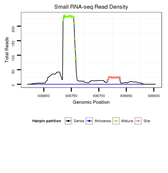
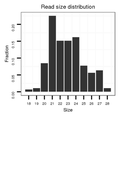
ID	Coordinate	Confidence	Class	Genome Locale
dvi_24633	**scaffold_13047:936647-936780 -**	**candidate-rescued**	**Canonical miRNA**	**intron**

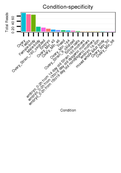
[View on UCSC Genome Browser (Crated Mirror)]

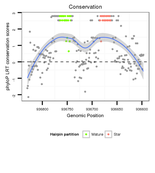
Legend: Mature Star Predicted 5' Arm Predicted 3' Arm

Predicted structure









Show Alternate Folds

FlyBase annotation

mirna:[Dvir\GI2704-aj]

No Repeats stream found

Sense Strand Reads

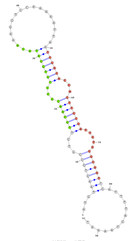
Sort by reads show red mismatch reads

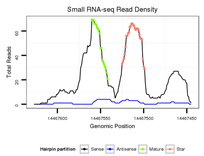
| Seq | Read # | Hit | Total | WGAT embryo female body | 2R0000477 Angel_ovarian_total | 2R0000481 Angel_testes_total | 2R0000476 Dubg_ovarian_total | 2R0290014 Dvera_Hiss_105_ovaliveed | 2R0290055 Dvera_Mis_K2 | 2R0290056 Dvera_Mis_K8 | 2R0290057 Dvera_Mis_T5 | 2R0290074 Dw105_ovarian_total | 2R0290059 Dvera_Mis_105 | 2R0290054 Dw105_ovarian_total | 2R0290058 105_testes_total | 2R0290076 Dw105_testes_total | 2R0290079 105ad_testes_total | 2R0290013 Dvera_Hiss_K_ovaliveed | 2R0290053 Dw105_testes_total | 2R0290052 Argentina_testes_total | 2R0290051 Dubg_testes_total | 2R0290050 A_mela_ovarianess_total | 2R0290049 105ad_testes_total | 2R0290048 Dsilicia mela | 2R0290044 105_mela_ovarianess_total | 2R0290043 105_female_ovarianess_total | 2R0290047 105_female_testesness_total | Y047 | Y114 | Y114 W061 embryo body | 2R0400460 embryo head | 2R0400461 Argentina_ovarian_total | 2R0290471 Dw105_mela_ovarianess_total | 2R0290475 Dw105_ovarian_total | 2R0400462 Dsil_K_D1 | 2R0290470 D1_embryos_total | 2R0290469 A_testes_total | 2R0290254 105ad_female_ovarianess_total | 2R0290252 Dw105_female_ovarianess_total | 2R0290253 105_testes_total | 2R0290255 105_ovarian_total | 2R0290488 | W118 | 2R0290493 head | 2R0290494 A_female_ovarianess_total | 2R0290495 105ad_female_testesness_total | 2R0290256 Dvera_Mis_T6 | 2R0290257 105_testes_total | 2R0400463 105_D1 | 2R0290468 D1_embryos_total | 2R0290467 105ad_mela_ovarianess_total | 2R0400472 A_ovarian_total | 2R0290465 Dubg_D1 | 2R0400467 D1_embryos_total | 2R0290466 105_testes_total | 2R0115672 embryo 105 female | 2R0115672 embryo 14- days female | 2R0290260 Dvera_Mis_105 | 2R0290261 Argentina_105 female | 2R0290262 embryo_D1 female | 2R0290263 105 female | 2R0290264 105ad_female | 2R0290265 embryo |
|---|---|---|---|---

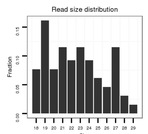
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_24646	**scaffold_12963:14467495-14467577 -**	**candidate-rescued**	**Canonical miRNA**	**intergenic**
				[View on UCSC Genome Browser (GenoMiMatz)]

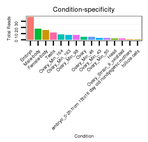
Legend: mature star mismatch to alignment mismatch to hairpin

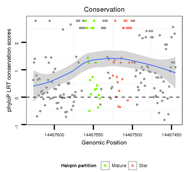
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatible elements found

