGAGTCAA	18	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
...CATGAGCTGCGCCAGGGCAA	20	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
...AGTGGAGCTGCAGCAGGT	18	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
...CCATCAGAGTCAACAACAAATAGT	24	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
...TTTAACGATCTCTTTGTGCTTGCAG	25	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...ACGATCTCTTTGTGCTTGCAG	21	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...ATCAGAGTCAACAACAAAT	19	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
...GTGGAGCTGCAGCAGGTCATCA	22	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0

Anti-sense strand reads

TGAGACCGTACTCGACGCGGTCCCGTTTGACGGGCTCCTCAAGTATTTGT[CACTCGGTAGTCTCAGTTGTTGTTTATCAGGTTTTTGATAAAATTGCTAGAGAAACACGA]ACGTCGTTAGAGTCACCTCGACGTCGTCCAGTAGTTCACGTACTACAGCGGGCTT	Read # size	# Mismatch	Hit Count	Total Norm	Total	SRR060682 9x140_0-2h_embryos_total	M047 female body	SRR060686 Argx9_0-2h_embryos_total	SRR060684 140x9_0-2h_embryos_total	SRR060687 9_0-2h_embryos_total	SRR060681 Argx9_testes_total	M027 male body	M061 embryo	M028 head	SRR060673 9_ovaries_total	V116 male body	SRR060685 9xArg_0-2h_embryos_total	SRR2096080 embryo_0-2h from 15to16 day old nondysgenic mothers	SRR060680 9xArg_testes_total	SRR060678 9x140_testes_total	V053 head	SRR1106728 larvae	SRR2096081 embryo_0-2h from 15to16 day old nondysgenic mothers	SRR060663 160_0-2h_embryos_total	SRR060666 160_males_carcasses_total	SRR060676 9xArg_ovaries_total	SRR1106729 mixed whole adult body	SRR060667 160_females_carcasses_total	SRR1106730 embryo_16-30h	V047 embryo	SRR060659 Argentina_testes_total	SRR060662 9x160_0-2h_embryos_total
...CTCGACGTCGTCCAGTAGTTC	21	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...GTCACTCGGTAGTCTCAGTTGT	22	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...TTTGATAAAATTGCTAGAGA	20	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_13049:8321840-8322004 -	dvi_18967	ACTCTGGCATGAGCTGCGCCAGGGCAAACTGCCCGAGGAGTTCATAAACA[TGAGCCA----TC---AGA---GT--CAAC----------AA----CA-AA]TAGTCCAAAAACTA-TTTTAAACG---ATCT-----CTT-TGTGCTTGCAGCAATCTCAGTGGAGCTGCAGCAGGTCATCAAGTGCATGATGTCGCCCGAA
droMoj3	scaffold_4680:11975589-11975790 -		GT-TGGCATGAGCTGCGCCAGGGCAACTGCCCGAGGAGTTCATAACATGAGCAA----TT--AA-A--T--TCAACCATATT----------G-GAATATA-A----------AA--TAATAACATGTA---T--CTT-TGCGCTTGCAGCAATCTCAGTGAGCTGCAGCAGGTCATGACTGCATGATGTCGCCCGAG
droGri2	scaffold_15110:7350695-7350864 -		ACTCTGGCATGAGCTGCGCCAGGGCAACTGCCCGAGGAGTTCATAAACATGAGCA-----GC-ATTT-AT-CATT-TCAATTTGT---------GGTCACCAT-G----------GA--C-TAAAATATA--T--T-GAGCTGACTATCTGCAGCAATCTCAGTGAGCTGCAGCAGGTCATAAGTGCATGATGTCGCCCGAG
droWil2	scaffold_11000000044511:3745121-3745287 +		G-TTGGCATGAGCTGCGCCAGGGCAACTGCCCGAGGAGTTGATACATGAGCTA----T---C---AT--AT-----ACATAAAAGCGAGGACGGAG-----T--AT---GCATGTCATTTCCACATTTCGTGCATTTCGCAGCAATCTCGTGGATCTGAGCAGGTCATGAAGTGCATGATGATCCCGAG
dp5	XR_group6:9780095-9780158 +		GCTCTGGCATGAGCTGCGCCAGGGCAACTGCCCGAGGAGTTCATAGCATGAGCAC--A-G--AC--A--C-----------------C-----C--A-----------------C-------C-----C---C-----C---GAG
droPer2	scaffold_6125078-55141 +		GCTCTGGCATGAGCTGCGCCAGGGCAACTGCCCGAGGAGTTCATAGCATGAGCAC--A-G--AC--A--C-----------------C-----C--A-----------------C-------C-----C---C-----C---GAG
droAna3	scaffold_13337:1276922-12769385 +		TTT-TGGCATGAGCTGCGCAAGGGCAACTGCCCGAGGAGTTCATAAACATGAGCA-----GC-AG-T-TA-T-ATTT--ATTTTTGA----------GG----CA-G----------T--GTTTCAATTGTATTTAAATCCACCATAGCAATCTCAGTGAGCTGCAGCAGTCATAGTGCATGATATCCCGAG
droBip1	scf718000039589:1253655-1253810 -		TTT-TGGCATGAGCTGCGCAAGGGCAACTGCCCGAGGAGTTCATAAACATGAGCA-----AGT--T-TTT-T--TGT-------T----------GT----TT-CA----------A-TT--TA---ATGTC--ATTTAATCCACCATAGCAATCTCAGTGAGCTGCAGCAGTCATAGTGAACC-CA-G
droKik1	scf718000030268:69247-69406 -		G-TTGGCATGAGCTGCGCCAGGGCAACTGCCCGAGGAGTTCATAACATGAGCGTGTATGC-AAGC---GT--GCGATCTTTAT----------TT----CA-G----------CTTTAATAA---T-C--T---CC--T--TTTTG-AGAT-TC-CTGGAGCTGCAGCAGATTACATCAAGTCATGATGATCCCGAG
droPic1	scf718000045392:1844746-1844907 +		ACTTGGCATGAGCTGCGCAAGGGCAACTGCCCGAGGAGTTATAAACATGAGCTTT----C-AA--AAAA--T--TCAATATTT----------GC----ACA----------G--CA-CA---TT-C--T--T-TGG-CTGCAGCTGCAGCAGTAATACATCAAGTCATGATGATCCCGAG
droEle1	scf718000049126:1263952-1264113 -		ACTTGGCACCCATGATCAAAGGGCAACTGCCCGAGGAGTTCATAAACATGAGCTTC----C-AA--GGCAAT--TT--CCCCGAT----------GC----CA-AAG----------G--CA-AA---AT-C--T--T-TGG-CTGCAGCTGCAGCAGTAATACATCAAGTCATGATGATCCCGAG
droRho1	scf718000076885:150093-150254 -		ACTATGGCATGATCTGCGCAAGGGCAACTGCCCGAGGAGTTCATAAACATGAGCTTA----A-A--G--G-A-T--T-TATTTGGGT----------GG----AG-T----------G--T--TAA-TA---AT-A-T---TTTTCAT-G-GCACCGCAGCAATCTCAGTGGAGCTGCAGCCGGTCAAGTCATGATGATCCCGAG
droBia1	scf718000030219:3274266-3274424 -		G-TTGGCATGAGCTGCGCAAGGGCAACTGCCCGAGGAGTTCATAAACATGAGTTT----TC--TT-TG-GA--TG--ATTTGAT----------G----CA-T----------G--T--TAA-T---GCG-----CTT-CTTTACCATAGCAATCTCCTGGAGCTGCAGCCGGTCAAGTCATGATGATCCCGAG
droTak1	scf718000041586:475844-475996 -		ACTTGGCATGAGCTGCGCAAGGGCAACTGCCCGAGGAGTTCATAAACATGAGCTTT----C-AA--GGT-A--TGCC------T----------AA----CA-AA----------A--T--AACGTGACGATCTTTCCATCACCATAGCAATCTCAGTGAGCTGCAGCCGGTCATCAAGTCATGATGATCCCGAG
droEug1	scf718000040946:1541374-1541530 -		ACTTGGCACGAGCTGCGCAAGGGCAACTGCCCGAGGAGTTCATAACATGAGCTTC----C-AAT--GGAA--A-CTTTTTAGAT----------A----G-T----------A--T--AAG---AAC--T--T-TGG-CTGCTGAACAGCAATCTCCTGGAGCTGCATATCAAGTCATGATGATCCCGAG
dm3	chr3L:5771575-5771736 -		ACTTGGCACGATCTGCGCAAGGGCAACTGCCCGAGGAGTTCATAAACATGAGCTTC----C-GA--CTAGCT--GCCCTACTTAAAT----------GC----CA-G----------G--T--GCTA---AGGCC--T--T-TGG-CTGCGCAGCAATCTCATGGAGCTGCAGCCGGTCAAGTCATGATGATCCCGAG
droSim2	311:5684561-5684721 -		ACTTGGCACGATCTGCGCAAGGGCAACTGCCCGAGGAGTTCATAAACATGAGCTTC----C-GAC--TAGCT--GCCCTACTTAAAT----------GC----CA-G----------G--T--GCTA---AGGCC--T--T-TGG-CTGCGCAGCAATCTCATGGAGCTGCAGCCGGTCAAGTCATGATGATCCCGAG
droSec2	scaffold_21:708419-5708579 -		ACTTGGCACGATCTGCGCAAGGGCAACTGCCCGAGGAGTTCATAAACATGAGCTTC----C-GAC--TAGCT--GCCCTACTTAAAT----------GC----CA-G----------G--T--GCTA---AGGCC--T--T-TGG-CTGCGCAGCAATCTCATGGAGCTGCAGCCGGTCAAGTCATGATGATCCCGAG
droYak3	3L:6341070-6341232 -		G-TTGGCACGATCTGCGCAAGGGCAACTGCCCGAGGAGTTCATAAACATGAGCTAT----C-CTAT--TGGAT--TGCTTTTTAGAT----------GC----CA-G----------G--T--GCTA---AGGCC--T--T-TCG--CTGAACCAGCAATCTCATGGAGCTGCAGCCGGTCAAGTCATGATGATCCCGAG
droEre2	scaffold_4784:8462192-8462353 -		ACTTGGCACGAGCTGCGCAAGGGCAACTGCCCGAGGAGTTCATAAACATGAGCTTC----C-AA--A-CTAT--TGCTACTTAGAT----------GC----CA-G----------G--T--GCTA---AGGCC--T--T-TCG--CTGAACCAGCAATCTCATGGAGCTGCAGCCGGTCAAGTCATGATGATCCCGAG

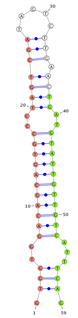
Generated: 09/08/2015 at 07:12 PM

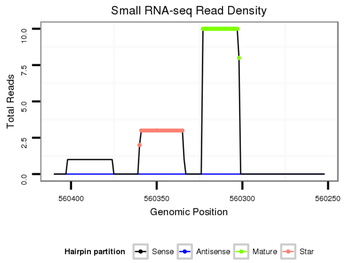
	PASS/FAIL
crit.star	0
crit.star	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.gap1	0
crit.gap3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.pairing	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

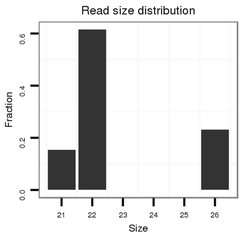
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_9393	**scaffold_12932:560302-560360 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

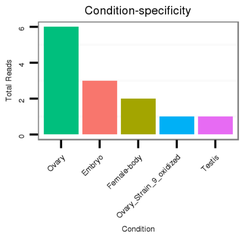
Legend: mature star mismatch in alignment mismatch in read

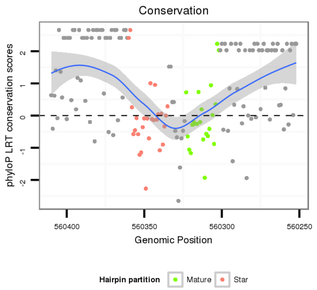
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dvir/GJ14771-in]; CDS [Dvir/GJ14771-cds]; CDS [Dvir/GJ14771-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CACAGAAGCGCCGCAAGGTGCCCGTCGACTACTATGCGCTGAAGGCCAAGGTGGTGGACAGCAGTGCCCTAGTCGATAGTCTTGAACTGATGTATTGTTGTCATTTCAGGTCTCGCTGCTTGAGCGGCGCCATTCAGAGCGGGAGGAGCGGCTGCATAT	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060676 9xArg_ovaries_total	SRR2096059 Ovary_Min_164	SRR060677 Argx9_ovaries_total	SRR060678 9x140_testes_total	SRR2096057 Ovary_Min_50	SRR060667 160_females_carcasses_total	SRR060682 9x140_0-2h_embryos_total	SRR2096013 Ovary_Strain_9_oxidized	SRR060661 160x9_0-2h_embryos_total	SRR060662 9x160_0-2h_embryos_total	SRR060669 160x9_females_carcasses_total	SRR060674 9x140_ovaries_total	SRR060684 140x9_0-2h_embryos_total	SRR2096014 Ovary_Strain_160_oxidized	SRR2096060 Ovary_Min_193	GSM1528803 follicle cells	SRR060668 160x9_males_carcasses_total	M027 male body	SRR060686 Argx9_0-2h_embryos_total
**********.((((..((((((((((..(((((((.....)))).)))))..))))))))))...)))).**********	22	0	1	8.00	8	2	0	2	0	0	0	0	1	0	0	0	1	1	1	0	0	0	0	0
.....TGATGTATTGTTGTCATTTCAG.....	23	1	1	3.00	3	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	1	0	0	0
.....TGATGTATTGTTGTCATTTCAGA.....	23	1	1	2.00	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGGTGGACAGCAGTGCCCTAGTCGA.....	26	0	1	2.00	2	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
.....TGATGTATTGTTGTCATTTCA.....	21	0	1	2.00	2	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
.....CGCCGCAAGGTGCCCGTCGACTACTAT.....	27	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGGTGGACAGCAGTGCCCTAGTCGAT.....	26	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

GTGTCTTCGCGGCGTTCCACGGGCAGCTGATGATACGCGACTTCCGGTTCCACCACCTGTCGTCACGGGATCAGCTATCAGAACTTGACTACATAACAACAGTAAAGTCCAGAGCGACGAACTCGCCGCGGTAAGTCTCGCCCTCCTCGCCGACGTATA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR2096056 Ovary_Min_46	SRR060672 9x160_females_carcasses_total	SRR060666 160_males_carcasses_total	SRR060682 9x140_0-2h_embryos_total	SRR1106729 mixed whole adult body	SRR060661 160x9_0-2h_embryos_total
**********.((((..((((((((((..(((((((.....)))).)))))..))))))))))...)))).**********	27	0	1	1.00	1	0	0	0	0	0	0

Show Alignment With Reads

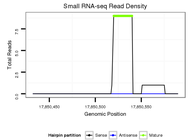
Re-alignment of all predicted orthologs

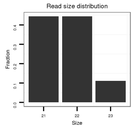
Species	Coordinate	ID	Alignment
droVir3	scaffold_12932:560252-560410 -	dvi_9393	CACAGAAGCGCCGCAAGGTGCCCGTCGACTACTATGCGCTGAAGGCCAAGGTGGTGGA----------CAGCA---------G----------TGCCCTAGTCGATAGTC---TTGAACTGATGTATTGT-TG----------TCATTTCAGGTCTCGCTGCTTGAGCGGCGCCATTCAGAGCGGGAGGAGCGGCTGCATAT
droMoj3	scaffold_6473:985610-985772 +		C-TAGAAAGCGCGCAAGGTGCCCGTCGATACTATGC-CTGAAGGCAAGGCAAGCG----------CGAC---------TAAACATATGCATACCCCAATGTCACTTGGTAAACTGT---------GAA----------TGCTCGAGGTCTCGCTGCTCGAGCGCCGCATCCGAGCGCGAGGAGCGGCTGCAGAT
droGri2	scaffold_14853:173059-173287 -		CACAGAAGCGCCGCAAAAA-CCCCGTCGACTACTATGC-CTGAAGGCAAGGCATATATATATATATATATATATATAGAT----------G----------GAGAATATATCAATCACAAATCCAAA---------ATCCAAACAGATATCATTTTGTATACAAGTTCTACAGTGATAGATTGAATATATGTTTTTAATG----------TTTTCAAGGTCTCGCTGCTTGAGCGCCGCATTCCGAGCGGGAGGAGCGCATTGCATAT
droWil2	scf2_1100000004909:7348988-7349149 -		CACAAAAGCGCCGCAAGTGCCCGTCGATACTATGCACTGAAAGCTAAGGCAAGCAA----------AT-CTT----------G-----TGAAAATAATAAT----------TT---------AAATTAAAAAAACATG----------TTTTCAAGGTCTCGCTGCTTGAGCGCCGCATTCCGAGCGGGAGGACCGTTGCATAT
dp5	XL_group1a:2159669-2159720 -		CACAGAAAGCGCCGCAAGGTGCCCGTCGACTACTATGCGCTGAAGGCCAAGGT--
droPer2	scaffold_28:585836-585887 -		C-TAGAAAGCGCGCAAGGTGCCCGTCGACTACTATGCGCTGAAGGCCAAGGT--
droAna3	scaffold_13117:115363-1115515 +		C-TAGAAAGCGCGCAAGGTGCCCGTCGACTACTATGCGCTGAAGGCCAAGGTGGCAATGT----------C---------AATA----------GACTCC---------GAATCCAGC----------ACTATCC--------CCAT-CGAT----CTTCCCAATTTCTCGTTGAGCGCCGCATCCGAGCGGGAGGAGCCATGCATAT
droBip1	scf7180000396425:1001226-1001413 +		C-TAGAAGCGCGCAAGGTGCCCGTCGATACTATGCGCTGAAGGCCAAGGCAAAGC----------G----------CACTCCAGATCCATTTGGGGTTCCAGCCC

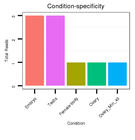
ID:	Coordinate:	Confidence:	Class:	Genome Locale:	
dvi_17414	**scaffold_13047:17850482-17850540 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser (GenB Mirtrons)]

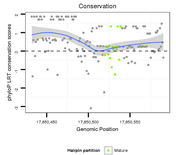
Legend: Exons Introns 5 p-arm 3 p-arm mismatch/error

Predicted structure









Show Alternate Folds

Flybase annotation

intron:[Dvir(GI34425-aj),CDS:[Dvir(GI34425-ak],CDS:[Dvir(GI34425-ak]

No Repeatmiks elements found

Sense Strand Reads

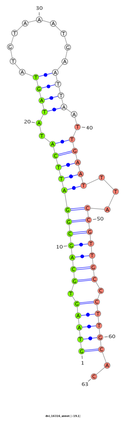
Node 3p reads | show mid mismatch reads

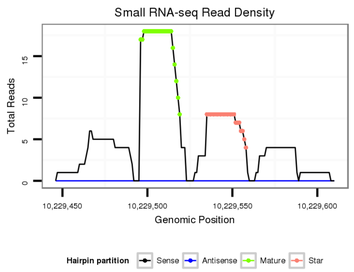
| | | |

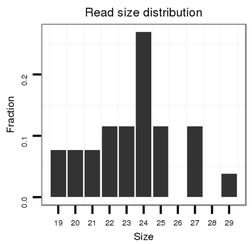
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_16316	**scaffold_13047:10229496-10229560 +**	**confident-exception**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

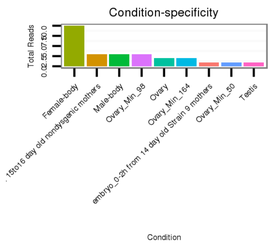
Legend: mature star mismatch in alignment mismatch in read

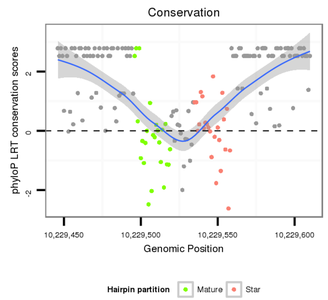
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dvir\GJ24175-in]; CDS [Dvir\GJ24175-cds]; CDS [Dvir\GJ24175-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TGAGCTCTCTGTCCATAGACTCCGAGGATGATACCAATTTGCTGAGTCAAGTAAGTGCAGCGGATTCATATAGTATGTAAATGAATTAATTGAATTTACCGTTGCCCTTGCACAGGCTATTGCCGCCGGCTGCAATAGACCCAAGTCGAATCTTGGCTTCAGCAC							SRR2096081							SRR2096072							SRR2096079			
					M047		embryo_0-2h from 15to16 day old nondysgenic mothers	SRR060667	V116	SRR060672	SRR060675	SRR060688		embryo_0-2h from 15to16 day old dysgenic mothers	M027	SRR060669	SRR060678	SRR060679	SRR2096038 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096050 embryo_0-2h from 14 day old Strain 160 mothers	SRR2096055	SRR2096056	SRR2096057	embryo_0-2h from 15to16 day old dysgenic mothers	SRR2096080 embryo_0-2h from 15to16 day old nondysgenic mothers	V053 head	SRR060684 140x9_0-2h_embryos_total
**********	Read size	# Mismatch	Hit Count	Total Norm	Total	female body	SRR2096058 Ovary_Min_98	160_females_carcasses_total	male body	9x160_females_carcasses_total	140x9_ovaries_total	160_ovaries_total	SRR2096059 Ovary_Min_164	male body	160x9_females_carcasses_total	9x140_testes_total	140x9_testes_total	Strain 9 mothers	Strain 160 mothers	Ovary_Min_43	Ovary_Min_46	Ovary_Min_50				
.....GTAAGTGCAGCGGATTCATATAGT.....	24	0	1	4.00	4	1	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGTGCAGCGGATTCATATAGTATG.....	27	0	1	3.00	3	0	0	1	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0
.....GTAAGTGCAGCGGATTCATAT.....	21	0	1	2.00	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGTGCAGCGGATTCATATA.....	22	0	1	2.00	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCCGCCGGCTGCAATAGACCC.....	22	0	1	2.00	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGTGCAGCGGATTCAT.....	19	0	1	2.00	2	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGTGCAGCGGATTCATA.....	20	0	1	2.00	2	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCCGAGGATGATACCAATTTGCTGAG.....	26	0	1	2.00	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
.....GTAAGTGCAGCGGATTCATATAG.....	23	0	1	2.00	2	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0
.....TTGAATTTACCGTTGCCCTTGCAC.....	24	0	1	2.00	2	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
.....ACTCCGAGGATGATACCAATTTGCTG.....	26	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATTGCCGCCGGCTGCAATAGACCCA.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AAGTGCAGCGGATTCATATAGTATG.....	25	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTACCGTTGCCCTTGCACA.....	21	1	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTGAATTTACCGTTGCCCTTGCAC.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTGAATTTACCGTTGCCCTTGC.....	22	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATTAATTGAATTTACCGTTGCCCTT.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGTGCAGCGGATTCATA.....	21	1	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
.GAGCTCTCTGTCCATAGACTC.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GCCGGCTGCAATAGACCC.....	18	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
.....ATAGACTCCGAGGATGATACC.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
.....GTCGAATCTTGGCTTCAG.....	18	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
.....TTGAATTTACCGTTGCCCTTGCAC.....	25	1	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
.....GAATTAATTGAATTTACCGTTGCC.....	24	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CTCCGAGGATGATACCAATTTGCTGA.....	26	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
.....TTGAATTTACCGTTGCCCTTGCA.....	23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
.....ATTAATTGAATTTACCGTTGCCCTTGCAC.....	29	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0

Anti-sense strand reads

ACTCGAGAGACAGGTATCTGAGGCTCCTACTATGGTTAAACGACTCAGTTCATTCACGTCGCCTAAGTATATCATACATTTACTTAATTAACTTAAATGGCAACGGGAACGTGTCCGATAACGGCGGCCGACGTTATCTGGGTTCAGCTTAGAACCGAAGTCGTG														SRR2096072
						SRR060679	V047	SRR060680		V053	M028	SRR060670		embryo_0-2h from 15to16 day old dysgenic mothers	M027
**********	Read size	# Mismatch	Hit Count	Total Norm	Total	140x9_testes_total	embryo	9xArg_testes_total		head	head	9_testes_total			male body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_13047:10229446-10229610 +	dvi_16316	TGAGCTCTCTGTCCATAGACTCCGAGGATGATACCAATTTGCTGAGTCAAGTAAGTGCAGCGGA----------TTCATA--TAG---ATGTAAATGAATT----------A-------ATTGAATTTACCGTTG---CCCTTGC---ACAGGCTATTGCCGCCGGCTGCAATAGACCCAAGTCGAATCTTGGCTTCAGC---AC
droMoj3	scaffold_6540:28378713-28378874 +		TGAGCTCTTGTCCATTGACTCCGAGGATGACACCAATTTGCTGAGTCATGTGCC--C----------A-AT-GGAATATCATATTAAGTATGTGCCCG----------CTAATCCGTTT---T-------------------TGTTTCAAGCAGGCTATTGCCGCCGGCTGCAATAGACCCAAGTCGAATCTTGGCTTCAGCGGCAC
droGri2	scaffold_15074:3832715-3832876 -		TGAGCTCTTGTCCATTGACTCCGAGGATGACACCAATTTGCTAGTCAGTAAAA--T----------CATT-GAGCGA---ATGCATTCG----------A-T-----TTTATTTAACCA-CGATT-TTTGT---AGGCTATTGCCGCCGGCTGCAATAGACCCAATCGAATCTTGGCTTCAGC---AC
droWil2	scf2_1100000004902:9366442-9366602 -		TGAGCTCTCTTCCATTGACTCCGAGGATGATACCAATTTGCTGAGTCAGTAG--------------------AAATATATTCCGAAGTGT---ATGCCAAGCT----------AGAA--T-TTTCAT---T-------TTTTTTTTTTTGTTTGCTTTGTTGCCGCCGGCTGCAATAGACCAAATCGAATCTTGGCTTCAGC---TC
dp5	2:13754786-13754953 +		TGAGCTCTCTTCCATTGACTCCGAGGATGACACCAATTTGCTGAGTCAGTAAAA--G-TTTGATTCGATCCCTTCCGCTTTTGAGGGGAAC-GATTT--T----------T-------TTTTTTTC-AC-CTCTT-TGTTC---GTAGGCTATTGCCGCCGGCTGCAATAGACCCAATCGAATCTTGGCTTCAGC---TC
droPer2	scaffold_01692648-6692815 -		TGAGCTCTCTTCCATTGACTCCGAGGATGACACCAATTTGCTGAGTCAGTAAAA--T-ATTCATTCGATCCCTTCCGCTTTTAGAGGGGAAC-GATTT--T----------T-------TTTTTTTC-AC-CTCTT-TGTTC---GTAGGCTATTGCCGCCGGCTGCAATAGACCCAATCGAATCTTGGCTTCAGC---TC
droAna3	scaffold_13340:17459878-17460041 -		TGAGCTCTCTTCCATTGACTCCGAGGATGACACCAATTTGCTGAGTCAGTAGAA--T-----------------------------TTCAC-TCACC-GATGTCGATTT--CCATTGA-TTCTATGGTGTT----------GAT--T-------TTTTTTTTTTTGTTTGCTTTGTTGCCGCCGGCTGCAATAGACCCAATCGAATCTTGGCTTCAGC---TC
droBip1	scf7180000396424:961721-961881 -		TGAGCTCTCTTCCATTGACTCCGAGGATGACACCAATTTGCTGAGTCAGTACA--A-----------------------------TTCAT-C--TCCCCCCATTGTCGATTT--CCATTGAACGTTGTGC----------TCTT---T-------TTTTTTTTTTTGTTTGCTTTGTTGCCGCCGGCTGCAATTGACCCAAGTCGAATCTTGGCTTCAGC---TC
droKik1	scaffold_0000302639:2727988-2728151 +		TGAGCTCTCTTCCATTGACTCCGAGGATGACACCAATTTGCTAGTCAGTAAACAAAATTTAGC----------AAA--T--TTT--TATTTAAATTTATT----------TTAAA----AAATTTATAAACGC---GATTTT--CAGGCTATTGCCGCCGGCTGCAATACGCCCAATCGAATCTTGGCTTCAGC---TC
droFic1	scf7180000454073:3689130-3689292 +		TGAGCTCTCTTCCATTGACTCCGAGGATGACACCAATTTGCTAGTCACT--T-----------------------------CCGT-GAAACCCCCTAAATAAATAATT----------GTTTCAAA----GGGGAAA----CAAT-GAATTTT--CAGGCTATTGCCGCCGGCTGCAATACGCCCAAGTCGAATCTTGGCTTCAGC---TC
droEle1	scf7180000491280:3241599-3241763 +		TGAGCTCTCTTCCATTGACTCCGAGGATGACACCAATTTGCTGAGTCAGTAAGTCT--T-----------------------------AAACACACCTTTAATTAAATGATT----------TAAAACCATGTTTAAAACCTT---------T-------TTTTTTTTTTTGTTTGCTTTGTTGCCGCCGGCTGCAATAGACCCAATCGAATCTTGGCTTCAGC---TC
droRho1	scf7180000779501:395714-395873 -		TGAGCTCTCTTCCATTGACTCCGAGGATGATACCAATTTGCTGAGTCAGTAACCA--T-----------------------------AACATTAACCCAAATGTAATAATT----------TCAAAAGATTTATTT---T-------TTTTTTTTTTTGTTTGCTTTGTTGCCGCCGGCTGCAATAGACCCAATCGAATCTTGGCTTCAGC---TC
droBia1	scf7180000302075:2098708-2098868 -		TGAGCTCTCTTCCATTGACTCCGAGGATGACACCAATTTGCTAGTCAGTAACTCT--T-----------------------------GAGCTTAAACCCGAATGTAAACCCA----------TTAAATGACA-------T-------TTTTTTTTTTTGTTTGCTTTGTTGCCGCCGGCTGCAATAGACCCAATCGAATCTTGGCTTCAGC---TC
droTak1	scf7180000415700:208505-208665 -		TGAGCTCTCTTCCATTGACTCCGAGGATGACACCAATTTGCTGAGTCAGTAACTCT--C-----------------------------T--TACACAAAAATATAAATTAATT----------TAAAATTTATTAA------TTTT--ATGCTTTT--CAGGCTATTGCCGCCGGCTGCAATAGACCCAAATCGAATCTTGGCTTCAGC---TC
droEug1	scf7180000409787:921930-922090 +		TGAGCTCTCTTCCCATAGACTCCGAGGATGATACCAATTTGCTGAGTCAGTAATCA--T-----------------------------AAATTTAATCGAAATGCAAATAAATAATT----------TTAAATGATTTCTTA--T-------TTTTTTTTTTTGTTTGCTTTGTTGCCGCCGGCTGCAATAGACCCAATCGAATCTTGGCTTCAGC---TC
dm3	chr3R:24662159-24662318 -		TGAGCTCTCTTCCATTGACTCCGAGGATGACACCAATTTGCTGAGTCAGTAGCA--T-----------------------------AAATTGAAACAAAATATCAATAACCATGGA----------TTAAGCCATTTCTTT--T-------TTTTTTTTTTTGTTTGCTTTGTTGCCGCCGGCTGCAATAGACCCAATCGAATCTTGGCTTCAGC---TC
droSim2	3r:24023926-24024085 -	dsi_5542	TGAGCTCTCTTCCATTGACTCCGAGGATGACACCAATTTGCTGAGTCAGTAGCA--T-----------------------------A-TTGAAACACCAATATTAAATATGT----------TTAAGCCATTTCTTT--T-------TTTTTTTTTTTGTTTGCTTTGTTGCCGCCGGCTGCAATAGACCCAATCGAATCTTGGCTTCAGC---TC
droSec2	scaffold_4:3525650-3525809 +		TGAGCTCTCTTCCATTGACTCCGAGGATGACACCAATTTGCTGAGTCAGTAGCA--T-----------------------------A-TTGAAACACCAATATTAAATATGT----------TTAAGCCATTTCTTT--T-------TTTTTTTTTTTGTTTGCTTTGTTGCCGCCGGCTGCAATAGACCCAATCGAATCTTGGCTTCAGC---TC
droYak3	3R:21843032-21843191 +		TGAGCTCTCTTCCATTGACTCCGAGGATGACACCAATTTGCTGAGTCAGTAGCA--T-----------------------------AAACGAAACACCAATATTAAATATGCTT----------TTAAACCATTTGCTT--T-------TTTTTTTTTTTGTTTGCTTTGTTGCCGCCGGCTGCAATAGACCCAATCGAATCTTGGCTTCAGC---TC
droEre2	scaffold_4820:3375443-3375602 +		TGAGCTCTCTTCCATTGACTCCGAGGATGACACCAATTTGCTGAGTCAGTAGCA--T-----------------------------AAATGAACATTATATAATCAATATA----------TTAAACCATTTCTTT--T-------TTTTTTTTTTTGTTTGCTTTGTTGCCGCCGGCTGCAATAGACCCAATCGAATCTTGGCTTCAGC---TC

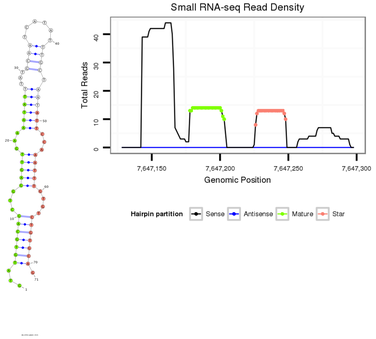
Generated: 09/08/2015 at 07:12 PM

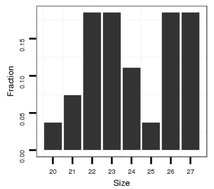
	PASS/FAIL
crit.star	1
crit.loop	0
crit.stem	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptp3	1
crit.uri	1
crit.gap	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

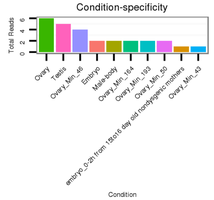
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_13512	**scaffold_12970:7647178-7647248 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

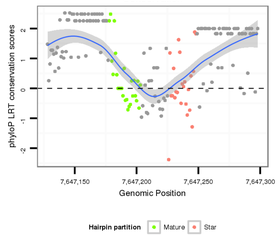
Legend: mature star mismatch in adjoining mismatch in star

Predicted structure









Show Alternate Folds

Flybase annotation

intron [Dvir/GJ19365-in]; CDS [Dvir/GJ19365-cds]; CDS [Dvir/GJ19365-cds]; utr3 [utr3_minus_11146]; utr3 [utr3_minus_11145]; utr5 [utr5_minus_13002]; utr5 [utr5_minus_13001]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TGACGCCTACATATTCCAGTACGACGATGTACACGAGACACATTGCCGGGTATGTGCAGCTGGAGTTGAAAATATTTATGCAATCATATTTGCTAATATTCCAAATTTGTGTCTGTGCAGGTTTACAATATAGTACCCTCGATAAGTGCAATTACTGGTGTTAGTCCGCA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060678 9x140_testes_total	SRR060681 Argx9_testes_total	SRR2096056 Ovary_Min_46	SRR060679 140x9_testes_total	M047 female body	SRR060670 9_testes_total	SRR060673 9_ovaries_total	SRR060680 Â 9xArg_testes_total	SRR060682 9x140_0-2h_embryos_total	SRR060657 140_testes_total	SRR060660 Argentina_ovaries_total	SRR060676 9xArg_ovaries_total	SRR2096057 Ovary_Min_50	SRR2096059 Ovary_Min_164	SRR2096040 Ovary_Min_193	V047 embryo	SRR060654 160x9_ovaries_total	SRR060666 160_males_carcasses_total	SRR060667 160_females_carcasses_total	SRR060686 Argx9_0-2h_embryos_total	SRR2096038 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096055 Ovary_Min_43	SRR2096072 embryo_0-2h from 15to16 day old dysgenic mothers	SRR2096081 embryo_0-2h from 15to16 day old nondysgenic mothers	V116 male body	SRR2096013 Ovary_Strain_9_oxidized	SRR060663 160_0-2h_embryos_total
**********	24	0	1	21.00	21	10	3	0	1	0	3	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..TCCAGTACGACGATGTACACGAGA	23	0	1	12.00	12	5	4	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..TCCAGTACGACGATGTACACGAG	26	0	1	5.00	5	2	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
..GTATGTGCAGCTGGAGTTGAAAATAT	27	0	1	5.00	5	0	1	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
..ATTCCAAATTTGTGTCTGTGCAG	23	0	1	5.00	5	0	0	2	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
..TTCCAAATTTGTGTCTGTGCAG	22	0	1	4.00	4	0	1	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
..TCCAGTACGACGATGTACACGA	22	0	1	4.00	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..GTATGTGCAGCTGGAGTTGAAAAT	24	0	1	2.00	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
..CACGAGACACATTGCCGG	18	0	1	2.00	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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..TATAGTACCCTCGATAAGTGCAATT	25	0	1	1.00	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..TCCAGTACGACGATGTACACGAGACACA	28	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..TACGACGATGTACACGAGACA	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0
..TAAGTGCAATTACTGGTGTTAGTCC	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..TATTCCAAATTTGTGTCTGTGCAG	24	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..ATAGTACCCTCGATAAGTGCAATT	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..ACGACGATGTACACGAGACACATTGC	26	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..TCCAGTACGACGATGTACACGAGACAC	27	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..TAAGTGCAATTACTGGTGTTAGTC	24	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..TCCAGTACGACGATGTACACGAGACACA	29	1	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..CCTCGATAAGTGCAATTACTGGT	23	1	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
..TACGACGATGTACACGAGAC	20	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
..TCCAAATTTGTGTCTGTGCAG	22	1	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..TCCAAATTTGTGTCTGTGCA	20	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
..ATGTGCAGCTGGAGTTGAAAA	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

ACTGGCGGATGTATAAGTCATGCTGCTACATGTGCTCTGTGTAACGGCCCATACACGTCGACCTCAACTTTTATAAATACGTTAGTATAAACGATTAAAGUTTAAACACAGACAGTGCCAAATGTTATATCATGGGAGCTATTCACGTTAATGACCACAATCAGGCGT	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060673 9_ovaries_total	SRR2096013 Ovary_Strain_9_oxidized	SRR060658 140_ovaries_total	V047 embryo	SRR060678 9x140_testes_total	SRR060685 9xArg_0-2h_embryos_total	SRR2096026 embryo_0-2h from 14 day old Strain 9 mothers	SRR060666 160_males_carcasses_total
**********	24	0	1	21.00	21	10	3	0	0	0	0	0	0

Show Alignment With Reads

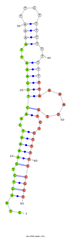
Re-alignment of all predicted orthologs

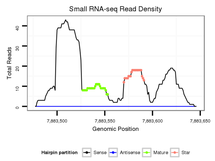
Species	Coordinate	ID	Alignment
droVir3	scaffold_12970:7647128-7647298-	dvi_13512	TGAC-CGCCTACATATTCCAGTACGACGATGTACACGAGACACATTGCCGGGTATGTGCAGCTGGAG----TTGAAAATA------TTATGCAATCATATTTG--CTAATACCCCCCCCCCTCCC--------AAATTTGTGTCTGTGCAGGTTTACAATATAGTACCCTCGATAAGTGCAATTACTGGTGTTAGTCCGCA
droMoj3	scaffold_6482:2037409-2037568 -		TGAC-CGCCTAC-T-TTCCAGTACGACGATGTACACGAGACACATTGCCGGGTATGTGCAGCTGGAGTTGAAAATATT-----ATTGTATGGATTT-T-------TATA-----TTGAAACATTTATTGAAGATAC---------T-TCTTTGTAGGTTTATGATATAACCCTCGATAAGTGCAATTACTGGTGTTAGTCCGCA
droGri2	scaffold_15203:6971363-6971530 -		TGAC-CGCCTAC-T-TTCCAGTACGACGATGTACACGAGACACATTGCCGGGTATGTG---------GCATGTATGCATGTATGGAATGCATTAA----GCT-TACTTTACTAATAA---------TATTTTTGTATGGCAGGTTTATACTATATAGTACCCTCGATAAGTGCATTACTGGTGTTAGTCCGCA
droWil2	scaf_1500000004909:7135085-7135253 -		TGAC-CGCCTAC-T-TTCCAGTACGACGATGTACACGAGACACATGCCGGGTATGTG----CAATTTCCAAACATTTGTGTCTGTGCAAGCATTTTAA----CATTACTTAAAAAGCTGCCCTCTGTTCTTTT

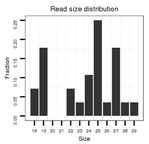
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_15944	**scaffold_13047:7883527-7883596 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Comb5 Mimic)]

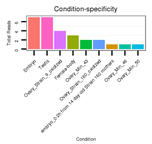
Legend: seed, loop, mature-3p, mature-5p, mismatch, mismatch-loop

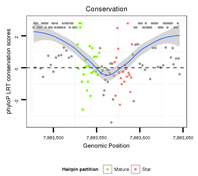
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dvir(GI24941-u)], CDS [Dvir(GI24941-cds)], CDS [Dvir(GI24941-cds)]

Repeatable elements

Name	Class	Family	Strand
AT_rich/Low_complexity	Low_complexity		+

Sense Strand Reads

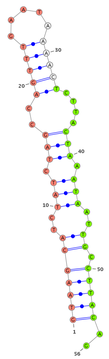
Hide 5p reads Show mid mismatch reads

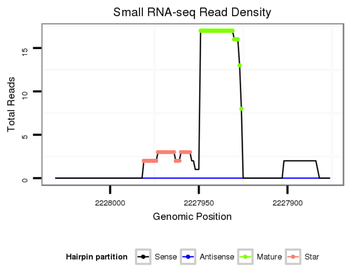
Read #	Hit Count	Total Hits	Total Reads	MD47 female body	SRR040685 Dvir_0-2h_embryos	MD41 embryos	SRR2296013 Ovary_Strain_9_ovaries	SRR2296014 Ovary_Strain_140_ovaries	SRR040686 Arge8-2h_embryos	embryo_0-2h 24 day old Strain 8 mothers	SRR2296050 SRR040672 Dvir140_females_carcasses	SRR040681 Arge8_males_testes	SRR040682 Dvir140_0-2h_embryos	SRR2296055 Ovary_Mix_43 cells	GSM1529803 follicle cells	SRR040673 9_ovaries	SRR040680 Dvir8_testes	embryo_0-2h 24 day old Strain 8 mothers	SRR040684 embryo_0-2h_embryos	SRR040674 Dvir8_ovaries	SRR2296054 Ovary_Mix_46	140_0-2h_embryos	SRR040663 Dvir140_testes	SRR040655 140_testes	SRR040657 140_testes	SRR040675 140s9_ovaries	SRR040678 Dvir140_ovaries	SRR040689 140s8_testes	SRR1106722 embryos_12-13h Ovary_Mix_50	SRR2296057 Ovary_Mix_51	SRR2296041 embryos_0-2h 24 day old Strain 140 mothers	SRR2296080 Mom 15to16 day old head+thorax mothers	SRR040658 140_ovaries	SRR040659 Argentina_testes	SRR040661 140s8_0-2h_embryos	SRR040662 3s140_0-2h_embryos	SRR040667 140_females_carcasses	SRR040670 9_testes	SRR040687 9_0-2h_embryos	SRR1106719 embryo_0-2h	SRR2296026 embryo_0-2h 24 day old Strain 9 mothers	SRR2296059 Ovary_Mix_164	SRR2296072 embryo_0-2h from 15to16 day old mothers	SRR2296079 embryo_0-2h from 15to16 day old dysgenic mothers	SRR2296081 embryo_0-2h from 15to16 day old nondysgenic mothers	SRR040671 Dvir140_males_carcasses	SRR040679 Dvir140_testes_total
alias	Mismatch	Count	Hom	Total																																													
.....	0	1	11.00	11	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	0	1	4.00	4	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	0	1	3.00	3	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	0	1	6.00	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	0	1	5.00	5	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	0	1	2.00	2

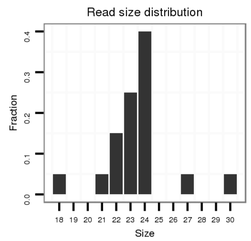
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_22216	**scaffold_13246:2227926-2227981 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

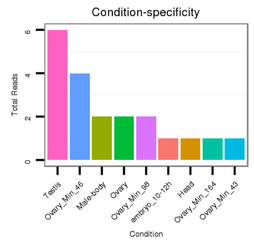
Legend: mature star mismatch in alignment mismatch in read

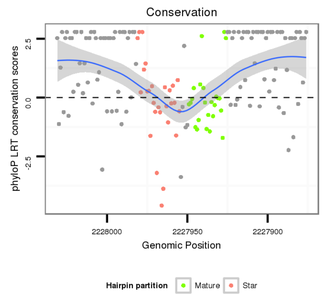
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dvir/GJ16134-in]; CDS [Dvir/GJ16134-cds]; CDS [Dvir/GJ16134-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

						SRR2096056	SRR060679 140x9_testes_total	SRR060678 9x140_testes_total	SRR2096058	SRR2096038 embryo_0-2h from 14 day old Strain 9	SRR2096055	M047 female body	GSM1528803 follicle	M028 head	M061 embryo	SRR060664 9_males_carcasses_total	SRR060668 160x9_males_carcasses_total	SRR060676 9xArg_ovaries_total	SRR060677 Argx9_ovaries_total	SRR060681 Argx9_testes_total	SRR1106722 embryo_10-12h	SRR2096057	SRR2096059	V053 head	SRR060670 9_testes_total	SRR060685 9xArg_0-2h_embryos_total	SRR2096060	V116 male	SRR060674 9x140_ovaries_total	SRR2096079 embryo_0-2h from 15to16 day old dysgenic	mothers
GTCTGGTTGGCAAATATAGCCACTGTACGCCCGGCCTGCTCTTTGATTATGTAAGCATCTATCTAGCCAGTTTGAATAAAACTCTTACTAAATAATTGCCTTACAGATCCTGGTTCAGATTCAAATTTATGACAACTTAATCGGACCCGTCTGCGA	Read # size	Hit size	Total Mismatch	Count	Norm	Total	Ovary_Min_46					Ovary_Min_98	mothers	Ovary_Min_43		cells														Ovary_Min_50	Ovary_Min_164				Ovary_Min_193	body		mothers
**********	24	0	1	8.00	8	2	0	0	2	0	1	0	0	0	0	0	0	1	1	0	0	0	1	0	0	0	0	0	0	0	0
**********	23	0	1	5.00	5	0	3	0	0	0	0	0	0	0	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0
**********	22	0	1	3.00	3	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**********	25	1	1	2.00	2	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**********	30	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
**********	27	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**********	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**********	20	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
**********	19	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
**********	18	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

						SRR060687 9_0-2h_embryos_total
CAGACCAACCGTTTATATCGGTGACATGCGGGCCGGACGAGAAACTAATACATTCGTAGATAGATCGGTCAAACTTATTTTGAGAATGATTTATTAACGGAATGTCTAGGACCAAGTCTAAGTTTAAATACTGTTGAATTAGCCTGGGCAGACGCT	Read # size	Hit size	Total Mismatch	Count	Norm	Total
**********						

Show Alignment With Reads

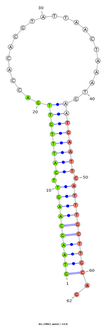
Re-alignment of all predicted orthologs

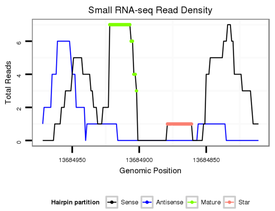
Species	Coordinate	ID	Alignment
droVir3	scaffold_13246:2227876-2228031 -	dvi_22216	GTCTGGTTGGCAAATATAGCCACTGTACGCCCGGCCTGCTCTTTGATTATGTAAGCATCTATCTAGCCA-GTTTGA------AT---AAAACTCTTACTA-AAT----------AATTGCCTTACAGATCCTGGTTCAGATTCAAATTTATGACAACTTAATCGGACCCGTCTGCGA
droMoj3	scaffold_6500:26339104-26339267 -		GTCTGTTTGGCAAATATAGCCACTGCAGGCCGGCTGCTTTGATTATGTAAGCATCTATCGCGTTTA-GTGTCTC------GC---GCGTTG-A-GTAA-GCA-AATTGCGA---- ATTGTA---TGCAGATCCTGTTCAATCAAATTTATGACAAGTTGATGGCGCGTCTGCGA
droGri2	scaffold_15126:3741541-3741709 +		-GCATTGTGGCAAATATAGCCACTGCTGGCCGGCATGCTCTTTGATTATGTAACTGA-ATATA-AGTCGCTGTCGGG---AAA---T---G-AACAC-A-AAT----A-TAA--CCCCC---------GCTCAT----------TGCTTTGTTAGAATCCTGCAGAACAAATTATGACAAGTTAATGGACCCGTTGCGA
droWil2	scf2_1100000004521:2144245-2144401 -		GTCTGTTTGGCAAATATAGCCACTGCCGCACCGGCATGTCTTTGATGATGTAAGTGAG-ATAAGTA-AGTGT---TGAATCACAC---AAA----ACTCT-AAATG---A-TCC---C----------TTGCTTTGTGCATCCTGCAGAACAAATTATGACAAGTGATGGACCCGTTGCGA
dp5	4_group1:6298110-6298349 +		GTCTGTTTGGCAAATATAGCCACTGCTGGCCGGCATGCTCTTTGATTATGTAAGCA-CAAGA-ATCGCG---CATTTAT---TG-TG-G-AC---GC GGGGT ATC---CCCCA---------GCTTTTTGTGCCTCGTGCAACATCGTAAAGAGTTAATGAGTCTATCTTTAAAATGTATGTCGTTTTAAACCCTTTTTGTCTGAGTAGCAAGCGATCGACCGTCTGCGA
droPer2	scaffold_1:5780356-5780605 +		GTCTGGTTGGCAAATATAGCCACTGCTGGCCGGCATGCTCTTTGATTATGTAAGCA-CAAAGA-ATCGCG---CATTTAT---TG-TG-G-AC---GC GGGGT ATC---CCCACCATAGAAGAGCTTTTCGTGCCTATTGCAACATCGTAAAGAGTTAATGAGTCTATCGTTAAAATGTATGTCGTTTAAACCCTTTTTGTCTGAGTAGCAAGCGATCGACCGTCTGCGA
droAna3	scaffold_12916:6332187-6332351 +		GTCTGTTTGGCAAATATAGCCACTGCTGGCCGGCATGTCTTTGATTATGTAAGCGGA-TGTGA-T-G-GTGTCTT---AAA---CG-CT-A-GGCT-AAAAATATC-TCC---C----------CCTATC-T-GTAGATCCTGCAGAACAAATTATGACAAGTGATTGCGA
droBip1	scf1800000396568:489666-489831 -		GTCTGGTTGGCAAATAGCTACTGTGCCCGGCATGCTCTTTGATTGATCGTAAGTGGA-TGATAA-T-ACTCGTCTTT---AAA---GGATTC-TAACCT-AACGTGTTAGTCC---T----------CCCCAA--CCTGATCTGTTGTCAAATCAAATCTATGACAAGTGATGGCCCGTTGCGA
droKik1	scf1800000302408:376974-377136 +		GTCTGTTTGGCAAATAGCCACTGTGCCCGGCCTGCTCTTTGATGATGTAGTTGTCGTTGTTGTTGTCC------AAA---TGCTTCTGTTGAACGT---TCCCTTAAA----------TTCATCGTGATCCTGCAGAACAAATTATGACAAGTGGCCCGTCTGCGA
droFic1	scf1800000453924:21389-21550 -		-GCATGGTTGGCAAATAGAGCCACTGTCGGCCGGCATGCTCTTTGATTATGTAAGTTTCTGTGACCA-TGTGTGGCGT---AAA---CCAAT-TTTCCTT-AACGT---C-TCC---C----------TCTAATATCAGTGATCCTGCAGAACAAATTATGACAAGTGCCCGTCTGCGA
droEle1	scf1800000491273:1148831-1148985 +		GTCTGTTTGGCAAATAGCCACTGTGCCAGGCATGCTCTTTGATATGTGAGTTTA-AGTGTA-TGTTGTTGTTT---AAA---TTATA-----TGTAGTTTGTTGAACGT---TCC---C----------TTCCTTTCAGTATCCTGCAGAACAAATTATGACAAGTGCCCGTCTGCGA
droRho1	scf1800000759283:17132-17292 -		-GCATGGTTGGCAAATAGAGCCACTGTCGGCCGGCCTGTCTTTGATTATGTGAGTTTA-AGTAGTTTTTTTGG------AA---GATTTTGAAACA-AAT----TCCTTT---T----------TCCCATTTTGACATCTGTTGTCAAATCAAATTTATGACAAGTGATCGGACCCGTCTGCGA
droBia1	scf1800000302408:356495-356657 +		-GCATGGTTGGCAAATAGAGCCACTGTCGGCCGGCATGCTCTTTGATTATGTGAGTTTA-AGTAGATTTTTTTGGTGGTT----AAA---TGAATGCTTGTTGAACGT---TCCAGTAAG----------TTCCCTTTCAGTATCCTGCAGAACAAATTATGACAAGTGCCCGTCTGCGA
droTak1	scf1800000415779:629245-629408 -		-GCATGGTTGGCAAATAGAGCCACTGTCGGCCGGCCTGCTCTTTGATTATGTGAGTTTA-AGTAGAGCTTTAAGTATGCA----AAA-ATAA---A-TTCTTTAATTTCTTCC---C----------TTCCTTTCAGTATCCTGCAGAACAAATTATGACAAGTGCCCGTCTGCGA
droEug1	scf1800000409554:3917234-3917397 -		-GCATGGTTGGCAAATAGAGCCACTGTCGGCCGGCATGCTCTTTGATTATGTAAGTTTCTGTGAGTATGTGTGTGTGTTTGTGTGTG