Sense Strand Reads

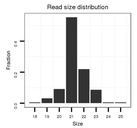
hide 3p reads show mid mismatch reads

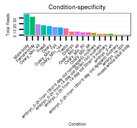
Read Seq	Size	Mismatch	Count	Mom	Total	MD41 embryo	V047 embryo	SRR040679 140w3 testes_total	SRR2296060 Ovary_Mis_193	SRR040665 9_female carcasses_total	SRR040681 Arge3 testes_total	SRR2296059 Ovary_Mis_164	MD47 female body	SRR2296058 Ovary_Mis_98	SRR040648 140w5 males carcasses_total	SRR040672 9_ovaries_total	SRR040667 140 females carcasses_total	SRR2296055 Ovary_Mis_43	SRR2296056 Ovary_Mis_46	SRR040671 9w140 males carcasses_total	V114 male body	SRR040664 9_males carcasses_total	SRR040673 9_ovaries_total	SRR040674 9dcr2 ovaries_total	MD27 female body	SRR040677 Arge3 ovaries_total	SRR2296013 Ovary_Strain_9_unfdissed	SRR1104729 mixed whole adult body	SRR2296057 Ovary_Mis_30	MD28 head	SRR040666 140 males carcasses_total	SRR040676 9w140 ovaries_total	SRR040669 140w5 testes_total	SRR1104730 embryo_0-20h	GSM1329803 follicle cells	SRR040654 140w5 ovaries_total	SRR040656 9w140 ovaries_total	SRR040657 140 testes_total	SRR040659 Argentina testes_total	SRR040663 140_0-20h embryo_total	SRR040649 140w5 females carcasses_total	SRR040670 9 testes_total	SRR040675 140w5 ovaries_total	SRR040678 9w140 testes_total	SRR040680 140 ovaries_total	SRR2296040 embryo_0-2h from 14V053 mosaic mothers	SRR2296050 embryo_2-2h from 14V053 mosaic mothers	SRR040661 140w8_0-20h embryo_total
((((((((.((((((.(((((((.(((((((.(((((((.....))))))).)))))))).)))))))).)))))).)))))))....																																															
.....TCCACCCCTTCGCACCCCT.....	19	0	1	4.00	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCCACAGGATTCGATTCTGGGCAGT.....	27	0	1	4.00	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTTGCGATTCTGGCAGGGT.....	27	0	1	4.00	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTACTGCCCCTTCGCACCCCT.....	23	0	1	4.00	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCCACCCCTTCGGATACAAGGTC.....	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	0	0	0	0	0	0	0	0
.....GTTAACACTGGGAGATCTCACC.....	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	0	0	0	0	0	0	0	0
.....ACGATTTGCGATTCTGGCC.....	20	0	1	3.00	3	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	0	0	0	0	0	0	0	0
.....TCCACCCCTTCGGATACAAGGTCCA.....	27	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	0	0	0	0	0	0	0	0
.....ACGATTTGCGATTCTGGGC.....	19	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	0	0	0	0	0	0	0	0	0
.....TCCACAGGATTCGATTCTGGGCAGT.....	27	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	0	0	0	0	0	0	0	0	0
.....GGTCTTGCAGCGCCTGTGGA.....	21	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	0	0	0	0	0
.....GGTCTTGCAGCGCCTGTGGA.....	21	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	0	0	0	0	0
.....GTACTGCCCCTTCGCACCCCTCT.....	25	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	0	0	0	0	0	0	0	0	0
.....ATTTAACACTGGGAGATCTCACC.....	24	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	0	0	0	0	0
.....TTGCAACCCCTCTGGATA.....	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	0	0	0	0	0	0	0	0	0
.....ATTTTAACGTGTCCACAGT.....	21	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	0	0	0	0	0
.....TATGCACATGTAAACATCGGA.....	21	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	0	0	0	0	0
.....GCGAGTTCGATTCTGGGCAGT.....	27	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	0	0	0	0	0
.....ACGATTTGCGATTCTGGGCA.....	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	0	0	0	0	0	0	0	0	0	0	0	0
.....ACGATTTGCGATTCTGGGCAGTT.....	20	0	1	2.00	2	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
.....AAACACTGGGAGATCTCACC.....	20	0	1	2.00	2	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
.....GTCCACATTTAACACT.....	19	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	0	0	0	0	0
.....GACTTGCCCCTTCGCACCCCT.....	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	0	0	0	0	0	0	0	0	0
.....TATCCACACGATTTGCGATTCTGGGCA.....	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	0	0	0	0	0	0	0	0	0
.....GATTTGCGATTCTGGGCAGTT.....	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	0	0	0	0	0
.....ACGATTTGCGATTCTGGGCAGTT.....	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	0	0	0	0	0
.....TCTTCCACGCCTCTGGATACAAGGTC.....	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	0	0	0	0	0	0	0	0	0
.....GCGATTCTGGGCAGTTGATTT.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATGCACATGTAAACATCGGA.....	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	0	0	0	0	0
.....TTTCACAAATCTTTATGCACATT.....	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	0	0	0	0	0
.....GCGATTCTGGGCAGTTGATTT.....	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	0	0	0	0	0
.....TCCACAGGATTCGATTCTGGGCAG