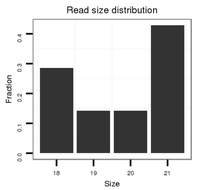
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_19862	**scaffold_13049:13684861-13684922 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

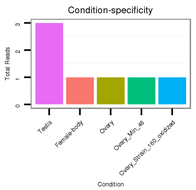
Legend: mature star sub-mat b in alignment mismatch in read

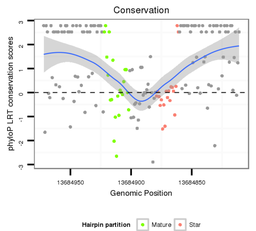
Predicted structure











Show Alternate Folds

Flybase annotation

intron [DvirGI11827-in]; CDS [DvirGI11827-cds]; CDS [DvirGI11827-cds]

No Repeatable elements found

mature	star
	1. scaffold_13047:3648536-3648544 - 2. dvi_19862 scaffold_13049:13684861-13684879 -

Sense Strand Reads

hide 3p reads show mid mismatch reads

TGTCCCTGGCAGCCACTCATCCACACCTGTTGCCGACGCATATTCAATCGTAAGCAAGTTGATTTGTTGACCACACGTATTAACTAAATGAATGAATCAATTTGCTTGCAGCACATTAAACATAATCTCGACTCATTGGTTAATCAGTTGTGCAATCACG	Read #	Mismatch	Count	Hit Norm	Total Total	SRR060678 9x140_testes_total	SRR2096056 Ovary_Min_46	SRR060681 Arg9_testes_total	SRR2096014 Ovary_Strain_160_oxidized	SRR2096038 embryo_0-2h from 14 day old mothers	SRR2096024 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096055 Ovary_Min_43	SRR060665 9_females_carcasses_total	M047 female body	SRR060677 Arg9_ovaries_total	SRR060679 140x9_testes_total	SRR2096057 Ovary_Min_50	V047 embryo male body	V116 female body	SRR060669 160x9_females_carcasses_total	SRR060664 9_males_carcasses_total	SRR060667 160_females_carcasses_total	SRR060668 160x9_males_carcasses_total	SRR060676 9xArg_ovaries_total	SRR060686 Arg9_0-2h_embryos_total	SRR2096058 Ovary_Min_98	SRR2096061 embryo_0-2h from 14 day old Strain 160 mothers	SRR2096072 embryo_0-2h from 15to16 day dysgenic mothers	SRR060646 160_males_carcasses_total	SRR060663 160_0-2h_embryos_total	SRR1106726 16h	SRR2096059 embryo_14-16h	SRR060684 140x9_0-2h_embryos_total	M027 male body	SRR060685 9xArg_0-2h_embryos_total
**********	size																																		
.....GTAAGCAAGTTGATTTGTTGACT.....	23	1	1	3.00	3	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGCAAGTTGATTTGTTGA.....	21	0	1	3.00	3	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
.....ATAATCTCGACTCATTGGTTA.....	21	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGCAAGTTGATTTGT.....	18	0	1	2.00	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGAATTCATTGCTTGCAG.....	20	1	2	1.50	3	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....ATAATCTCGACTCATTGGT.....	19	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ACATAATCTCGACTCATTGGT.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
.....GGTTAATCAGTTGTGCAAT.....	19	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATCTCGACTCATTGGTTAATCAGT.....	24	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATTGGTTAATCAGTTGTGCAA.....	21	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGCAAGTTGATTTGTTG.....	20	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ACTCATCCACACCTGTTGCCGAGC.....	24	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TAATCAGTTGTGCAATACACG.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CATCCACACCTGTTGCCGA.....	19	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGCAAGTTGATTTGT.....	19	1	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CACCCACTCATCCACACCTGT.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ACACCTGTTGCCGAGCGAT.....	19	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CTGTTGCCGAGCGATATTCAATCGT.....	27	2	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AATCGGTAAGCAAGTTGATTT.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CACCTGTTGCCGAGCGATATTCAATCG.....	27	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGAATTCATTGCTTGCAG.....	19	0	2	1.00	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

ACAGGGACCGTCGGTGAGTAGGTGTGGACAACGGCTCGCTATAAGTTAGCCATTCGTTCAACTAAACAACTGGTGTGCATAATTGATTTACTTAACTTAAGTAAACGAACGTCCTGTAATTTGTATTAGAGCTGAGTAACCAATTAGTCAACACGTTATGTGC	Read #	Mismatch	Count	Hit Norm	Total Total	SRR060659 Argentina_testes_total	SRR2096057 Ovary_Min_50	V116 female body	M047 female body	SRR060664 9_males_carcasses_total	SRR060683 160_testes_total	SRR2096059 Ovary_Min_164	SRR2096072 embryo_0-2h from 15to16 day old dysgenic mothers	M027 male body	SRR2096014 Ovary_Strain_160_oxidized
**********	size														
.....CGGTGAGTAGGTGTGGACAAC.....	21	0	1	2.00	2	0	0	1	0	1	0	0	0	0	0
.....CCGTCGGTGAGTAGGTGT.....	18	0	1	2.00	2	0	0	0	0	0	0	0	0	0	0
.....AATTTGTATTAGAGCTGAGTA.....	21	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0
.....GCTCGCTATAAGTTAGCCATTCG.....	23	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
ACAGGGACCGTCGGTGAGTAG.....	21	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0
.CAGGGACCGTCGGTGAGTAGG.....	21	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0

Show Alignment With Reads

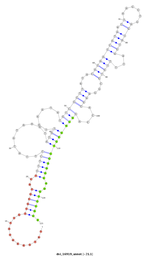
Re-alignment of all predicted orthologs

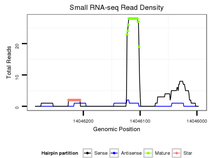
Species	Coordinate	ID	Alignment
droVir3	scaffold_13049:13684861-13684922 -	dvi_19862	TGTCCCTGGCAGCCACTCATCCACACCTGTTGCCGAGCGATATTCAATCGTAAGCA--AGTTGA----------T--------T-TGTTGCCACACGTATTA----------ACTAAATGAA------TGAATTCA-----TTTGC----CTTGCAGCACATTAAACATAATCTCGACTCATTGGTTAATCAGTTGTGCAATCACG
droMoj3	scaffold_6682:1366158-1366735. +		TGTCATCCACACCTGTTGCCGACGCTATTCAATCGTAAGCGAA-----------ATT----------CA--------T-TGTTGCTAATGAGCGTA----------ACTAATAT------TTTTTAAYCGCGCCAAGGGACATAAACATAATCTCACTCATTGGTTAATCAGTTGTGCAATACCG
droGri	scaffold_15110:1551983-1552139. +		TGTCCTTGGCAGCCACTCATCCACACCTGTTGCTGGCAGCGATATTCAATCGTAAGCAAGCAATTGCAAT----------ACTAAA----------TAAAAAAAAAATATGAGTTGCAATAATCTCACTCATTGGTTAATCAGTTGTGCAATCACG
droWil2	scaffold_110000:0:1110087-1110259. +		TGTCCTTGGCAGCCACTCATCCACACCTGTTGCTGGCAGCGATATTCAATCGTAAGCAAAGCAA----------TTT----------CCCATTCAAC----------CAAGATTGTGTTGATGCTCTTTTGTAGTGTCCCAGCAGCCAAGGGATATAAACATAATCTCACTCATTGGTTAATCAGTTGTGCAATACCG
dp5	AE_group61:3218174-3218871 -		TGTCCTTGGCAGCCACTCATCCACACCTGTTGCTGGCCGAGCGATATTCAATCGTAAGCAGCCCGAGTGCGGCATTTTCACTTAGAGGTTACTAATTTAC----------C----------CCCC

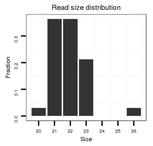
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_16919	**scaffold_13047:14046047-14046235 -**	**candidate**	**5p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser (Cortell Mirror)]

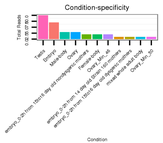
Legend: **mature** star **Mismatch in alignment** **mismatch in star**

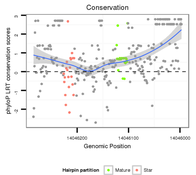
Predicted structure











Show Alternate Folds

Flybase annotation

intron [D=rnGI22835-aj; CDS [D=rnGI22835-cds],CDS [D=rnGI22835-cds]

No Repeatable elements found

Sense Strand Reads

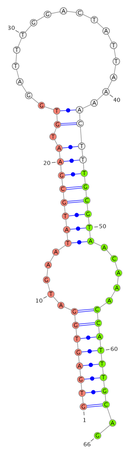
hide 3p reads show mid mismatch reads

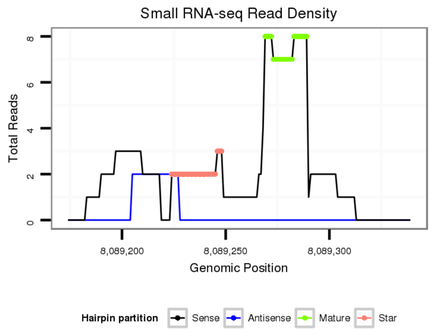
Read #	Align Mismatch	Hit Count	Total Score	Total	SRR040679 14dw9_testes_total	SRR040682 9w140_3-2h_embryos_total	V116 male body	SRR040681 Arge9_testes_total	SRR294059 Ovary_Mix_164	M47 female body	M041	SRR040643 140_2-embryos_total	SRR040678 9w140_testes_total	SRR294050 embryos_0-2h from 14 day old Strain 140 mothers	SRR294056 Ovary_Mix_66	SRR294080 embryos_0-2h from 15tock day old nondypsenic 2h_embryos_total	SRR294057 Ovary_Mix_50	SRR040684 14dw9_0-mothers	GSM1528603 follicle cells	SRR040657 140_testes_total	SRR040662 9w140_3-2h_embryos_total	SRR040665 9_females_carcasses_total	SRR040667 140_females_carcasses_total	SRR040674 9w140_ovaries_total	SRR040675 14dw9_ovaries_total	SRR040676 9abrg_ovaries_total	SRR040687 9_0-mothers	SRR040688 140_ovaries_total	SRR040689 14dw9_testes_total	SRR1104729 mixed whole adult body	SRR294058 Ovary_Mix_98	SRR294041 embryos_0-2h from 14 day old Strain 140 mothers	SRR294072 embryos_0-2h from 15tock day old dypsenic mothers	SRR294079 embryos_0-2h from 15tock day old nondypsenic mothers	SRR294081 embryos_0-2h from 15tock V047 day old nondypsenic mothers	SRR040666 140_males_carcasses_total	SRR040669 14dw9_females_carcasses_total	SRR040685 9abrg_0-2h_embryos_total	SRR040672 9w140_females_carcasses_total	SRR294024 embryos_0-2h from 14 day old Strain 9 mothers
.....	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	0	1	1.00	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	0	1	2.00	2	0	0

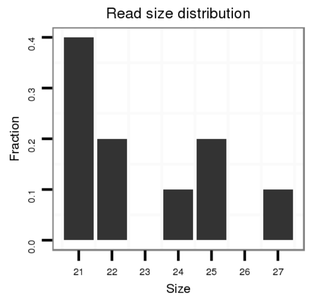
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_10845	**scaffold_12963:8089224-8089289 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

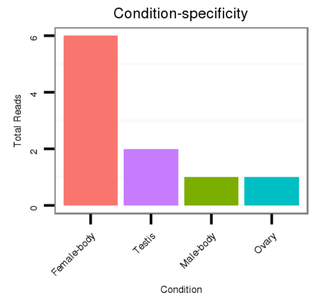
Legend: mature star **mismatch in alignment** mismatch in read

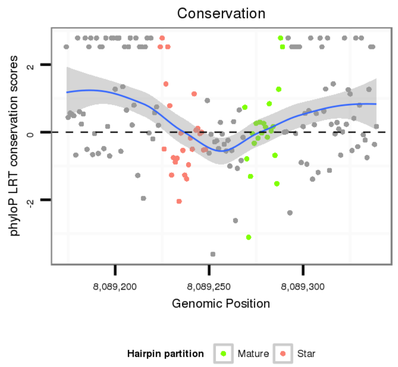
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dvir\GJ17181-in]; CDS [Dvir\GJ17181-eds]; CDS [Dvir\GJ17181-eds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GGCATGTTTGTGGTCCTGCCCATATTCATAGGCGAAATTGCCGACAACAGGTGAGTGGATGAATATGCGAATGTGGATTTGGACTATTAAAACTTTGCGTAACAAACCATTTGCAGCATACGTGGTCGGCTGTGCTCCTTCTTCACCCTGGCCGTCAATACGGGCA **********(((((((.....(((((((.((.....)))))))))).....)))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M047 female body	SRR060679 140x9_testes_total	SRR2096055 Ovary_Min_43	SRR060689 160x9_testes_total	V116 male body	M027 male body	SRR060669 160x9_females_carcasses_total	SRR060676 9xArg_ovaries_total	SRR060678 9x140_testes_total	SRR060683 160_testes_total	V053 head	SRR060685 9xArg_0-2h_embryos_total	SRR060682 9x140_0-2h_embryos_total	V047 embryo	SRR060684 140x9_0-2h_embryos_total	SRR060687 9_0-2h_embryos_total
.....TGCGTAACAAACCATTTGCAGC.....	22	1	1	5.00	5	1	2	0	1	1	0	0	0	0	0	0	0	0	0	0	0
.....TGCGTAACAAACCATTTGCAG.....	21	0	1	4.00	4	2	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....GTGAGTGGATGAATATGCGAATGTG.....	25	0	1	2.00	2	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
.....TTGCGTAACAAACCATTTGCAG.....	22	0	1	2.00	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
.....TTTGCAGCATACGTGGTCGGC.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
.....GTGGATTTGGACTATTAAAACTTTGCG.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GCGTAACAAACCATTTGCAGC.....	21	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CTTTGCGTAACAAACCATTTGCAG.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCGTAACAAACCATTTGCAGCC.....	23	2	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATACGTGGTCGGCTGTGCTCCT.....	22	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
.....ATTCATAGGCGAAATTGCCGAC.....	22	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
.....GTGGTCCTGCCCATATTCATAGGCGAA.....	27	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCCCATATTCATAGGCGAAATTGCCGAC.....	29	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

CCGTACAAACACCAGGACGGGTATAAGTATCCGCTTTAACGGCTGTTGTCCACTCACCTACTTATACGCTTACACCTAAACCTGATAATTTTGAAACGCATTGTTTGGTAAACGTCGTATGCACCAGCCGACACGAGGAAGAAGTGGGACCGGCAGTTATGCCCGT **********(((((((.....(((((((.((.....)))))))))).....)))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M047 female body	SRR2096055 Ovary_Min_43	V053 head	SRR060655 9x160_testes_total	SRR060689 160x9_testes_total	V116 male body	V047 embryo	SRR060686 Argx9_0-2h_embryos_total
.....CGCTTTAACGGCTGTTGTCCACT.....	23	0	1	2.00	2	0	2	0	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12963:8089174-8089339 +	dvi_10845	G-GCATGTTTGTGGTCCTGCCCATATTCATAGGCGAAATTGCCGACAACAGGTGAGTGG---ATGA---AT--ATGC----GA----------ATGTGG-ATTTGGACT---ATT----------AAA-ACTT---TGCGT--AACAAACCATTTGCAGCATACGTGGTCGGCTGTGCTCCTTCTTCACCCTGGCCGTCAATACGGGCA
droMoj3	scaffold_6500:708628-708801 +		G-GCATGTCCCTGGTGCTGCCCATGTTCATTGGCGAAATGCGAGACGCAGGTGAGTGA---ATT---GGGATGA-ATTGATGATGAATCTTTGGCCG-----------GCCTGT---------GAC-ACTT---TGAGTGACTCCAT-TTGCAGCATTGCGGGCGATGTGTGCTCCTTCTTCAA-TTGGCCTTCAATCTAGGCA
droGri2	scaffold_15252:7521789-7521961 +		G-GCATGTTTCATGGTGCTACCCATGCGTTCATTGGCGAAATGCCGCACAACAGGTAAGTGA---ATA---ATCA-CA-ATTGATGTTGATAACGAAACG-----------GACTGAAGGC----------AAC-TGAA---CGA--TGCATGAA-TTTCAGCATCGCGGCAGATTGTGCTCCTTATGCAGTCTGGCGATGAATTTGGGCA
droWil2	scf2_1100000004945:755011-755168 +		G-GCATGTTTGTGGTGTGCCGATGTTCATTAATGAAATTGCCGAAAAAGGTAAGCAA---TGGATTTATACAT-----------CACAAAG-----------TAA----------TGG-AATC---ATT--CAATCCAT-TTTGCAGTGTCGTGGCGGTTTCGTTCCTTTTTT-ATTGGTTATCAAGCAAGGGCA
dp5	4_group3:6254874-6255029 -		G-GTGCAGTGTGTCCTGCCCAGATTCATTATGCGAATTGCGAGAGCATGAGTGCT---TGCA---AG-----------CG-----GAGAGACG---ATC----------ATTGGCT---CTCAATTTTTTT-GCCACAGCATTGCGGCGTGCGCTCGATGATTTTCTGTCCGTCAATACGGGCG
droPer2	scaffold_1:7748175-7748330 -		G-GTGCAGTGTGTCTGCCCAGATTCATTATGCGAATTGCGAGAGCATGAGTGCT---TGCA---AG-----------CG-----GAGAGACG---ATC----------ATTGTCT---CTCAATTTTTTT-GCCCAGCATTGCGGCGTGCGCTCGATGATTTTCTGTCCGTCAATACGGGCG
droAna3	scaffold_12916:13399362-13399534 -		GGCTGTTAGTGTGTCCTTGCGACCTTCATAGCGAAATGCGAGACGCAAGTAGTGC---CGA---GCCTAG--ACGGATGA----------CTG-GCGAAAAAGTGATA----------TACTAAG---GGCT--TGTAAAGCAGCGCAGCGTACGCGGTCGGCTGCGCTCGAAACGTTCTTGTGAGTGAATAAGGGGG
droBip1	scf7180000396580:97331-97501 +		G-GTGCAGTGTGTCCTTGCGACCTTCATCAGCGAAATGCGAGACGCAAGTAGCGTAC---A----GTGCCGAGAGGCATG----------ACT-GCACAAAATGTATA----------ACTCCAG---AAT--TTTAAAGCACCGCAGCGTACGCGGCCGATGCGCTCGAAACGTTCTTGTGAGTGAAGACGGGCG
droKik1	scf7180000302679:1517038-1517190 -		G-G--GAATGTGGTGCTGCCAATTTTATCAGCGAAGTTGCCGACAGCGGTGAGATTTTTGTG---GTGAAAA----------ATGTG-A--------T---A----------AAA-TATT---ATT--T-CGTT-CCATAGCATTGCGCGCTGTCACTTCGATGGTGATGTTATCCGTCCATTTGGGAA
droFic1	scf7180000453924:1310940-1311111 +		G-GTGCAGTGTGTCCTGCCGACCTTCATCAGCGAATTGCGAGACGCAGTGAGTGAAGTCAA---TGTGAGT----------AA--------CGTGCTG-GATGGGAAACAGCT----------GAT-AAC---GGGC--CATAAAGT-TTGCGAGTGTCGCGGTCGTCGCGCTCGATATCTTCTGTGCGTGAAGACGGGCG
droEle1	scf7180000491046:2032178-2032348 +		G-GTGCAGTGTGGTGTGCCGACCTTCATCAGCGAATTGCCGACAGCAGTGAGTGT---TGTTTTCCTAAAG-----------CGTGCTG-AA--------TGATTAACTAC----GAT-TATCCACGTGTC--CATAAAGT-ATTAGAGCGTGCGCGGTCGTCGCGCTCGAAACGTTCTTATGCGTGAAGACGGGAG
droRho1	scf7180000777227:176781-176940 +		G-GTGCAGTGTGGTGTGTCCGACCTTCATCAGCGAATTGCGAGACGCAGTGAGTGT---TGTAA--TGGAG-----------CGTGCTG-AA--------TGATA----------AAC-TACT---TGTCC--TGTAAAGT-TTCAGAGCGTGCGCGGTCGTCGCGCTCGATATCTTCTATGCGTGAACTCGGGAG
droBia1	scf7180000301468:1204949-1205106 -		G-CTGGCAGTGGTGGTGCCCATTTCATCAGCGAGGTGCCGACAGCAGGTGAGTGC---CGCT---GC---CT-----------GTTAG-AAAA---TAACATC----------ACA-AAAA---ATT--CACAAA---CTTAGAGCATTGCGGGGCCTCACTTCGATGGTGATGCTATTGTCGATTTGGGTA
droTak1	scf7180000413924:17178-17335 -		G-GTGCAGTGTGGTCCTGCCGACCTTCATTAGCGAATAGCCGACAGCAAGTGAGTGT---TATTTTTGTGGAG-----------CGTGCTG-------------ATT----------AAC-TAAC---TGGC--CATAAAGT-TTGCGAGCGTGCGCGGTCGTCGCGCTCGATATCGTGAAGACGGGCG
droEug1	scf7180000409554:2765834-2766000 -		G-GTCCTAGTGGTCCTGCCGACCTTCATAAGCGAATAGCCGACAGCAAGTGAGTAA---TAT---AAACGCGC----------GCGGAG-TGATTAGGTA--------CTAGTTAAC-TACT---TGGC--CATAAAGT-TTGCAGGGTGCGCGGTCGGCTGCGCTCGATATCGTATGTCGTGAAGACGGGTG
dm3	chr2L:3331495-3331661 +		G-GTGCAGTGTGTCCTTGCGACCTTCATAAGCGAAATGCGAGACGCAAGTAAGTCT---CAA---AGTGATGT----------GTGCTATGATTATACACGATT----------AAC-TAAT---TGCT--CATAAAGT-TTTGCAGTGTGCGCGGTCGCGCTAGCGTCGATATCTTCTATGCGTGAACACGGGTG
droSim2	2L:3191651-3191816 +		G-GTGCAGTGTGTCCTTGCGACCTTCATAAGCGAAATGCGAGACGCAAGTGAGTCT---CAA---AGTGATGT----------GTGCTG-AAGTATACTATGCATT----------AAC-TAAT---TGCT--CATAAAGT-TTTGCAGTGTGCGCGGTCGCGCTAGCGTCGATATCTTCTATGCGTGAACACGGGTG
droSec2	scaffold_5:1474346-1474511 +		G-GTGCAGTGTGTCCTTGCGACCTTCATAAGCGAAATGCGAGACGCAAGTGAGTCT---CAA---AGTGATGT----------GTGCTG-AAGTATACTATGCATT----------AAC-TAAT---TGCT--CATAAAGT-TTTGCAGTGTGCGCGGTCGCGCTAGCGTCGATATCTTCTATGCGTGAACACGGGTG
droYak3	2L:3315872-3316037 +		G-GTGCAGTGTGTCCTTGCGACCTTCATAAGCGAAATGCGAGACGCAAGTGAGTCT---CAA---AGTGATGT----------GTGCTG-AAATATACTATGCATT----------AAC-TAAT---TGCT--CATAAAGT-TTTGCAGTGTGCGCGGTCGCGCTAGCGTCGATATCGTATGTCGTGAACACGGGTG
droEre2	scaffold_4929:3361637-3361808 +		G-GTGCAGTGTGTCCTTGCGACCTTCATAAGCGAAATGCGAGACGCAAGTGAGTCT---CAA---AGTTGTGT----------GCCTG-AATATACTACGATTAACTAC----GAT-TAAT---TGCT--CATAAAGT-TGTGCAGTGTACGCGGTCGCGCTAGCGTCGATATCTTCTATGCGTGAACACGGGTG

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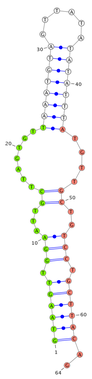
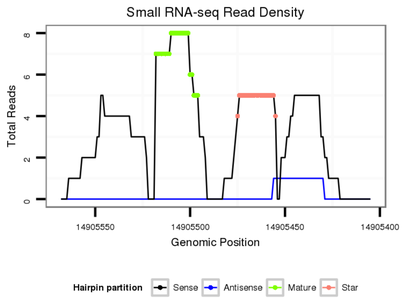
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

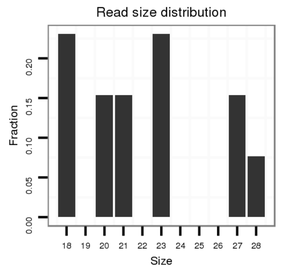
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_11959	**scaffold_12963:14905455-14905518 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

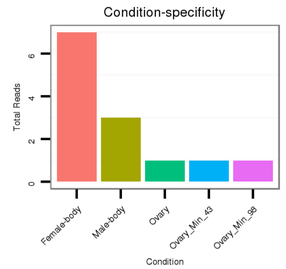
Legend: mature star mismatch in alignment mismatch in read

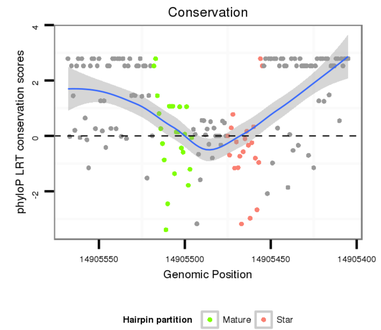
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dvir\GJ21225-in]; CDS [Dvir\GJ21225-cds]; CDS [Dvir\GJ21225-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TGGGCGACTGCAACAAGGAGCGCGGCTTTATCTGTGAAATGGATCCGAGAGTAAGTTGGAATTGCTTAGTGTTAAATGTAGTTATATATATTTATGTTGCTGTCCTGCTTACAGGTCATCATCGATCCGTTGTCGTGGCGCGCGGACATTTTTGCCATAAGTAT	Read size	# Mismatch	Hit Count	Total Norm	Total	M047 female body	V116 male body	M027 male body	SRR2096056 Ovary_Min_46	SRR2096038 embryo_0-2h from 14 day old mothers	SRR060658 Strain_9	SRR060664 140_ovaries_total	SRR060667 9_males_carcasses_total	SRR060675 160_females_carcasses_total	SRR060676 140x9_ovaries_total	SRR060678 9xArg_ovaries_total	SRR2096055 9x140_testes_total	SRR2096058 Ovary_Min_43	SRR2096059 Ovary_Min_98	SRR2096060 Ovary_Min_164	SRR060668 Ovary_Min_193	V053 160x9_males_carcasses_total	SRR060666 head	160_males_carcasses_total
**********(((((((.(((.(...((.....((((((((.....))))))))....))..))))..))))))).**********																								
.....GTAAGTTGGAATTGCTTAGTGTT.....	23	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CATCATCGATCCGTTGTCGTG.....	21	0	1	2.00	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGTTGGAATTGCTTAGTGTTAAAT.....	27	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGTTGGAATTGCTTA.....	18	0	1	2.00	2	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0
.....GCGGCTTTATCTGTGAAATGGATCC.....	25	0	1	2.00	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GCGCGGCTTTATCTGTGAAATGGATC.....	26	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
.....ATGTTGCTGTCCTGCTTACAG.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGTTGGAATTGCTTAGT.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CATCGATCCGTTGTCGTGGC.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GAATTGCTTAGTGTTAAA.....	18	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
.....ATGTTGCTGTCCTGCTTACAGA.....	22	1	1	1.00	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....TCGATCCGTTGTCGTGGCGCGCGGAC.....	26	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
.....AACAAGGAGCGCGGCTTTATCTGTGA.....	26	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....CGACTGCAACAAGGAGCGC.....	19	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGTTGGAATTGCTTAGA.....	20	1	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
.....TGTTGCTGTCCTGCTTACAG.....	20	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTATGTTGCTGTCCTGCTTACAG.....	23	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATGTTGCTGTCCTGCTTACA.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
.....GATCCGTTGTCGTGGCGC.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATATTTATGTTGCTGTCCTGCTTACAG.....	28	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

ACCCGCTGACGTTGTTCCTCGCGCCGAAATAGACACTTTACCTAGGCTCTCATTCAACCTTAACGAATCACAATTTACATCAATATATATAAATACAACGACAGGACGAATGTCCAGTAGTAGCTAGGCAACAGCACCGCGCCTGTAAAAACGGTATTCATA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060655 9x160_testes_total	SRR2096059 Ovary_Min_164	SRR2096057 Ovary_Min_50	SRR2096013 Ovary_Strain_9_oxidized	V047 embryo
**********(((((((.(((...((.....((((((((.....))))))))....))..))))..))))))).**********										
.....TCCAGTAGTAGCTAGGCAACAGCACCG.....	27	0	1	1.00	1	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12963:14905405-14905568 -	dvi_11959	TGGGCGACTGCAACAAGGAGCGCGGCTTTATCTGTGAAATGGATCCGAGAGTAAGTTGG----------AATTGCTTAG---------TGT-TAA----------A----------TG-TAGTTA-TA-TATATTTATGTTGCT----------G------TCC---T-GCTTACAGGTCATCATCGATCCGTTGTCGTGGCGCGCGGACATTTTTGCCATAAGTAT
droMoj3	scaffold_6500:17859380-17859540 -		TGGCAGGACTGCACGAAGGAGCGCGGCTTGATCTGGAAATGGATCCGAGGGTAAAGAACA----AAGGT--ACAAT------------TG---AAA----------TAA----------G----------AG--TAAA-AATT---GA--CA----------GC---CTTTCC---A-CTGCTTAGGTCATCATGATCCGTTGTCGTGGCGCGCGGACATTTTTGCCATAAGTAT
droGri2	scaffold_8080:644-810 +		TGGCAGGACTGCAACAAGGAGCGAGGCTTGATCTGTGAAATGGATCCAAGGTAAGGTG----------CAATCATTAAGTATATGCTCG-CT-TA----------G----------TA-TTATTTA-TA-------AA----------AT-CCTG-TCC---A-TTTCGTAGGTCATCATCGATCGATTTTCGCGCGCGGACATTTTTGCCATAAGTAT
droWil2	scf2_1100000004521:9256677-9256844 -		TGGCAAGATGGGCAAGAAAGGGTTGATCTGTGAAATGGATCCAAGGTAAGAAATT----------AAAAA----------TATA---TATTCTAATA--TATTCT----------AAA-TAA-C-ACTG---ATT--GA--CTC----------G---GTC---CTGTTCTAGGTCATCATGATCGTTGTCTGGCGCGCGGACATTTTTGCCATAGATAT
dp5	4_group3:4924568-4924726 -		TGGCAAGACTGGCCAAGGAAAGGGTTGATCTATCGAAATGGATCCAGAGTAAGTCTATTCAGCAGAGG----CAAT------------CC---------G----------G---TGAGC-TGTA---ATT--CA-GAAT----------C------CGT---TTTCCTTAGGTCATCATGATCGTTGTCTGGCGCGCGGACATTTTTGCCATCAGTAT
droPer2	scaffold_1:6415217-6415375 -		TGGCAAGACTGGCCAAGGAAAGGGTTGATCTATCGAAATGGATCCAGGGTAAGTCTATTCAGCAGAGG----CAAT------------CC---------G----------G---TGAGC-TGTA---ATT--CA-GAAT----------C------CGT---TTTCCTTAGGTCATCATGATCGTTGTCTGGCGCGCGGACATTTTTGCCATCAGTAT
droAna3	scaffold_12916:1806397-1806558 +		TAAGGACTGCGGCAAGGAGCGGGTTGATCTGGAGATGGATCCGAGGGTGACCATCTA-ATAA---TGGAA---CATCAA----------AT-AT----------A----------A-T-T----------A----------ATG-TAATCG--T-------GCGAACT----------T------ATT---CCACACGTAGGTCATGATCGATCCGTTGTCGTGGCGCGCGACATTTTTGCCATCAGTAT
droBip1	scf7180000396728:464449-464613 +		TAAGGACTGCGGCAAGGAGCGGGTTGATCTGGAGATGGACCGAGGGTGACCATCTA-AAAG---TCGAA---AAT-CCA----------TCT-T----------A----------A-T-T----------A----------ATG-TAATCG-CCG--------AC----------CGCTTTT---CCCGACGAAGGTCATGATCGATCCGTTGTCGTGGCGCGCGACATTTTTGCCATCAGTAT
droKik1	scf7180000302401:722569-722758 +		TGAGGATGTGCAACAAGGAGCGCGGTTGATCTGTGAAATGGATCCGAGGGTAAGTTGATCGAACAA---TTGAA---AT----------AAA---TTTGATAGCAGTATTAA----------AAATGAAA--TC---TAGA-GA-ATTCAATAATAATTAAAGCAAATTCAGTTGAAGTCATCATGATCCGTTGTCGTGGCGCGCGACATTTTTGCCATCAGTAT
droFic1	scf7180000453924:1781303-1781452 +		TGGCAGGATGCACGCAAGGAGCGCGGTTGATCTGGAAATGGATCCAGAGGTAGGAACAAA----------AAAAA----------AAATG-------A----------ACC-TAAAC-CCTT---AGT--AA----------C------TGT---T-TTCATCAGGTCATCATGATCGCTTGTCGTGGCGCGCGACATTTTTGCCATCAGTAT
droEle1	scf7180000490728:558121-558375 +		TGGCAGGATGCACGCAAAGAGCGGGTTGATCTGGAAATGGATCCAGGGTAAGAATATC----------AAAAA----------TTAAATTTTTGTTTATTTTTTATGTTTTACATTATATTTATTTATTCTTTATAGCACCATCTTGGTGCTACAAGAG----------AATCATTTATTTAATGCACTAGTTAGAAATTGTAAC-ACT---CGTT--AAGAAAT----------T------TTATATTTTGTTAGGTCATCATGATCGCTTGTCGTGGCGCGCGACATTTTTGCCATCAGTAT
droRho1	scf7180000779430:65486-65648 -		TGGCAGGATGCACGCAAGGAGCGCGGTTGATCTGGAAATGGATCCAGGGTAAGATATTG----------AAAAA----------TTT-AAACT----------AAT-----TTACAG----------A----------AAC-TAAAC-ACTT---CGTT--AAGAAC----------C------ACA---CTTGCAAGGTCATCATGATCGCTTGTCGTGGCGCGCGACATTTTTGCCATCAGTAT
droBia1	scf7180000302261:2188720-2188878 +		TGGCAGGATGCGGCAAGGAGCGCGGTTGATCTGGAAATGGATCCAGGGTAGAGCTC----------AAAAA----------G-TT----------AAGGACCTTAAGGAG----------A----------A-T--AAG-CCTT---GCT--AAGAAT----------C------ATT---CTTTCGCAAGGTCATCATGATCGCTTGTCGTGGCGCGCGACATTTTTGCCATCAGTAT
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droEug1	scf7180000409554:2274273-2274431 -		TGGCAGGACTGCGCAAAGAGCGCGGTTGATCTGTGAAATGGATCCAGGGTAAGGAACTC----------AAAAA----------CC-T-----------AAGGTTCACTAAGAG----------A----------A--T--AAC-AATG---ATT--AAGCAG----------A------AGT---CTTTCTAGGTCATCATGATCGCTTGTCGTGGCGCGCGACATTTTTGCCATCAGTAT
dm3	chr2L:3800772-3800929 +		TGGCAGGATGCAACAAGGAGCGCGGTTTTATCTGGAATCGGATCCGAGGGTAAAAAGTC----------AAAAA----------AAA---AAA----------AAGA---AATAATAG----------A----------AAA-TCAAC-ATTG---CGTT--AGCAACT----------G------TGA---T-CTTTCAGGTTATCATTGATCGCCTATCCTGGCGCGCGACATTTTTGCCATCAGTAT
droSim2	21:3652891-3653044 +		TGGCAGGATGCAACAAGGAGCGCGGTTGATCTGGAATCGGATCCGAGGGTAAAAAAAC----------AAAAA----------T-T---AAA----------AAGA---AATACTAG----------A----------A--T--AAT-ATTG---CGTT--AGGAACT----------G------TGT---T-CTTTCAGGTTATCATTGATCGCCTATCCTGGCGCGCGGACATTTTTGCCATCAGTAT
droSec2	scaffold_51:902861-1903014 +		TGGCAGGATGCACGAAGGAGCGCGGTTGATCTGGAATCGGATCCGAGGGTAAAAAAC----------AAAAA----------AAA---AAA----------AAGA---AATAATAG----------A----------A--T--AAT-ATTG---CGTT--AGAAACT----------G------TGT---T-CTTTCAGGTTATCATTGATCGCCTATCCTGGCGCGCGACATTTTTGCCATCAGTAT
droYak3	2L:3802464-3802621 +		TGGCAGGATGCAACAAGGAGCGCGGTTGATCTGGAATCGGATCCGAGGGTAAAACC----------AAAAA----------AAA---AAA----------AAGA---AATTAAAG----------A----------A--T--AAT-ATTG---CGTT--AGAAACT----------G------TAT---TCCTTTCAGGTTATCATTGATCGCTTATCCTGGCGCGCGACATTTTTGCCATCAGTAT
droEre2	scaffold_4929:3846223-3846381 +		TGGCAGGATGCAACAAGGAGCGCGGCTTTATCTGGAATCGGATCCGAGGGTAAAATT----------AAAAA----------AAA---CAA----------AAGC---AACAATAG----------A----------AAA-TAACAATTG---CGTT--CGTAACT----------G------TGT---T-CGCTTTAGGTTATCATTGATCGCTTATCCTGGCGCGCGACATTTTTGCCATCAGTAT

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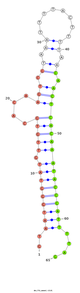
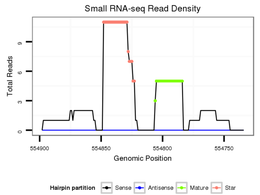
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.ptop3	0
crit.uri	1
crit.back	0
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

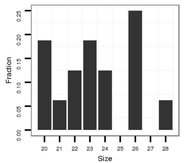
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_751	**scaffold_10324:554784-554848 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

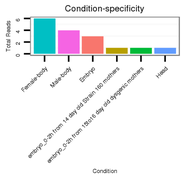
Legend: sense star antisense/5 in alig non-st mismatch in star

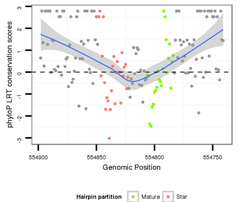
Predicted structure











Show Alternate Folds

Flybase annotation

intron [DvirGI14987-nd]; CDS [DvirGI14987-cds]; CDS [DvirGI14987-cds]

No Repeatable elements found

Sense Small Reads

hide 3p reads show mrd mismatch reads

Read #	Hit Count	Total Norm	Total	V116 male body	M047 female body	M061 embryo	V053 160_0-hour head	SRR060643 2h_embryos_total	SRR060672 9x160_females_carcasses_total	SRR2096014 Ovary_Strain_160_oxidized	SRR2096079 embryo_0-2h from 15to16 day old mothers	SRR060684 140x9_0-2h_embryos_total	SRR060682 9x140_0-2h_embryos_total	SRR060686 Arg9_0-2h_embryos_total	SRR1106722 embryo_10-12h	SRR2096081 embryo_0-2h from 15to16 day old nondygenic 14h	SRR1106724 embryo_12-14h	SRR1106726 16h	SRR1106728 larvae	SRR2096041 embryo_0-2h from 14 day old Strain 160 mothers	SRR2096013 Ovary_Strain_9_oxidized	SRR060687 9_0-2h_embryos_total	SRR060685 9xArg_0-2h_embryos_total	SRR060670 9_testes_total	M027 male body	SRR2096080 embryo_0-2h from 15to16 day old nondygenic mothers	SRR060655 9x160_testes_total	SRR060676 9xArg_ovaries_total
size	Mismatch																											
26	0	1	4.00	4	0	1	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	0	1	3.00	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
23	0	1	3.00	3	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	1	1	3.00	3	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
17	1	1	3.00	3	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0
22	0	1	2.00	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	1	2.00	2	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
18	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	2	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
23	1	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

Read #	Hit Count	Total Norm	Total	M027 male body	SRR060686 Arg9_0-2h_embryos_total	SRR060685 9xArg_0-2h_embryos_total	M047 female body	SRR060675 140x9_ovaries_total	SRR060684 140x9_0-2h_embryos_total	SRR060682 9x140_0-2h_embryos_total	SRR060676 9xArg_ovaries_total	SRR060674 9x140_ovaries_total	SRR060687 9_0-2h_embryos_total	M028 head	SRR060667 160_females_carcasses_total	SRR060677 Arg9_ovaries_total	SRR060668 160x9_males_carcasses_total	SRR060683 160_testes_total	SRR1106728 larvae	SRR2096026 embryo_0-2h from 14 day old Strain 9 mothers	SRR060649 140x9_females_carcasses_total	SRR060664 9_males_carcasses_total	SRR060671 9x160_males_carcasses_total	SRR060679 140x9_testes_total	SRR060681 Arg9_testes_total	SRR2096038 embryo_0-2h from 14 day old male Strain 9 mothers	V116 male body	SRR2096072 embryo_0-2h from 15to16 day old dysgenic mothers	V053 head	SRR060658 140_ovaries_total	SRR060657 140_testes_total	SRR060688 160_ovaries_total	SRR060666 160_males_carcasses_total	SRR060659 Argentina_testes_total	SRR2096057 Ovary_Min_50
size	Mismatch																																			
26	0	1	4.00	4	0	1	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	0	1	3.00	3	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	0	1	3.00	3	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	1	1	3.00	3	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
17	1	1	3.00	3	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	1	2.00	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	1	2.00	2	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
18	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
28	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	2	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	1	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Show Alignment With Reads

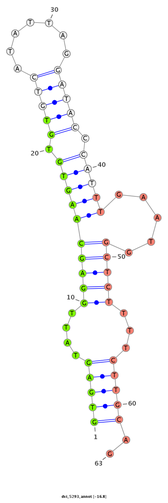
Re-alignment of all predicted orthologs

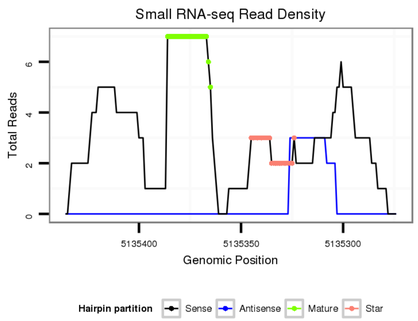
Species	Coordinate	ID	Alignment
droVir3	scaffold_10324:554784-554831,-	dvi_751	CAGGATCATTAAATTGCGCAAGACGGCAATGGAGGAGCTCAAAGTAATG-GTATGTTGTGCACAAGTCGTAAATTTACTTTTAACAACTCACAAATACCATTTTAGAGGCCAACATGAAGTTTCTGGAGCACCTGAAGAGGAAATGGACGAGAAA----------TAC--T----------T--TTAAC----AACTC--A
droMoj3	scaffold_6496:238589-238603,-		CAAGATCATGAATTGCGCAAGACGGCAATGGAGGAGCTCAAAGTAATGGTATGTTGTACCTCAAATACTGCAAT--T--G-GGGCAAATAACTGAG--T--AATAAGTC----T--C-----CTCCTCTTA----------TA-G-TATTTGAGCGCAATG-A-G-TGAAG-T-TTGGAGCACCTGAAGAGGAAATGGACGAGAAA
droGri2	scaffold_13245:827852-827869,-		CAC-ATCATCCCATTGCGCAAGACGGCAATGGAGGAGCTCAAAGTAATGGTATGTTGTACCTCAAATCTATGCAAT--C-CAA-A-TGTCTC----------TC-TATAA-----TAAC-----C-----TC-TTTTTAAC-TC-CATGA-G-TGTAG-G-T-TGAAGAGCACCTGAAGAGGAAATGGACGAGAAA
droWil2	scaffold_14000000045162:47756-47853,-		G-GATCATGAATTGCGCAAGACGGCAATGGAGGAGCTCAAAGTAATGGTATGTTGTACCTCAAATCTATGCAAT-GTGCAAATATGCAAGCTCTCTTTT

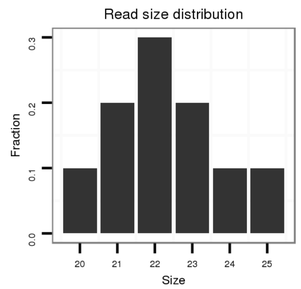
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_5293	**scaffold_12875:5135324-5135386 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Comell Mirror]]

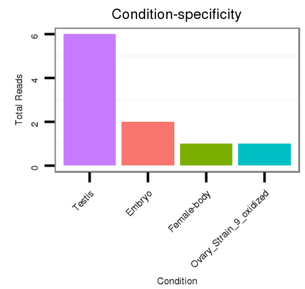
Legend: mature star mismatch in alignment mismatch in read

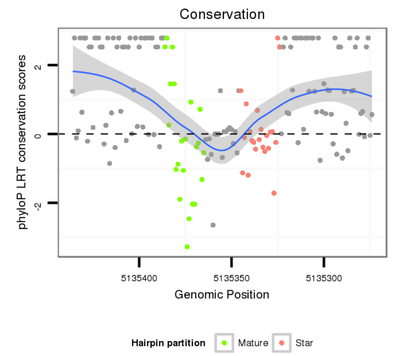
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dvir\GJ20879-in]; CDS [Dvir\GJ20879-cds]; CDS [Dvir\GJ20879-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GAGGAGAATCGTTTTGCCCTATTGCAGCCAGAGCTGGAAATTAATCCAAAGTGAGTATTGGAGCAAGTGTGTGTCATATTAGGATACCCATTTGAATGGCTCTTTTCTTGCAGACATCCCATCATAAAGAAGCTGCATTCCTTGCGTACAAGCGAACCGGAAT	Read size	# Mismatch	Hit Count	Total Norm	Total	M047 female body	M061 embryo	SRR060655 9x160_testes_total	SRR060678 9x140_testes_total	SRR060679 140x9_testes_total	SRR060681 Argx9_testes_total	V047 embryo	SRR060668 160x9_males_carcasses_total	SRR060669 160x9_females_carcasses_total	SRR060674 9x140_ovaries_total	SRR060677 Argx9_ovaries_total	SRR060687 9_0-2h_embryos_total	SRR2096013 Ovary_Strain_9_oxidized	SRR2096026 embryo_0-2h from 14 day old Strain 9 mothers	V053 head
**********(((((.....(((((((((.(((((.....)))))).)))))).....)))))...)))))..**********																				
.....GTGAGTATTGGAGCAAGTGTGT.....	22	0	1	2.00	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
.....AGCCAGAGCTGGAAATTAATCCAAA.....	25	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....TTTGCCCTATTGCAGCCAGAGCTGGAA.....	27	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
.....CCCTATTGCAGCCAGAGCTGGAA.....	23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
.....TGCATTCCTTGCGTACAAGCGAACC.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTGAATGGCTCTTTTCTTGCAG.....	22	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
.....GTGAGTATTGGAGCAAGTGTGTG.....	23	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
...GAGAATCGTTTTGCCCTATTGC.....	22	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTTGAATGGCTCTTTTCTTGCAG.....	23	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
.....TTGCCCTATTGCAGCCAGAGCTG.....	23	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTATTGGAGCAAGTGTGTGC.....	24	1	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
.....ACATCCCATCATAAAGAAGCTGCATTCC.....	28	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
.....GTGAGTATTGGAGCAAGTGT.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTATTGGAGCAAGTGTGTGTC.....	25	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
.....GACATCCCATCATAAAGAAGCTGC.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CATTCCTTGCGTACAAGC.....	18	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AGGATACCCATTTGAATGGCT.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
.....CATAAAGAAGCTGCATTCCT.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..GGAGAATCGTTTTGCCCTATTGC.....	23	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GCTGCATTCCTTGCGTACA.....	19	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTATTGGAGCAAGTGTGTGT.....	24	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
.....GTGAGTATTGGAGCAAGTGTG.....	21	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0