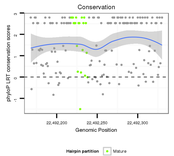
ID:	Coordinate:	Confidence:	Class:	Genome Locale:
dvi_158	**scaffold_13049:22492218-22492280 +**	**candidate-rescued**	**Canonical miRNA**	**CDS** [View on UCSC Genome Browser (GoogleMotif)]

Legend: loop; 5p; 3p; mismatch in a hairpin; mismatch in loop

Predicted structure:







Show Alternate Folds

Flybase annotation

CDS [Dvir(GEN75.c4)]

No Repeatable elements found

Sense Strand Reads

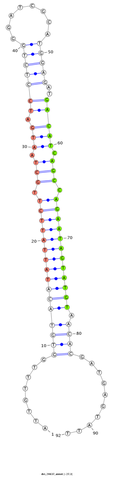
Hide 3p reads | Show mid mismatch reads

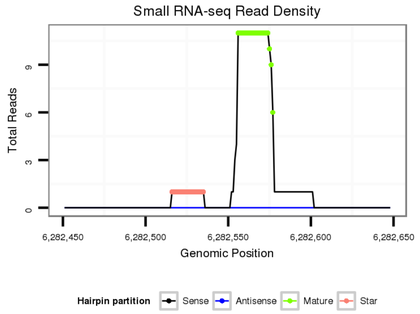
| | | |

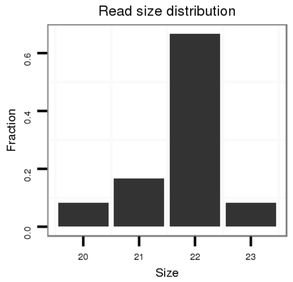
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_24637	**scaffold_12855:6282501-6282598 +**	**Known Ortholog**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser [Cornell Mirror]]

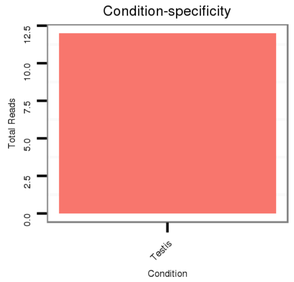
Legend: mature star mismatch in alignment mismatch in read

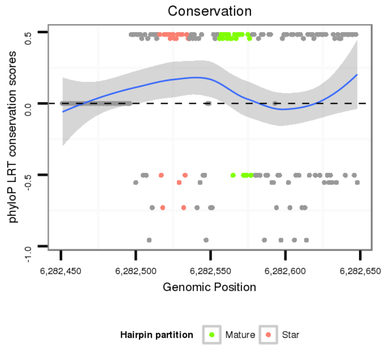
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [DviriGJ10228-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TCTGAGAAAGTTCAAGAAGAAAACCTAAGTATTTGAAGTACCTTGGATATATTGTTTGGTGTACATATTATTCTTGCTAATGATCCTCTGGGATCGCATGGAGATGACATCAGCCAGAATAGTATGTAACACGATGAGTATTAGGCGGTTATATAGGTTAAGGCAGTTCAATCTTATTAGTTCTTGGTTAAAATTGTT	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060670 9_testes_total	SRR060659 Argentina_testes_total	SRR060678 9x140_testes_total	SRR060681 Argx9_testes_total	SRR060679 140x9_testes_total	SRR060689 160x9_testes_total	SRR2096056 Ovary_Min_46	SRR060665 9_females_carcasses_total	V047 embryo	SRR060682 9x140_0-2h_embryos_total	SRR060686 Argx9_0-2h_embryos_total	SRR060664 9_males_carcasses_total	V053 head
**********.....((((((((((((((((.((((.((((.(((((((.....)))))..)))))).))).))))))))))).))))..**********																		
.....GACATCAGCCAGAATAGTATGT.....	22	0	1	5.00	5	1	3	1	0	0	0	0	0	0	0	0	0	0
.....GACATCAGCCAGAATAGTATG.....	21	0	1	2.00	2	0	0	1	1	0	0	0	0	0	0	0	0	0
.....ATGACATCAGCCAGAATAGTAT.....	22	0	1	2.00	2	1	0	0	1	0	0	0	0	0	0	0	0	0
.....AGATGACATCAGCCAGAATAGTA.....	23	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0
.....TGACATCAGCCAGAATAGTATG.....	22	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0
.....GTAACACGATGAGTATTAGGCGGTTA.....	26	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0
.....TATTATCTTGCTAATGATC.....	20	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0
.....GACATCAGCCAGAATAGTATGTG.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

AGACTCTTTCAAGTTCTTCTTTTGGATTCATAAACTTCATGGAACCTATATAACAAACCACATGTATAATAAGAACGATTACTAGGAGACCCTAGCGTACCTCTACTGTAGTCGGTCTTATCATACATTGTGCTACTCATAATCCGCCAATATATCCAATTCCGTCAAGTTAGAATAATCAAGAACCAATTTTAACAA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060684 140x9_0-2h_embryos_total	SRR060687 9_0-2h_embryos_total	V053 head	SRR2096038 embryo_0-2h from 14 day old Strain 9 mothers
**********.....((((((((((((((((.((((.((((.(((((((.....)))))..)))))).))).))))))))))).))))..**********									
.....TGTGCTACTCATAATCCGCCAATATATCCAATTCCGTCAAGTTAGAATAATCAAGAACCAATTTTAACAA.....	35	0	1	1.00	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12855:6282451-6282648 +	dvi-mir-9538	TCTGAGAAAGTTCAAGAAGAAAACCTAAGTATTTGAAGTACCTTGGATATATTGTTTGGTGTACATATTATTCTTGCTAATGATCCTCTGGGATCGCATGGAGATGACATCAGCCAGAATAGTATGTAACACGATGAGTATTAGGCGGTTATATAGGTTAA-GGCAGTTCAATCTTAT-----------------TAGTTCTTGGTTAAAATTGTT-----
droMoj3	scaffold_6540:629877-630050 -	dmo_74	----------ATTATATTCTTGCTGATGTGTCCTCTGGATCTATTAGAATAGGCGCAATACGATAATCGGTTTAATATTGATGTATGTAAATCTAATGCATGGTTCAAATTATATGTAT

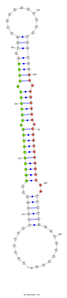
Generated: 09/11/2015 at 09:31 PM

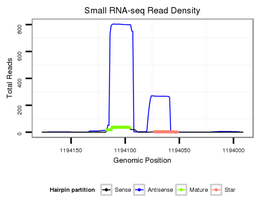
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	1

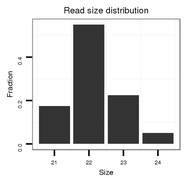
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_24638	**scaffold_13047:1194041-1194127 -**	**candidate-rescued**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Comell/Mimo)]

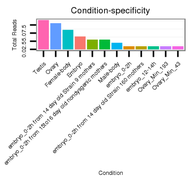
Legend: mature star non-seen hairpin arm mismatch in read

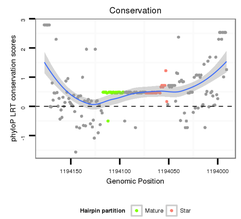
Predicted structure











Show Alternate Folds

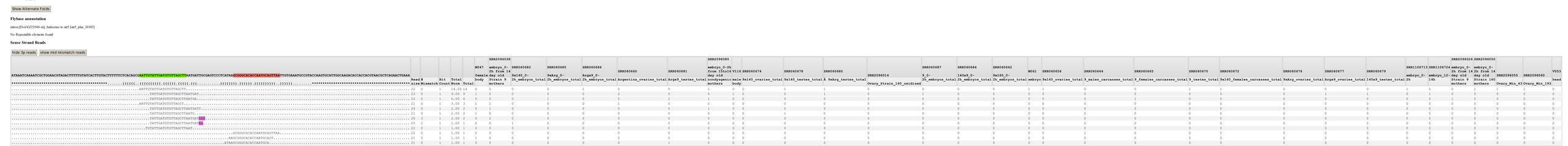
Flybase annotation

intron [Dvir/GI23540-ia], Antisense to ut5 [ut5_plus_10185]