Anti-sense strand reads

CTCCTCTTAGCAAAACGGGATAACGTCGGTCTCGACCTTTAATTAGGTTTCACTCATAACCTCGTTCACACACAGTATAATCCTATGGGTAAACTTACCGAGAAAAGAACGTGTGTAGGGTAGTATTTCTTCGACGTAAGGAACGCATGTTCGCTTGGCCTTA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060656 9x160_ovaries_total	V116 male body	SRR060658 140_ovaries_total	M061 embryo	SRR060686 Argx9_0-2h_embryos_total	GSM1528803 follicle cells	SRR2096060 Ovary_Min_193	SRR2096055 Ovary_Min_43	SRR060665 9_females_carcasses_total	SRR060671 9x160_males_carcasses_total	V053 head	SRR060668 160x9_males_carcasses_total
**********(((((.....(((((((((.(((((.....)))))).)))))).....)))))...)))))..**********																	
.....GTCTGTAGGGTAGTATTTCTTCG.....	23	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0	0
.....GTCTGTAGGGTAGTATTT.....	18	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12875:5135274-5135436 -	dvi_5293	GAGGAGAATCGTTTTGCCCTATTGCAGCCAGAGCTGGAAATTAATCCAAAGTGAGTATTGGAGCAAGTGTGTGTCATATTAGGATACCCATT----------TGAATGG----------CTCTTTTC--------TTGCAGACATCCCATCATAAAGAAGCTGCATTCCTTGCGTACAAGCGAACCGGAAT
droMoj3	scaffold_6496:24956809-24956965 +		GAAGAGAATCGTTTTGCCTTATTGCAGCCAGAGCTGGAAATCAATCCAAGTGAGTCCCCATCTTCCCCTAATACC---------- ---TAACCTTT--------TTTGATTAATC---G-GTTA---TTTTTC--------CCACAGACATCCCATCATAAAGAAGTGCTTTTCCTTGCGTACAAGCGAACCCGAAC
droGri2	scaffold_15112:160746-160997 -		GAAGAGAATCGTTTTGCACTGCTGCAGCCGAGCTGGAAATCAATCCAAGTGAGTAAA--TGTCTATTTTT---A---TTTATATTTATTTAAAATATATATTATATTAAATAATATTCAACATTCCGATACTCTTTTTAAACTAAATTTAAGATAGCTTGCATATTA---GTTAAATTCATAATTCTAACGTC----------TTTGTA-------TTTTTCTA--------TTGCAGACATCCCATCATCAAGAAGCTGCATTCCTGCGCACGAGCGAACCTGAAT
droWil2	scf2_1100000004510:1948416-1948580 -		GAAGAGAATCGATTTGCCTTTGCTCCAGCCGGAACTTGGAAATCAATCCAAAGTATCATATACATTTA----------AGTCAGTATTT---------- ----------CC-ATCAT---------TTTA--TTTATTTTTC---G-------TTTATTTTGCAGACATCCCATCATCAAGAAGTCAATTTCATTGCGTGTCGAGCGATCCGAGATT
dp5	31:18223477-18223643 -		GAGCAGAACCGCTTTGCTTTGCTGCAGCCGGAACTTAGAGATCAATCCAAAGTGAGTGGGAC-----A---------- ----------CCTCTGTTGTCT---GTTATCCTCAGCCCTTAATCC----------TTCGGT----TTGCGCCT--------TTTCAGACATCCCATCATCAAGAAGCTGATCAAGCTGCGCGAGAGTGCACGCGAGT
droPer2	scaffold_34:166523-166689 -		GAGCAGAACCGCTTTGCTTTGCTGCAGCCGGAACTTAGAGATCAATCCAAAGTGAGTGGGAC-----A---------- ----------CCTCTGTTGTCT---GTTATCCTCAGCCCTTAATCC----------TTCGGT----TTGCGCCT--------TTTCAGACATCCCATCATCAAGAAGCTGATCAAGCTGCGCGAGAGTGCACGCGAGT
droAna3	scaffold_13266:18508069-18508224 +		GAGCAGAATCCATTTGCACTCCTGCAGCCGAGCTTAGAAATCAAACCAAAGTGAGTGTATTTC----------A---------- ----------TTATATTTT----------TTAAAATAAA-TTT--TTTTTA---C---AAACATGTCTTGCAGCTACCTATCATCAAAAAGCTCATCAAGAAGCTGCCGAGAGCGACGCAGGAGC
droBip1	scf7180000395549:17913-18068 -		GAGCAAAATCCATTTGCTCTTTGCAGCCGAGCTTGGAAATTAATCCAAAGTGAGTTATTTT----------G---------- ----------TATATTAT----------TTGAAATCA-GTT--TTTTCA---C---AAACATGTCTTGCAGCTACCTATCATCAAGAAGCTCATCAAGCTGCGTGAAGCGACGCAGGAGC
droKik1	scf7180000302470:89016-89175 -		GAGCAGAACCGCTTTTGCACTCCTGCAGCCGAGCTGGACTATAACCCAAAGTGAGTATTCTCTATCCT-------G---------- ----------TTCTCATCTTCAGCACTTAA--CGT--------CATT----CTACTTTT--------ATTCAGCACCCCATCATCAAGAAGCTGATCAAGCTGCGCGAAGCGACGCAGGAGC
droFic1	scf7180000453955:787916-788074 +		GAAGCAAAACCGATTTGCCCTCCTTCAGCCGGAGCTGGACGATCAACCCAAAGTAAGTAGGCCTTTTTCCCCTCGCGCCT---------- ----------TTCATACCTT----------CACAACCGA-----T----CCAATCCC--------AAATAGCCACGCCATCATCAAGAAGCTGATCAAGCTGCGCGAGAGCGACAAGGAGC
droEle1	scf7180000491217:497899-498057 +		CAAGAGAACCGATTTGCCCTCCTGCAGCCAGAGCTGGACGATCAACCCAAGTGAGTAACCTATTTACCCTGCGTGC---------- ----------TTTTGATTT----------TATGCCC-----AACTT-----TCACCCCT--------TTCCAGCCACCCATCATCAAGAACTGATCAAGCTGCGCGAGACCGAAGAAGGATC
droRho1	scf7180000766409:407392-407551 -		GAAGAGAATCGATTTGCCTTGCTTCAGCCAGAGCTGGACGATCAACCCAAGTCAGTAGTCCTAGTTTCCCTGCATTT---------- ----------TTATTGCTTT----------AATAACC-----TACTT-----CCACCCTA--------TTAAGACACCCCATCATCAAGAACGTAATCAAGCTGCGCGAGACCGAAGAAGGATC
droBia1	scf7180000302292:3632465-3632626 +		GAGCAGAATCCATTTGCCCTCCTTCAGCCAGATCTGGACGATCAACCCAAGTGAGTAGTCCTATTTC----------ATTTTCCCAGT---------- ----------GCAACCG----------CTAA--CATACTTTA----------TACATTT--------TTCAAGCACACCCATCATCAAGAAGCTGATCAAGCTGCGCGAGAGCGACAAGGAGC
droTak1	scf7180000415609:157724-157886 -		GAAGAGAATCCATTTGCCCTCCTGCAGCCAGATCTGGACGATCAACCCAAGTGAGTGGCCGCTGTTACCCCGGCATTT---------- ----------AGTCAACCTTA----------CTTACTTTTTA---C-CTA--TTTTCTT--------CTTAAGACACCCATCATCAAGAAGCTAATCAAGCTACCGAGAGCGACAAGGATC
droEug1	scf7180000409758:249740-249900 -		GAAGAGAACCGATTTGCCCTCCTTCAGCCAGAGCTTGACGATCAACCCAAGTGAGTACTCACAGTTTCCCAGCATTG---------- ----------ATTGCATA----------TTGATATTAAC---T-TATTT--TTTCATTT--------TTAAAGCCATCCCATAATCAAGAAGAGCTAATCAAGTTGCGCGAAAGCGATACGGAGC
dm3	chr2R:2521404-2521565 -		GAAGAGAATCGATTTGCCCTGCTTCAACCAGATCTGGACGATCAACCCAAAGTGAGTGCCCCTCCTCACCTTTCCTTTC---------- ----------ATTGCCTTT----------CTTATTTTGCA---T-TTTT---CCTTACCCCATCATCAAGAAGCTAACAAGCTCGTGAGAGCGACAAGGAGC
droSim2	2r:3385090-3385251 -		GAAGAGAATCGATTTGCCCTGCTTCAACCAGATCTGGACGATCAACCCAAAGTGAGTGCCCCTCTGTCACCTTTCCTTTC---------- ----------ATTGCCTTT----------CTTATTTTGCA---T-TTTT---CCTTACCCCATCATCAAGAAGCTAACAAGCTCGTGAGAGCGACAAGGAGC
droSec2	scaffold_1:185012-185173 -		GAAGAGAATCGATTTGCCCTGCTTCAACCAGATCTGGACGATCAACCCAAAGTGAGTGCCCCTCGTCACCTTCCTTTC---------- ----------ATTGCCTTT----------CTTATTTTGCA---T-TTTT---CCTGACCCCATCATCAAGAAGCTAACAAGCTCGTGAGAGCGACAAGGATC
droYak3	2L:15267440-15267602 -		GAAGAGAATCCATTTGCCCTCCTTCAACCAGATCTGGAAATCAATCCAAAGTGAGTGCCGCCTTGTGACCCTACTTTC---------- ----------ATTGCCTTT----------TTTAGTGGCA---T-TGTTT---CCCTTACCCCATCATCAAGAAGCTGACAAGCTCGCGTGAGAGCGACAAGGATC
droEre2	scaffold_4929:20023536-20023698 +		GAAGAGAATCCATTTGCCCTCCTTCAACCAGATCTGGACGATCAACCCAAAGTGAGTACTCCTTGTCACCCTACTTTC---------- ----------ATTGCTTCT----------CTTAGTGGCA---T-TGTTT---CCCTTACCCCATCATCAAGAAGCTAACAAGCTGCGAGGCAGCGACAAGGATC

Show Alignment With Reads

Generated: 09/08/2015 at 10:44 PM

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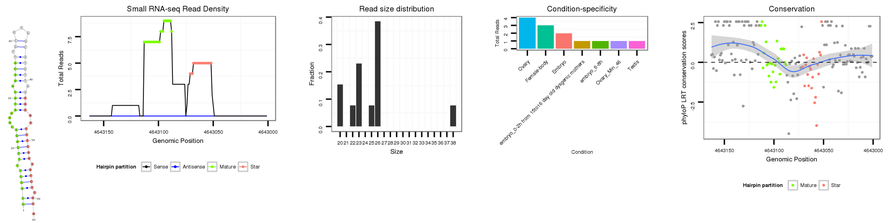
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	0
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_5249	**scaffold_12875:4643051-4643113 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: **mature** **star** **sub-mature** **in its arfg name or** **mismatch in star**

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dvir/GI20890-ra], CDS [Dvir/GI20890-cds], CDS [Dvir/GI20890-cds]

No Repeatmbr elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	Hit Count	Total Mism	Mism Rate	Total Mism	M041 embryo head	V053 female body	M047 female PaAng_ovaries_total	SRR060474	SRR060686 Arga9_0-2h_embryos_total	SRR060687 9_0-2h_embryos_total	SRR060666 140_males_carcasses_total	SRR060677 Arga9_ovaries_total	SRR060681 Arga9_testes_total	SRR1106718 embryo_6-8h	SRR2096054 Ovary_Min_46	SRR2096079 embryo_0-2h from 15to16 day old dysgenic mothers	SRR060659 Argentina_testes_total	SRR2096059 Ovary_Min_144	SRR060657 140_testes_total	SRR060658 140_ovaries_total	SRR2096058 Ovary_Min_98	SRR060660 Argentina_ovaries_total	V047 embryo
24	0	1	5.00	5	0	0	0	3	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
23	1	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0
23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
25	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
20	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	1	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

Read #	Hit Count	Total Mism	Mism Rate	Total Mism	140x9_0-2h_embryos_total	9_0-2h_embryos_total	9x140_0-2h_embryos_total	140x9_0-2h_embryos_total	M028 head	SRR060659 Argentina_testes_total	SRR060663 140_0-2h_embryos_total	SRR060666 140_males_carcasses_total	V116 male body	SRR060679 140x9_testes_total	SRR060686 Arga9_0-2h_embryos_total	SRR060661 140x9_0-2h_embryos_total	SRR060672 9x140_females_carcasses_total	SRR060664 9_males_carcasses_total	V047 embryo	SRR060668 140x9_males_carcasses_total	M047 female body	SRR060669 140x9_females_carcasses_total	SRR060671 9x140_males_carcasses_total	SRR2096014 Ovary_Strain_140_oxidised	SRR060665 9_females_carcasses_total	SRR060667 140_females_carcasses_total	SRR2096056 Ovary_Min_46	SRR2096080 embryo_0-2h from 15to16 day old nondysgenic mothers	SRR2096059 Ovary_Min_144	SRR060658 140_ovaries_total	SRR060675 140x9_ovaries_total	SRR060685 PaAng_0-2h_embryos_total	SRR2096057 Ovary_Min_50	SRR060678 9x140_testes_total	M027 male body	SRR2096060 Ovary_Min_193	SRR060660 Argentina_ovaries_total	SRR060677 Arga9_ovaries_total	SRR2096026 SRR2096081 embryo_0-2h from 14 from 15to16 day old nondysgenic mothers	SRR2096082 embryo_0-2h from 15to16 day old nondysgenic mothers
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21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
38	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dvivi4	scaffold_12875:4643051-4643113:-	dvi_5249	GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
drobo3	scaffold_6898:2567788:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
drosim12	scaffold_15291:3239:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
dp3	scaffold_1483:1531818:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
drepe2	scaffold_2763:205:1:2:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
drehe3	scaffold_1256:1862823:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
drejp	scaffold_2333:34417:32393:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
drelk1	scaffold_1:2302817:2309817:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
drelk2	scaffold_1:2302817:2309817:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
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drelk4	scaffold_1:2302817:2309817:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
drelk5	scaffold_1:2302817:2309817:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
drelk6	scaffold_1:2302817:2309817:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
drelk7	scaffold_1:2302817:2309817:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
drelk8	scaffold_1:2302817:2309817:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
drelk9	scaffold_1:2302817:2309817:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
dmel	scaffold_4:1364141-1364218:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
drebo1	scaffold_2:2864740:2864837:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
drebo2	scaffold_2:2864740:2864837:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
drebo4	scaffold_2:2864740:2864837:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
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drefa2	scaffold_2:2864740:2864837:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
drefa3	scaffold_2:2864740:2864837:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
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drelu5	scaffold_2:2864740:2864837:-		GCGCTGGACACCGAATATGAGGATATGTTTGATCAGATGCCCACCGTGG-GTAGGTTTTGAGACAAAATATAAACATTGGCTGGCATGTTAATATATCCTCAATATCTCACA-GTGACAGCGATGATGAGGCGGTCGAGAAGCAGAACGCCGGTGCCACAAAGC
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Generated 09/08/2015 at 06:27 PM

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ch.arf	1
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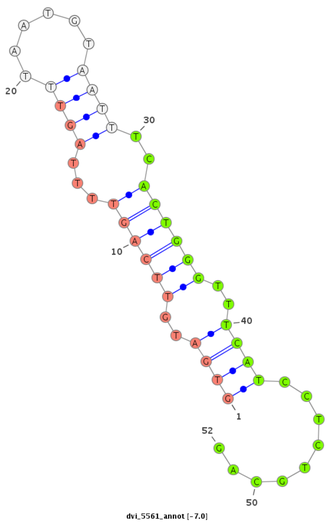
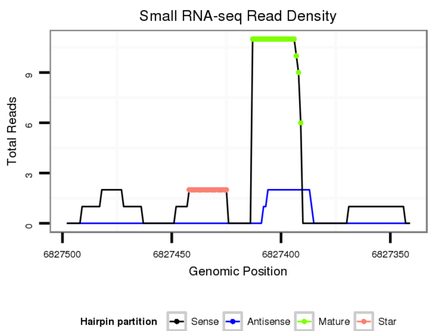
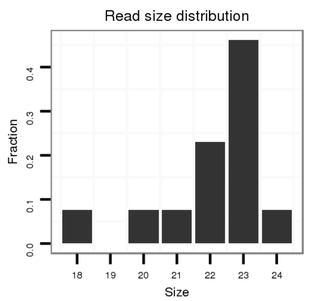
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_5561	**scaffold_12875:6827391-6827448 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

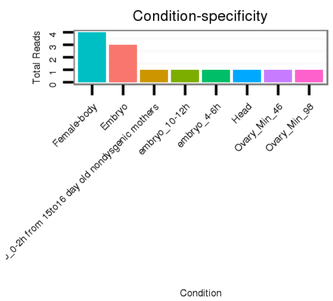
Legend: mature star **mismatch in alignment** mismatch in read

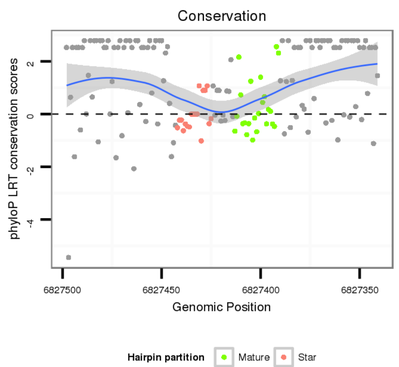
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dvir\GJ20764-in]; CDS [Dvir\GJ20764-cds]; CDS [Dvir\GJ20764-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GTCCGCCGGATTTGATTATGGAGCGCGTTGAGTCCAATCCGCATCAGAAGGTGGGTGTGATGTTCAGTTTTAGTTTAATGTAATTTCACTGGGTTTCATCCTCTGCAGCTTGTGGCGGCTTTGACCAACATTAAACCAGTGAATAAAACGGATGCCGT						M047	M061	M028	M027	SRR060657	SRR060687	SRR1106715	SRR1106722	SRR2096050			SRR2096080	V053	SRR060664	SRR060686	V116	SRR060663	SRR060666	SRR060655
**********(((((..(((((((...((((.....))))..))))))..))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	female body	embryo	head	male body	140_testes_total	9_0-2h_embryos_total	embryo_4-6h	embryo_10-12h	embryo_0-2h from 14 day old Strain 160 mothers	SRR2096056 Ovary_Min_46	SRR2096058 Ovary_Min_98	embryo_0-2h from 15to16 day old nondysgenic mothers	head	9_males_carcasses_total	Argx9_0-2h_embryos_total	male body	160_0-2h_embryos_total	160_males_carcasses_total	9x160_testes_total
.....TCACTGGGTTTCATCCTCTGCA.....	22	0	1	3.00	3	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCACTGGGTTTCATCCTCTGC.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGATGTTCAGTTTTAGT.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGGGTGTGATGTTCAGTTTTAGT.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GGATTTGATTATGGAGCGC.....	19	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATGGAGCGCGTTGAGTCC.....	19	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCACTGGGTTTCATCCTCTG.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATTAAACCAGTGAATAAAACGGATGC...	26	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

CAGGCGGCCTAAACTAATACCTCGCGCAACTCAGGTTAGGCGTAGTCTTCCACCCACACTACAAGTCAAAATCAAATTACATTAAAGTGACCCAAAGTAGGAGACGTCGAACACCGCCGAAACTGGTTGTAATTTGGTCACTTATTTTGCCTACGGCA						SRR060673	SRR060672	SRR2096058	SRR2096060	SRR2096056	SRR060682	SRR060687	SRR060668	V047
**********(((((..(((((((...((((.....))))..)))))))..))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	9_ovaries_total	9x160_females_carcasses_total	Ovary_Min_98	Ovary_Min_193	Ovary_Min_46	9x140_0-2h_embryos_total	9_0-2h_embryos_total	160x9_males_carcasses_total	embryo
.....CAAAGTAGGAGACGTCGAAC.....	20	0	1	1.00	1	0	1	0	0	0	0	0	0	0
.....CCCAAAGTAGGAGACGTCGAACA.....	23	0	1	1.00	1	0	0	1	0	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12875:6827341-6827498 -	dvi_5561	GTCCGCCGGATTTGATTATGGAGCGCGTTGAGTCCAATCCGCATCAGAAGGTGGGTG-TGATGTTCAG--TTTT----------AG----TTTAATG----------TAATTTC----------ACT--GGGTTT-----CA----TCCTC-TGCAGCTTGTGGCGGCTTTGACCAACATTAAACCAGTGAATAAAACGGATGCCGT
droMoj3	scaffold_6496:13404271-13404426 +		GTTCCCCAGACTTGATTATGGAGCGTGTGAGTCCAATCCGCATCAGAAGGTGTGTAA---ACC----CTT----------AGAGTGTTTAAATGTTCTT----------\-------\----------AT--ATT-CA-----TA----A-T-CATAGCTTGTAGCGGCTTTGACCAACATTAAGCCGTGAACAAAACAGATGCTGT
droGri2	scaffold_15112:1695343-1695501 -		GTCCACCAGACTTGATTATGGAAGCGTGTGAATCTAATCCACATCAAAGGTAGGTA--TTT----TTTG----TAGATATGCATCCATC-----ATTCTTTATATCA----------\-------\----------\---AC-----\-------T----TCTC-CAGAGCTTGTAGCGCCTTAACAACATTAAGCCAGTGAATAAAACGGATGCAGT
droWil2	scf2_1100000004558:487484-487583 +		GTTCGCCAGATTTAATAATGGAGCGTGTGAATCGAATCCTCATCAGAAA-------\----------\----\----------\----\-------\----------\-------\----------\---\--\-----\----\--\----\-----\-----TTGTGTAGCGTTGACCAACATTAAGCCGTAAATAAAACGGATGCAGT
dp5	1:2750257-2750432 +		GGCCACCGGATTTGATTATGGAACCGTGTGAATCGAATCCGCATCAAAGGTGCAGTACACAA-----TGTTATCAAATATGTTGACTCCTAAATATGCTCATAATATTAATAATG--------\-------\----------\---\--C---\-----\--TTGTGTGATCTTAGCGTGTGGCTGCTGTACCAACATCAAGCCGTGTAACAAAACGGATGCCGT
droPer2	scaffold_21:2940264-2940439 +		GGCCACCGGATTGATTATGGAACCGTGTGAATCGAATCCGCATCAAAGGTGCAGTACACAA-----TGTTATCAAATATGTTGACTCCTAAATATGCTCATAATATTAATAATG--------\-------\----------\---\--C---\-----\--TTGTGATCTTAGCGTGTGGCTGCTGTACCAACATCAAGCCGTGTAACAAAACGGATGCCGT
droAna3	scaffold_13266:5342138-5342289 +		GGCCACCGGATTGATTATGGAACCGTGTAGAGTCTAATCCGCATCAAAGGTGAAGAA----------\----------\----\-------\----------ATATCTAATAAATGC----TGTACGGTTAAAA-ACAAC--TC----T----T--AT-TCAGCTGTGTACTGCTGCACCAACATTAAGCCGTGAACAAAACAGAGCGCGT
droBip1	scf7180000395751:1124360-1124514 +		GTCCACCGGATGTGATTATGGAAGCGTAGAGTCTAATCCGCATCAAAGGTGAAGAA----------\----------\----\-------\----------CAATAGAATAATTAAAGTGCAAGAGTAAAAAAGAG-ATC-CC-----TG----\----T-TCAGCTTGTTACGCTTTAACCAACATAAAACCGTCAATAAAACAGAGCGCGT
droKik1	scf7180000302411:825806-825958 -		GGCCGCCGAGATCTGATCATGGAGCGTGTGAGTCCAATCCGCATCAGAAGGTAATHA----------\----------\----\-------\----------TGATGAATACG-AATTGGTTTCCCGGAACTGT--A-----CTCC-----GT-TCAGCTGTGGCACTTTGACCAACATCAAACCAGTGAACAAAACGGATGCCGT
droPic1	scf7180000453778:493293-493454 -		GGCCGCCGGATTTGATCATGGAGCGTGTGAATCTAACCCACATCAAAGGTAATGC----------\----------\----\-------\----------TAGTGATGATAATTCCCGCTTTTGGCATAATCAGAGAACCA-----A----TGCT-TCAGCGTGTGGCTGCTGTACCAACATCAAGCCAGTGAACAAAACAGATGCCGT
droEle1	scf7180000491349:76714-76872 -		GGCCACCAGATTTGATCATGGAGCGTGTGAGTCCAATCCGCATCAAAGGTAATTG----------\----------\----\-------\----------CTATAAAGTACTCACTTTTAACCATACTGATGAATA--ACCTTA-----AA----TG--TTTAGCGTGTGGCTGCCTAACCAACATCAAGCCGTGAACAAACAGATGCCGT
droRho1	scf7180000777695:56563-56721 -		GGCCTCCAGATTTGATCATGGAGCGTGTGAGTCCAACCCGCATCAAAGGTAGTAA----------\----------\----\-------\----------TGATTAAATTGCCACCATTAACCATACTGATGAATA--ACT-CA-----TA----TG-T-TTAAGCTGTGGCTGCTGTACCAACATCAAACCGTGAACAAAACGGATGCAGT
droBia1	scf7180000301754:1878021-1878177 -		GGCCGCCAGATTTGATCATGGAGCGTGTGAGTCCAATCCGCATCAAAGGTACTGG----------\----------\----\-------\----------TTGTGAATACG-CATCA--------GGTGATGAATA--AT-TAAGTCAAG----TG-TTTCAGCTTGTGGCTGCTGTACCAACATCAAGCCGTGAACAAACGGACGCCGT
droTak1	scf7180000415091:99864-100021 +		GGCCACCGGATTTGATCATGGAGCGTGTGAGTCCAATCCGCATCAGAAGGTATCAG--C-------\----------\----\-------\----------TTGTGATGAAATACG-T------TTCATAATGATGAATA--ACCTTA-----AA----TGCTTTCAGCTATGGCTGCTGTACCAACATCAAGCCGTGAACAAACGGATGCCGT
droEug1	scf7180000409462:2074159-2074324 -		GACCGCCAGATTTAATTATGGAACCGTGTGAGTCAAACCCGCATCAGAAGGTATAHA--T-------\----------\----\-------\----------TTGTAATAGAATTCCCTATTTTGCCTTAGTGATGAACA--ACCTTA-----CATTTTTGTTTTTAGCTTGTGGCTGCTGTACCAACATCAAACCAGTTAACAAAACGGATGCCGT
dm3	chr2R:10741011-10741168 +		GTCCGCCAGATTTGATCATGGAGCCGTGGAGTCTAATCCACACAGAAGGTACCCA----------\----------\----\-------\----------TGTTTACATTGCCCAGTATCCGCCACTGTAATGCCATA--ATC-CC-----AA----TGTCCCATAGCTAGCTGGCTGCTGCACCAACATCAAGCCGTGAACAAACGGATGCCGC
droSim2	2r:11444140-11444297 +	dsi_14606	GGCCGCCAGATTTGATCATGGAGCCGTGGAGTCTAATCCACATCAGAAGGTACCCA----------\----------\----\-------\----------TGACGAAATTGCCAGTATCCGCCATTGTAATGCCATA--ATC-CA-----AA----TGTCCCATAGCTAGCTGGCTGCTGCAACCAACATCAAGCCGTGAATAAACACGGATGCCGC
droSec2	scaffold_1:8263586-8263743		GTCCGCCAGATTTGATCATGGAGCCGTGGAGTCTAATCCACATCAGAAGGTACCCA----------\----------\----\-------\----------TGATGAAATTTCCAGTATCCGCCATTGTAATGCCATA--ATC-CA-----AA----TGTCCCATAGCTAGCTGGCTGCTGCACCAACATCAAGCCGTGAACAAACTGATGCTGC
droYak3	2R:10678608-10678765 +		GTCCGCCAGATTTGATCATGGAGCCGTGGAGTCTAATCCACATCAGAAGGTACACA----------\----------\----\-------\----------TGATGAAATTCACGCGTATAGTCATTGTAATGCCATA--ACC-CA-----AA----TGTCCCTTAGCTAGCTGGCTGCTGCACCAACATCAAGCCGTGAACAAACGGATGCGCC
droEre2	scaffold_4845:15101334-15101493 -		GACCGCCAGATTTGATTATGGAGCCGTGGAGTCGAATCCACATCAGAAGGTACTCA----------\----------\----\-------\----------TGATGAAATTCCACACTATCCGCCATTGTAATGCCATA--ACC-CA-----AA----TGTCCCTTAGCTTGCTGGCTGCTGCACCAACATCAAGCCGTGAACAAACAGATGCGCC

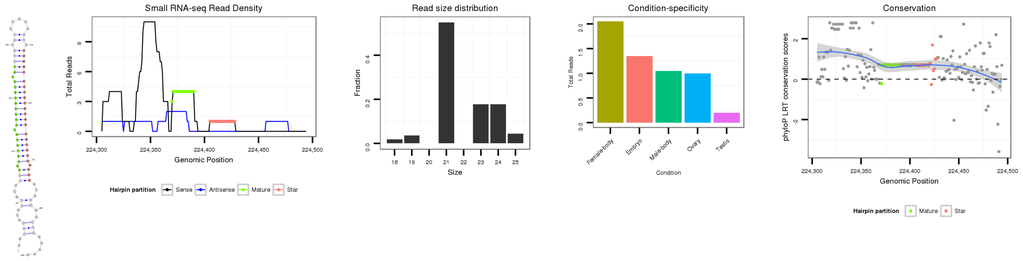
Generated: 09/08/2015 at 10:45 PM

	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:	
dvi_24639	**scaffold_10324:224355-224444 +**	**candidate**	**Canonical miRNA**	**5pUTR**	[View on UCSC Genome Browser (CompEl Mitos)]

Legend: mature star 5p mismatch in alignment mismatch in star

Predicted structure



Show Alternate Folds

Flybase annnotation

utr5 [utr5_plus_3623]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GCGCAGCGCTTTGTTGGTGGTGGTTTTTCTAGTGAACTTTGCCTGAAACGACAGACACTACATGTACATGTGTATGCATATGTGTGTGTGTATGCATTTACACCATGTGTATCATGTGTGAGCAATAAGAACTGAAGAAAAAAAAAAAAAAACGTGTACCAATCGAAACTTACACAAAATGAAAAAAAA	Read # size	Mismatch	Hit Count	Total Norm	Total	GSM1528803 follicle cells	SRR2096056 Ovary_Min_46	M047 female body	SRR060667 160_females_carcasses_total	SRR2096057 Ovary_Min_50	SRR2096060 Ovary_Min_193	SRR060682 9x140_0-2h_embryos_total	SRR060665 9_females_carcasses_total	SRR060671 9x160_males_carcasses_total	M061 embryo	SRR060676 9xArg_ovaries_total	SRR2096055 Ovary_Min_43	V047 embryo	SRR2096080 embryo_0-2h from 15to16 day old nondygenic mothers	SRR2096081 embryo_0-2h from 15to16 day old nondygenic mothers	SRR060666 160_males_carcasses_total	SRR060684 140x9_0-2h_embryos_total	SRR060664 9_males_carcasses_total	SRR060679 140x9_testes_total	SRR060686 Arg9_0-2h_embryos_total	SRR060659 Argentina_testes_total	SRR2096058 Ovary_Min_28	SRR060672 9x160_females_carcasses_total	SRR060655 9x160_testes_total	SRR060643 160_0-2h_embryos_total	SRR060687 9_0-2h_embryos_total	SRR1106739 V116 embryo_16-old male body	SRR2096072 embryo_0-2h from 15to16 day old dygenic mothers	SRR2096026 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096038 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096050 embryo_0-2h from 14 day old Strain 160 mothers
.CGCAGCGCTTTGTTGGTG	18	0	1	3.00	3	0	0	0	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TACATGTGTATGCATATGTGT	21	0	1	3.00	3	0	0	0	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTTGCCTGAAACGACAGACACTAC	24	0	1	3.00	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAACTTTGCCTGAAAC	18	0	1	2.00	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTGCCTGAAACGACAGAC	18	0	2	1.50	3	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TACACCATGTGTATCATGTGAGCA	24	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GAACTTTGCCTGAAACGACA	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAACTTTGCCTGAAACGACAGAC	25	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ACATGTGTATGCATATGTGTGTG	23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TAGTGAACTTTGCCTGAAACG	21	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CTTTGCCTGAAACGACAGAC	20	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.GCTTTGTTGGTGGTGGTTT	19	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATGTGTATGCATATGTGTGTGTGTG	25	0	4	0.25	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGTGTGTGTGTGTACGATT	19	0	5	0.20	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTATGCATATGTGTGTGTGTG	21	0	10	0.10	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCATATGTGTGTGTGTG	18	0	20	0.05	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
.....ATGCATATGTGTGTGTGT	18	0	20	0.05	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

CGCGTCGCGAAACAACCACCACCAAAAAAAGATCACTTGAAACGGACTTTGCTGTCTGTGATGTACATGTACACATACGTATACACACACATGCTAAATGTGGTACACATAGTACACTCGTTATTCTTGACTTCTTTTTTTTTTTTTTTTGCACATGGTTAGCTTTGAATGTGTTTTACTTTTCTTT	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR060681 Arg9_testes_total	SRR2096013 Ovary_Strain_9_oxidised	M047 female body	SRR060674 9x140_ovaries_total	SRR060677 Arg9_ovaries_total	SRR060678 9x140_testes_total	SRR060687 9_0-2h_embryos_total	SRR060676 9xArg_ovaries_total	SRR060675 140x9_ovaries_total
.....TGTACATGTGTACACATAGCGTAT	21	0	1	1.00	1	0	0	0	1	0	0	0	0	0
.....CCAAAAAAGATCACTTGAAACGGACT	24	0	1	1.00	1	1	0	1	0	0	0	0	0	0
.....GTATGCATATGTGTGTGTGTG	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0
.....GTCTGTGATGTACATGTACACATACGT	27	0	1	1.00	1	0	1	0	0	0	0	0	0	0
CGCGTCGCGAAACAACCACC	20	0	1	1.00	1	0	0	0	0	0	1	0	0	0
.....ACCATATACACACACACACA	19	0	20	0.05	1	0	0	0	0	0	0	0	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_10324:224355-224439:-	dvi_24639	GCG-CA------GC-GCTTT----GTTGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---AAACGACAGA----CACTACATGTACATGTGTATGCATATGTGTGTGTGTATGCATTTACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GAAAAA-AAAAAA-AAA----------ACGTGT--ACCAA-TCGAAA-C----TTACA-CAA---------AATG----AAAAGAAA----
droMoj3	scaffold_6486:2847543:2847633:-	dmo_102	GC-T-G------GT-G-TTT----GTTGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATTTACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------G-G-AAA-AAA-GGAAAAA----AAA----------ACGTGT--GA-G-A---GTTTAAAGCTGTCGA-CAA---------AAGAAA----AAAGAAA----
droGri	scaffold_14245:15422543:15422733:-		GCG-CA-GGGCGC-GC-GCTTT----G-TGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATTTACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GGG-G--------CAA----------ACGTGT--CAAA-TCGAAA-TTTC----TTA-CAA---------AAGAAGAAAAGAAA----
droWil1	scaffold_14000000045133:3301342:3301487:-		GC-GGG------GG-G-TTGGGCTAC-TGGTGGTGGTGGTTTTT--CTAGTGAACTTTGCCT-G---G-AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATGCATACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GAAAGATACAC-GGG--GAAAAGAGAGAAAAA----------G-AAA-TGAAAGAGAAAAA----------AAAAAA----AAAGAAA----
dpo	Un:1582305:15882403:+		G-GG-A------G-G-TTT----GTTGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---G-AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATGCATACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GAAA-GGG-G-AAAAGTTTTA----------ACGTGT--G-AAG-TCGAAA-TTTC----TTA-CAA---------AAGAAA----AAAGAAA----
dsePer2	Scaffold_4:4835340:4835647:-		G-GG-A------G-G-TTT----GTTGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---G-AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATGCATACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GAAA-GGG-G-AAAAGTTTAA----------ACGTGT--G-AAG-TCGAAA-TTTC----TTA-CAA---------AAGAAA----AAAGAAA----
droAna3	scaffold_13246:184819:184938:-		GAG-G------G-G-TTGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---G-AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATGCATACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GAAA-GGG-G-AAAAGTTTAA----------ACGTGT--G-AAG-TCGAAA-TTTC----TTA-CAA---------AAGAAA----AAAGAAA----
droBip1	Scf7180000039670:1206148:1206263:-		TTG-T------G-G-------G-G-G-----------G-TGGTGAACTTTGCCT-G---G-AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATGCATACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GAAA-G-AAA-CCGAA----------CAGCGGACACCGCATTGG-G--CAAA-TCGAAG-G----TTGC----------G-ACATGTGTCTGT-----
droRik1	Scf7180000030247:828224:828341:+		GAG-G------G-G-------G-G-G-----TTGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---G-AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATGCATACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GAAA-GGG-G-AAAAGTTTAA----------ATCGTTAAAGCGAA----------G-G-AAA-TCGAA-TTTC----TTA-CAA---------AAGAAA----AAAGAAA----
droFic1	Scf7180000453858:1268635:1268724:-		GAG-G------G-G-------G-G-----GTTGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---G-AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATGCATACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GGG-G-AAA-GGGAAAAAGAGAAAAA----------AAAAAA----AAAGAAA----
droEle3	Scf7180000489107:1673862:1673955:-		GAG-G------G-G-------G-G-G-----TTGGTGGTGGTTTTTT--CTGTGAACTTTGCCT-G---GCGT-G-GAA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATGCATACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GAAA-GC-GGG-G-AAA----------AAAAAA----AAAGAAA----
droBoh3	Scf7180000377217:325864:325962:+		GAG-G------G-G-------G-G-G-----TTGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---CCTCG--AAG--AACT--GAA----------GAAA-GGG-G-AAA----------AAAAAA----AAAGAAA----
droBia3	Scf7180000301506:128173:128215:-		GAG-G------G-G-------G-G-G-----TTGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---G-AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATGCATACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GAAA-GGG-G-AAA----------AAAAAA----AAAGAAA----
droTak1	Scf7180000415401:439432:439509:+		GAG-G------G-G-------G-G-G-----TTGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---G-AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATGCATACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GAAA-GGG-G-AAA----------AAAAAA----AAAGAAA----
droEug1	Scf7180000459203:72620:72690:-		GAG-G------G-G-------G-G-G-----TTGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---G-AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATGCATACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------AAAAAA-GGG-G-AAA----------AAAAAA----AAAGAAA----
dm3	chr2R:5460567:5460644:+		GAG-G------G-G-------G-G-G-----AAGTGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---G-AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATGCATACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GAAA-GGG-G-AAA----------AAAAAA----AAAGAAA----
droSim1	Scf2R2430:4231338:4231423:+		GAG-G------G-G-------G-G-G-----AAGTGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---G-AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATGCATACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GAAA-GGG-G-AAA----------AAAAAA----AAAGAAA----
droSec2	Scaffold_13055219:3055316:3055411:-		GAG-G------G-G-------G-G-G-----AAGTGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---G-AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATGCATACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GAAA-GGG-G-AAA----------AAAAAA----AAAGAAA----
droYak3	Sc:1807:583:1807:583:+		GAG-G------G-G-------G-G-G-----AAGTGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---G-AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATGCATACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GAAAA-GGG-G-AAA----------AAAAAA----AAAGAAA----
droEre2	Scaffold_4929:8916600:8916705:-		GAG-G------G-G-------G-G-G-----AAGTGGTGGTGGTTTTTT--CTAGTGAACTTTGCCT-G---G-AAACGACAGA----CACATGTGTATGCATATGTGTGTGTGTGTATGCATGCATACACCATGTGTATCATGTGTGAGCAT--AAG--AACT--GAA----------GAAA-GGG-G-AAA----------AAAAAA----AAAGAAA----

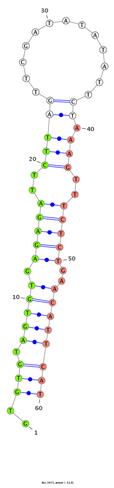
Generated: 09/08/2015 at 08:44 PM

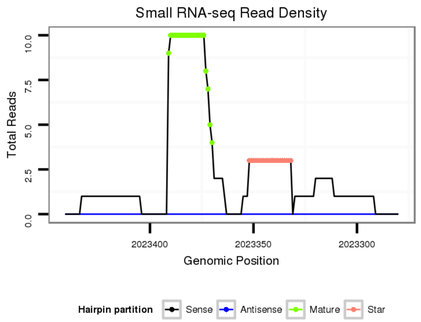
	PASS/FAIL
crit.star	0
crit.star5	0
crit.star	0
crit.half	0
crit.mid	0
crit.paring	1
crit.mp3	1
crit.mp5	0
crit.uri	0
crit.back	0
rescue.star	0
rescue.dominant	0
rescue.star5	0
rescue.confident	1
rescue.candidate	1

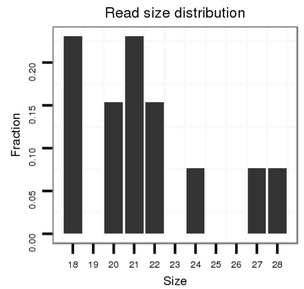
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_3475	**scaffold_12855:2023330-2023391 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

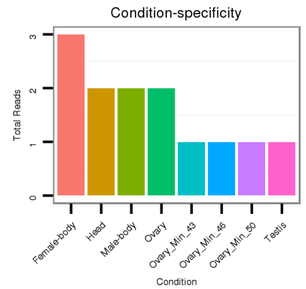
Legend: mature star **mismatch in alignment** mismatch in read

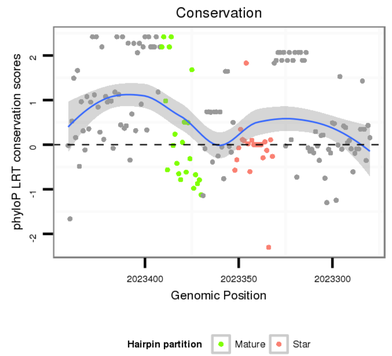
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dvir\GJ10475-in]; CDS [Dvir\GJ10475-cds]; CDS [Dvir\GJ10475-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read size	# Mismatch	Hit Count	Total Norm		Total	SRR060667 160_females_carcasses_total	SRR060659 Argentina_testes_total	SRR060676 9xArg_ovaries_total	V053 head	V116 male body	M047 female body	M061 embryo	SRR060666 160_males_carcasses_total	SRR060668 160x9_males_carcasses_total	SRR060675 140x9_ovaries_total	SRR060681 Argx9_testes_total	SRR1106727 larvae	SRR2096055 Ovary_Min_43	SRR2096056 Ovary_Min_46	SRR2096057 Ovary_Min_50	V047 embryo	M027 male body
AACAGCAGCGGGCTATCAGGCGCCAAATGTGGAGCACGAGGAGAGCGAAGGTGTGTAGTGTGAGAGATTCTTAGTTCGATATATATTCTAAAGTTTCTCTGAACATTCATAGATGATGAGGACATGGAGGACATGACTGCGGCGCCAGCTGTGCTTACAGCC																						
**********																							
.....GTGTGTAGTGTGAGAGATTCTT	22	0	1	2.00	2	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGTGTAGTGTGAGAGAT	18	0	1	2.00	2	1		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AAAGTTTCTCTGAACATTCAT	21	0	1	2.00	2	0		0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0
.....GTGTGTAGTGTGAGAGATTC	20	0	1	2.00	2	0		0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
.....CGGGCTATCAGGCGCCAAATGTGGAGCAC	29	0	1	1.00	1	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGTGTAGTGTGAGAGATTCTTAGTTC	27	0	1	1.00	1	0		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
.....GTGTGTAGTGTGAGAGATTCT	21	0	1	1.00	1	0		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGTGTAGTGTGAGAGATTCTTAGTTCG	28	0	1	1.00	1	0		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
.....TCTAAAGTTTCTCTGAACATTCAT	24	0	1	1.00	1	0		0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
.....TGTGTAGTGTGAGAGATT	18	0	1	1.00	1	0		0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
.....ACATGGAGGACATGACTGCGGCGCCAGCT	29	0	1	1.00	1	0		0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
.....GTGTGTAGTGTGAGAGAT	18	1	1	1.00	1	0		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
.....GATGATGAGGACATGGAGG	19	0	1	1.00	1	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0

Anti-sense strand reads

	Read size	# Mismatch	Hit Count	Total Norm		Total	SRR060684 140x9_0-2h_embryos_total	GSM1528803 follicle cells
TTGTCGTCGCCCGATAGTCCGCGGTTTACACCTCGTGCTCCTCTCGCTTCCACACATCACACTCTCTAAGAATCAAGCTATATATAAGATTTCAAAGAGACTTGTAAGTATCTACTACTCCTGTACCTCCTGTACTGACGCCGCGGTCGACACGAATGTCGG								
**********								
...(((.(((((.(((((..(((((.....)).))).)..)))))..))))))))	21	0	1	2.00	2	0		
...(.(((((.(((((..(((((.....)).))).)..)))))..))))))	20	0	1	2.00	2	0		
...(.(((((.(((((..(((((.....)).))).)..)))))..))))))	29	0	1	1.00	1	1		
...(.(((((.(((((..(((((.....)).))).)..)))))..))))))	27	0	1	1.00	1	0		
...(.(((((.(((((..(((((.....)).))).)..)))))..))))))	21	0	1	1.00	1	0		
...(.(((((.(((((..(((((.....)).))).)..)))))..))))))	28	0	1	1.00	1	0		
...(.(((((.(((((..(((((.....)).))).)..)))))..))))))	24	0	1	1.00	1	0		
...(.(((((.(((((..(((((.....)).))).)..)))))..))))))	18	0	1	1.00	1	0		
...(.(((((.(((((..(((((.....)).))).)..)))))..))))))	29	0	1	1.00	1	0		
...(.(((((.(((((..(((((.....)).))).)..)))))..))))))	18	0	1	1.00	1	0		
...(.(((((.(((((..(((((.....)).))).)..)))))..))))))	19	0	1	1.00	1	0		

Show Alignment With Reads

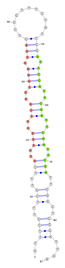
Re-alignment of all predicted orthologs

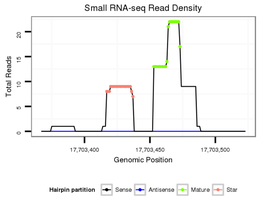
Species	Coordinate	ID	Alignment
droVir3	scaffold_12855:2023280-2023441 -	dvi_3475	AACAG----------CAG---CGGGCTATCAGGCGCCAAATGTGGAGC--------ACGAGGAGAGCGAAGGTGTGTAGTGTGA---GAGATTC----------TTAGTTCGAT---ATATATT--CTAAA----G----------TTT--------CTCTGAACATTCATAGATGATGAGGACATGGAGGACATGACTGCGGCGCCA----------GCTG---TGCTTACAGCC
droMoj3	scaffold_6540:32315394-32315553 -		A----------T-CTATGGGCTATCAGGCGCCAATGTGGAGCAGGA----G-AAGAGCGAAGGTGTGTGCC---GTAGAAAGTCTGC-AGCGAT----A---------T--TAATC--TAGCT---G----------AGTCGATCTTCTC----ATTGACAGATGATGAGGACATGGAGTGCCTGTGC------GCTAGCTA---CAGCCACAGCC
droGri2	scaffold_14830:396617-396682 -		GGCAA----------CG---TG-CATATCAGCGCCAATGTGCA---ACCAAGAGGAAAGCGAAGGTACTAGACGA---------GA----------
droWil2	scf2_1100000004902:3814172-3814220 +		A----------GATGATGAGGAATGGAGGCACAACGAGACA---
dp5	2:3925779-3925982 +		AGCAGCCAGGCCT---CGATCTGTGGCCGCCAG---CTACTATCCGATGCCGAACCGGGACC--GACTACAAGGAGGAAGCGAAGGTGCTGCGCG--ATTGCGATTCTTCGGCGGTTCTC----TTGAGA------T--TAATTCTTTTC----G----------TTTCGTTTCC-TGCC-----C-AACAGATGATGAGGAATGGAGGCGGAAGCGAGATAACCC
droPer2	scaffold_7:424560-424768 -		AGCAGCCAGGCCT---CGATCTGTGGCCGCCAG---CTACTATCCGATGCCGAACCGGGACC--GACTACAAGGAGGAAGCGAAGGTGCTGCGCG--ATTGCGATTCTTCGGCGGTTCTC----TTGAGA------T--TAATTCTTTTC----G----TTTCG--------TTTCGTTTCC-TGCC-----C-AACAGATGATGAGGAATGGAGGCGGAAGCGAGATAACCC
droAna3	scaffold_13340:19121088-19121323 -	dan_3168	ACAGTCCGCCCGGCTGATCTTTGGC---CT----CAACTTTGGGATTCCGAATTGGACATGGACTACAACGAGGACAGCGAAGGTGCTTTGTGAGACA A AAAACCAT--TGAGAT-----TGTTAATTCTGATTATTTATATA--ATAATG----G----------TTTGGACTT-TGTT----GCTTCAGATGATGAGAATGGAGCCAGAGCGTGTTGCTTACTCCAATCAACAGCAGCGCGACTGCAACGAACAGGAGC---------C
droBip1	scf7180000395652:60871-61075 +		AGCAGTCCGCCCCGGCTGATCTTTGGC---CTA---CAACTATCGGATTCCGAATTGGACATGGACTACAACGAGGASAGCGAAGGTGCTTGAAA--CAAAGAAAATTTGC-AAGAAAAACCATTCATA------T--TAATA--ATAATG----G----------TTTGGATTT-TGT----GCGTTAGATGATGAGAATGGAGCCAGAGCGTGAGTCATCCTGTCAACAGCA----------C
droKik1	scf7180000302697:845550-845631 +		AATT----------CAG---CAACTATCGGATTCCGAATTGGACATGGACTACAACGAGGACAGCGAAGGTGCTGCGCG--ATTGCGATTCTTCGGCGGTTCTC----TTGAGA------T--TAATTCTTTTC----G----------TTTTTCTTT-TCT----TCCATCAGATGAGGAGCATGGAGTCGGACGCATATACGACCTCTGAGCAGCAGCTTCACCT--------C
droFic1	scf7180000454055:538304-538363 -		C----------AG---CACTATCGCGATGCCGAATTGGACATCGACTTCAACGAGGACAGCGAAGGTGCTGT-------C-------T----------T----------T---T----C----C----C

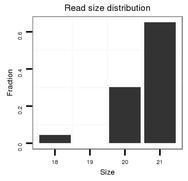
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_132	**scaffold_13049:17703417-17703473 +**	**candidate**	**Canonical miRNA**	**5pUTR**	[View on UCSC Genome Browser [Cornell Mirror]]

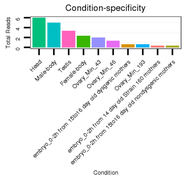
Legend: mature star mismatch to alignment mismatch in seed

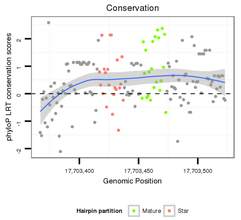
Predicted structure











Show Alternate Folds

Flybase annnotation

utr5 [utr5_plus_8094]

Repeatable elements

Name	Class	Family	Strand
(ATTCCG)n	Simple_repeat	Simple_repeat	+

mature	star
1 scaffold_12970:2916631-2916651 - 2 scaffold_130473:1402447-1402467 + 3 dvi_132 scaffold_13049:17703453-17703473 +	

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGCTGACTGCAATCAGCAGTGGTTCGCCTTGTTTCGTTTCGTTTCGTTTCGTTTCGCTCCTGGGCTCG	Read # size	Mismatch	Hit Count	Total Norm	Total	M028 head	SRR2096056 Ovary_Min_46	SRR2096059 Ovary_Min_144	M027 male body	SRR2096055 Ovary_Min_43	SRR2096057 Ovary_Min_50	V053 head	SRR060658 140_ovaries_total	SRR060660 Argentina_ovaries_total	SRR060673 9_ovaries_total	SRR060678 9x160_testes_total	SRR1106727 larvae	SRR060664 9_males_carcasses_total	SRR060668 160x9_males_carcasses_total	SRR060679 140x9_testes_total	SRR060681 4xp9_testes_total	SRR2096060 mothers body	SRR2096072 embryo_0-2h from 15to16 day old dysgenic mothers	SRR060655 male 9x160_testes_total	SRR060659 Argentina_testes_total	SRR060665 9_females_carcasses_total	SRR060667 160_females_carcasses_total	SRR060671 9x160_males_carcasses_total	SRR060672 9x160_females_carcasses_total	SRR060683 160_testes_total	SRR2096050 embryo_0-2h from 14 from 15to16 day old Strain 160 mothers	SRR2096081 embryo_0-2h from 15to16 day old nondysgenic mothers	SRR2096014 GSM1528810 Ovary_Strain_160_oxidized	SRR2096079 embryo_0-2h from 15to16 day old dysgenic mothers	follicle cells	SRR2096080 embryo_0-2h from 15to16 day old nondysgenic mothers	embryo
ATTCCATTCGATTCGATTCGA	21	0	3	8.33	25	0	0	0	0	3	0	0	4	0	0	0	0	0	2	2	2	1	0	2	0	1	1	1	1	1	1	1	1	1	0	0	0
TTCGATTCGATTCGGCTCGGGCTCG	22	0	1	7.00	7	0	0	3	0	0	0	2	0	1	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
GTTTCGCTTCGCCTGGGCTCG	21	0	1	6.00	6	2	1	0	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATTCCATTCGATTCGATTCGA	20	0	3	5.67	17	8	1	0	0	0	1	3	0	0	0	0	0	0	0	0	0	1	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0
GTTTCGCTTCGCCTGGGCTC	20	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCGATTCGATTCGGCTCGGAT	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TTCGTTTCGCTTCGCCTGGGCT	22	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCGCTTCGCCTGGGCTCG	18	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATTCGATTCGATTCGGCTCGATTGA	26	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCAATCAGCAGTGGTTCG	18	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TTTTTCGTTTCGTTTCGTTTT	25	0	4	0.25	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
GTTTCGTTTCGTTTCGTTT	23	0	14	0.21	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0
GTTTCGTTTCGTTCGCTT	19	0	5	0.20	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