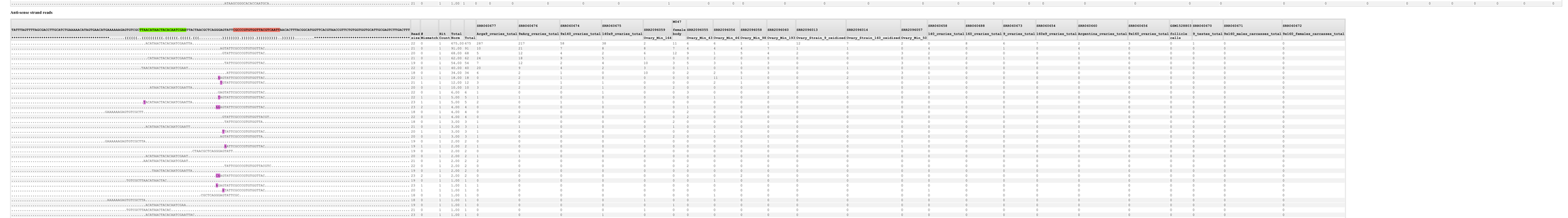
No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mrd mismatch reads



Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

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

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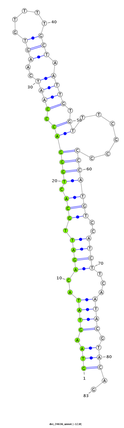
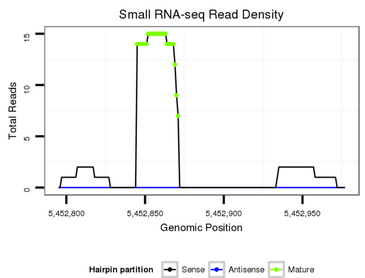
crit.mm	0
crit.bef	0
crit.seed	0
crit.gap1	0
crit.gap3	0
crit.bmp3	1
crit.bmp5	1
crit.back	0
rescue.total	1
rescue.mature	1
rescue.known	1
rescue.conflicts	1
rescue.candidate	1

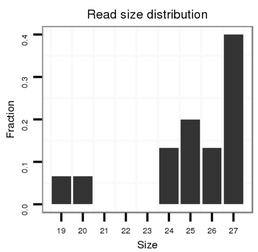
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_24636	**scaffold_13047:5452845-5452927 +**	**candidate**	**MiRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

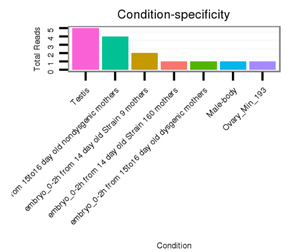
Legend: mature star mismatch in alignment mismatch in read

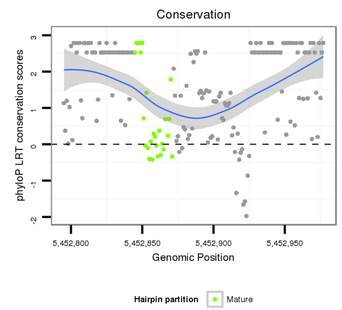
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DviriGJ23911-in]; CDS [DviriGJ23911-cds]; CDS [DviriGJ23911-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GCAACACAACAACAATGTATCCCGCACCGGTGCGTCACCCCGGCCGCCGGGGTAAGTATACAGATTGCACTGGGACCCAATCAAGTGTTTTGCTAATTGTGTTTCGCCCCCATGTCCATCTTCAATACGTACAGGGACCACCACCTCAGGGTCCAATCAAATTTACCATTGCCGATACACTGGA						M047	SRR060681	SRR060679	SRR2096080	SRR2096081			SRR060662	SRR060666	SRR060678	SRR060686	SRR1106730	SRR2096026	SRR2096038	SRR2096050		SRR2096079		
**********	Read # size	Mismatch	Hit Count	Total Norm	Total	female body	Argx9_testes_total	140x9_testes_total	embryo_0-2h from 15to16 day old nondysgenic mothers	embryo_0-2h from 15to16 day old nondysgenic mothers	GSM1528803 follicle cells	M027 male body	9x160_0-2h_embryos_total	160_males_carcasses_total	9x140_testes_total	Argx9_0-2h_embryos_total	embryo_16-30h	embryo_0-2h from 14 day old Strain 9 mothers	embryo_0-2h from 14 day old Strain 9 mothers	embryo_0-2h from 14 day old Strain 160 mothers	SRR2096060 Ovary_Min_193	embryo_0-2h from 15to16 day old dysgenic mothers	SRR2096058 Ovary_Min_98	SRR2096056 Ovary_Min_46
********(((.((((..((((.(((.(((((((.((((..(((.....))).))))).))).....))))))).))))...)))).))).**********	27	0	1	6.00	6	0	0	0	1	1	0	0	0	0	0	0	0	0	1	1	1	1	0	0
.....	25	0	1	3.00	3	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	26	0	1	2.00	2	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	24	0	1	2.00	2	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0
.....	17	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	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
.....	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
.....	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
.....	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
.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....	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