TCGACTGACGTTAGTCGTCACCAAGCGGACAAAGCAAAGCAAAGCAAAGCAAAGCGAAGCGAAGCCGAGCCCAGGCAAAGATAAGCTAAGGTAAACTAAGCTAAGCGAAGCCGAGCCTAACTCAAAGACAAATGCCGGCTAAAAGCTCACGACGCTG	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR2096060 Ovary_Min_193

Show Alignment With Reads

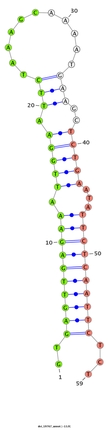
Re-alignment of all predicted orthologs

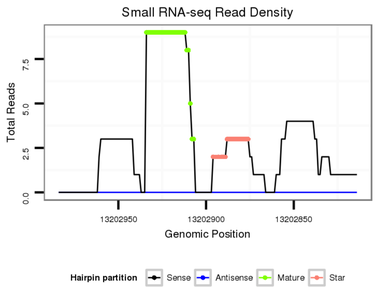
Species	Coordinate	ID	Alignment
droVir3	scaffold_13049:17703383-17703523+	dvi_132	AGCTGACTGC---AATCAGCA--GTGGTTCGCC----------TTGTTTCGTTTCGTTTCGTTTCGTTTCGCTCCTGGGCTCG---GGGCT----------CG---TCCG----------TTTCTATTGC-ATTCCA-------TTC------GATTCGAT-----------TCGA-----TCGGC----------TCGGATTGAGT--TTCTG-TTT--ACGGCCGATTTTCGAGTGCT---GCGAC----------
droMoj3	scaffold_6680:22756334-22756496+		AGCTGACTGC---AATCAGCA--TGGTTCGCC----------TTTTCGTTTCGTTCGCTCGCTCGTTTCGCTCGTTTCGCTCTGCGCGCTCTTCGCCTCG---TCCG----------TTTCTATTGCATTCC-------TTC------GATTCGAT-----------TCGA-----TCGGC----------TCGGATTGAGT--TTCTG-TTT--ACGGCCGATTTTCGAGTGCT---GCGAC----------
droGri	scaffold_15110:1447538?-1447615?+		AGCTGACTGC---AATCAGCA--GTGGTTCGCTTCGTTTCGTTTCGTTTCGTTTCGCTCCTGGGCTCGTTTCGCTCGTTTCGCTCTTCTACTTCTTGTCGCTTTTCGCTCGCGCTCGCGCTCG

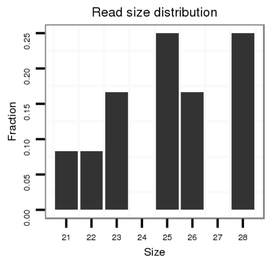
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_19767	**scaffold_13049:13202864-13202934 -**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

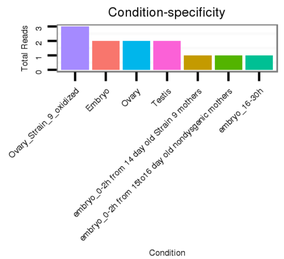
Legend: mature star **mismatch in alignment** mismatch in read

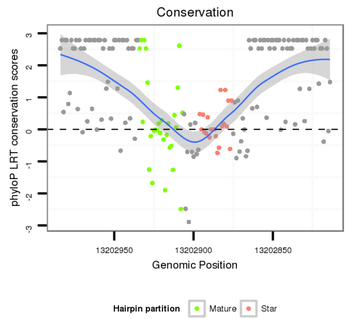
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dvir\GJ11870-in]; CDS [Dvir\GJ11870-cds]; CDS [Dvir\GJ11870-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CAATATTTGCACTCGCACAAGATCATACACAGAGATCTGAAAAGTCCGAAGTGAGTTGAGAAATTGGAATTCTAAAGCAAAATGAAGCTCTGAATATTCTCAATTCTCTTGAATCCCCCAGCATACTGATTAGTACAAACGAAGTGGTGAAGATCAGCGACTTTGGCACCA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR2096013 Ovary_Strain_9_oxidized	SRR060663 160_0-2h_embryos_total	GSM1528803 follicle cells	SRR2096026 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096057 Ovary_Min_50	SRR2096060 Ovary_Min_193	M047 female body	M027 male body	SRR060658 140_ovaries_total	SRR060659 Argentina_testes_total	SRR060665 9_females_carcasses_total	SRR060677 Argx9_ovaries_total	SRR060679 140x9_testes_total	SRR060685 9xArg_0-2h_embryos_total	SRR1106730 embryo_16-30h	SRR2096079 embryo_0-2h from 15to16 day old dysgenic mothers	SRR2096081 embryo_0-2h from 15to16 day old nondysgenic mothers	V047 embryo	V116 male	SRR060660 Argentina_ovaries_total
..GTGAGTTGAGAAATTGGAATTCTAAAGC..	28	0	1	3.00	3	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..GTGAGTTGAGAAATTGGAATTCTAA..	25	0	1	3.00	3	0	1	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
..ACAGAGATCTGAAAAGTCCGAAGTG..	24	2	1	2.00	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..CATACACAGAGATCTGAAAA..	20	0	1	2.00	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..GTGAGTTGAGAAATTGGAATTCTAAA..	26	0	1	2.00	2	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
..GATTAGTACAAACGAAGTGGT..	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
..TCTGAATATTCTCAATTCTCT..	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
..TCTGAATATTCTCAATTCTCTTG..	23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
..TAGTACAAACGAAGTGGTGAAGATC..	25	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
..GTGAGTTGAGAAATTGGAATTCT..	23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
..ATACACAGAGATCTGAAAAGTCC..	23	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..AGATCAGCGACTTTGGCACCA..	21	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..GATTAGTACAAACGAAGTG..	19	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
..ACTGATTAGTACAAACGAAGTGGT..	24	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
..TTCTCAATTCTCTTGAATCCCC..	22	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0

Anti-sense strand reads

GTTATAAACGTGAGCGTGTTCTAGTATGTGTCTCTAGACTTTTCAGGCTTCACTCAACTCTTTAACCTTAAGATTTCGTTTTACTTCGAGACTTATAAGAGTTAAGAGAACTTAGGGGGTCGTATGACTAATCATGTTTGCTTCACCACTTCTAGTCGCTGAAACCGTGGT	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR2096013 Ovary_Strain_9_oxidized	SRR2096026 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096038 embryo_0-2h from 14 day old Strain 9 mothers	SRR060686 Argx9_0-2h_embryos_total	SRR060666 160_males_carcasses_total	SRR2096014 Ovary_Strain_160_oxidized	SRR060677 Argx9_ovaries_total

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_13049:13202814-13202984 -	dvi_19767	CAATATTTGCACTCGCACAAGATCATACACAGAGATCTGAAAAGTCCGAAGTGAGTTGAGAAA-T--------TGGAA-----TTC-TAAAGCAAAAT----------G-AAGCTCTGAATATTCTCAATT----------CTCTTGA----A-TCCCCCAGCATACTGATTAGTACAAACGAAGTGGTGAAGATCAGCGACTTTGGCACCA
droMoj3	scaffold_6680:14160352-14160513 +		CAATATTTGCACTCACACAAGATCATACACAGAGATCTAACAGTCCGAAGTGAGTTCAGGAGGGGAGTCTC-----TTGCAAACG-CTT----------ATGGCTCTGAAT---GAAGTGGTGAAGATCAGCGACTTTGGCACCA
droGri2	scaffold_15110:18640778-18640947 -		CAATATTTGCACTCACACAAGATCATACACAGAGATCTAACAGTCCGAAGTGAGTAT-ATTAA--------ACG-----CTCCAC-AT-TAGT----------ATAAA----------TATTTACATATTTGATTTGGTTGC-----ATTTGTTAGCATACTGATTAGTACAAACGAAGTGGTGAAGATCAGCGACTTTGGCACCA
droWil2	scf2_1100000004762:4731508-4731687 -		CAATATTTGCACTCACACAAGATCATACACAGAGATCTAACAGTCCGAAGTGAGTGTTAAAT-G--------CAAAAAAAAA---T--AAAAAAAA----------AATTGGTTAACTAACAAAAACACATTGTGTTTGTTTT--------------------------------GTTTTAGCATACTGATTAGTACAAACGAGTGGTGAAATATAGTGACTTTGGCACCA
dp5	XR_group8:7695170-7695354 +		CACTATTTGCACTCCACAAGATCATACACAGAGATCTGAACAGTCCGAAGTGAGTGCC---T--------CCCA-----TCC-AGC--------A----------T--------------GTTGATTCCTCCATATAGATTCGGATTTAACGTATCCTGTTTGTGCGGGATATCCTTTCAGCATACTGATTAGTACAAACGAGTGGTGAAGATCAGCGACTTTGGCACCA
droPer2	scaffold_48:473632-473816 -		CACTATTTGCACTCCACAAGATCATACACAGAGATCTGAACAGTCCGAAGTGAGTGCC---T--------CCCA-----TCC-AGC--------A----------T--------------GTTGATTCCTCCATATAGATTCGGATTTAACGTATCCTGTTTGTGCGGGATATCCTTTCAGCATACTGATTAGTACAAACGAGTGGTGAAGATCAGCGACTTTGGCACCA
droAna3	scaffold_13337:17267592-17267757 +		CACTATCCTGCACTCCACAAGATATATCACAGGATCTGAACAGCCCGAAGTGATATATTTCAACAC--------CAGAA-----CTCCAGTATCCAGGTCTCCAGAAT----------CCTATTCCGATC--------------------------------------CTTTCAGCATCTGATTAGTACAAACGAGTGGTGAAGATCAGCGACTTTGGCACCA
droBip1	scf7180000396741:564628-564788 +		CACTATCCTGCACTCCACAAGATCATACACAGGATCTGAACAGCCCAAGTGATATTCTAACCTGAAACC-T-ATA-----GCT-AGCATACCCAATCTAAC----T----------AAAATCCTTTCAGCATACTGATTAGTACAAACGAGTGGTGAAGATCAGCGACTTTGGCACCA
droKik1	scf7180000302694:165405-165571 -		CACTATCTGCACTCCACAAGATGATACACAGGATCTGAACAGTCCGAAGTAGTTGAGAAA-G--------CTCCT-----TTGTAAAGCCTTGTCACAGTAAT----------CCATATGT---------TCAATT----------G-------TTTCCCCAGCATACTGATTAGTACAAACGAGTGGTGAAGATCAGCGACTTTGGCACCA
droFic1	scf7180000453831:176356-176515 -		CACTATCTGCACTCCACAAGATCATGCACAGGATCTAACAGCCCGAAGTAGTCACATAAA-AAAG-----CAACA-----CTGCCAAAAATTG-A--------ATTACTTTTTGT---ATCT----------T--------A----------T----------T-CTTTTTAGCATACTGATTAGTACAAACGAAGTGGTGAAGATCAGCGACTTTGGCACCA
droEle1	scf7180000491249:6927389-6927559 -		CACTATCTGCACTCCGCACAAGATCATACACAGAGATCTGAACAGTCCGAAGTGAGTCACATGAAA---ACT--ATGCACA---T-GCAAACGAAATA-ATAAT--AATAATTGGGATACTTGTTT--------T--------G----------T----------T----------T-TTTCAGCATACTGATTAGTACAAACGAGTGGTGAAGATCAGCGACTTTGGCACCA
droRho1	scf7180000779665:26339-26500 +		CAATATCTGCACTCCACAAGATCATACACAGAGATCTGAAAAGTCCGAAGTGAGTCATAGAAA-A--------ATCCACA---T-GCAAAAGATTTG--------TTTAATTGGGACTATTATTT--------T--------A----------T----------T----------T-TTTTCAGCATACTGATTAGTACAAACGAGTGGTGAAAGATCAGCGACTTTGGCACCA
droBia1	scf7180000302377:1985556-1985717 +		CACTATCTGCACTCCACAAGATCATGCACAGGATCTGAAAAGTCCGAAGTAGTCATAAAAA-A--------CATCG-----GCAAAAAGAGCG--------ATTAATTGGTATAATTATTA--------T--------A----------T----------T----------T-TATTCCAGCATACTGATTAGTACAAACGAGTGGTGAAGATCAGCGACTTTGGCACCA
droTak1	scf7180000415276:146602-146763 -		CACTATCTGCACTCCACAAGATCATACACAGAGATCTAAAAGTCCGAAGTAGTTATAAAAA-A--------CATCGAAAAAT---T--AAAAAAGCG--------AATAATTGGTGTAATAATT--------T--------A----------T----------T----------T-ATTTCCAGCATACTGATTAGTACAAACGAAGTGGTGAAGATCAGCGACTTTGGCACCA
droEug1	scf7180000409472:169475-169633 -		CACTATCTGCACTCCACAAGATCATACACAGAGATCTAACAGTCCGAAGTAGTGATAAAA-A--------CATCACAAAG---T--AATGTAAAT--------ATTAATTGGTGTA----TTT--------T--------A----------T----------T----------T-TATTCAGCATACTGATTAGTACAAACGAGTGGTGAAGATCAGCGACTTTGGCACCT
dm3	chr3L:19621148-19621301 -		CACTATCTGCACTCCACAAGATCATACACAGAGATCTAACAGTCCGAAGTAGTTAAAGAAA-A--------CAACA-----CGCAAAATGATATG-T--------ATAAATCTGCGT---------T--------T----------T----------T----------T-ATTTTTAGCATACTGATTAGTACAAACGAGTGGTGAAGATCAGCGACTTTGGCACCA
droSim2	3L:19271703-19271856 -		CACTATCTGCACTCCACAAGATCATACACAGAGATCTAACAGTCCGAAGTAGTTAAAGGAA-A--------CACCA-----CGCAAAAGGATATG-T--------ATAAATCTGCGT---------T--------T----------T----------T----------T-ATTTTTAGCATACTGATTAGTACAAACGAGTGGTGAAGATCAGCGACTTTGGCACCA
droSec2	scaffold_29:324489-324642 +		CACTATCTGCACTCCACAAGATCATACACAGAGATCTAACAGTCCGAAGTAGTTAAAGAAA-A--------CACCA-----CGCAAAAGGATATG-T--------ATAAATCTGCGT---------T--------T----------T----------T----------T-ATTTTTAGCATACTGATTAGTACAAACGAGTGGTGAAGATCAGCGACTTTGGCACCA
droYak3	3L:20922458-20922611 +		CACTATCTGCACTCCACAAGATCATACACAGAGATCTAACAGTCCGAAGTAGTTAATAGAAA-A--------CATCA-----TTAAAAAGGAAATG-T--------ATTAATCTGCGT---------T--------T----------T----------T----------T-ATTTTTAGCATACTGATTAGTACAAACGAGTGGTGAAGATCAGCGACTTTGGCACCA
droEre2	scaffold_4784:19420311-19420464 -		CACTATCCTGCACTCCACAAGATCATACACAGAGATCTAACAGTCCGAAGTAGTTAAAGAAA-A--------CATCA-----TCAAAAAGGAAATG-T--------ATTAATCTGCGT---------T--------T----------T----------T----------T-ATTTTTAGCATACTGATTAGTACAAACGAGTGGTGAAGATCAGCGACTTTGGCACCA

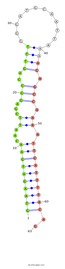
Generated: 09/08/2015 at 07:17 PM

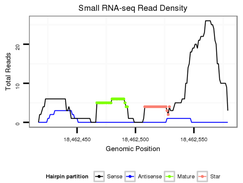
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.ptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

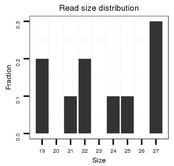
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_17513	**scaffold_13047:18462467-18462529 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

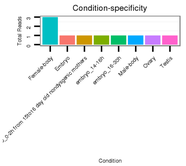
Legend: exon intron mismatch in alignment mismatch in seed

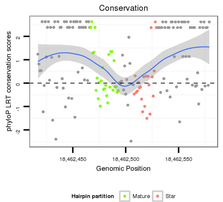
Predicted structure











Show Alternate Folds

Flybase annotation

intron [DroVigG24648-in], CDS [DroVigG24648-cds], CDS [DroVigG24648-cds]

No Repeatible elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CAGGTGCTGGACGCGCTATTGGCCATCTCTGTGGTTATTCACACCCATTG	GTAAGATGAACAATTCGAGGCCAGTTG	GGGATGCAATTAAA	ACAGCCAAAATTCATTTTACAG	GGGCGTTGAAGCTATGATTGTCGACTACCTGCGTCCAGGTGTCGTGGGCA
Read #	Hit	Total		
Aligns Mismatch Count	Score	Total		
**********	((((((((((...(((...(((...((((.....)))).))).)).))))))))))	**********		

Read # Aligns	Mismatch Count	Hit Score	Total Total	M047 female body	SRR060667 160_females_carcasses_total	M061 embryo	M027 male body	M028 head	SRR060659 Argentina_testes_total	SRR060670 9_testes_total	SRR2096014 Ovary_Strain_160_oxidized	V047 embryo	V116 male body	SRR060672 9x160_females_carcasses_total	SRR1106730 embryo_16-30h	V053 head	SRR060665 9_females_carcasses_total	SRR060669 160x9_females_carcasses_total	SRR060671 9x160_males_carcasses_total	SRR060682 9x140_0-2h_embryos_total	SRR060666 160_males_carcasses_total	SRR060660 Argentina_ovaries_total	SRR060661 160x9_0-2h_embryos_total	SRR060664 9_males_carcasses_total	SRR060674 9x140_ovaries_total	SRR060678 9x140_testes_total	SRR060679 140x9_testes_total	SRR060681 Argx9_testes_total	SRR060684 140x9_0-2h_embryos_total	SRR1106725 embryo_14-16h	SRR2096050 embryo_0-2h from 14 day old Strain 160 mothers	SRR2096058 Ovary_Min_88	SRR2096081 embryo_0-2h from 15to16 day old 160_9-nondypenic mothers	SRR060663 2h_embryos_total	SRR060658 140_ovaries_total	SRR060657 140_testes_total	SRR060655 9x160_testes_total	SRR060686 Argx9_0-2h_embryos_total
GTAAGATGAACAATTCGAGGCCAGTTT	27	0	1	3.00	3	0	0		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATGATTGTCGACTACCTGCGTCCAGGT	22	0	1	2.00	2	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ACAGCCAAAATTCATTTTACAG	22	0	1	2.00	2	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0
GCGTCCAGGTGTCGTGGGCA	20	0	1	2.00	2	1	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TTTCCTGACTACCTGCGTCCAGGT	20	0	1	2.00	2	0	0		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GATGTCCGACTACCTGCGTCCAGGT	25	0	1	2.00	2	1	0		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTCACCTGCGTCCAGGTGTCGTGGGC	18	0	1	2.00	2	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTACCTGCGTCCAGGTGTCGTGGGC	25	0	1	2.00	2	0	1		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AGCCAAAATTCATTTTACAG	21	1	1	2.00	2	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GGGCGTTGAAGCTATGATTGTCGA	26	1	1	1.00	1	0	0		0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTCTGTGGTTATTCACACC	19	0	1	1.00	1	0	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ACAGCCAAAATTCATTTTA	19	0	1	1.00	1	0	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TGCGTCCAGGTGTCGTGGGCA	21	1	1	1.00	1	0	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTGGGCGCGCTATTGGCCATC	23	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATGATTGTCGACTACCTGCGTCCAGGT	27	0	1	1.00	1	0	0		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTTTGAAGCTATGATTGTCGA	21	0	1	1.00	1	0	0		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GGGCGTTGAAGCTATGATTGTCGA	24	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCTATGATTGTCGACTACC	19	0	1	1.00	1	0	0		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTGCGTCCAGGTGTCGTGGGC	21	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATTGTCGACTACCTGCGTCCA	21	0	1	1.00	1	0	0		1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TGCGTCCAGGTGTCGTGGGC	20	0	1	1.00	1	0	0		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GATGTCCGACTACCTGCGTCCAGGT	25	1	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AGCCAAAATTCATTTTACAG	21	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GTGCTGGACGCGCTATTGGCC	21	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CAGCCAAAATTCATTTTACAGG	24	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATGATTGTCGACTACCTGCGTC	22	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ACAGCCAAAATTCATTTTAC	20	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CAGCCAAAATTCATTTTACAG	22	1	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GATGTCCGACTACCTGCGTCCAG	23	1	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCGTCCAGGTGTCGTGGGC	19	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GTTATTCACACCCATTGG	23	1	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTCACCTGCGTCCAGGTGTCGTGGG	23	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TTGTCGACTACCTGCGTCCAGGTGT	25	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GGGGCGTTGAAGCTATGATTGTC	23	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GACTACCTGCGTCCAGGTGT	20	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GGGGCGTTGAAGCTATGATTGTCG	24	0	1	1.00	1	0	0		0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ACCTGCGTCCAGGTGTCGTGGGC	23	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TTTGAGGCCAGTTTGGGAT	19	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GTTGAAGCTATGATTGTCGACTAC	24	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
GTAAGATGAACAATTCGAGGCCAG	24	0	1	1.00	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GATGTCCGACTACCTGCGTCCAGG	24	1	1	1.00	1	0	0		0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTACCTGCGTCCAGGTGTCGTGGG	24	0	1	1.00	1	0	0		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

GTCCACGACCTCGCGATAACCGGTAGAGACACCAATAAGTGTGGGTAACCATTCTACTTGTTAAGCTCCGGTCAAACCCTACGTTAATTTGTCCGGTTTTAAGTAAAATGTGTCCCGCAACTTCGATACTAACAGCTGATGGACGCAGGTCCACAGCACCCGT																																							
Read # Aligns	Mismatch Count	Hit Score	Total Total	SRR060657 140_testes_total	SRR060672 9x160_females_carcasses_total	SRR060683 160_testes_total	SRR060686 V116 male body	Argx9_0-2h_embryos_total	SRR2096013 Ovary_Strain_9_oxidized	M061 embryo	SRR060679 140x9_testes_total	SRR2096056 Ovary_Min_46
**********	((((((((((...(((...(((...((((.....)))).))).)).))))))))))	**********										
GTCCCCGCAACTTCGATACTA	21	0	1	1.00	1	0	1	0	0	0	0	0	0
TCGCGCGATAACCGGTAGAGC	21	0	1	1.00	1	0	0	0	0	0	0	0	0
CCTGCGCGATAACCGGTAGAG	21	0	1	1.00	1	0	0	0	0	0	0	0	0
GGATAACCGGTAGAGACACC	20	0	1	1.00	1	0	0	1	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
DroVig2	scaffold_13047:18462467-18462529 +	dvi_17513	CAGGTGCTGGACGCGCTATTGGCCATCTCTGTGGTTATTCACACCATTGTAAGATGAACAATTCGAGGCCAGTTGGGATGCAATTAAAACAGCCAAAATTCATTTTACAGGGGCGTTGAAGCTATGATTGTCGACTACCTGCGTCCAGGTGTCGTGGGCA
DroMo3	scaffold_6540:2935883-2936066 +		[illegible]
DroGri2	scaffold_15074:238143-238253 +		[illegible]
DroWil2	scaffold_180000004211:3360023-3360186 +		[illegible]
Dp5	Dp:2820084:1280248 +		[illegible]
DroPer2	scaffold_8:762756:762731-762		[illegible]
DroAna3	scaffold_13347:1394787-1394844 +		[illegible]
DroBip1	scaffold00039:6413:2446371-2446348 +		[illegible]
DroFik1	scaffold00032:2635:2392275-2392445 +		[illegible]
DroFic1	scaffold00453:8201:1756793-1756833 +		[illegible]
DroEle1	scaffold00484:7:637450-637511 +		[illegible]
DroNok1	scaffold00077:205:371396-371296 +		[illegible]
DroBla1	scaffold00302:2075:1541703-1541738 +		[illegible]
DroTak1	scaffold00481:5765:1139387-1139441 +		[illegible]
DroEug1	scaffold00403:7381:802183-802236 +		[illegible]
Dm3	Chr3R:19853581:19853756 +		[illegible]
DroSim2	Dro:19139431:19139597 +		[illegible]
DroSec2	scaffold_21:1393836-1393855 +		[illegible]
DroTer4	Dro:2432616:2642267 +		[illegible]
DroPse2	scaffold_4825:1438784-1438784 +		[illegible]

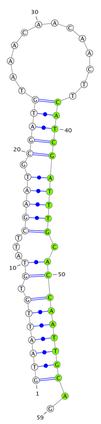
Generated: 09/08/2015 at 07:17 PM

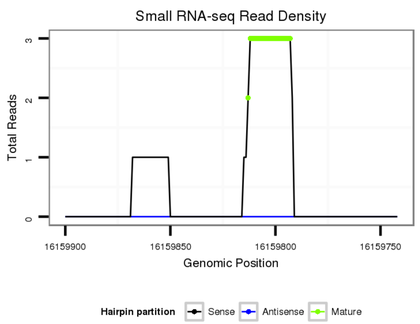
	PASSPAR
cch.star	0
cch.loop	0
cch.stem	0
cch.half	1
cch.end	1
cch.gap	0
cch.bp1	0
cch.bp2	0
cch.pos	1
cch.uri	1
rescue.score	1
rescue.total	1
rescue.homol	1
rescue.length	1
rescue.confidence	1
rescue.candidate	1

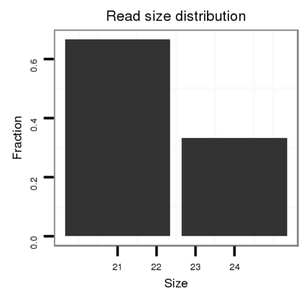
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_17138	**scaffold_13047:16159792-16159850 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

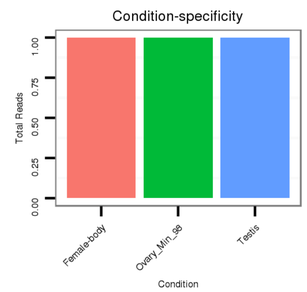
Legend: mature star mismatch in alignment mismatch in read

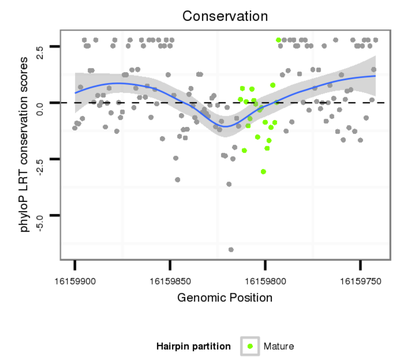
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dvir\GJ22728-in]; CDS [Dvir\GJ22728-cds]; CDS [Dvir\GJ22728-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AGGATTGGATATTTAAGCGTGAACAAGGCTACGAAAGTGTCACAACTGAGGTAATTGTGTATTCGAATGCGATGTAAACAACAACTTCATCGATTTGCACCAATTGCAGCTCAAGTGGGTTTGCGACAAATCGCATCACTCGGCTGTCGGCCAATCGTT						SRR060681	M047 female body	SRR060665	SRR060671	SRR060672	SRR060676	SRR060683	SRR2096058	V116 male	V053 head	SRR060663 160_0-2h_embryos_total	SRR060679	GSM1528803	SRR060669	M061
	Read size	# Mismatch	Hit Count	Total Norm	Total	Argx9_testes_total		9_females_carcasses_total	9x160_males_carcasses_total	9x160_females_carcasses_total	9xArg_ovaries_total	160_testes_total					140x9_testes_total	follicle cells	160x9_females_carcasses_total	embryo
(((((((.((...(((((.(((((.....))))))))).))))))))..	22	1	1	2.00	2	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0
.....ATCGATTTGCACCAATTGCAGH.....	21	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CATCGATTTGCACCAATTGCA.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GAAAGTGTCACAACTGAG.....	23	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
.....CATCGATTTGCACCAATTGCAGH.....	24	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
.....TTCATCGATTTGCACCAATTGCAG.....	24	1	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....TCATCGATTTGCACCAATTGCAGH.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATCGATTTGCACCAATTGCAG.....																				

Anti-sense strand reads

TCCTAACCTATAAATTCGCACTTGTTCCGATGCTTTCACAGTGTTGACTCCATTAACACATAAGCTTACGCTACATTTGTTGTTGAAGTAGCTAAACGTGGTTAACGTCGAGTTCACCCAAACGCTGTTTAGCGTAGTGAGCCGACAGCCGGTTAGCAA **(((((((.((...(((((.(((((.....))))))))).))))))))..**																		SRR1106729
	Read size	# Mismatch	Hit Count	Total Norm	Total	V053 head	SRR060666 160_males_carcasses_total	M027 male body	SRR060684 140x9_0-2h_embryos_total	SRR060682 9x140_0-2h_embryos_total	SRR060672 9x160_females_carcasses_total	M028 head	SRR060667 160_females_carcasses_total	mixed whole adult body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_13047:16159742-16159900 -	dvi_17138	AGGAT---TGGATATTTAAGCGTGAACAAGGCTACGAAAGTGTCACAACTGAGGTAATT--GTGTATTCGAATGCGATG----------TAA----------ACAA--CAACTTC-------ATCGATTTG----------CACCAATTGCAGCTCAAGTGGGTTTGCGACAAATCGCATCACTCGGCTGTCGGCCAATCGTT
droMoj3	scaffold_6540:12467941-12468094 -		AGAAC---TGGATATTTAAGCGTGAACAGGCTACGAAGTATCACCAACGAGGTAGTGC--AGCAG----------C----------CTCG----CTC----------AAG--ACTTGCGAA---------A-TTGGCCTAA------TGTTCATTGCAGCTCAAATGGGTCTGCGACAACTCGCATCACTCGGCGTCGCAGTCGTT
droGri2	scaffold_15116:1027929-1028093 -		AGAAC---TGGATATTTAAGCGTGAACAGGCTATGAGAGTGTTACAACTGAGGTATTT--TGCCT----------CT-G----ACAATTTATTT--AGCAA---------- ----------TCAGG------A-CTTCTTAC-A-CTTA----------CA-TTACAGAGCTCAAATGGGTCTGCGACAACTCACATCATCAACGCGCGTGTGGCCAATCGTT
droWil2	scf2_1100000004902:2611223-2611387 -		GCGATCGCTGGATATTCATTTATGATTTTGGCTATAAGAGATGATACTGAGGTAATGA--TCTTATTCTAATGTTTG----------TA----------AAAA--GTTTGATTAT---------CTTGTATT-TTTTCTCTCTACAGGTTAATTGGGTCTGTGAGTCAGCTCAAACGCGCCTGTCGGCCAATCATT
dp5	2:29935980-29936145 +		CCGAT---TGGATATTCATACCGATAGGGGGCTCGAGAGCATCACCACCGAGGTCCTT--AAT----------CCAT----------GCCC--TGCAACTTG----------G-GCATCTCATA-AT---C-C-ATTTCCACCTT----------TTCCTTTCAGGTCAATTGGGTCTGTGAGAACTCCATCACCCGCGTCTGGCACATCCTT
droPer2	scaffold_6:5305136-5305298 +		CCGAT---TGGATATTCATACCGATAGGGGGCTCGAGAGCATCACCACCGAGGTCCTT--AAT----------CCAT----------GCCC--TGCAACTTG----------G-GCATCTCTCA-T---C-C-ATTTCCACCTT----------TTCCTTTCAGGTCAATTGGGTCTGTGAGAACTCCATCACCCGCGTCTGGCACATCCTT
droAna3	scaffold_13340:14974011-14974164 -		CCAAC---TGGATATTTAAGCGAAAGTGGCTATGAGAGATCACCACCGAGGTACCCTTT----------CT----------GACT--TGCTTCCTA----------ATCA--ACTCTATC-----CTCACCT----------TATTCCCTTTCTTAAAGTGGGTCTGTGACAACTCCATCACCACCGCGTCTGGCACATCCTT
droBip1	scf7180000395971:220551-220705 +		ACTGT---TGGCAATACGAAACGGAAGAAAACTATGAAAGCATCACAAGAGATGAATT--TTT----------ACAC----------ACAAT-TA----TGA----------T-GTT--TATTTT---ATCA-------AATTAT----------TGTTATATTGGCTCGATTGGGTCTGCGACGAACCTTTAACGTGGCTGTTGGCCAATCCTT
droKik1	scf7180000302666:193404-193560 -		AGGAC---TGGATTTCAAGCGGATATGGCTACGAAAGTATCACCACTGAGGTATGGC--AAATA----------CAC----T------GTCC--TCTAACCCG----------AAG--AGTTATTAGT---------GTTGA-------TGTTCAACGAGCTCAAGTGGGTCTGCGCAAATCTGACACTCTGGCGTCGGCAGTCCTT
droFic1	scf7180000454126:419366-419529 +		GGAAT---TGGATTTCAAGAGGAAAGGGGCTACGAAAGGATCACCACTGAGGTAAGT--ATATAT----------A--AT------TT-TTTA----CAACAAAAAAA----TTTG-TTA-------TGATTAT----------TATTTTTTTTTTCAGCTCAAATGGGTTTGTGACAAACGGCATCACTCATGCATTGGCAATCGTT
droEle1	scf7180000486474:70815-70977 -		AGAAC---TGGATCTAGAATCTACGATTTTGGCTACTGAAGATCATACCGAGGTAAGT--GTGGTT----------C----TTAATCAACTC--ATCAAT---------- ----CGGTTGT------A-CT-TC-ATGATTAA----------CTTTTATTTGGTAAATGGGTCTGTGAGTCGGCGTCAAACGCACGCATTGGCCATCTGCCT
droRho1	scf7180000779431:10750-10922 -		GGGAT---TGGATTTCCAGAGGAAAGTGGCTACGAAAGATTACCACTGAGGTACGATTAAT----------CAAT----------TAGA-------TTAA--AACACTTATTTTC-CAA-ATCTA-T----A-A-ATTTTACCTTTA----------TTTGCTGCAGCTCAAATGGGTCTGTGAGCAATCCATCAACCGGCAGTCGGCCATCCTT
droBia1	scf7180000302402:1200609-1200770 +		AAGAT---TGGATTTCAAAAGGAAGAGGGGCTATGAAAGATCACCACCGAGGTTCCTT--AACAA----------AG--AAT----------TTTTA----TTT----------AAAA--TCCTATTTT---CCTATACGCGACTT----------TCCAACTTCAGCTCAAATGGGTCTGTGACAAATCCATCAACCGCGAGTCGGCAATCCTT
droTak1	scf7180000415710:405782-405944 -		GACAT---TGGATTTCAAGAGGAGAGTGGCTACGAAAGCATCACCACCGAGGTAACCCAATT----------ATAAATAAC----------TTTTA----TC----------AGAA--ATTATATTTT---------TTTAAAATCCTTTTATTCCCTAGCTCAAATGGGTCTGCGACAAATCCCATCACCAGCGGCGTCGGCAATCCTT
droEug1	scf7180000409804:1713783-1713942 +		AGAAT---TGGATTTCAAGAGGAGGTGGCTATGAAAGATCACCACCGAGGTACCAC--AACTA----------AA----------GCCTCTTA----CT----------TTG-CATTTTTATTCTTACTCA-------TTTTTTTTTTGCTTAAGCTCAAATGGGTCTGCGACAAATCCATCACTCATCGCATTGGCCATCCTT
dm3	chr3R:15426740-15426898 +		GGAAT---TGGATTTTTAACAGGAGAGGGGCTACGAAAGATACCACCGAGGTATCAA--AGCCATTGAAAAAGGTG----------TAC----------AAAA--GTTTATAAAT---------TATAGAAA-----AGCCCTCTCAGCTCAAATGGGTTTGTGACAAATCGCATCACTCATCGCATTCGGCCAATCCTT
droSim2	3r:5839485-5839647 -		GGAAT---TGGATTTCAAACAGGAAAGGGGCTACGAAAGATACCACCGAGGTATAA--AGCCATTGAAAAATGTA----------CTC----------AGAA--ACTTTATAAT---------TTTGAAAAA--CAAAGCCCTCTCAGCTCAAATGGGTTTGTGACAAATCGCATCACTCATCGCATTCGGCCAATCCTT
droSuz2	scaffold_26:350037-350199 -		GGAAT---TGGATTTCAAACAGGAAAGGGGCTACGAAAGATACCACCGAGGTATAA--AGCCATTGAAAAATGTG----------CTC----------AGAA--ACTTTATAAT---------ATTGTAAA--C--AAGCCCTCTCAGCTCAAATGGGTTTGTGACAAATCGCATCACTCATCGCATTCGGCCAATCCTT
droYak3	3R:4180717-4180873 +		GTAGC---TGGATTTCGCACAGGAGAGGGGCTACGAAAGATACCACCGAGGTATAA--AGCCATTAA-AAATATA-TG----------CTC----------AAGA--AGTGAATACT---------TTTGATG-----T-CCCCCTCAGCTCAAATGGGTCTGTGACAAATCGCCCATCACTCATCGCATTCGGCCAATCCTT
droEre2	scaffold_4770:6214317-6214474 -		GGAGC---TGGATTTCAACAGGAGAGGGGCTACGAAAGATACCACCGAGGTACAA--GCCCATAGGAAACT-TGG----------CTC----------GAAA--AGCTTATAAT---------GTTGACA-----T-CCCCCTCAGCTCAAATGGGTCTGTGACAAACTCTACACCGGCGATCGGCCAATCCTT

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

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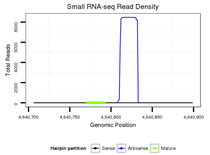
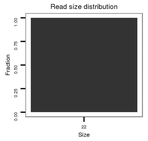
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

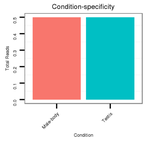
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_24640	**scaffold_12723:4640756-4640849 +**	**candidate**	**Canonical miRNA**	**intergenic**	View on UCSC Genome Browser (Cosmil Mirror)

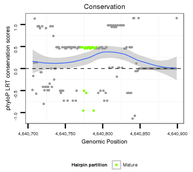
Legend: Sense 5p Arm/Loop 3p Arm/Loop 5' mismatch/Arm 3' mismatch/Arm

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

markers	star
4: dvi_24640 scaffold_12723:4640775-4640792 ...	
5: scaffold_19963:2284645-2284663 ...	

Sense Strand Reads

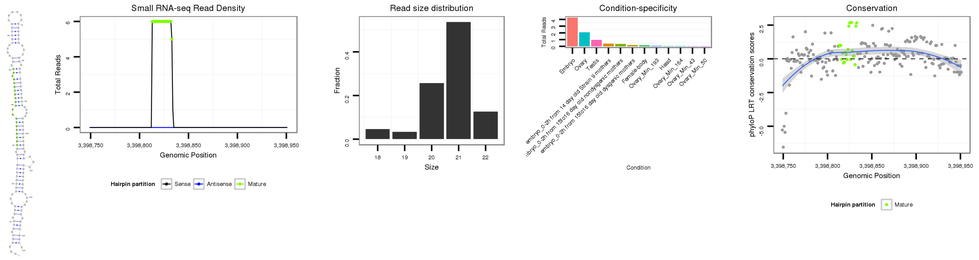
hide 3p reads show red mismatch reads

| | | |

ID:	Coordinate:	Confidence:	Class:	Genome Locale:	
dvi_24664	**scaffold_12928:3398799-3398901 +**	**Candidate**	**Unknown**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in star

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
TG26	Simple_repeat	Simple_repeat	+

mature

1. scaffold_12726:816909-816928 +
2. scaffold_12756:342043-342063 +
3. scaffold_12822:1110660-1110680 +
4. scaffold_12822:4033986-4033906 +
5. scaffold_12855:9847493-9847501 +
6. scaffold_12875:32963572-32963592 +
7. scaffold_12875:33299786-33299726 +
8. scaffold_12875:20187636-20187668 +
9. dvi_24664 scaffold_12928:3398833-3398833 +
10. scaffold_12963:5245569-5246589 +
11. scaffold_12963:7217159-7217179 +
12. scaffold_12963:6597538-6597558 +
13. scaffold_12963:17325684-17325704 +
14. scaffold_12970:3332702-3332722 +
15. scaffold_12970:3332357-3332395 +
16. scaffold_13047:1165831-1165851 +
17. scaffold_13047:1062879-1062829 +
18. scaffold_13047:1166811-1166831 +
19. scaffold_13047:1165939-1165919 +
20. scaffold_13047:1445465-1445467 +
21. scaffold_13047:1547436-1547438 +
22. scaffold_12773:5713885-5713905 +
23. scaffold_12854:63138-63108 +
24. scaffold_12963:5372015-5720833 +
25. scaffold_12963:8854846-8854866 +
26. scaffold_12970:10307861-10307881 +

Sense Strand Reads

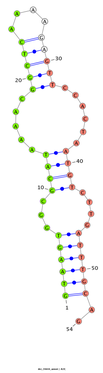
hide 3p reads show mid mismatch reads

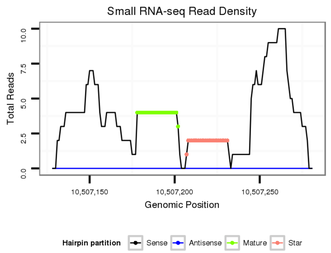
GCGAAACCGCTCAAAAAAACTTCTGAGAAGCGTTGCAAGGCATTCAGATGTTTGTGTTTGTGGCTGTCTGTTTAATCACGATTTTGGTTGCTTGCATTGCTCTACGCACGCATGCCAAGCACATTTAATCAGAGCGTTCACGCCCTTAATATACCGCCCCTTCACCAAATAG						M047	SRR060687	SRR060662	SRR060682		SRR2096059	SRR060673	SRR060685	SRR060656	SRR060670	SRR060676	SRR060675	SRR2096060	SRR060681	SRR2096026	SRR2096038	SRR2096080	SRR060680	SRR060655	SRR2096079	SRR2096081	SRR060674	SRR060679	SRR060677	SRR1106729	SRR060454	SRR060465	SRR060661	SRR060678	SRR060686	SRR2096055	SRR2096057	SRR2096072	
**********	Read # Size	Mismatch	Hit Count	Total Norm	Total	female 9 body	0-2h_embryos_total	9w160_0-2h_embryos_total	9w140_0-2h_embryos_total		9_ovaries_total	2h_embryos_total	9w160_ovaries_total	9_testes_total	9wArg_ovaries_total	140w9_ovaries_total		Ovary_Min_164	Arge9_testes_total	embryo_0-2h from 14 day old Strain 9 mothers	embryo_0-2h from 14 day old Strain 9 mothers	embryo_0-2h from 15to16 day old nondygenic mothers	9wArg_testes_total	9w160_testes_total	embryo_0-2h from 15to16 day old dygenic mothers	embryo_0-2h from 15to16 day old nondygenic mothers	9w140_ovaries_total	140w9_testes_total	Arge9_ovaries_total	adult body	whole mixed	160w9_0-2h_embryos_total	9_females_carcasses_total	160w9_0-2h_embryos_total	9w160_testes_total	2h_embryos_total	Ovary_Min_43	Ovary_Min_50	embryo_0-2h from 15to16 day old dygenic mothers	V053 head
..(((.((.((.(.....(((((((((.(((((((((.....(((((((.(((.(.(.....(((((.....))))))).....)).)))))))))).....))))))).)).)))))))))).))).))))))))

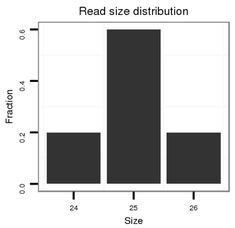
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_24644	**scaffold_12875:10507178-10507231 +**	**candidate**	**MiRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

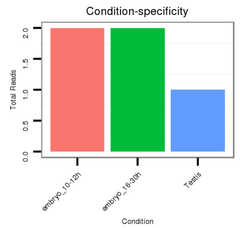
Legend: mature star mismatch in alignment mismatch in read

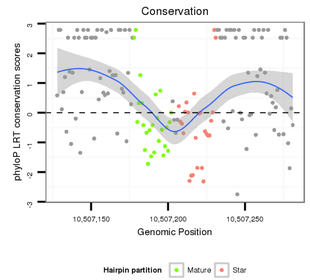
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DviriGI21763-in]; CDS [DviriGI21763-cds]; CDS [DviriGI21763-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AATACCGCAGGCATCAGTGGATCCCGAGCAGGTTATGACCAATCTGCATGGTAAGTGGCGCATAAAACGGCTCAAAAAGAGTTCCACTAATGTCTTGATTTGCAGATCCCCAGAAGTCGATAGCAGTTGTCAATGAGGTGCAAAAGGCGTCTGCC	Read #	Mismatch	Hit Count	Total Norm	Total	SRR060661 160x9_0-2h_embryos_total	SRR1106730 embryo_16-30h	V047 embryo follicle cells	GSM1528803	SRR1106722 embryo_10-12h	SRR2096058 Ovary_Min_98	M047 female body	SRR060654 160x9_ovaries_total	SRR060658 140_ovaries_total	SRR060663 160_0-2h_embryos_total	SRR060664 9_males_carcasses_total	SRR060666 160_males_carcasses_total	SRR060674 9x140_ovaries_total	SRR060675 140x9_ovaries_total	SRR060676 9xArg_ovaries_total	SRR060678 9x140_testes_total	SRR1106725 embryo_14-16h	SRR1106726 embryo_14-16h	SRR2096014 Ovary_Strain_160_oxidized	SRR2096059 Ovary_Min_164	SRR2096079 embryo_0-2h from 15to16 day old dysgenic mothers	SRR060672 9x160_females_carcasses_total	V116 male body	SRR060687 9_0-2h_embryos_total
...ACCGCAGGCATCAGTGGATCCCGAG	25	0	1	2.00	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GATAGCAGTTGTCAATGAGGT	21	0	1	2.00	2	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GTAAGTGGCGCATAAAACGGCTCAA	25	0	1	2.00	2	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TTATGACCAATCTGCATG	18	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATCCCGAGCAGGTTATGACCAATCTGC	27	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CCCCAGAAGTCGATA	15	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
GATAGCAGTTGTCAATGAGGTGC	27	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
TTCCACTAATGTCTTGATTTGCAG	25	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GATAGCAGTTGTCAATGAGGT	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GTAAGTGGCGCATAAAACGGCTCA	24	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
GTAAGTGGCGCATAAAACGGCTCAAA	26	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GATAGCAGTTGTCAATGAGGTGC	23	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
GTCAATGAGGTGCAAAAGGC	20	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TTGTCAATGAGGTGCAAAAGGCGTC	25	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GTTCCACTAATGTCTTGATTTGCAG	25	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CGCAGGCATCAGTGGATCCC	20	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
ATAGCAGTTGTCAATGAGGT	20	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CCCGAGCAGGTTATGACCA	19	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GAGGTGCAAAAGGCGTCT	18	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
AGGCATCAGTGGATCCCGAGC	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
AGCAGTTGTCAATGAGGTGCAA	22	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
ATCCCGAGCAGGTTATGA	18	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0

Anti-sense strand reads

TTAGGCGTCCGTAGTCACCTAGGGCTCGTCCAATACTGGTTAGACGTACCATTCACCGCGTATTTTGCCGAGTTTTCTCAAGGTGATTACAGAACTAAACGTCTAGGGGTCTTCAGCTATCGTCAACAGTTACTCCACGTTTTCCGCAGACGG	Read #	Mismatch	Hit Count	Total Norm	Total	GSM1528803 follicle cells	V116 male body	SRR2096014 Ovary_Strain_160_oxidized	SRR060665 9_females_carcasses_total	M061 embryo	SRR2096058 Ovary_Min_98	M047 female body	SRR1106721 embryo_10-12h
GTTGTCAATGAGGTGCAAAAGGCGTCT	27	0	1	1.00	1	0	0	0	0	0	0	0	0
GTCAATGAGGTGCAAAAGGC	20	0	1	1.00	1	0	0	1	0	0	0	0	0
TTGTCAATGAGGTGCAAAAGGCGTC	25	0	1	1.00	1	0	0	0	0	1	0	0	0
ATAGCAGTTGTCAATGAGGT	20	0	1	1.00	1	0	1	0	0	0	0	0	0
GAGGTGCAAAAGGCGTCT	18	0	1	1.00	1	0	0	0	0	0	0	0	0
AGCAGTTGTCAATGAGGTGCAA	22	0	1	1.00	1	0	0	0	0	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12875:10507128-10507281 +	dvi_24644	AATACCGCAGGCATCAGTGGATCCCGAGCAGGTTATGACCAATCTGCATGGTAAGTGG---CGCAT-AAAAC--GGC-TCAAAAGAGTT-C----------CA-CTAAT---G-TC---TTGATTTGCAGATCCCCAGAAGTCGATAGCAGTTGTCAATGAGGTGCAAAAGGCGTC---TGCC
droMoj3	scaffold_6496:16437909-16473070 -		AATACCGCAGGCATCAGTGGATCCGAGCAGTTATGACCAATCTGCATGGTAAGTGAATGATCATCAATT-TTT-------TTT-G-T-----TCTTCATTTTCTCAC-TTTCCCC-----G-GCTTCTGGTTGTAGATCCCCAGAATTCGATTGTCAATGAGGTGCAAAGGC-TC---TCCC
droGri2	scaffold_15245:3627002-3627171 -		AATACCGCAACGCATCGTGGATCCCGAGCAGGTTATGACCAATCTGCATGGTAGTGG---CC-TC-AACT-AATC-CAAAAAGAGTTCCAAT-TTC-------TTTTCCCAGAAGTCGATGTGTGTCAATGAGGTGCAAGACATTATATAT-----CGCC
droMil2	scf2_1100000004514:2790755-2790919 +	dwi_108	GTATAATTTCAATATTCATGGATCCCGAAGAGGTGTTATCATAATTGAATGTATAGTGGT---ATTT-CAAATT-TTT-------TATCGATAGGGGTCTTTTTTCTTATAGATCCCGATAATTCGTTTGTCTTATGGTGTATGAATTCAAAAATCCTTC---TATG
dp5	Il1064756:1064770 +		GTATAATTTCATATTCATGGATCCCGACAGGTTATGATTAATCTCATATCATGTATGGGGT-C-TCTTTTTTTTATTTGTGT-TTATGCTTGA-------TCT-----------AATCTAATTTTATATTCCTCCCAAATAGATCCCTAGAATTCGATAGTCAGCGTTGTCATATGAGGTGCAAGCGTC---TTCC
droPer2	scaffold_4597670:597686 +		GTATAATTTCATATTCATGGATCCCGACAGGTTATGATTAATCTCATATCATGTATGGGGT-C-TCTTTTTTTTATTTGTGT-TTATGCTTGC-------TCT-----------AATCTAATTTTATATTCCTCCCAAATAGATCCCTAGAATTCGATAGTCAGCGTTGTCATATGAGGTGCAAGCGTC---TTCC
droAna3	scaffold_13266:10620824-10620985 +		AATAATTTCATATTCATGGATCCCGACAGTATTATCATCAATCTATATCATGTATGGGGTTCTTTATTTTTCAAAATGTATAGTTCTATCGGGGTCTTTTTTCTTATAGATCCCGATAATTCGTTGTCATATGAGGTGCAAGCGTC---TTCC
droBip1	scf718000039642 8:1048100-1048262 +		GTATAATTTCATATTCATGGATCCCGATACGTATTATCCCATCTGTATGGTTGTGGGTTTTTCTTTTTAAAATTGGGAAGTTCCT-------CATTAT-----------AATCTGTTTTTTATTATTCATCGTCGAATAGATCCCGATAATTCGTTGTCATATGAGGTGCAAGCGTC---TTCC
droKik1	scf718000030285:312724-312878 -		GTATAATTTCATATTCATGGATCCCGACAGTATTATCCCAATCTATATGGTTGAGTATTTAGCTTTTTTTT