Anti-sense strand reads

CGTTGTGTTGTTGTTACATAGGGCGTGGCCACGCAGTGGGGCGGCGGCCCCATTCATATGTCTAACGTGACCCTGGGTTAGTTCACAAAACGATTAACACAAAGCGGGGGTACAGGTAGAAGTTATGCATGTCCCTGGTGGTGGAGTCCCAGGTTAGTTTAAATGGTAACGGCTATGTGACCT						SRR060664 9_males_carcasses_total	SRR060670 9_testes_total	SRR060667 160_females_carcasses_total	SRR060687 9_0-2h_embryos_total	V047 embryo	GSM1528803 follicle cells	V053 head	V116 male body
********(((.((((..((((.(((.(((((((.((((..(((.....))).))))).))).....))))))).))))...)))).))).**********	Read # size	Mismatch	Hit Count	Total Norm	Total								

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_13047:5452795-5452977 +	dvi_24636	G---C----------AACACAACAACAATGTATCCCGCACCGGTGCGTCACCCCGGCCGCCGGGGTAAGTA--TAC-AGATTGCACTGGGACCC----------A----------ATCA--AGTGT----------TTT----GCTAATTGTGTTTCG----------CCCCCA----------TG----------TCCATCTT----------CAATACG-TACAGGGACCACCACCTCAGGGTCCAATCAAATTTACCATTGCCGATACACTGGA
droMoj3	scaffold_6540:15826563-15826746 +	dmo_1964	G---C----------AACACAACAACAATGTATCCCGCACCGGTGCGTCACCCCGGCCGCCGGGGTAAGTATT-TAAGATTGCAATGGGACCC----------A----------ATCA--AGTGT----------TA----ACTAATTGTGTTTCG----------CCCCCA----------TG----------TCCATCTT----------CAATACG-TACAGGGACCACCACCTCAGGGCCAATCAAATTTACCATTGCCGATACATGGA
droGri2	scaffold_14906:10827906-10828099 +		-CAAA----ATCAAC-CAACAACAACAATGTATCCCGCACCGGTGCGTCACCCCGGCCGCCGGGGTAAGTATTAACGGATTGCAATGGGACCC----------A----TCC----------ATCA--AGTGT----------TTT----GCTAATTGTGTTTCG----------A--CC----------CA----------TG----------TCCATCT----------A-TCT-T-TTAGGGACCACCACCTCAGGGCCAATCAAATTACCATTGCCGATACATGGA
droWil12	scf2_1100000004943:15498544-15498762 +		-CA-A----------CAAAAACAACAATGTATCCCGCACCGGTGCGTCACCCCGCCGCCGGGGTAAGTACC-TC--------------TCCTACAACTAC-----A--TCC-----TACACCTAGTGTT-ATGTCAACCA-ATTCAT----------A----------TCTCTCTG----------A----------CTTT-TGTAT-TCC----------TAA--A----------A----------AT---G-AT-TAGGGACCACCACCTCAGGGCCAATCAAATTTACCATTGCCGATACATGGA
dp5	Z:19171210-19171485 +		-A--A----------A---TAACAAC-ATGTATCCCAACCGGTGCGTCACCCCGCCGCCGGGGTAAGTACCA-CCAAT----------CCACTCCATAG-GCCCCGCAGAGCCGAGACCCG-CAG-TTGTTGTCCACACTCTCTGGGGCCTCTCCTCCCCTCCCCCCACCGA--A-TT----GCTAATTGTGTTTCG----------A--CCTTTTTCTCACTCCCTCTGG----------CGGCGGA----------A----------A----TGTT-------A-ATCCCCCCCGCACTTGG----CACAG-TTGAGGGACCACCACCTCAGGGCCAATCAAATTTACCATTGCCGATACATGGA
droPer2	scaffold_2:1916524-1916798 +		-A--A----------A---TAACAAC-ATGTATCCCAACCGGTGCGTCACCCCGCCGCCGGGGTAAGTACCA-CCAAT----------CCACTCCATAG-GCCCCGCAGAGCCGAGACCCG-CAG-TTGTTGTCCACACTCTCTGGGGCCTCTCCTCCCCTCCCCCCACCGA--A-TT----GCTAATTGTGTTTCG----------A--CCTTTTTCTCACTCCCTCTGG----------CGGCGGA----------A----------A----TGTT-------A-ATCCCCCCCGCACTTGG----CACAG-TTGAGGGACCACCACCTCAGGGCCAATCAAATTTACCATTGCCGATACATGGA
droAna3	scaffold_13340:11273901-11274084 -		G---CATAACGT-AGATAACAAC-ATGTATCCCAACCGGTGCGTCACCCCGCCGCCGGGGTAAGTACCA-CCAAT-G-TT----------A----------A--TCA-TGGTCACTCGCTGTCGGGCACCCC----------A----A-TAGTGTCAC-A----------A--CTTCTATCC----------A----------CAA--A----------A----------A----TGTT-------A-ATCCCCCCCGCACTTGG----AT-TTA-TTAGGGACCACCACCTCAGGGCCAATCAAATTTACCATTGCCGATACATTGGA
droBip1	scf7180000396691:183495-183684 -		-TAGA----------ATAAAAACAAC-ATGTATCCCAACCGGTGCGTCACCCCGCCGCCGGGGTAAGTACCA-CTAG-T-CA-CTATGGT-T-A----------A----------A----A----A----A----A----A----ACTGCCTGTCGGTC----------A----A----CTAATTGTGTTCC-T----------CTTTTTT----------CCCCCA----------TC-----TATCCATCT----------A----A-TAG-TTGAGGGACCACCACCTCAGGGCCCATTAAGTTTACCATTGCCGATACATTGGA
droKik1	scf7180000302261:84617-84828 -		G---T----------AGA-TAACAAC-ATGTATCCCAACCGGTGCGTCACCCCGCCGCCGGGGTAAGTACCA-CCAGCA-TTTGACA-C------A----A---GGGTA----A----A----A----A----A----TCTTGACCG----------A----T-GCCCGCTAATGATGGT-GT----------A--TCTCTCTG----------A--TT-----AT--GTCT-CCCCCACCCAG-GTGTC----------CACC--TA-CC-------A----A----A----GA----A----GGCATT-T-A-TAGGGACCACCACCTCAGGGCCAATCAATTTACCATTGCCGACACATGGA
droFic1	scf7180000454055:1778669-1778919 +		G---C----------CTAACAACAAC-ATGTATCCCAACCGGTGCGTCACCCCGCCGCCGGGGTAAGTACCA-TATTA-C--A-A-AAAAT-GA----------A----A----A----A----A----A----GACCG----------CAAGTCCG----GCTAATTGTGTTTCA----------A--TCTCCCCTCTCTCCCTCTCTCCCTCTCT----------A----A----CC----CCCG--TG--GCCTCATGTGTGCCCACTTACT----------A----A----CGAC----CACCCACC--C----------A----A----A----TTTGGTTGG-GG-GGTAGGGACCACCACCTCAGGGTCCAATCAATTTACCATTGCCGACACATGGA
droEle1	scf7180000491261:839865-840099 +		G---C----------CTAACAACAAC-ATGTATCCCAACCGGTGCGTCACCCCGCCGCCGGGGTAAGTACCA-ACTCT----------A----A----A----A----A----A----GACCG----------CCAAATG-T----GCTAATTGTGTTTCA----------A--TCTCTATG----------A----A----AC---CCCG--CCGCCTTGCCATTGTGCCGCCCACCATA----------A----A----TTGAG----CCGCCACC-C----------A----A----A----TCAAGATTTT-GG-CAGGGACCACCACCTCAGGGTCCAATCAATTTACCATTGCCGACACATGGA
droRho1	scf7180000780074:219482-219716 +		G---C----------CTAACAACAAC-ATGTATCCCAACCGGTGCGTCACCCCGCCGCCGGGGTAAGTACCA-CTCCGATT-TATGGGTGTA-A----------A----A----A----A----A----A----GACCG----------CCAGATCCG----GCTAATTGTGTGCCA----------A--TCTCTCTG----------A----A----CC----TCCG--CCACCGGCCATGTTTCCGCCCACCCTT----------A----A----A----TTGAG----CACGCACC--A----------A----A----A----TCC-TATT-T-GG-CAGGGACCACCACCTCAGGGTCCAATCAATTTACCATTGCCGACACATGGA
droBia1	scf7180000302113:2070749-2070960 +		G---C----------CTAACAACAAC-ATGTATCCCAACCGGTGCGTCACCCCGCCGCCGGGGTAAGTACCA-CTACCC-----------CC----------A----A----A----A----A----A----GAGCG----------CCGAATCCG----GCTAATTGTGTTTCA----------A--TTTCTCCG----------A----A----CTCC--CTC---CG--ACGCCATGTGATCCGCCCGC----------CACA----------A----A----A----TG-----GA----A----A----A----TGT-CGCCT-C-ACAGGGACCACCACCTCAGGGTCCAATCAATTTACCATTGCCGACACATGGA
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droEug1	scf7180000409682:743887-744127 -		G---C----------CTAACAACAAC-ATGTATCCCAACCGGTGCGTCACCCCGCCGCCGGGGTAAGTACCA-CACCCTGCCGCCCGGGTAAGTACCA-CTACCC-----C-GCCTGGGACCA----A----A----A----A----A----A----GACCG----------TTAAATCCG----GCTAATTGTGTTTCA----------A--TCTCTCTG----------A----A----CC-----CATT-A-AG--GCGGCCATT-GTACCACCCACTCATT----------CATCTATTGAACACGGCCCACT--C----------A----A----A----A----A----A----CTTAGTTGG-GG-TAGGGACCACCACCTCAGGGTCCAATCAAATTTACCATTGCCGACACATGGA
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droSim2	Ur:21366041-21366274 +		CCAG----------CT---AACAAC-ATGTATCCCAACCGGTGCGTCACCCCGCCGCCGGGGTAAGTACCA-CACCCAT---A-GGGGGTGCCC----------A----A----A----A----A----A----GACCG----------CCGAATCCG----GCTAATTGTGTTTAT----------A--TCTCTCTG----------A----A----CC-----CACG--CG--GGGCCATT-GTGCCGCCCACGTACGGAACACCAACCACG----------A----A----A----TG-----TA----A----A----A----TTCAGATTTA-TAGGGACCACCACCTCAGGGTCCAATCAATTTACCATTGCCGACACATGGA
droSec3	scaffold_13563565:663393 +		CCAG----------CT---AACAAC-ATGTATCCCAACCGGTGCGTCACCCCGCCGCCGGGGTAAGTACCA-CACCCAT---A-GGGGGTGCCC----------A----A----A----A----A----A----GACCG----------CCGAATCCG----GCTAATTGTGTTTAT----------A--TCTCTCTG----------A----A----CC-----CACG--CG--GGGCCATT-GTGCCGCCCACGCATGTAACGCCAACCACG----------A----A----A----TG-----TA----A----A----A----TTCAGATTTA-TAGGGACCACCACCTCAGGGTCCAATCAATTTACCATTGCCGACACATGGA
droTer4	18:24605979-24606239 -		G---C----------CTAACAACAAC-ATGTATCCCAACCGGTGCGTCACCCCGCCGCCGGGGTAAGTACCA-CACCCAT---A-GGGGGTGCCC----------A----A----A----A----A----A----GACCG----------CCGAATCCG----GCTAATTGTGTTTAT----------A--TCTCAACAACACT-TG----------A----A----CC-----CACG--CG--GGGCCATT-GTGCCGCCCACGCATGGAACACAAAAACCTCACCTATTTAC----------A----A----A----TG-----TA----A----A----A----TTCAGATTTA-TAGGGACCACCACCTCAGGGTCCAATCAATTTACCATTGCCGACACATGGA
droEre2	scaffold_4820:6176657-6176898 -		G---C----------CTAACAACAAC-ATGTATCCCAACCGGTGCGTCACCCCGCCGCCGGGGTAAGTACCA-CACCCAT---A-GGGGGTGCCC----------A----A----A----A----A----A----GACCG----------CCGAATCCG----GCTAATTGTGTTTAT----------A--TCTCTCTG----------A----A----CC-----C-CGACCG--GTGCCACATGTGCCGCCCACGCATGGAACACCAACCACG----------A----A----A----T--A----TC-AG----------A---AATCAGT-CGA-A-TAGGGACCACCACCTCAGGGTCCAATCAATTTACCATTGCCGACACATGGA

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

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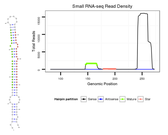
crit.ptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	1

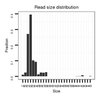
ID	Coordinate	Confidence	Size	Genome Locus
dv1_24632	**scaffold_12447:131-223 +**	**confident exception**	**Canonical miRNA**	**intergenic**

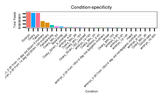
Show on UCSC Genome Browser (Linked Bases)

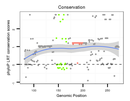
Legend: Stem Loop Mature Star Adapter Stem

Predicted structure:









Show Alignments Folder

Flybase annotation

dm6a.gtf.ncRNA.ncLCG.TE.4.4.1

In Repeatmasker Genome Grange

Genome	Name
1 scaffold_4810[50:470 +	1 scaffold_4810[50:470 +
2 scaffold_10[1000:1400 +	2 scaffold_10[1000:1400 +
3 scaffold_2[1000:1400 +	3 scaffold_2[1000:1400 +
4 scaffold_2[28:91:93 +	4 scaffold_2[28:91:93 +
5 scaffold_2[1:1:1: