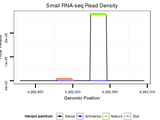
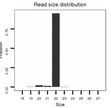
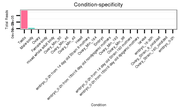
ID	Coordinate	Confidence	Class	Genome Locale	
dvi_14	**scaffold_12855:6282879-6282946 +**	**confident**	**Testes-restricted**	**antheme_to_intron**	Click on LCSC Genome Browser (Cantell Mouse)

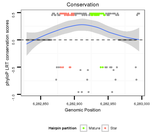
Length: **68nt** (**Genome: 68nt**, **mature: 68nt**)

Predicted structures









Show Alternate Folds

Flybase annotation

Antisense to dmel:FBrf0218229.mj

No flyanadb clusters found

Sense Strand Reads

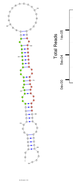
Hide 3p reads Show mid mismatch reads

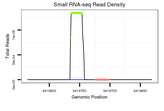
| TCGACTCCGTCATCACTTTCCTTGACCTGAACTCCTTGCCTTCTCCTTCCTTCTCCTTCCTTCTCCTTCTCCTTC

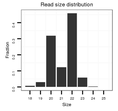
ID	Coordinate	Confidence	Class	Genomic Locale
dvi_264	**scaffold_12970:9419681-9419786 -**	**confident**	**Testes-restricted**	**intergenic**

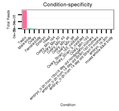
Search: **Hide All** | **Show Canonical** | **Show Novel**

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annotation

intergenic

No Repeatmb elements found

Some Strand Reads

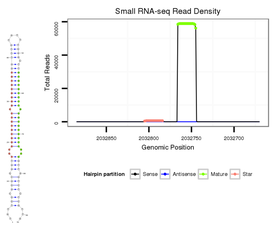
Hide Sp reads | Show Mid mismatch reads

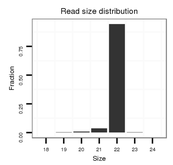
| Sequence | Strand | Pos | Total | 28802672 | 28802929 | 28802991 | 28803025 | 28803089 | 28803283 | 28803478 | 28803579 | 28803657 | 28803840 | MIAT Genic Intron | 28803858 | 28804023 | 28804054 | 28804088 | 28804260 | 28804276 | 28804277 | 28804278 | 28804279 | 28804280 | 28804281 | 28804282 | 28804283 | 28804284 | 28804285 | 28804286 | 28804287 | 28804288 | 28804289 | 28804290 | 28804291 | 28804292 | 28804293 | 28804294 | 28804295 | 28804296 | 28804297 | 28804298 | 28804299 | 28804300 | 28804301 | 28804302 | 28804303 | 28804304 | 28804305 | 28804306 | 28804307 | 28804308 | 28804309 | 28804310 | 28804311 | 28804312 | 28804313 | 28804314 | 28804315 | 28804316 | 28804317 | 28804318 | 28804319 | 28804320 | 28804321 | 28804322 | 28804323 | 28804324 | 28804325 | 28804326 | 28804327 | 28804328 | 28804329 | 28804330 | 28804331 | 28804332 | 28804333 | 28804334 | 28804335 | 28804336 | 28804337 |
|---|---|---|---|---

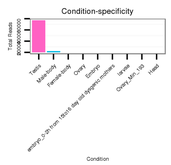
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_189	**scaffold_13042:2032720-2032835 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

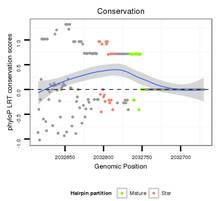
Legend: **mature** star **star-loop** **star is n/g-seq** **mismatch in read**

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

No Repeatmile elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	alignment	Hit	Total	Norm	Total	Arge9_testes_total	9a140_testes_total	140a9_testes_total	9akrg_testes_total	140a9_testes_total	140_testes_total	9_testes_total	9a160_testes_total	male body	160_testes_total	Argentina_testes_total	male body	female body	W027	W027	SRR060458	SRR060454	SRR060688	SRR060673	SRR060684	SRR060656	SRR060660	W061	SRR060664	SRR060668	SRR060676	SRR1106728	SRR2096060	SRR2094079	SRR060672	SRR060674	SRR060682	SRR2096038	SRR2096072	SRR2096081	V053
						SRR060681	SRR060678	SRR060679	SRR060680	SRR060689	SRR060657	SRR060670	SRR060655	V116	SRR060683	SRR060659									SRR060684																
						Arge9_testes_total	9a140_testes_total	140a9_testes_total	9akrg_testes_total	140a9_testes_total	140_testes_total	9_testes_total	9a160_testes_total	male body	160_testes_total	Argentina_testes_total	male body	female body	W027	W027	140_ovaries_total	140a9_ovaries_total	160_ovaries_total	9_ovaries_total	2h_embryos_total	9a160_ovaries_total	Argentina_ovaries_total	W061	embryos_0-2h_from 15to16 day old dgenesis mothers	SRR060672	9a160_females_carcasses_total	140a9_males_carcasses_total	9akrg_ovaries_total	larvae	Ovary_Mix_193	embryos_0-2h_from 15to16 day old mothers	9a140_ovaries_total	2h_embryos_total	embryos_0-2h_from 15to16 day old Strain 9 mothers	embryos_0-2h_from 15to16 day old dgenesis mothers	embryos_0-2h_from 15to16 day old nondgenesis mothers	embryo head
AATGTATAAGCTCTACACCTCCATGTTCACTTTGATTTCGTTGACTTTCAGCTTTTGCTTGGCATATTGGCAGACGAAATGCGGGCATGTCCAAGACATATATTTTATTTTGAACTTATATGTTTTAGACGTGTTCAGGATTATGTCTCTCATTAGTCCACCTCCATGTTCACTTTAATCAATAGCTCGTGACTGAAAGAGGCCAGATTAGTCG																																										
ATATGTTTAGACGTGTTCAGG	22	0	1	55541.00	55541	13376	13024	8805	3670	3502	3229	2548	2057	2155	1439	1413	51	1	20		16		7	4	6	4	2		2	1	1	1	0	2	1	1	0	0	0	0	0	1
ATATGTTTAGACGTGTTCAGG	23	1	1	2031.00	2031	546	512	369	159	179	2	126	69	13	47	6	0	0	0		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0
TGCGGGCATGTCCAAGACATA	23	1	1	797.00	797	203	168	116	46	70	19	50	24	27	30	43	1	0	0		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATATGTTTAGACGTGTTCAGG	20	0	1	333.00	333	95	68	87	30	22	0	12	12	1	5	1	0	0	0		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATATGTTTAGACGTGTTCAGG	22	0	1	175.00	175	20	24	87	5	7	10	6	1	4	2	4	1	0	0		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATATGTTTAGACGTGTTCAGG	23	0	1	171.00	171	42	34	42	11	13	2	3	3	7	6	4	1	0	0		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATATGTTTAGACGTGTTCAGG	19	0	1	142.00	142	36	28	31	16	15	0	6	4	0	7	1	0	0	0		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0
TATGTTTAGACGTGTTCAGG	21	0	1	116.00	116	25	32	22	6	3	0	3	1	2	3	1	0	0	0		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0
TGCGGGCATGTCCAAGACATATA	22	0	1	111.00	111	39	37	0	11	3	0	13	3	0	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
ATATGTTTAGACGTGTTCAGG	22	0	1	92.00	92	27	23	2	10	8	0	6	8	2	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
ATATGTTTAGACGTGTTCAGG	20	0	1	84.00	84	23	21	7	4	3	4	7	5	3	1	3	0	0	0		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATATGTTTAGACGTGTTCAGG	22	1	1	74.00	74	21	25	5	4	5	1	4	2	5	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
TGCGGGCATGTCCAAGACATATA	23	0	1	70.00	70	25	22	0	5	1	0	8	0	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
ATATGTTTAGACGTGTTT	18	0	1	51.00	51	9	11	9	5	4	2	5	1	0	5	0	0	0	0		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0
CGGGCATGTCCAAGACATAT	20	0	1	49.00	49	19	13	0	4	0	0	3	3	0	4	1	0	0	0		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0
TGCGGGCATGTCCAAGACAT	21	0	1	40.00	40	11	11	0	4	1	0	4	4	0	2	2	0	0	1		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATATGTTTAGACGTGTTCAG	22	1	1	39.00	39	12	5	0	1	5	2	8	1	2	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
ATATGTTTAGACGTGTTCA	21	1	1	37.00	37	8	9	13	2	0	1	3	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
CGGGCATGTCCAAGACATATA	21	0	1	37.00	37	14	8	0	4	1	0	3	1	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
TGTTTAGACGTGTTCAGG	19	0	1	34.00	34	3	8	7	3	5	0	1	1	0	1	2	2	0	1		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0
TATATGTTTAGACGTGTTCA	21	0	1	33.00	33	13	5	0	0	6	0	0	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
ATATGTTTAGACGTGTTCAGG	23	1	1	33.00	33	17	7	5	1	1	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	0
ATATGTTTAGACGTGTTCAG	20	0	1	33.00	33	8	11	3	6	0	0	0	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
TATGTTTAGACGTGTTCAGG	22	1	1	30.00	30	7	4	13	0	0	1	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
ATATGTTTAGACGTGTTCAG	24	2	1	23.00	23	8	5	1	0	4	0	0	1	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
GTTTAGACGTGTTCAG	18	0	1	22.00	22	5	8	2	2	2	1	1	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
TGCGGGCATGTCCAAGACATATA	24	0	1	20.00	20	9	5	0	0	0	0	0	0	0	0	0	0	0	0		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATATGTTTAGACGTGTTCAGGAT	23	0	1	17.00	17	5	4	1	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
ATATGTTTAGACGTGTTCAGG	23	1	1	16.00	16	5	6	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
ATATGTTTAGACGTGTTCAGG	22	1	1	15.00	15	2	5	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
TGCGGGCATGTCCAAGACATA	22	1	1	15.00	15	7	4	0	0	0	0	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
ATATGTTTAGACGTGTTCAG	22	1	1	15.00	15	3	4	0	0	0	0	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
TATGTTTAGACGTGTTCAGG	22	1	1	14.00	14	3	5	0	0	0	0	0	0	0	0	0	0	0	0		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0
ATATGTTTAGACGTGTTCA	22	3	2	1.00	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

Show Alternate Folds

Flybase annotation

intergenic

No Repeatmile elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	alignment	Hit	Total	Norm	Total	SRR2096014	SRR060686 Arge9_0-2h_embryos_total	SRR060679 140a9_testes_total	SRR060687 9_0-2h_embryos_total	SRR060663 140_0-2h_embryos_total
TTCACATATTCGAGATGTGGAGGTACAAGTGAAACTAAACCACTGAAACTGAAACCTAAAGCAACGAACCGTATAACCGTCTGCTTAACGCCCGTACAGGTTCGTATATTAAATATAAACTTGAATATAACAAACTGCACAAGTCCTAATCAGAGAGTAATCAGGTGAGGTACAAGTGAAATTAGTTATCGAGACGACTGACTTTCTCCGCGCTCTAATCAGC									
...GGGTTCAGGTGAAACTAAAGCAACTG	27	0	1	1.00	1	0	0	1	0	0
AATATACAAAACTGCACAAGT	23	1	1	1.00	1	0	0	0	0	0

Show Alignment With Reads

Anti-sense strand reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dvi(v1)	[scaffold_13042:2032720..2032835, 2032681..2032835]	[dvi_189]	AAGTGTATAAGCTCTACACCTCCATGTTCACTTTGATTTCGTTGACTTTCAGCTTTTGCTTGGCATATTGGCAGACGAAATGCGGGCATGTCCAAGACATATATTTTATTTTGAACTTATATGTTTTAGACGTGTTCAGGATTATGTCTCTCATTAGTCCACCTCCATGTTCACTTTAATCAATAGCTCGTGACTGAAAGAGGCCAGATTAGTCG
Sp5	[Unknown group 5653:9235, 9270..0]		AAG[illegible]
droEle1	[scf1180000302686:913647..914218:-]		[illegible]
droRho1	[scf1180003738085:264743..264888:-]		[illegible]
droTak1	[scf1180004133733:453270..453318:-]		AAGTGTA[illegible]

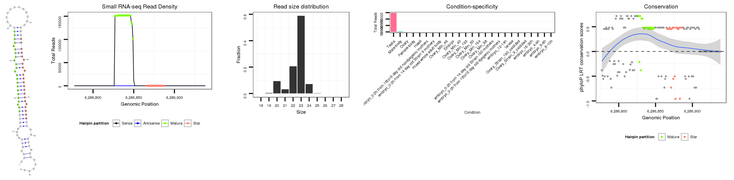
Generated: 09/08/2015 at 08:54 PM

	PASSFAIL
cvb.star	1
cvb.loop	1
cvb.mature	1
cvb.half	1
cvb.duplex	1
cvb.partdup	1
cvb.hairS	1
cvb.hairL	1
cvb.arm	1
cvb.flank	1
rescue.total	0
rescue.star	0
rescue.loop	0
rescue.mature	0
rescue.candidate	0

ID	Coordinate	Confidence	Class	Genome Locale	
dvi_197	**scaffold_12855:6286827-6286888 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser (Cured/Mdmr)]

Legend: Sense Antisense Mature Star

Predicted structure



Show Alternative Folds

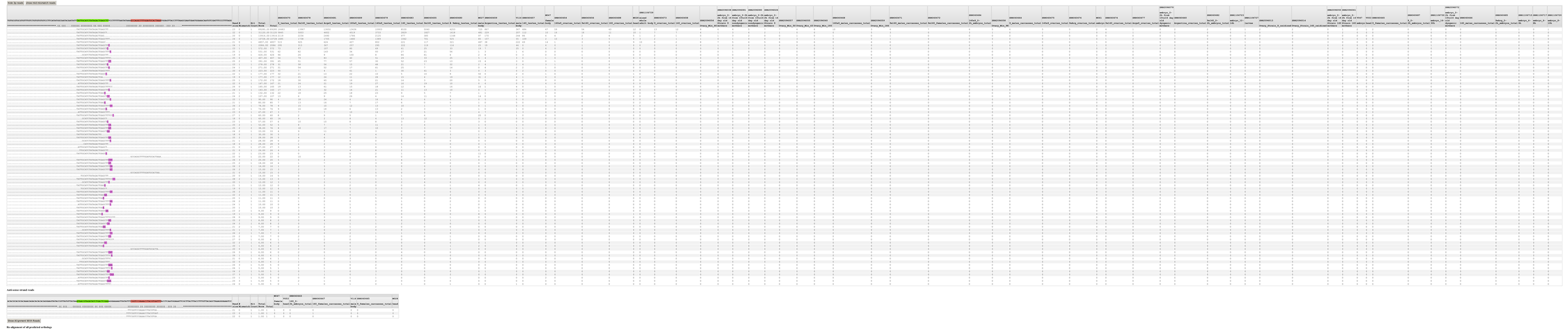
Flybase annotation

Antisense to dmel:FBrf0221628:vig

No flyanatlas cluster found

Sense Strand Reads

Hide Sp reads | Hide mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

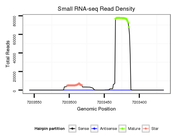
Species Coordinate	ID	Alignment
dmel|X:12855:+:12855:+:12855:+	dvi_197	
dsim|Scf_2L:2L:+:2L:+:2L:+	dsim_197	
dyak|Scf_2L:2L:+:2L:+:2L:+	dyak_197	
dvir|Scf_1:1:+:1:+:1:+	dvir_197	

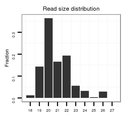
Generated 09/06/2025 at 08:04 PM

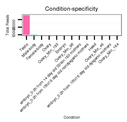
ID	Coordinate	Confidence	Class	Genome Locale	
dvi_23425	**scaffold_12963:7203415-7203507 -**	**Candidate**	**Unknown**	**antisense_to_intron**	[View on UCSC Genome Browser (Linear/Minus)]

Legend: [illegible]

Predicted structure







No conservation details.

Show Alternate Fields

Flybase annotation

Antisense to intron [FlyFAT:FBFO:adj intron [FlyFAT:FBGN:adj

No Repeatible element found

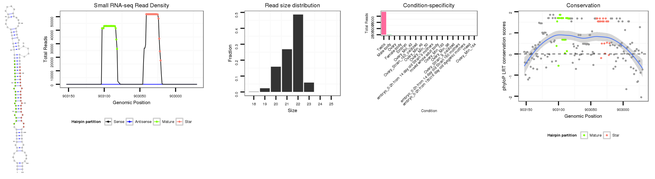
Sense Strand Reads

Hide 3p reads | show mid mismatch reads

| Read # | Size | Mismatch | Count | Nom | Total | Total | 28M00478 | 28M00481 | 28M00479 | 28M00480 | 28M00489 | 28M00470 | 28M00483 | 28M00455 | 28M00457 | 28M00459 | W1118 female body | W1118 male body | WGT 10Dsd female body | WGT 10Dsd male body | 28M00454 | 28M00468 | 28M00458 | 28M00471 | 28M00484 | 28M00477 | 28M00488 | 28M00514 | 28M00464 | 28M00454 | 28M00465 | 28M00460 | 28M00466 | 28M00472 | 28M00473 | 28M1104720 | 28M00469 | 28M00475 | 28M00476 | 28M00482 | 28M29450 | 28M29454 | 28M29453 | V103.WGS | 28M00465 | 28M00466 | 28M00474 | 28M00458 | 28M00487 | 28M29513 | 28M29438 | 28M29436 | 28M29441 | 28M29437 | 28M29439 | 28M29435 |
|---|---|---|---|---|---

ID	Coordinate	Confidence	Class	Genomic Locale
dvi_45	**scaffold_13042:903020-903103 -**	**confident**	**Testes-restricted**	**intergenic**
Legend: Stem 5p 3p Terminal Loop Internal Loop				Click on UCSC Genome Browser (Crash Mirror)

Predicted structure



Show Alternate Folds

Flybase annotation

mergem

No Repeatitle elements found

Sense Strand Reads

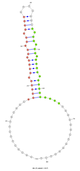
Hide Sp reads | Show mid mismatch reads

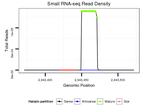
| Read # | Size | Mismatch | Count | Total | 28M04681 Argo1_testes_total | 28M04678 Ago2_testes_total | 28M04679 Ago3_testes_total | 28M04670 Piwi_testes_total | 28M04680 Rahu_testes_total | 28M04689 iCOA_testes_total | 28M04683 iKO_testes_total | 28M04685 Argonaute_testes_total | 28M04659 wild_testes_total | 28M04657 Female_body | 28M04656 male_body | 28M04673 Argo1_ovarian_total | 28M04677 Ago2_ovarian_total | 28M04671 Ago3_ovarian_total | 28M04654 Piwi_ovarian_total | 28M04668 iKO_ovarian_total | 28M04658 Argonaute_ovarian_total | 28M04655 wild_ovarian_total | 28M04688 iCOA_ovarian_total | 28M04675 Rahu_ovarian_total | 28M04676 Female_ovarian_total | 28M04674 male_ovarian_total | 28M04666 Argonaute_ovarian_total | 28M04684 iCOA_2- 2h_embryos_total | 28M04657 Female_2- 2h_embryos_total | 28M04655 male_2- 2h_embryos_total | 28M11167720 28M04687 mixed whole 0_2- 2h_embryos_total adult body | 28M29613 Piwi_2- 2h_embryos_total | 28M29462 28M29463 embryo_2- 4h_embryos_total Piwi_2- 4h_embryos_total | 28M29458 Argo1_2- 4h_embryos_total | 28M29460 Ago2_2- 4h_embryos_total | 28M1 Piwi_4h_embryos_total | 28M04672 Female_4h_embryos_total | 28M04662 male_4h_embryos_total | 28M29464 28M29465 embryo_6- 8h_embryos_total embryo_8-10h_embryos_total Piwi_6- 8h_embryos_total Piwi_8-10h_embryos_total | 28M04667 Ago2_6- 8h_embryos_total | 28M04669 Piwi_10-16h_embryos_total | 28M04664 Argo1_6- 8h_embryos_total | 28M29467 28M29466 embryo_10-16h_embryos_total Argonaute_embryo_total | 28M04665 Female_10-16h_embryos_total | 28M04663 male_10-16h_embryos_total | 28M29469 28M29468 Piwi_0-24h_adult_total Argonaute_ovarian_total | 28M29470 Female_adult_total | 28M29471 male_adult_total |
|---|---|---|---|---

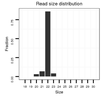
ID	Coordinate	Confidence	Class	Genome Locus
dvi_15 | scaffold_12855:2943421-2943472 +		confident	Canonical miRNA	CDS

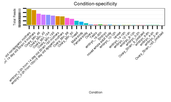
Legend: Mature Loop Star Miscellaneous

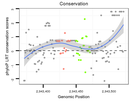
Predicted structure











Show Alternate Forms

Flybase annotation

CG40 [FlyCorEx/Flan.sq]

Ts Drosophila clarens Small

Some Strand Reads

Note: 3p reads show PAS mismatch reads

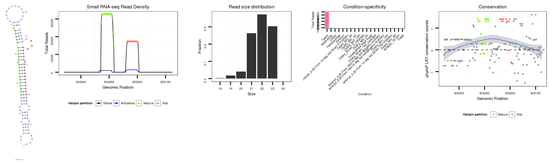
| Read # | Mrk | Total | Total | 3MM3T4G | 2MM3T5G | 2MM3T6G | 2MM3T8G | 2MM3T9G | 2MM3T10G | 2MM3T11G | 2MM3T12G | 2MM3T13G | 2MM3T14G | 2MM3T15G | 2MM3T16G | 2MM3T17G | 2MM3T18G | 2MM3T19G | 2MM3T20G | 2MM3T21G | 2MM3T22G | 2MM3T23G | 2MM3T24G | 2MM3T25G | 2MM3T26G | 2MM3T27G | 2MM3T28G | 2MM3T29G | 2MM3T30G | 2MM3T31G | 2MM3T32G | 2MM3T33G | 2MM3T34G | 2MM3T35G | 2MM3T36G | 2MM3T37G | 2MM3T38G | 2MM3T39G | 2MM3T40G | 2MM3T41G | 2MM3T42G | 2MM3T43G | 2MM3T44G | 2MM3T45G | 2MM3T46G | 2MM3T47G | 2MM3T48G | 2MM3T49G | 2MM3T50G | 2MM3T51G | 2MM3T52G | 2MM3T53G | 2MM3T54G | 2MM3T55G | 2MM3T56G | 2MM3T57G | 2MM3T58G | 2MM3T59G | 2MM3T60G | 2MM3T61G | 2MM3T62G | 2MM3T63G | 2MM3T64G | 2MM3T65G | 2MM3T66G | 2MM3T67G | 2MM3T68G | 2MM3T69G | 2MM3T70G | 2MM3T71G | 2MM3T72G | 2MM3T73G | 2MM3T74G | 2MM3T75G | 2MM3T76G | 2MM3T77G | 2MM3T78G | 2MM3T79G | 2MM3T80G | 2MM3T81G | 2MM3T82G | 2MM3T83G | 2MM3T84G | 2MM3T85G | 2MM3T86G | 2MM3T87G | 2MM3T88G | 2MM3T89G | 2MM3T90G | 2MM3T91G | 2MM3T92G | 2MM3T93G | 2MM3T94G | 2MM3T95G | 2MM3T96G | 2MM3T97G | 2MM3T98G | 2MM3T99G | 2MM3T100G | 2MM3T101G | 2MM3T102G | 2MM3T103G | 2MM3T104G | 2MM3T105G | 2MM3T106G | 2MM3T107G | 2MM3T108G | 2MM3T109G | 2MM3T110G | 2MM3T111G | 2MM3T112G | 2MM3T113G | 2MM3T114G | 2MM3T115G | 2MM3T116G | 2MM3T117G | 2MM3T118G | 2MM3T119G | 2MM3T120G | 2MM3T121G | 2MM3T122G | 2MM3T123G | 2MM3T124G | 2MM3T125G | 2MM3T126G | 2MM3T127G | 2MM3T128G | 2MM3T129G | 2MM3T130G | 2MM3T131G | 2MM3T132G | 2MM3T133G | 2MM3T134G | 2MM3T135G | 2MM3T136G | 2MM3T137G | 2MM3T138G | 2MM3T139G | 2MM3T140G | 2MM3T141G | 2MM3T142G | 2MM3T143G | 2MM3T144G | 2MM3T145G | 2MM3T146G | 2MM3T147G | 2MM3T148G | 2MM3T149G | 2MM3T150G |
|---|---|---|---|---

ID	Coordinate	Confidence	Class	Genome Locale
dvi_187	**scaffold_13042:903188-903280 -**	**confident**	**Totes-restricted**	**intergenic**

[View on UCSC Genome Browser (Local Mirror)]

Legend: Stem Loop Terminal Loop Mature Arm

Predicted structure



Show Alternate Folds

Fisher ensemble

Hairpin

No Repeatable stems found

Sense Strand Reads

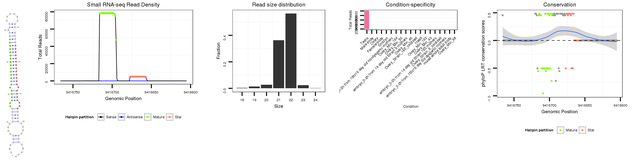
Hide Sp reads | Show read mismatch reads

| Read # | Strand | Total | Total | Scgr0_Vertex_total | Sscr0_Vertex_total | Lfish_Vertex_total | Ofish_Vertex_total | Ocin_Vertex_total | Ocin_Vertex_total | Ocin

ID	Coordinate	Confidence	Class	Genome Locale
dv1_40	**scaffold_12970:9416655-9416716** +	**confident**	**Testes-restricted**	**intergenic**

Source: **dme** in **Drosophila melanogaster** genome build

Predicted structure



Show Alternate Forms

Flybase annotation

intergenic

No Reputedly chimeric found

Sense Strand Reads

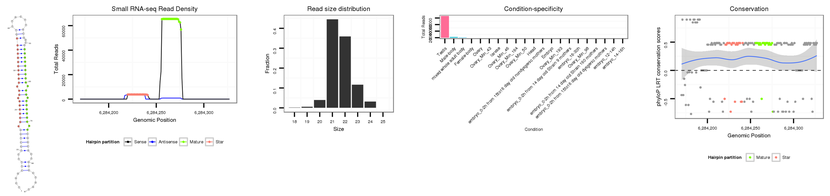
Order By reads show mid mismatch reads

| Read # | M/A | Total | Total | 28MD05081 | 28MD05079 | 28MD05059 | 28MD05079 | 28MD05070 | 28MD05057 | 28MD05080 | 28MD05055 | 28MD05089 | 28MD05083 | 28MD05058 | 28MD05073 | 28MD05074 | 28MD05060 | 28MD05054 | 28MD05077 | 28MD05056 | 28MD05072 | 28MD05076 | 28MD05075 | 28MD05090 28MD05091 webcyc_D-Dh from 15cut from 15cut day old day old | 28MD05088 | 28MD05087 15cut day old | 28MD05068 | 28MD05014 | 28MD05024 webcyc_D- 2h from 14 day old | 28MD05079 webcyc_D- 15cut day old | 28MD05092 webcyc_D- 15cut day old | 28MD05072 | 28MD05073 webcyc_D- 15cut day old | 28MD05033 | 28MD05071 | 28MD05098 28MD05081 webcyc_D- 2h from 14 Dh from 14 day old day old | 28MD05082 | 28MD05084 webcyc_D- 15cut day old | MOL | 28MD05064 | 28MD05084 15cut_D- 2h from 14 day old | 28MD05011 | 28MD05067 | 28MD05062 | 28MD05065 | 28MD05085 webcyc_D- 2h day old | 28MD05097 | 7047 | 28MD05062 | 28MD05063 | 28MD11475A mixed stage | 28MD05066 | MOUE | 28MD05069 | 28MD05068 |
|---|---|---|---|---

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_31	**scaffold_12855:6284220-6284277 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser (GenomUMtest)]

Legend: mature star mismatch in alignment mismatch in loop

Predicted structure



Show Alternate Fields

Flybase annotation

Antisense to intron [FlyAtlas2:FBGN:0]

No Repeatable elements found

Sense Strand Reads

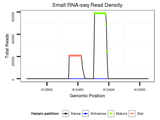
hide 2p reads show mid mismatch reads

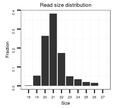
| Read # | Mismatch | Mismatch Count | Hit Num | Total Hits | Arga0_testes_total | 14Dsf_testes_total | 3_testes_total | 0hbrg_testes_total | 1Dsf_testes_total | 14D_testes_total | Argcelica_testes_total | which body | male body | female body | Ovary_Mix_43 | Ovary_Mix_44 | Ovary_Mix_144 | Ovary_Mix_192 | Ovary_Mix_193 | mothers | 0-2h from 15to16 day old mothers | 2h embryos total | 14Dsf_ovaries_total | 14D_ovaries_total | 0Dsf_ovaries_total | 0D_ovaries_total | 0Dsf_testes_total | 0D_testes_total | 0Dsf_females_testes_total | 0D_females_testes_total | 14Dsf_females_testes_total | 14D_females_testes_total | 0Dsf_females_testes_total | 0D_females_testes_total | 14Dsf_testes_total | 14D_testes_total | 0Dsf_testes_total | 0D_testes_total | 0hbrg_testes_total | 0Dsf_ovaries_total | 0D_ovaries_total | 14Dsf_ovaries_total | 14D_ovaries_total | 0Dsf_ovaries_total | 0D_ovaries_total | 0Dsf_ovaries_total | 0D_ovaries_total | 0Dsf_ovaries_total | 0

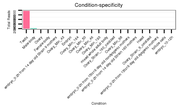
ID	Coordinate	Confidence	Class	Genome Locale	
chr_185	**scaffold_13042:912386-912483 -**	**confident**	**Textos-restricted**	**antisense_to_intron**	View on UCSC Genome Browser (Grand Hilton)

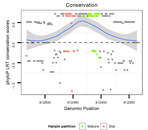
Legend: **Mature** **Star** **Antisense** **Antisense Mature** **Antisense Star**

Predicted structure









Show Alternate Folds

Fly base annotation

Antisense to intron [FlyBase:FBGN7 ng]

No Repeatmiller elements found

Genome	Gene
1	dm_dl: scaffold_13042:912386-912483
2	dm_dl: scaffold_13042:912386-912483

Sense Strand Reads

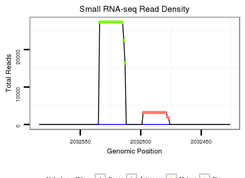
Hide 3p reads | Show mid mismatch reads

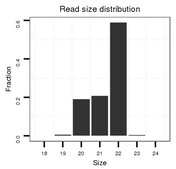
| Read ID | Strand | Mismatch | Count | Score | Total | 3p | 5p | 5p | 3p | 3p | 5p | 5p | 3p | 3p | 5p | 5p | 3p

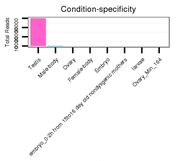
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_63	**scaffold_13042:2032476-2032534 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

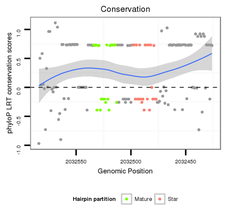
Legend: **miRNA** **Hairpin** **mismatch in alignment** **mismatch in miRNA**

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATTTGCTTAAATGAAGCTTTTATGCCCACAAATATTGGCAGCTGAATTGTGATCGCGTCTAAGACATATAAGTTTATACTTGACTTATATGCAGTAGATGTGATCGCGTTTCGTGCGAGCTCCAGTGCTCACCTCCATGTTCGTTGTG	Read #	Hit	Total	SRR060681 Arge9_testes_total	SRR060679 140x9_testes_total	SRR060678 9x140_testes_total	SRR060680 9xArg_testes_total	SRR060670 9_testes_total	SRR060689 160x9_testes_total	SRR060683 160_testes_total	SRR060655 9x160_testes_total	SRR060659 Argentina_testes_total	V116 male body	SRR060657 140_testes_total	M027 female body	SRR060658 140_ovaries_total	SRR060654 160x9_ovaries_total	SRR060688 160_ovaries_total	M047 female body	SRR060668 160x9_males_carcasses_total	SRR060677 Arge9_ovaries_total	SRR060656 9x160_ovaries_total	SRR060664 9x140_0-2h_males_carcasses_total	SRR060673 9_ovaries_total	SRR060674 9x140_ovaries_total	SRR060682 140x9_0-2h_embryos_total	SRR060684 140x9_0-2h_embryos_total	SRR060671 9x160_males_carcasses_total	SRR1106727 larvae	SRR2096059 Ovary_Min_144	SRR2096079 embryo_0-2h 13stx14 day old dyspanic mothers	SRR2096080 embryo_0-2h from 13stx14 day old nondyspanic mothers	SRR060666 embryo_160_males_carcasses_total	SRR060672 9x160_females_carcasses_total	SRR060665 9_females_carcasses_total
**********	size	Mismatch	Count	Norm	Total																															
...(((.(((((.(((((((((((.....(((((((.(((.....))).))))))).....))))))))))))))).))).)))....	24	0	1	16325.00	16325	4812	4441	3292	1167	347	624	476	268	53	160	53	10	1	0	5	2	3	0	2	3	0	0	1	0	1	0	0	0	0	0	0
.....TGATCGCGTCTAAGACATATAA.....	21	0	1	6053.00	6053	1699	1637	1104	436	349	293	221	137	54	58	51	9	2	1	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....TGATCGCGTCTAAGACATAT.....	20	0	1	4694.00	4694	1225	1165	622	350	350	287	304	151	90	48	87	7	3	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGATCGCGTCTAAGACATATA.....	24	0	1	2758.00	2758	800	815	657	188	188	136	111	53	35	56	68	32	1	2	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0
.....ATATGCAGTAGATGTGATCGCG.....	22	0	1	1647.00	1647	302	380	297	70	179	89	65	94	87	36	45	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0
.....ATATGCAGTAGATGTGATCGCGT.....	23	0	1	1136.00	1136	220	185	118	47	131	41	39	45	173	44	92	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGATCGCGTCTAAGACATATAAA.....	24	2	1	299.00	299	85	95	55	23	10	5	8	0	3	14	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATATGCAGTAGATGTGATCGC.....	21	0	1	254.00	254	56	43	47	13	27	20	7	4	15	4	6	10	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
.....TGATCGCGTCTAAGACATA.....	19	0	1	153.00	153	34	49	22	17	5	5	4	6	7	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....ATATGCAGTAGATGTGATCGCGT.....	23	0	1	104.00	104	20	22	13	3	3	4	11	5	5	3	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGATCGCGTCTAAGACATATA.....	22	1	1	83.00	83	30	13	14	7	3	2	4	5	1	3	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGATCGCGTCTAAGACATAT.....	22	0	1	52.00	52	10	17	11	4	3	1	2	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATATGCAGTAGATGTGATCGC.....	22	1	1	48.00	48	6	9	8	0	10	1	0	2	1	3	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGATCGCGTCTAAGACATATAAT.....	23	0	1	46.00	46	4	10	4	4	8	2	6	2	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGATCGCGTCTAAGACATATAG.....	22	1	1	42.00	42	7	3	7	3	16	3	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
.....TGATCGCGTCTAAGACATATAAAA.....	25	3	1	32.00	32	5	16	3	5	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATATGCAGTAGATGTGATCG.....	19	0	1	27.00	27	4	12	2	4	1	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
.....TGATCGCGTCTAAGACATATAG.....	20	1	1	25.00	25	5	9	2	6	1	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
.....TGATCGCGTCTAAGACATATG.....	22	1	1	25.00	25	6	3	4	2	2	4	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
.....TGATCGCGTCTAAGACATATAT.....	24	2	1	24.00	24	4	7	5	1	1	3	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGATCGCGTCTAAGACATATG.....	23	1	1	22.00	22	6	9	2	3	1	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGATCGCGTCTAAGACAT.....	18	0	1	19.00	19	3	11	0	4	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
.....TGATCGCGTCTAAGACATATG.....	21	1	1	18.00	18	3	1	1	0	0	5	0	3	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GCGTCTAAGACATATAG.....	18	1	1	15.00	15	1	2	0	0	0	7	0	0	4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GATCGCGTCTAAGACATATAG.....	21	0	1	14.00	14	2	4	1	1	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
.....TGATCGCGTCTAAGACATATAAG.....	23	1	1	11.00	11	3	3	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
.....ATATGCAGTAGATGTGATCGCGTAG.....	23	1	1	10.00	10	2	3	1	1	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
.....ATATGCAGTAGATGTGATCGTAG.....	21	1	1	10.00	10	4	4	1	0	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
.....ATATGCAGTAGATGTGATCGTAGT.....	21	1	1	9.00	9	1	2	1	0	1	0	0	1	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGATCGCGTCTAAGACATATAG.....	21	0	1	7.00	7	1	0	0	1	4	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
.....TATGCAGTAGATGTGATCGCGG.....	21	0	1	7.00	7	1	0	0	0	1	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
.....TGATCGCGTCTAAGACATATAATG.....	24	2	1	7.00	7	2	1	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
.....TGATCGCGTCTAAGACATATAATG.....	24	2	1	6.00	6	3	0	1	0	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
.....TGATCGCGTCTAAGACATATAGG.....	23	2	1	6.00	6	1	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
.....ATATGCAGTAGATGTGATCGCG.....	22	1	1	6.00	6	1	0	0	0	1	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATGCAGTAGATGTGATCGT.....	19	0	1	5.00	5	1	0	0	0	2	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
.....TGTGATCGCGTCTAAGACATA.....	21	0	1	5.00	5	1	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
.....TGATCGCGTCTAAGACATATA.....	19	0	1	5.00	5	0	1	1	0	1	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
.....TGATCGCGTCTAAGACATAA.....	22	2	1	5.00	5	0	1	0	0	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
.....ATCGCATAGATGTGATCGCGTT.....	22	0	1	5.00	5	1	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	0	0	0	0	0
.....ATATGCAGTAGATGTGAT.....	18	0	1	4.00	4	0	3	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
.....TATGCAGTAGATGTGATCGCGG.....	22	0	1	4.00	4	2	0	0	0	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
.....ATCGCGTCTAAGACATATAA.....	20	0	1	3.00	3	1	0	0	0	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
.....TGATCGCGTCTAAGACATATAG.....	23	2	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
.....TGATCGCGTCTAAGACATATGG.....	22	1	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
.....ATATGCAGTAGATGTGATCGCGT.....	22	1	1	3.00	3	0	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
.....ATGCAGTAGATGTGATCGCG.....	20	0	1	3.00	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
.....GATCGCGTCTAAGACATA.....	20	0	1	3.00	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
.....TGATCGCGTCTAAGACATATAAAA.....	25	3	1	3.00	3	0	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	0	0	0	0
.....TGATCGCGTCTAAGACATATG.....	21	0	1	3.00	3	0	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
.....TGATCGCGTCTAAGACATATAT.....	24	2	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
.....ATATGCAGTAGATGTGATCGCGT.....	23	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
.....ATATGCAGTAGATGTGATCGCGTTT.....	25	0	1	2.00	2	0	0	0	0	1	1	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
.....ATATGCAGTAGATGTGATCGCGTG.....	24	1	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	0	0	0	0	0	0	0
.....TGATCGCGTCTAAGACATATAAAG.....	25	3	1	2.00	2	0	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	0	0	0	0
.....TATGCAGTAGATGTGATCGCGG.....	22	1	1	2.00	2	1	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	0	0	0	0
.....ATATGCAGTAGATGTGATCGCGTT.....	22	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	0	0	0	0	0	0	0	0	0	0	0
.....ATATGCAGTAGATGTGATCGCGT.....	22	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	0	0	0	0	0	0	0	0	0	0	0
.....TTATATGCAGTAGATGTGATC.....	21	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	0	0	0	0	0	0	0	0	0	0	0
.....TGTGATCGCGTCTAAGACATA.....	23	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	0	0	0	0	0	0	0	0	0	0	0
.....TGATCGCGTCTAAGACATATATT.....	24	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	0	0	0	0	0	0	0	0	0	0	0
.....TGTGATCGCGTCTAAGACAT.....	20	0	1	2.00	2	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
.....TGATCGCGTCTAAGACATATATAA.....	24	0	1	2.00	2	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
.....TGATCGCGTCTAAGACAT.....	19	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
.....ATATGCAGTAGATGTGATC.....	19	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
.....TGATCGCGTCTAAGACATATAAAA.....	24	3	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
.....TGATCGCGTCTAAGACATATAG.....	25	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
.....ATGCAGTAGATGTGATCGCGT.....	22	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
.....TATGCAGTAGATGTGATCGCGTT.....	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	0	0	0	0	0	0	0	0	0	0	0
.....GATCGCGTCTAAGACATAT.....	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
.....TGATCGCGTCTAAGACATATAAG.....	25	3	1	1.00	1	0	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
.....TGATCGCGTCTAAGACATATG.....	20	2	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
.....AATATATGCAGCTGAATTG.....	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	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

TAAAACGAATTTACTTCGAAAATACGGGTGTTTATAACCGTCGACTTAACACTAGCGCAGATTCTGTATATTAAATATGAACTGAATATACGTCATCTACACTAGCGCAAAGCAGCGTCGAGGTACGAGTCTAACCCGAGTGGAGGTACAAGCAAACAC	Read #	Hit	Total	SRR060675 female body 140x9_ovaries_total	SRR2096058 male body Ovary_Min_98	SRR2096060 Ovary_Min_193	V116	SRR060664 9_males_carcasses_total	SRR060666 160_males_carcasses_total
**********	size	Mismatch	Count	Norm	Total				
...(((.(((((.(((((((((((.....(((((((.(((.....))).))))))).....))))))))))))))).))).)))....	24	0	1	4812	4812	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species Coordinate	ID	Alignment
DroYi3 scaffold_13042:2032426-2032534-	dvi_63	ATT--TTTGCTTAAATGAAGCTTTTATGCCCACAAATATTGGCAGCTGAATTGTGATCGCGTCTAAGACATATAAGTTTATACTTGACTTATATGCAGTAGATGTGATCGCGTTTCGTGCGAGCTCCAGTGCTCACCTCCATGTTCG----------TTTGTG
DroGri2 scaffold_15245:3115683-3115800-		AT--TTTGCTTAATGTGAAGCT**----------**
DroMel2 chr2L:14000000045111:5133930:-5133993:-1		AC--TTTGT**----------**
DroBip1 scaffold0003987351:1679081-1679148:-1		ATG-TCATC**-----TTTGTTAACTCCATCTCACTTCTCCT**********----------**
DroFic1 scaffold0004540721:117410:-117473:-		G--CA**-----GTATGTACCACA**********----------**
DroNoa1 scaffold0007398517:5367:-5432:-		G--TTGAGCCCCCGAAGAGAG**********TATTGCGGCAACCCTACCATATCGCTGTAGGCGGTAGCATAATCTAGTGTGATGTCTTAAAATTGTGTC**********GGGGCAAAAACACCACCCCACCAACTTGTTGTTCTTGTG
DroTak1 scaffold0004154483:458:435:-1		ATA-TTGCCCAAGCGCCCCGTCGTCCAAATAT**----------**

Generated 09/08/2015 at 08:56 PM

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cr3.stop	0
cr3.loop	0
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cr3.half	0
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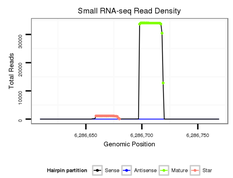
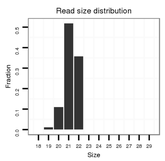
cr3.arm	0
rescue.loop	0
rescue.stem	0
rescue.dominant	0
rescue.recessive	0
rescue.confident	0
rescue.candidate	0

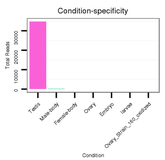
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_77	**scaffold_12855:6286659-6286719 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser (Cosmil Mirror)]

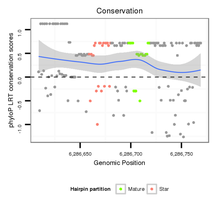
Legend: **Sense** **Star** **mismatch in alignment** **mismatch in star**

Predicted structure









Show Alternate Folds

Flybase annotation

Antisense to intron [Dvir/GI10228-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read # size	Mismatch	Count	Hit Score	Total Score	Total	SRR060681 Arge3_testes_total	SRR060678 9x140_testes_total	SRR060679 140x9_testes_total	SRR060680 9Arg_testes_total	SRR060689 160x9_testes_total	SRR060670 9_testes_total	SRR060683 140_testes_total	SRR060655 9x160_testes_total	SRR060657 160_testes_total	SRR060659 Argentina_testes_total	V116 female	M047 male body	M027 male body	SRR060654 160x9_ovaries_total	SRR060671 9x160_males_carcasses_total	SRR060658 140_ovaries_total	SRR060668 160x9_males_carcasses_total	SRR060656 9x160_ovaries_total	SRR060673 9_ovaries_total	SRR060676 9Arg_ovaries_total	SRR060684 2h_embryos_total	SRR060682 embryo-2h	M061 140x9_0-9x140_0-	SRR060688 160_ovaries_total	SRR1106729 mixed whole adult body	SRR2096014 Ovary_Strain_160_sexBiased	SRR060664 9_males_carcasses_total	SRR060666 160_males_carcasses_total	SRR060667 160_females_carcasses_total	SRR060672 9x160_females_carcasses_total	SRR060674 9x140_ovaries_total	SRR060677 Arge9_ovaries_total	SRR060685 2h_embryos_total	SRR1106727 larvae	SRR2096080 embryo_0-2h from 15to16 day old nondygenic mothers	Ovary_Mis_133
21	0	1	17551.00	17551	4846	4338	2859	2147	1154	1029	635	397	24	11	74	12	0	8	3	1	3	1	0	1	1	1	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0
22	0	1	12470.00	12470	3989	3863	2341	1332	366	366	250	140	121	10	0	26	15	2	1	2	3	0	0	1	2	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
20	0	1	3218.00	3218	776	580	458	296	421	241	227	171	7	10	18	7	0	0	1	0	0	2	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	1	1	543.00	543	153	180	122	56	13	8	5	4	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
20	0	1	534.00	534	10	27	34	4	24	34	11	28	159	165	20	1	16	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	320.00	320	5	13	7	0	10	13	8	15	157	80	12	0	0	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	299.00	299	48	56	61	29	31	18	37	11	1	5	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
21	0	1	286.00	286	95	75	51	39	8	4	2	3	2	5	0	1	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
20	1	1	249.00	249	0	0	0	0	4	17	6	5	89	127	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
22	1	1	215.00	215	57	45	45	47	27	4	7	1	3	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
22	1	1	167.00	167	57	36	24	27	7	9	3	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
23	2	1	104.00	104	36	23	21	9	4	5	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
21	1	1	98.00	98	24	20	17	13	6	10	5	1	0	0	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
20	0	1	92.00	92	22	24	20	9	3	7	2	1	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
22	1	1	74.00	74	3	4	3	1	2	10	1	10	0	16	21	0	1	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	0	1	73.00	73	0	1	1	0	0	2	1	0	39	22	4	0	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
22	2	1	55.00	55	16	9	12	4	5	3	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
21	1	1	54.00	54	1	1	3	1	10	31	8	15	0	0	0	0	0	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	52.00	52	1	4	4	0	2	5	4	3	7	20	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
22	0	1	48.00	48	17	8	18	5	0	0	0	0	0	0	0	0	0	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	46.00	46	14	20	8	2	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
20	1	1	37.00	37	1	1	0	2	9	13	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
23	1	1	36.00	36	13	11	3	5	0	3	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
22	1	1	36.00	36	12	10	8	5	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
21	1	1	33.00	33	11	3	2	5	4	4	3	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
24	2	1	32.00	32	14	7	8	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
23	2	1	30.00	30	6	7	9	5	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	0	0	0
18	0	1	27.00	27	0	5	5	2	0	0	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
19	0	1	25.00	25	0	2	0	1	2	6	1	2	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
20	0	1	23.00	23	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
20	1	1	20.00	20	1	0	0	0	0	3	0	4	2	4	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
22	1	1	19.00	19	0	1	2	0	0	0	0	0	0	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
21	0	1	19.00	19	0	4	3	0	1	3	2	0	0	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
20	1	1	17.00	17	0	5	2	1	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	0	0
23	3	1	16.00	14	1	5	2	1	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
21	3	1	13.00	13	2	5	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
28	0	1	12.00	12	3	4	1	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
23	3	2	12.00	24	5	10	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

Anti-sense strand reads

hide 3p reads show mid mismatch reads

Read # size	Mismatch	Count	Hit Score	Total Score	Total	SRR2094059	SRR2094080 embryo_0-2h from 15to16 day old nondygenic mothers	Ovary_Mis_133

Show Alignment With Reads

Re-alignment of all predicted orthologs

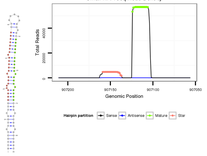
Species	Coordinate	ID	Alignment
drePV1-3	scaffold_12855:6286659-6286719:-	dvi_77	CGTCAATTTGTAATTTGATTTATTTTTTTATTTTGTGCTTTTGCAGTTTGAGCGTCGGTTGGTGTTTGCTTGTCCGTGCACTTGATAAGCCAACAAACGCTTAAATTTACAAATGCCCAGTCGCCAGCGTCGATGATATATAGTGAA
droMoj3	scaffold_4540:1634573:-1634716 +	dmo_3127	CGTCAATTTGTAATTTGATTTATTTTTTATTTTGTGCTTTTGCAGTTTGAGCGTCGGTTGGTGTTTGCTTGTCCGTGCACTTGATAAGCCAACAAACGCTTAAATTTACAAATGCCCAGTCGCCAGCGTCGATGATATATAGTGAA
droVir2	scaffold_14924:7391720:-7394719 +		[illegible]
droGri1	scaffold_8800084:1341947925:-1342985 +		[illegible]

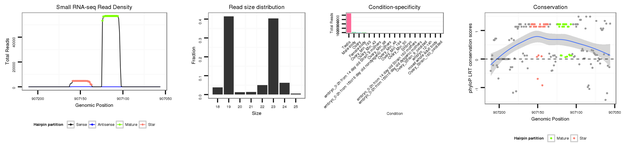
Generated: 09/09/2015 at 08:56 PM

ID	Coordinate	Confidence	Class	Genomic Locale	
dvi_343	**scaffold_13042:907106-907161 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser (Crandl/Mitsui)]

Layers: Sense Antisense Mature Star Hairpin Arms

Predicted structure





Show Alternate Folds

Flybase annotation

Antisense to intron [FlyAS:FBGN?.na]

No Repeatable elements found

Sense Strand Reads

hide 5p reads show red mismatch reads

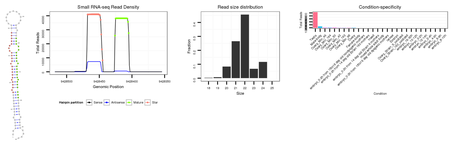
Read #	Mismatch	Count	Strand	Total	0610678	0610681	0610679	0610675	0610685	0610687	0610659	0610663	0610689	0610655	0610684	0610674	0610658	0610664	0610683	0610656	0610691	0610673	0610694	0610672	0610693	0610690	0610686	0610688	0610671	0610672	0610682	0610692	0610665	0610680	0610687	0610662	0610661	0610663	0610664	0610668	0610675	0610659	0610665	0610669	0610683	0610673	0610680	0610683	0610684	0610664	0610662	0610661	0610663
TTATCGATACGACATCGTACATCGATTGATTGATTGCAACATTCCTCTTCATTTTCGCAACTTCCTTCAATTCTCTTCTTCATTTTCGAGCAACTTCTTCTCGCTCATTCGATTCGATTTTCTTCGATTCGATTCGAT

ID	Coordinate	Confidence	Type	Genomic Locus
dvi_198_scaffold_12970:9428404-9428468	-	**confident**	**Trans-enriched**	**antisense_to_intron**

View on UCSC Genome Browser (Grail/Bibiser)

Strand: **Sense** **Antisense** **Both**

Predicted structure



No conservation details

Show Alternative Folds

Flybase annotation

Indicator is: dmel:FBGN0039445 ug

No Repeatitis Genome Trait

Sense Strand Reads

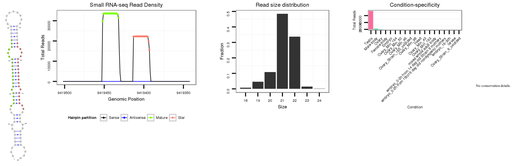
Scale Up Height Allow Hint Overlapping Reads

| Read Seq | Strand | Hits | Total Frequency | Dmel:FBgn0039445_Exon:Intron_Intron | Dmel:FBgn0039445_Exon:Exon_Intron | Dmel:FBgn0039445_Exon:Intron_Exon | Dmel:FBgn0039445_Exon:Exon_Exon | Dmel:FBgn0039445_Intron:Intron_Intron | Dmel:FBgn0039445_Intron:Exon_Intron | Dmel:FBgn0039445_Intron:Intron_Exon | Dmel:FBgn0039445_Intron:Exon_Exon

ID	Coordinate	Confidence	Class	Genome Locale
dvi_36	**scaffold_12970:9419392-9419452** +	**confident**	**Testes-restricted**	**intergenic**

Legend: **Mature** **Star** **Reads with mismatch** **Mismatches**

Predicted structure



No conservation details.

Show Alternate Folds

Flybase annotation

intergenic

No Repeatitis elements found

Sense Strand Reads

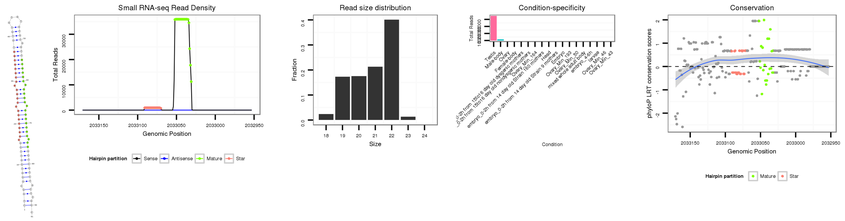
Sort by reads | show mismatch reads

| Read # | Hit. Mismatch | Total Count | Total Norm | 2R0004679 Tcf42_testes_total | 2R0004681 Arpt4_testes_total | 2R0004679 10Ub4_testes_total | 2R0004670 Tcf4_testes_total | 2R0004669 10Ub4_testes_total | 2R0004680 Bebog_testes_total | 2R0004655 Tcf20_testes_total | 2R0004659 Argonte_testes_total | 2R0004658 10Ub_testes_total | 2R0004657 10_testes_total | V116 Bebog testes body | WGT Female testes body | 2R0004674 Bebog_ovarian_total | 2R0004656 Tcf20_ovarian_total | 2R0004654 10Ub4_ovarian_total | 2R0004688 10_ovarian_total | 2R0004673 Tcf20_ovarian_total | 2R0004658 10_ovarian_total | 2R0004672 10Ub_ovarian_total | 2R0004675 Argonte_ovarian_total | 2R0004677 Tcf4_ovarian_total | 2R0004657 Ovary_Mix_18 | 2R0004658 Ovary_Mix_24 | 2R0004656 Ovary_Mix_41 | 2R0004654 Ovary_Mix_120 | 2R0004688 Ovary_Mix_125 | 2R0004674 Ovary_Mix_135 | 2R0004673 Ovary_Mix_138 | 2R0004672 Ovary_Mix_139 | 2R0004684 10ub4 P-ovary | MOEL Bebog | YOS2 2R0004660 Argonte_ovarian | 2R0004659 Argonte P-ovary | 2R0004662 Tcf20_female_carcasses_total | 2R0004672 Tcf20_female_carcasses | 2R0004613 Ovary_Stress_5_validated | 2R0104729 mixed whole adult body | WGS5 WGS7 | 2R0004662 Bebog P-ovary | 2R0004663 L2 P-ovary | 2R0004660 Argonte P-ovary | 2R0004686 Argonte P-ovary | 2R0004662 2R0004663 2R0004660 2R0004686 mebcyc_P-ovary 2h Zoom L4 Zoom L4 from 2Zoom mebcyc_2-2h day old day old day old day old mature mature mature mature | 2R0004664 2R0004666 2R0004671 2R0004665 2R0104757 2R0104758

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_190	**scaffold_13042:2033003-2033121 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Control Mmus)]

Legend: Sense Sense Antisense Antisense Mature Mature Star Star Mismatch in alignment Mismatch in star

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

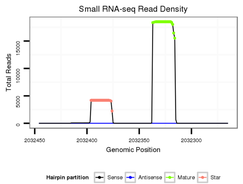
hide 3p reads show mid mismatch reads

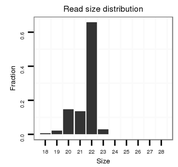
| Read # | size | M1 | Mismatch Count | Total Nuce | Total | SRR040679 | SRR040678 | SRR040681 | SRR040670 | SRR040669 | SRR040680 | SRR040655 | SRR040659 | SRR040683 | SRR040657 | V116 | M27 female body | SRR040658 | SRR2094072 embryo_0-15hr16 day old ovaries | SRR2094059 Ovary_Mix_164 | SRR2094080 embryo_0-2h from 15hr16 day old nondypgenic mothers | SRR2094056 Ovary_Mix_2 | SRR2094050 embryo_2-4h from 15hr16 day old mothers | SRR2094054 male body | SRR2094079 embryo_0-15hr16 day old dypgenic mothers | SRR2094081 embryo_0-2h from 15hr16 day old nondypgenic mothers | SRR040684 140w9_0-2h_embryos_total | SRR1104729 mixed whole adult body | SRR040677 Arga9_testes_total | SRR2094038 embryo_0-2h from 14 day old mothers | SRR2094057 Ovary_Mix_50 | SRR2094060 Ovary_Mix_193 | SRR2094041 embryo_0-2h from 14 day old Strain 160 mothers | SRR040673 9_ovaries_total | SRR040674 | SRR2094024 embryo_0-2h from 14 day old Strain 9 mothers | SRR1104728 larvae | SRR2094056 Ovary_Mix_46 | SRR040660 Argentina_ovaries_total | SRR040676 9akrg_ovaries_total | SRR040686 Arga9_0-2h_embryos_total | SRR1104715 embryo_4-6h | SRR1104716 embryo_6-8h | SRR2094055 Ovary_Mix_43 | V047 embryos head | V053 |
|---|---|---|---|---|---

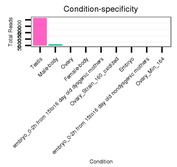
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_44	**scaffold_13042:2032315-2032396 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

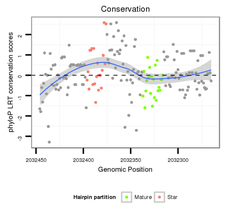
Legend: sense siRNA mismatch to alignment mismatch to miRNA

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
TTAA	Simple_repeat	Simple_repeat	+

Sense Strand Reads

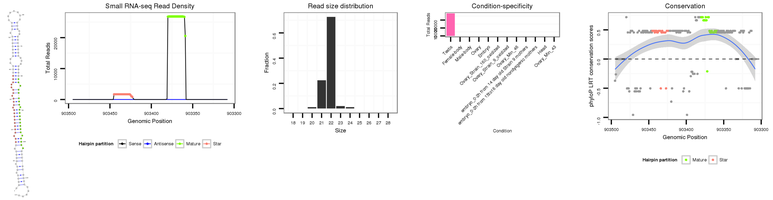
hide 3p reads | show mrd mismatch reads

| | | |

ID:	Coordinate:	Confidence:	Class:	Genome Locale:	
dvi_110	**scaffold_13042:903358-903445 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser [GeneID,Mirbase]]

Legend: mature star mismatch to the mature mismatch to star

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

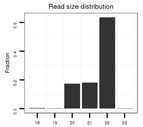
Hide 3p reads show mid mismatch reads

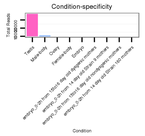
Read #	Wt	Total	SRR060481	SRR060478	SRR060479	SRR060480	SRR060469	SRR060470	SRR060483	SRR060455	SRR060459	SRR060457	M047 female body	V116 male body	SRR060477	SRR060454	SRR060475	SRR296013	SRR060464	SRR060471	SRR060484	SRR060456	SRR296014	SRR060488	W027	SRR060468	SRR060474	SRR060482	SRR060465	SRR060473	SRR060476	SRR296026	W041	SRR060463	SRR060458	SRR060469	SRR060472	SRR060467	SRR296038	SRR296080	SRR296081
size	Mismatch	Count	Norm	Total	Arga9_testes_total	Del40_testes_total	140e9_testes_total	8_bakcg_testes_total	140e6_testes_total	9_testes_total	140_testes_total	Del60_testes_total	Argentina_testes_total	140_testes_total	Arga9_ovaries_total	140e9_ovaries_total	140e9_females_carcasses_total	Ovary_Strain_9_unidiscd	9_males_carcasses_total	Del40_males_carcasses_total	140e9_9_embryos_total	Del40_ovaries_total	Ovary_Strain_140_unidiscd	140_ovaries_total	male body	140e9_males_carcasses_total	Del40_ovaries_total	male body	Del40_0-2h_embryos_total	bakcg_0-2h_embryos_total	9_ovaries_total	bakcg_ovaries_total	embryo_0-2h from 14 day old mutant mutbase	embryo_0-2h from 15to16 day old mutant mutbase	Ovary_Mix_45	embryo_9_females_carcasses_total	140_ovaries_total	140e9_females_carcasses_total	Del40_females_carcasses_total	9_0-2h_embryos_total	embryo_0-2h from 15to16 day old mutant mutbase	embryo_0-2h from 15to16 day old mutant mutbase	Ovary_Mix_41	mutbase	mutbase	mutbase
22	0	1	20445.00	20445	6810	5468	4064	1845	750	429	388	282	45	19	42	13	9	5	4	4	5	2	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	0	1	4000.00	4000	1054	1245	1163	420	494	424	323	146	52	28	10	12	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
25	1	1	1593.00	1593	314	282	161	78	82	72	59	35	5	0	0	5	0	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	690.00	690	185	171	124	47	45	40	32	14	4	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
23	0	1	482.00	482	133	140	112	42	17	17	10	3	4	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
21	0	1	455.00	455	92	133	91	26	15	13	8	11	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
24	0	1	334.00	334	97	120	56	19	13	17	10	4	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
23	0	1	278.00	278	54	45	44	15	16	11	27	11	24	45	0	0	0	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	148.00	148	43	37	29	4	11	12	8	3	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
22	0	1	121.00	121	22	48	24	7	2	3	3	3	5	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
26	2	1	115.00	115	38	20	9	10	7	8	13	6	1	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
23	1	1	101.00	101	36	29	15	9	2	4	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
23	2	1	100.00	100	17	18	22	4	10	14	8	3	2	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
29	0	1	96.00	96	38	25	14	4	4	5	5	3	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
24	1	1	75.00	75	29	13	14	4	4	5	3	3	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	68.00	68	17	15	10	4	4	1	3	13	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
20	0	1	53.00	53	14	5	5	3	11	2	1	3	1	1	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
25	0	1	43.00	43	9	11	13	3	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
22	0	1	36.00	36	10	8	9	4	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	0	0
22	1	1	31.00	31	5	9	5	1	13	11	6	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
24	2	1	31.00	31	13	4	5	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
21	0	1	30.00	30	5	6	5	1	1	1	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
23	0	1	30.00	30	5	4	5	1	1	1	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
23	0	1	28.00	28	7	4	1	2	4	4	1	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
19	0	1	27.00	27	3	4	2	1	1	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	0
21	0	1	20.00	20	6	3	2	1	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
21	0	1	19.00	19	4	2	4	1	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
23	1	1	16.00	16	5	5	3	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
23	0	1	14.00	14	6	1	1	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
19	0	1	14.00	14	4	1	1	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
24	0	1	13.00	13	4	1	1	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
21	1	1	12.00	12	3	4	1	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
23	1	1	12.00	12	2	2	1	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
28	3	1	12.00	12	6	3	1	0	1	2	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
24	1	1	11.00	11	1	3	1	1	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
19	0	1	11.00	11	1	3	1	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
27	0	1	10.00	10	1	3	1	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
21	0	1	8.00	8	1	3	1	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
22	0	1	7.00	7	1	3	1	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
22	0	1	7.00	7	1	3	1	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
21	0	1	7.00	7	1	3	1	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
20	0	1	7.00	7	1	3	1	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
20	0	1	7.00	7	1	3	1	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
23	1	1	6.00	6	1	2	1	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
24	0	1	6.00	6	1	2	1	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
24	1	1	6.00	6	1	2	1	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
22	2	1	6.00	6	1	2	1	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
22	1	1	5.00	5	1	2	1	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
28	1	1	5.00	5	1	2	1	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
24	3	1	5.00	5	1	2	1	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
22	1	1	5.00	5	1	2	1	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
26	2	1	4.00	4	1	2	1	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
22	1	1	3.00	3	1	2	1	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
22	1	1	3.00	3	1	2	1	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
25	1	1	3.00	3	1	2	1	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
24	1	1	3.00	3	1	2	1	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
21	1	1	2.00	2	1	2	1	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
21	1	1	2.00	2	1	2	1	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
25	1	1	2.00	2	1	2	1	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
23	1	1	2.00	2	1	2	1	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
24

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_43	**scaffold_12723:4641314-4641373 -**	**confident**	**Testes-restricted**	**intergenic**
				[View on UCSC Genome Browser (GenoB Mirror)]

Legend: sense, star, mismatch to sense, mismatch to star

Predicted structure





No conservation details.

Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

matures	star
1. dvi_43 scaffold_12723:4641352:4641373 - 2. dvi_18 scaffold_2596:1529969:1529986 +	

Sense Strand Reads

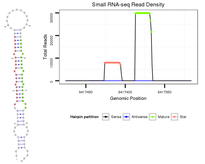
Hide 3p reads | Show mid mismatch reads

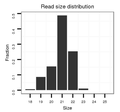
| Read # | Size | Mismatch | Count | Hit | Total | Total | SRR040678 | SRR040681 | SRR040679 | SRR040670 | SRR040655 | SRR040689 | SRR040690 | SRR040683 | V116 | SRR040657 | SRR040659 | M47 female adult | SRR040672 embryo_0-2h from 0-24 day old dgenic mothers | SRR040656 | SRR040658 | SRR040679 embryo_0-2h from 0-24 day old dgenic mothers | SRR040673 | SRR209638 embryo_0- 2h from 0-24 day old Strain 9 mothers | SRR209690 embryo_0-2h from 0-24 day old nondgenic mothers | V947 | M27 female adult | SRR040676 | SRR040626 embryo_0- 2h from 0-24 day old Strain 9 mothers | SRR040614 | SRR040688 | SRR040674 | SRR040654 | SRR040677 | SRR209081 embryo_0-2h from 0-24 day old nondgenic mothers | SRR040671 | SRR040684 | SRR209045 embryo_0- 2h from 0-24 day old Strain 160 mothers | SRR040660 | SRR040668 | SRR040672 | SRR040687 | SRR040661 | SRR040664 | SRR040675 | SRR040682 | SRR040685 | SRR040686 | SRR209014 | SRR209050 embryo_0- 2h from 0-24 day old Strain 160 head | V953 | W628 | SRR209045 |
|---|---|---|---|---

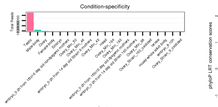
ID	Coordinate	Confidence	Class	Genome Locale
dvi_32	**scaffold_12970:9417366-9417426** +	**confident**	**Testes-restricted**	**Intergenic**

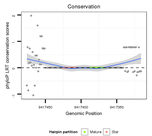
Legend: **Mature** **Star** **Sense** **Antisense** **Hairpin loop**

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

No Repeats chosen /Lost

Sense Strand Reads

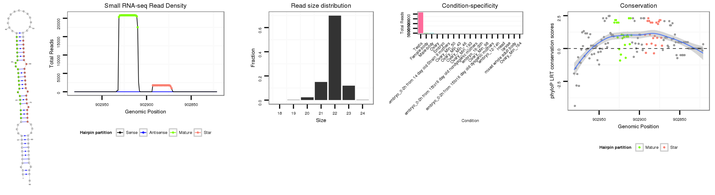
Sort By reads show mismatch reads

Read #	Dir	Total	2R:8455678	2R:8554561	2R:8554570	2R:8554629	2R:8554679	2R:8554690	2R:8554855	2R:8554857	2R:8554863	2L:14	2R:8554889	MOF	2R:8554928	2R:8554976	2R:8554984	2R:8554975	2R:8554973	MOL	2R:8554954	2R:8554960	2R:8554977	2R:8554988	2R:8554994	2R:8554993	2R:8554992	2R:8554990	2R:8554974	2R:8554958	2R:8554959	2R:8554956	2R:8554957	2R:8554961	2R:8554987	2R:8554986	2R:8554979	2R:8554980	2R:8554981	2R:8554982	2R:8554972	2R:8554962	2R:8554966	2R:8554968	2L:15729	2R:8554963	2R:8554964	2R:8554965	2R:8554973	2R:8554967	2R:8554971	2R:8554995	2R:15725	2R:15727
size	Mismatch	Count	Norm	Total	Drosophila_melanogaster_Testes_total	Argos9_testes_total	B_testes_total	Argentina_testes_total	18S4_testes_total	B_Dubg_testes_total	Ro30_testes_total	18S_testes_total	18S_testes_total	mela	18S4_testes_total	mela	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	mebrys	18S4_testes_total	Argentina_testes_total	18S_testes_total	Argos9_testes_total	18S_testes_total	18S_testes_total	Dubg_testes_total	Ro30_testes_total	18S4_testes_total	18S_testes_total	18S_testes_total	mebrys	18S4_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	18S_testes_total	larvae
21	0	14476.00	14476	1973	2373	2370	2949	1327	419	440	1473	417	562	420	219	18	25																																												
21	0	5101.00	5101	695	836	834	1039	468	148	155	519	147	198	148	77	6	9	1																																											
21	0	5101.00	5101	695	836	834	1039	468	148	155	519	147	198	148	77	6	9	1																																											
21	0	3976.00	3976	1345	1122	72	8	884	406	32	5	14	1	32	4	10	0																																												
21	0	2622.00	2622	908	704	34	6	517	268	17	1	9	1	24	1	12	18	0																																											
21	0	925.00	925	115	145	145	182	56	53	36	64	37	38	18	7	1	0																																												
21	0	370.00	370	87	86	8	1	33	15	2	0	1	0	2	0

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_76	**scaffold_13042:902871-902931 -**	**confident**	**Testes-restricted**	**intergenic**
				[View on UCSC Genome Browser (ConfidMmm)]

Legend: **Dicer** **Ago** **Dicer/Ago in Ovary** **mismatch/nt**

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

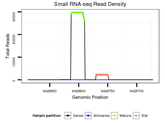
Hide 3p reads | Show mm mismatch reads

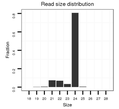
Sequence					SRR040478	SRR040481	SRR040479	SRR040480	SRR040470	SRR040469	SRR040483	SRR040455	W147 Female	SRR040459	V116	W127	SRR040457	SRR2094055	SRR2094057	W041	SRR040471	SRR2094024 embryo_0-2h from 14.0h embryo_2-4h from 14.0h day old adult male mothers	SRR2094039 embryo_0-2h from 14.0h embryo_2-4h from 14.0h day old adult male mothers	SRR040468	SRR2094056	SRR040464	SRR040477	SRR040454	SRR040472	SRR1106720 mixed whole body	SRR040467	SRR040473	SRR2094040	SRR040474	SRR040484 14wb_0-2h embryos	SRR2094041 embryo_0-2h from 15hr14.5V147 day old adult male mothers	SRR040475	SRR040469	SRR1106730 embryo_16-24h	SRR2094078 embryo_0-2h from 15hr14.5V147 day old adult male mothers	SRR2094081 embryo_0-2h from 15hr14.5V147 day old adult male mothers	SRR040465	SRR040456	SRR040466	SRR040476	SRR040467	V153	SRR040469	SRR040482	SRR040485	SRR1106724	SRR2094050 embryo_0-2h from 14 day old adult male mothers
TCCGGAGACGATGATTCTTGGATGATAACCCATGTGTCCACTTAACCTCATTGTCCGCATCGAACTCAGCTTCAATTCTTTTTCAA					Del40_testes_total	Argo8_testes_total	16Dv8_testes_total	Bxbq_testes_total	1_testes_total	10Dv8_testes_total	16D_testes_total	Del40_testes_total	Female Argentina_testes_total	male body	male 16D_testes_total body	male 16D_testes_total body		Ovary_Mix_49	Ovary_Mix_50	embryo	Del40_males_carcasses_total	0-2h from 14.0h embryo day old adult male mothers	2-4h from 14.0h embryo day old adult male mothers	10Dv8_males_carcasses_total	Ovary_Mix_46	8_males_carcasses_total	Argo8_ovaries_total	10Dv8_ovaries_total	Del40_females_carcasses_total	whole body	10D_females_carcasses_total	9_ovaries_total	Ovary_Mix_38	Del40_ovaries_total	2h_embryos_total	mothers	0-2h from 15hr14.5V147 day old adult male mothers	16-24h from 15hr14.5V147 day old adult male mothers	10Dv8_ovaries_total	10D_ovaries_total	30h	Ovary_Mix_38	mothers	3_females_carcasses_total	Del40_males_carcasses_total	Bxbq_ovaries_total	3_embryos_total	head	16Dv8_females_carcasses_total	Del40_ovaries_total	3_embryos_total	15h	Larvae	mothers	Ovary_Mix_164
**********	22	0	1	14495.00	14495	4724	4047	3420	1125	333	372	243	144	84	14	21	6	24	4	5	8	13	6	0	6	4	0	5	1	5	0	0	0	1	0	2	0	1	2	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GACTCGATTCCTCCTGTCAC	21	0	1	7913.00	7913	1915	2535	1373	826	200	199	128	112	67	10	29	83	0	16	0	3	1	2	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	0
....GACTCGATTCCTCCTGTCACA	21	0	1	2731.00	2731	676	704	629	240	65	152	78	47	49	5	13	1	6	0	3	1	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	0	0	0	0
....GACTCGATTCCTCCTGTCGCA	22	0	1	1024.00	1024	1	256	256	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GACTCGATTCCTCCTGTCGCAC	22	0	1	722.00	722	128	163	157	37	153	8	24	49	51	27	37	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
....GACTCGATTCCTCCTGTCACT	21	0	1	469.00	469	115	111	72	41	44	6	7	19	3	38	6	0	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
....TGGACGATTCCTCCTGTCGTCA	23	0	1	293.00	293	80	58	68	17	11	2	8	8	4	21	4	0	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GACTCGATTCCTCCTGTCGTCAC	23	0	1	228.00	228	79	56	50	15	7	10	0	1	5	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACGATTCCTCCTGTCGTCACT	24	0	1	366.00	366	91	74	51	31	11	1	1	11	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GACTCGATTCCTCCTGTCGTCACA	23	0	1	300.00	300	32	74	25	31	1	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	0	0	0	0	0	0	0
....TGGACGATTCCTCCTGTCGTCACT	24	0	1	179.00	179	19	36	17	14	16	4	12	23	4	8	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
....GACTCGATTCCTCCTGTCGTCACT	23	0	1	152.00	152	38	32	32	12	4	12	3	19	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	0	0	0
....GACTCGATTCCTCCTGTCGTCACT	23	0	1	142.00	142	49	54	27	11	10	4	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	0	0	0	0	0	0	0	0	0	0	0	0	0
....GACTCGATTCCTCCTGTCGTCACTT	24	0	1	94.00	94	16	26	18	5	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	0	0	0	0
....GACTCGATTCCTCCTGTCGTCACTC	24	0	1	94.00	94	16	26	18	5	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	0	0	0	0
....GACTCGATTCCTCCTGTCGTCACTCA	25	0	1	121.00	121	25	34	29	3	7	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GACTCGATTCCTCCTGTCGTCACTCA	24	0	1	112.00	112	29	35	23	7	4	5	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GACTCGATTCCTCCTGTCGTCACT	22	0	1	91.00	91	15	25	7	4	6	15	6	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	0
....GACTCGATTCCTCCTGTCGTCACTCAC	24	0	1	91.00	91	11	8	7	1	19	4	0	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	0	0	0	0	0	0	0	0	0
....GACTCGATTCCTCCTGTCGTCACTCA	21	0	1	81.00	81	9	19	7	1	10	0	0	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	0	0	0	0	0	0	0	0	0
....TGGACGATTCCTCCTGTCGTCACTC	23	0	1	51.00	51	9	21	5	1	1	0	0	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	0	0	0	0	0	0	0	0	0
....TGGACGATTCCTCCTGTCGTCACT	24	0	1	37.00	37	11	11	12	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	0	0	0	0	0
....TCGGACGATTCCTCCTGTCACT	19	0	1	36.00	36	6	5	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCC	22	1	1	36.00	36	8	5	1	2	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	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCCT	23	1	1	36.00	36	8	5	1	2	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	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCCTT	24	1	1	36.00	36	8	5	1	2	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	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCC	21	1	1	27.00	27	8	1	10	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTC	20	1	1	24.00	24	8	1	6	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCCT	21	1	1	24.00	24	8	1	6	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCCTA	22	1	1	20.00	20	8	1	4	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GACTCGATTCCTCCTGTCGTCA	23	1	1	18.00	18	8	1	2	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GACTCGATTCCTCCTGTCGTCAC	24	1	1	18.00	18	8	1	2	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GACTCGATTCCTCCTGTCGTCACA	25	1	1	17.00	17	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GACTCGATTCCTCCTGTCGTCACT	24	1	1	17.00	17	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCC	23	1	1	15.00	15	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCCT	24	1	1	15.00	15	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCC	22	1	1	12.00	12	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GACTCGATTCCTCCTGTCGTCA	21	1	1	9.00	9	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GACTCGATTCCTCCTGTCGTCAC	22	1	1	9.00	9	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCCTT	23	1	1	9.00	9	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCCTTT	24	1	1	9.00	9	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....ATGGCATCAAGGTGGGTTTC	20	1	1	8.00	8	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....ATGGCATCAAGGTGGGTTTCCT	21	1	1	8.00	8	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....ATGGCATCAAGGTGGGTTTCCTTT	22	1	1	8.00	8	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCCTTTA	23	1	1	8.00	8	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....ATGGCATCAAGGTGGGTTTCCTTTT	24	1	1	8.00	8	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCCTTTTA	25	1	1	8.00	8	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....ATGGCATCAAGGTGGGTTTCCTTTTT	26	1	1	8.00	8	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GACTCGATTCCTCCTGTCGTCACTCA	24	1	1	6.00	6	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....GACTCGATTCCTCCTGTCGTCACTC	25	1	1	6.00	6	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCCTTTCC	26	1	1	6.00	6	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCCTTTC	25	1	1	5.00	5	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCCTTT	24	1	1	5.00	5	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGGTTTCCTTTTT	25	1	1	5.00	5	8	1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TGGACATCAAGGTGGG

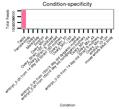
ID	Coordinate	Confidence	Class	Genome Locale	
dvi_293	**scaffold_12970:9428722-9428838 +**	**confident**	**Testes-restricted**	**antheme_to_intron**	Chloe on UCSC Genome Browser (Cram&Bam)

Legend: **Hairpin** **Mature** **Antisense** **Star**

Predicted structure







No conservation details

Show Alternate Folds

Flybase annotation

Antisense to intron:FBgn0023449:intj

No Repeatmasker elements found

Sense Strand Reads

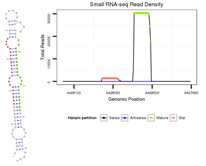
Hide Sp reads | Show mm2 mismatch reads

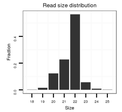
| Read # | Strand | Start | Mismatch Count | Reads | Total Reads | 2R:8479778 Sec20_testes_total | 2R:8481481 Argo8_testes_total | 2R:8481679 Ubl5_testes_total | 2R:8481680 Sdhb_testes_total | 2R:8481689 Ubl5_testes_total | 2R:8481670 Sdhb_testes_total | 2R:8481683 Ubl5_testes_total | 2R:8481655 Sec20_testes_total | MEF1 Female Argonaute_testes_total | 2R:8481659 Argonaute_testes_total | 3L:16 Ubl5_testes_total | 3L:16 Sdhb_testes_total | 3L:16 Sec20_testes_total | 3L:16 Argo8_testes_total | MET 3R:8481675 wuba Ubl5_ovarian_total | 3R:8481684 Sdhb_ovarian_total | 3R:8481686 Sec20_ovarian_total | 3R:8481674 Argo8_ovarian_total | 3R:8481677 wuba Ubl5_testes_total | MET 3R:8481675 Sdhb_testes_total | 3R:8481688 Sec20_testes_total | 3R:8481668 Argo8_testes_total | 3R:8481664 wuba Ubl5_malee_carcasses_total | 3R:8481673 Sdhb_malee_carcasses_total | 3R:8481676 Sec20_malee_carcasses_total | 3R:8481654 wuba Argo8_malee_carcasses_total | 3R:8481653 Ubl5_malee_carcasses_total | 3R:8481656 Sdhb_malee_carcasses_total | 3R:8481654 Sec20_malee_carcasses_total | 3R:8481653 Argo8_malee_carcasses_total | 3R:8481654 Ubl5_malee_carcasses_total | 3R:8481672 Sdhb_malee_carcasses_total | MYL1 Female wuba Ubl5_ovarian_total | 3R:8481654 Sec20_ovarian_total | 3R:8481656 Argo8_ovarian_total | 3R:8481657 Ubl5_testes_total | 3R:8481659 Sdhb_testes_total | 3R:8481667 Sec20_testes_total | 3R:8481665 Argo8_testes_total | 3R:8481687 Ubl5_malee_carcasses_total | 3R:8481685 Sdhb_malee_carcasses_total | 3R:8481655 Sec20_malee_carcasses_total | 3R:8481655 Argo8_malee_carcasses_total | 3R:8481655 Ubl5_malee_carcasses_total | 3R:8481671 Sdhb_malee_carcasses_total | 3R:8481658 Sec20_malee_carcasses_total | 3R:8481656 Ubl5_testes_total | 3R:8481655 Sdhb_testes_total | 3R:8481655 Sec20_testes_total | 3R:8481655 Argo8_testes_total | 3R:8481655

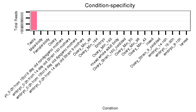
ID	Coordinate	Confidence	Class	Genome Locale	
dvi_59	**scaffold_12970:9428001-9428064** -	**Known Ortholog**	**Testes-restricted**	**anthene_to_intron**	[View on UCSC Genome Browser (GenoBEMers)]

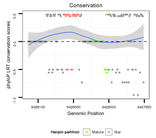
Target: Hairpin **Antisense** Loop **Sense** Mismatch Bulge

Predicted structure









Show Alternate Folds

Flybase annotation

Antisense to intron:[FlyE22TR609-a]

No Exporatdis clusters found

Sense Strand Reads

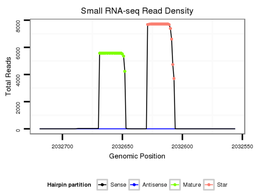
Note 3p reads show mid mismatch reads

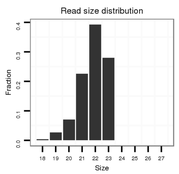
| Alt Gene/TSS/TTS/CTS/CAGE/DAS/Ch/Ch/Ch

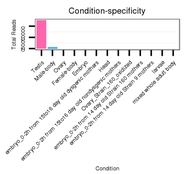
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_53	**scaffold_13042:2032606-2032669 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

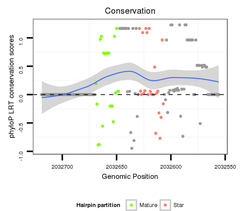
Legend: sense; 5bp mismatch in siRNA; one of mismatch in seed

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

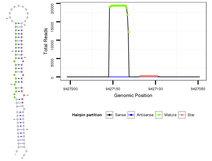
hide 3p reads show mrd mismatch reads

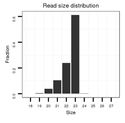
| ATGTTCACTTTAATCAATAGCTGTGACTGAAAGAGGCGCAGATTAGTCC | GAACCACAGCTAAACATATAAT | TTTTTTTTTACAAGTTCT | TATGTGTGTTAGCTGGGCTCATG | ATTCGTTTCGTTGTTCACTTTAATTTGCTTAAATGAAGCTTTTATGCCA | | |

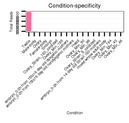
ID	Coordinate	Confidence	Class	Genome Locale	
dvi_94	**scaffold_12970:9427098-9427154 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser (GenomeMine)]

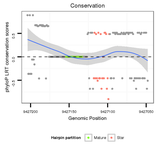
Layout: [illegible]

Predicted structure









Show Alternate Folds

FlyBase annotation

Antisense to intron [FBAP0239619-in]

No Repeatmiler element found

Sense Strand Reads

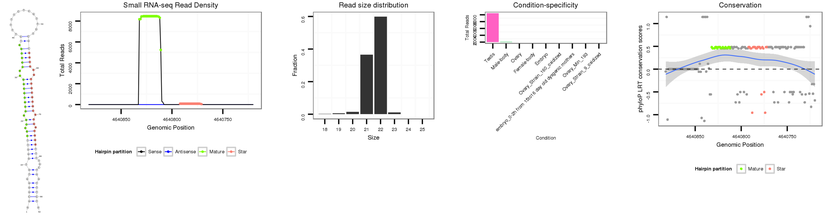
Hide 3p reads show mid mismatch reads

| | | |

ID:	Coordinate:	Confidence:	Class:	Genome Locale:
dvi_207	**scaffold_12723:4640770-4640832 -**	**confident**	**Testes-restricted**	**intergenic**
				[View on UCSC Genome Browser (Genes/Mapping)]

Legend: Sense Arm Mismatch in alignment Mismatch in seed

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

nearest		later	
1. dvi_207 scaffold_12723:4640770-4640832 -		1. dvi_207 scaffold_12723:4640770-4640832 -	
2. dvi_324 scaffold_12963:336489:336830 +		2. dvi_324 scaffold_12963:336489:336830 +	

Sense Strand Reads

hide 3p reads show mid mismatch reads

GAGCTTATCGATTCCGTTCCGAATTATGTCTGGCAAAACAAAATATAAAT	Read #	Hit Count	Total Score	Total	SRR060481 Arge9_testes_total	SRR060478 9x140_testes_total	SRR060479 140x9_testes_total	SRR060470 9_testes_total	SRR060480 Ankrg_testes_total	SRR060489 160x9_testes_total	SRR060483 140_testes_total	SRR060655 9x160_testes_total	SRR060459 Argentina_testes_total	SRR060657 140_testes_total	V114 male body	M047 female body	M027 male body	SRR060656 9x160_ovaries_total	SRR060654 160x9_ovaries_total	SRR060658 140_ovaries_total	SRR060673 9_ovaries_total	SRR060676 Ankrg_ovaries_total	SRR060668 160x9_males_carcasses_total	SRR060666 140_males_carcasses_total	SRR060684 140x9_0-2h_embryos_total	SRR060674 9x140_ovaries_total	SRR060677 Arge9_ovaries_total	SRR060688 160_ovaries_total	M061	SRR060664 embryo_9_males_carcasses_total	SRR2094014 Ovary_Strain_160_ovidized	SRR2094059 embryo_9x160_males_carcasses_total	V047	SRR060671 2h_embryos_total	SRR060686 Arge9_9-12h_embryos_total	SRR060687 9_12-24h_embryos_total	SRR2094013 Ovary_Strain_9_ovidized	SRR2094060 Ovary_Mix_160	SRR2094079 embryo_0-2h_from 13to16_day mutants	SRR060669 x16 Systemic mutants	SRR060667 160x9_females_carcasses_total	SRR060665 9_females_carcasses_total	SRR1154729 mixed whole adult body
**********	Seed #	Arm Mismatch	Count	Score	Total																																								
.....TGCCAAGTATGCAGCACGTTGA.....	22	0	2	4889.50	9779	2417	2130	2074	748	819	532	527	231	117	75	70	4	0	1	3	4	4	5	1	0	0	1	2	2	2	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGA.....	22	0	2	3097.05	6194	1320	1410	1314	756	434	390	243	237	182	150	32	4	0	1	2	3	0	1	0	0	0	0	1	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0
.....CCAAGTATGCAGCACGTTGATTG.....	22	0	1	195.00	195	80	43	32	0	31	0	0	1	3	2	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
.....TGCCAAGTATGCAGCACGTTGATCTT.....	23	0	1	105.00	105	38	40	39	25	25	19	18	16	8	3	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
.....TGCCAAGTATGCAGCACGTTGATT.....	23	0	1	65.00	65	24	21	6	0	7	4	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	0	0	0	0	0	0	0
.....AACGCATTGCATCATGACAA.....	22	0	1	40.00	80	5	38	26	1	4	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
.....TGCCAAGTATGCAGCACGTTGA.....	23	0	2	36.50	73	9	19	12	7	10	4	5	3	0	0	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
.....TGCCAAGTATGCAGCACGT.....	19	0	2	34.00	52	13	19	18	5	3	7	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
.....AACGCATTGCATCATGACAA.....	21	0	2	32.50	65	11	28	20	0	4	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
.....TGCCAAGTATGCAGCACGTTGATG.....	24	0	1	27.00	27	3	11	5	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CCAAGTATGCAGCACGTTGATGT.....	23	0	1	26.00	26	13	4	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	0	0	0
.....TGCCAAGTATGCAGCACGTTGAT.....	24	0	1	22.00	44	0	7	8	0	8	2	0	0	0	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
.....TGCCAAGTATGCAGCACGTTGA.....	22	1	2	18.50	37	0	0	0	19	0	3	10	5	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
.....TGCCAAGTATGCAGCACGTTGA.....	22	1	2	15.50	31	5	4	0	2	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	0	0
.....CCAAGTATGCAGCACGTTGA.....	20	1	2	12.50	25	3	7	4	0	4	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	0	0	0	0
.....CCAAGTATGCAGCACGTTGAT.....	21	1	2	12.00	12	3	1	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	0	0	0	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGA.....	18	0	2	11.50	23	0	1	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	0	0	0	0	0	0	0
.....AATGCATTGCATCATGACAA.....	18	0	2	11.00	22	2	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
.....AACGCATTGCATCATGACAAG.....	23	1	2	10.50	21	2	11	6	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	0	0	0	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGA.....	21	0	2	8.00	16	2	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	0	0	0	0	0	0	0	0
.....GCCAAGTATGCAGCACGTTGA.....	21	0	2	8.50	17	1	3	3	1	1	3	2	2	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
.....TGCCAAGTATGCAGCACGTTGATG.....	24	1	1	6.00	6	5	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	0
.....CCAAGTATGCAGCACGTTG.....	19	0	2	6.50	13	1	3	5	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	0	0	0	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGA.....	21	1	2	6.00	12	3	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGA.....	19	1	2	6.00	12	1	1	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
.....TGCCAAGTATGCAGCACGTT.....	21	1	2	5.50	11	2	2	1	4	0	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	0
.....CCAAGTATGCAGCACGTTGATTATG.....	24	1	2	5.00	5	0	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	0	0	0	0	0	0	0	0
.....CCAAGTATGCAGCACGTTGATGT.....	24	1	2	5.00	5	0	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	0	0	0	0	0	0	0	0
.....CAATGTATGCAGCACGTTGA.....	18	1	2	5.00	10	1	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
.....TGCCAAGTATGCAGCACGTTGATG.....	22	1	2	4.00	4	3	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
.....TGCCAAGTATGCAGCACGTTGA.....	22	1	2	3.50	7	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
.....TGCCAAGTATGCAGCACGTTGA.....	22	1	2	3.50	7	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
.....GCCAAGTATGCAGCACGTTGA.....	20	0	2	3.50	7	1	1	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
.....TGCCAAGTATGCAGCACGTTGATG.....	21	1	2	3.00	6	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	0	0	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGA.....	20	1	2	3.00	6	0	3	0	0	0	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	0	0	0	0	0
.....GCCAAGTATGCAGCACGTTGATG.....	23	1	2	2.00	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
.....TGCCAAGTATGCAGCACGTTGATG.....	24	1	2	1.50	3	0	0	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
.....TGCCAAGTATGCAGCACGTTGAT.....	23	1	2	1.50	3	0	0	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
.....CAATGTATGCAGCACGTTGATG.....	20	1	2	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	0	0	0	0	0	0
.....TATGCAGCACGTTGATGT.....	18	0	2	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	0	0	0
.....TGCCAAGTATGCAGCACGTTGATG.....	25	1	2	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	0	0	0	0	0	0
.....CCAAGTATGCAGCACGTTGATG.....	21	1	2	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	0	0	0	0	0	0
.....GCCAAGTATGCAGCACGTTGATG.....	23	1	2	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	0	0	0	0	0	0
.....TGCCAAGTATGCAGCACGTTGATG.....	24	1	2	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	0	0	0	0	0	0
.....CCAAGTATGCAGCACGTTGATGT.....	23	1	2	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	0	0	0	0	0	0
.....AACGCATTGCATCATGACAAG.....	24	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AACGCATTGCATCATGACA.....	20	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CAACGCATTGCATCATGACA.....	22	0	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ACAACGCATTGCATCATGACA.....	22	0	2	0.50	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	0	0	0
.....CAATGTATGCAGCACGTTGA.....	21	0	2	0.50	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	0	0	0
.....TGCCAAGTATGCAGCACGTTGA.....	20	1	2	0.50	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	0	0	0
.....TGCCAAGTATGCAGCACGTTGA.....	24	0	2	0.50	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	0	0	0
.....TGCCAAGTATGCAGCACGTTGA.....	22	0	2	0.50	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	0	0	0
.....CGCATTGCATCATGACAAA.....	20	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CAACGCATTGCATCATGACAAA.....	22	0	2	0.50	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	0	0	0
.....TGCCAAGTATGCAGCACGTT.....	22	0	2	0.50	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	0	0	0
.....TGCCAAGTATGCAGCACGTTGA.....	19	1	2	0.50	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	0	0	0
.....TGCCAAGTATGCAGCACGTT.....	22	1	2	0.50	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	0	0	0
.....CAACGCATTGCATCATGACAAA.....	23	0	2	0.50	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	0	0	0
.....TGCCAAGTATGCAGCACGTTG.....	22	0	2	0.50	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	0	0	0

Anti-sense strand reads

CTCGAATAGCTAAGCCAAGCCTAATACAGACCCTTTCTTTATTTTAAT	Read #	Hit Count	Total Score	Total	M047 female body	V114 male body	SRR060481 Arge9_testes_total	SRR060484 140x9_0-2h_embryos_total	SRR060666 140_males_carcasses_total	SRR060682 9x140_0-2h_embryos_total
**********	Seed #	Arm Mismatch	Count	Score	Total					
.....TAAACGGTTCATACGTCGTGCA.....	24	1	1	1.00	1	0	0	0	0	0
.....TTGCGTAACGTATACTGTTT.....	22	0	2	0.50	1	0	0	0	0	0
.....GTTGCGTAACGTATACTGTTT.....	22	0	2	0.50	1	0	0	0	0	0
.....AAACGGTTCATACGTCGTGCA.....	22	3	2	0.50	1	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

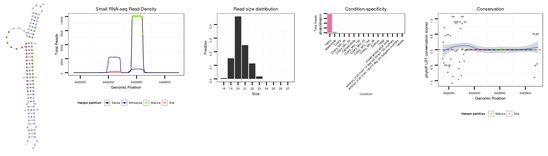
Species	Coordinate	ID	Alignment
Dvirilis	Scaffold_2_:21214662:21214662:-	Dvir_21	CGGCTTATCGATTCCGTTCCGAATTATGTCTGGCAAAACAAAATATAAAT-TGCCAAGTATGCAGCACGTTGA-TTTTTTCTCGTTGTCAACGCATTGCATCATGACAAGTTTTTCTATTTTTATT---CTGCTTGAAACATAAAG--TAATTATAATAGCAC-T
Dsimsim	Scaffold_4000:1991905:1992000:+	Dsim_21	***********************************-G-G-G-G-AAACGCATTGCATCATGACAAGTTTTTCTATTTTTATT-----G-G-G-G-G-G-G-G-AAGCGCATTGCATCATGACAAGTTTTTCTATTTTTATT---G-G-G-G-G-G-G-G-AAGCGCATTGCATCATGACAAGTTTTTCTATTTTTATT-----

ID	Coordinate	Strand	Genomic Locus
chr1_298_scaffold_12970:9426825-9426912_+	**chr1:9426825-9426912**	**Twizzle-overlexed**	**antisense_to_intron**

View on UCSC Genome Browser (Crawl Mirror)

Length: 88 | GC: 0.5682 (50.00%) | Structure: 100.00%

Predicted structure



Show Alternate Folds

Flybase annotation

Indexed on dmel (BDGP5.25)

No Drosophila ortholog found

Sense Strand Reads

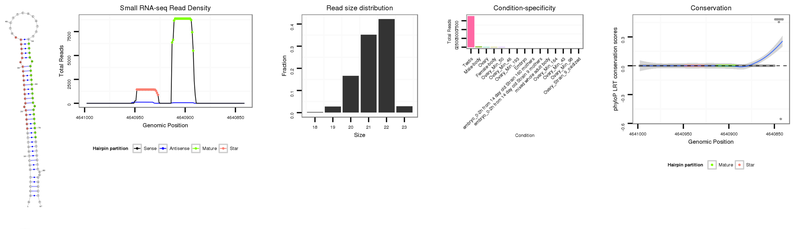
Hide 3p reads | Show mid-mismatch reads

| 5'Seq | Read ID | Strand | Total Reads | Total Genomic Reads | Total Genomic Loci | 5'Seq Nucleotide Counts | 5'Seq Nucleotide Counts | 5'Seq Nucleotide Counts

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_71	**scaffold_12723:4640891-4640948 -**	**confident**	**Testes-restricted**	**intergenic** [View on UCSC Genome Browser (Cornell Mirror)]

Legend: Sense Star Antisense 5' or 3' overhang Mismatch in loop

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatible elements found

number	blast
	1. dvi_71 scaffold_12723:4640927-4640941
	2. dvi_384 scaffold_12963:338290-338318 -

Sense Strand Reads

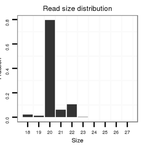
hide 3p reads show mid mismatch reads

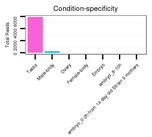
GACTGTTGGACGGATAACAAGTGATGGTGGCAATAAACTTAACTAATTA	TAGACAGCATCAAGCATTAATT	ACCTTACACATTTA	TTAAAGCTTGGTGCAGTCTGTAATTATGATTAGCAGACTTATGCAGACTTCCGTTCCGCATTATGTCTGGCAAAACAAA
**********	((((((((((((((((((((.((((((((((.((((((.(((((.((((((.((((.))))).))).))).

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_319	**scaffold_12963:329857-329951 +**	**confident**	**Testes-restricted**	**intergenic**	View on UCSC Genome Browser (Cornell Mirror)

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

Predicted structure





No conservation details.

Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

mature	star
1. dvi_43 scaffold_12725:4643317-4643336 + 2. dvi_319 scaffold_12963:329906-329925 +	1. dvi_43 scaffold_12725:4643352-4643371 + 2. dvi_319 scaffold_12963:329869-329890 +

Sense Strand Reads

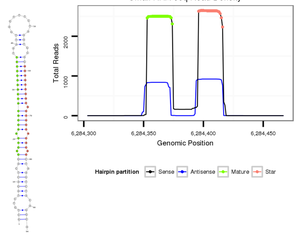
Hide 3p reads Show mid mismatch reads

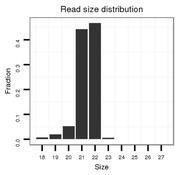
GTACTTTTGATCTACATGCACCTGTAAAGTTCAACTGCTAAAGTTCAACTTTCATGTTCCGGCAGCAAGCC	TCCAAATTGTTTTTCCTATTAG	TTATTTCAAATAGCTTAAACCGTTTAAACTCCTTAACTTTCCTGGAGAAGCAACCTAAAATAAAATGGTTTACATCTAGTTAATCCTTAATAATTATCTAATATGTGACA	Read #	Bit Count	Total Norm	Total	SRR060478	SRR060479	SRR060481	SRR060670	SRR060689	SRR060655	SRR060680	SRR060683	V116 SRR060659	SRR060657	W047 female body	W027 SRR060656	SRR060662 male body	SRR060660	SRR060667	SRR294050 embryo_0-2h_rep1 14 Strain 160 mothers	SRR060654	SRR060673	SRR060684 10x9_0-	SRR294038 embryo_0-2h_rep2 14 Strain 9 mothers	SRR294024 embryo_0-2h_rep1 14 dysgenic Strain 9 mothers	SRR060672	W041	SRR060658	SRR060668	SRR060675	SRR060676	SRR060688	SRR1106720 embryo_0-10h	SRR3396056 head	W028 SRR060671	SRR060677	SRR3396060	SRR294041 embryo_0-2h_rep1 14 Strain 160	SRR060687	SRR060682	SRR060686
**********	((((((.....((((((((((((((.....)))))))))))))).....)).)).))	**********	alice	Mismatch	Count	Norm		9x140_testes_total	14Dw3_testes_total	Arge3_testes_total	9_testes_total	140x9_testes_total	9x140_testes_total	140_testes_total	male Argentina_testes_total	140_testes_total	female body	male 9x140_ovaries_total	female body	2h_embryos_total	Argentina_ovaries_total	140_females_carcasses_total	Strain 160 mothers	10x9_ovaries_total	9_ovaries_total	2h_embryos_total	Strain 9 mothers	dysgenic Strain 9 mothers	Strain 9 mothers	9x140_females_carcasses_total	embryo	140_ovaries_total	10x9_males_carcasses_total	14Dw3_ovaries_total	9xArg_ovaries_total	140_ovaries_total	10h	Ovary_Mix_45	head	9x140_males_carcasses_total	Arge3_ovaries_total	Ovary_Mix_193	mothers	2h_embryos_total	2h_embryos_total	2h_embryos_total
....TCCAAATTGTTTTTCCTATTAG....			20	0	2	4893.00	9786	1690		1684	1659	988	865	747	651	550	268 324		345	4 1	3	0	0	0	0	0 2	1	1	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0
....TCCAACCGGAAGCAATTTGTCG....			21	0	1	575.00	575	147		114	49	37	28	36	28	12	48 30		21	2 0	0	0	0	0	0	0	0	0	0	28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TCCAACCGGAAGCAATTTGTCT....			21	0	1	303.00	303	82		69	41	17	20	20	24	4	13 4		4	2 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
....TCCAAATTGTTTTTCCTATTAG....			23	1	1	217.00	217	49		72	25	11	5	7	11	3	15 2		3	1 0	0	0	0	0	0	0	0	1	0	11	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
....TCCAAATTGTTTTTCCTATTAG....			23	1	2	168.00	336	135		69	75	1	8	2	28	8	0 0		1	7 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
....TCCAACCGGAAGCAATTTGTCG....			23	1	2	153.00	153	30		23	11	2	13	29	5	3	28 12		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
....TCCAACCGGAAGCAATTTGTCT....			19	0	2	136.50	273	50		78	52	21	4	7	26	18	0 12		4	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
....TCCAAATTGTTTTTCCTATTAC....			23	2	1	76.00	76	32		12	10	3	7	4	2	2	7 16 0		2	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
....TCCAAATTGTTTTTCCTATTAC....			22	0	2	70.00	140	63		24	10	1	5	0	10	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	0	0
....TCCAACCGGAAGCAATTTGTCT....			19	0	2	70.50	141	25		35	13	1	1	12	14	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
....TCCAACCGGAAGCAATTTGTCG....			21	0	2	45.50	91	13		35	13	1	1	11	14	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
....TCCAACCGGAAGCAATTTGTCT....			21	1	2	59.00	59	8		5	1	2	5	1	6	3	13 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
....TCCAAATTGTTTTTCCTATTAC....			21	1	2	58.50	117	38		32	25	2	3	3	15	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	0	0	0	0
....TCCAACCGGAAGCAATTTGTCG....			24	2	2	49.00	98	39		23	17	5	2	1	5	4	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
....TCCAACCGGAAGCAATTTGTCT....			23	1	2	40.00	80	19		16	12	3	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
....TCCAACCGGAAGCAATTTGTCTAT....			23	1	1	27.00	27	8		5	3	0	3	0	0	1	3 3 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
....TCCAACCGGAAGCAATTTGTCTAT....			24	2	1	17.00	17	4		4	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
....TCCAACCGGAAGCAATTTGTCT....			21	0	2	11.50	23	2		7	2	1	1	4	2	3	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
....TCCAACCGGAAGCAATTTGTCT....			22	1	1	11.00	11	2		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	0	0	0	0	0	0	0	0
....TCCAAATTGTTTTTCCTATTAG....			22	1	2	11.00	22	8		4	1	0	0	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
....TCCAAATTGTTTTTCCTATTAG....			25	3	2	10.50	21	10		4	2	0	0	1	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
....TCCAACCGGAAGCAATTTGTCTAG....			23	0	1	10.00	10	2		2	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
....TCCAACCGGAAGCAATTTGTCTG....			23	2	1	8.00	8	2		2	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	0	0	0
....TCCAACCGGAAGCAATTTGTCTC....			23	2	1	7.00	7	2		1	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
....TCCAACCGGAAGCAATTTGTCTCG....			23	2	1	7.00	7	2		1	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
....TCCAAATTGTTTTTCGATT....			20	0	2	7.00	14	3		3	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
....TCCAAATTGTTTTTCGATTAG....			22	1	2	5.50	11	3		3	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
....TCCAACCGGAAGCAATTTGTCT....			22	1	2	5.00	5	1		1	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
....TCCAAATTGTTTTTCCTATTACG....			24	2	2	4.50	9	5		1	2	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
....TCCAAATTGTTTTTCCTATTACT....			24	2	2	4.50	9	3		1	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
....TCCAAATTGTTTTTCCTATTT....			21	1	2	3.50	7	3		1	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
....TCCAACCGGAAGCAATTTGTCG....			22	0	2	3.00	6	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	0
....AACCGGAAGCAATTTGTCG....			22	0	2	3.00	6	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	0
....TCCAACCGGAAGCAATTTGTCTAC....			22	1	2	3.00	6	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	0
....TCCAACCGGAAGCAATTTGTCTAT....			19	0	2	3.00	6	0		4	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
....GAACCGGAAGCAATTTGTCG....			19	0	2	2.50	5	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	0	0	0	0	0	0
....TCCAACCGGAAGCAATTTGTCT....			21	1	2	2.50	5	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
....TCCAACCGGAAGCAATTTGTCTG....			23	2	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....TCCAACCGGAAGCAATTTGTCTAT....			24	2	1	2.00	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	0	0	0	0	0	0	0	0
....TCCAACCGGAAGCAATTTGTCTAT....			23	3	1	2.00	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	0	0	0	0	0	0	0	0
....TCCAAATTGTTTTTCGATTAG....			23	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....AACCGGAAGCAATTTGTCT....			20	0	2	1.50	3	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
....TCCAACCGGAAGCAATTTGTCTG....			20	1	2	1.50	3	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
....TCCAACCGGAAGCAATTTGTCTAT....			18	0	2	1.50	3	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
....TCCAACCGGAAGCAATTTGTCTA....			19	1	2	1.50	3	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
....TCCAAATTGTTTTTCCTATTACT....			24	1	2	1.50	3	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	0
....CCTCCAAATTGTTTTTCCTATTT....			22	0	2	1.50	3	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
....TCCAACCGGAAGCAATTTGTCTAT....			24	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....AACCGGAAGCAATTTGTCTAG....			24	3	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
....TCCAACCGGAAGCAATTTGTCTAT....			25	3	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
....AACCGGAAGCAATTTGTCTAG....			24	3	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
....TCCAACCGGAAGCAATTTGTCTAT....			24	3	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
....TCCAACCGGAAGCAATTTGTCTAT....			24	3	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
....GAACCGGAAGCAATTTGTCTG....			22	0	2	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
....TCCAACCGGAAGCAATTTGTCTAT....			20	1	2	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
....TCCAACCGGAAGCAATTTGTCTAT....			19

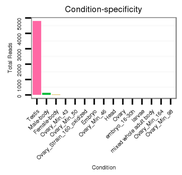
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_220	**scaffold_12855:6284353-6284417 +**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser (Comell Mirror)]

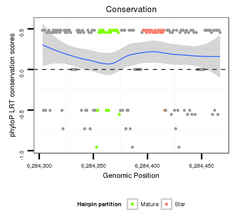
Legend: sense: 5p antisense: 3p mismatch in alignment mismatch in seed

Predicted structure









Show Alternate Folds

Flybase annotation

Antisense to intron [Dvir/GI10228-in]

No Repeatable elements found

Sense Strand Reads

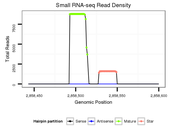
hide 3p reads show mid mismatch reads

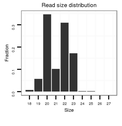
AAAGCGTGCCAGTGTTGTAAAGTGTTCGTAGTAGTGCTGTCTAGACTCAGCGGTGAACCACATCAATTTTCTTAATTGAGTTTCTAAATGCAGAAGTTGATGGTGGTACACAG CTAGTCTACAGGCAAAACAACATTTCAGATAACATAAAATACACAACAATTC	Read #	Mismatch	Hit Count	Total Norm	Total	SRR060681 Arg9_testes_total	SRR060678 9x140_testes_total	SRR060679 140x9_testes_total	SRR060680 Â 9xArg_testes_total	SRR060657 140_testes_total	M027 male body	SRR060670 9_testes_total	M047 female body	SRR060659 Argentina_testes_total	SRR060689 160x9_testes_total	SRR060655 9x160_testes_total	SRR060683 160_testes_total	SRR2094055 Ovary_Min_43	M061 embryo Ovary_Min_50	SRR2096057 body	V116 male Ovary_Strain_160_oxidized	SRR2094014	SRR2094054 Ovary_Min_46	M028	SRR060684 16x9_0-2h_embryos_total	SRR2096058 Ovary_Min_98	SRR2096059 Ovary_Min_164	SRR060658 140_ovaries_total	SRR060664 9_males_carcasses_total	SRR060674 9x140_ovaries_total	SRR1106728 larvae	SRR1106729 mixed whole adult body	SRR1106730 embryo_16-30h	SRR2096026 embryo_0-4h from 14 day old Strain 9 mothers	SRR060666 160_males_carcasses_total	V053 head	SRR060665 9_females_carcasses_total	SRR060686 Arge9_0-2h_embryos_total	SRR060663 160_0-2h_embryos_total
...CGGTGAACCACATCAATTTTCT...	22	0	1	2244.00	2244	779	712	469	245	1	1	6	6	0	9	7	2	0	0	0	5	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
...AAAGTTGATGGTGGTACACAG...	21	0	1	1869.00	1869	420	534	387	151	126	114	27	19	28	10	11	15	9	2	5	1	0	3	2	1	0	1	1	1	0	0	1	1	0	0	0	0	0	0	0
...CGGTGAACCACATCAATTTTCT...	23	1	1	337.00	337	113	110	65	37	0	0	2	4	0	1	4	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...AAAGTTGATGGTGGTACACAGCT...	23	0	1	252.00	252	62	62	52	13	20	5	10	4	13	4	3	2	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...AAAGTTGATGGTGGTACACA...	20	0	1	212.00	212	52	68	51	18	13	2	1	4	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...CGGTGAACCACATCAATTTTCTC...	24	2	1	169.00	169	68	38	34	24	0	0	1	3	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
...CGGTGAACCACATCAATTTTCT...	21	0	1	147.00	147	61	28	36	21	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
...TAATTGAGTTTCTAAATGCAG...	21	0	1	145.00	145	34	42	26	8	0	0	10	0	0	0	16	5	3	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
...AAAGTTGATGGTGGTACACAG...	19	0	1	90.00	90	17	24	21	5	0	0	5	1	1	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
...CGGTGAACCACATCAATTTTCT...	22	0	1	82.00	82	19	23	16	6	0	0	4	1	2	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...CGGTGAACCACATCAATTTTCT...	23	1	1	53.00	53	18	17	10	7	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
...AAAGTTGATGGTGGTACACAG...	22	1	1	35.00	35	8	10	7	2	0	0	0	1	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...AAAGTTGATGGTGGTACA...	18	0	1	33.00	33	8	5	8	3	6	0	1	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
...GGTGAACCACATCAATTTTCT...	21	0	1	31.00	31	8	14	4	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
...AAAGTTGATGGTGGTACACA...	21	1	1	30.00	30	10	7	7	1	4	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
...AAAGTTGATGGTGGTACACAGC...	24	1	1	21.00	21	7	2	3	3	3	0	1	0	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
...CGGTGAACCACATCAATTTT...	20	0	1	19.00	19	7	5	3	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
...CGGTGAACCACATCAATTTTCTT...	23	0	1	18.00	18	6	3	5	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
...GAAAGTTGATGGTGGTACACA...	21	1	1	16.00	16	5	6	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	0	0
...CGGTGAACCACATCAATTTTCTT...	24	1	1	16.00	16	12	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	0	0	0
...CGGTGAACCACATCAATTTT...	22	1	1	15.00	15	7	4	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	0	0
...AAAGTTGATGGTGGTACAA...	20	1	1	14.00	14	3	2	3	4	0	0	0	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
...GGTGAACCACATCAATTTTCTC...	23	2	1	12.00	12	5	4	1	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
...CGGTGAACCACATCAATTTTCTCC...	25	3	1	12.00	12	1	4	2	1	0	0	0	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
...ACCGGTGAACCACATCAATTTT...	22	0	1	12.00	12	5	3	3	3	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
...AAAGTTGATGGTGGTACACAG...	22	1	1	11.00	11	5	2	1	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	0
...AAAGTTGATGGTGGTACA...	19	1	1	10.00	10	1	4	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
...AAGTTGATGGTGGTACA...	20	0	1	10.00	10	3	1	2	1	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
...AAGTTGATGGTGGTACAGG...	20	0	1	9.00	9	3	1	1	0	0	0	1	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
...TGCAGAAAGTTGATGGTGGTA...	20	0	1	9.00	9	2	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
...ACCGGTGAACCACATCAATTTTC...	23	0	1	9.00	9	5	1	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
...TGCAGAAAGTTGATGGTGGTACA...	23	0	1	8.00	8	4	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
...AAAGTTGATGGTGGTACAA...	20	1	1	8.00	8	1	2	4	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
...AAAGTTGATGGTGGTACAGA...	21	1	1	7.00	7	2	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	0
...TGCAGAAAGTTGATGGTGGTA...	22	1	1	7.00	7	4	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
...TGCAGAAAGTTGATGGTGGTAC...	22	0	1	7.00	7	3	1	1	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	0	0	0	0	0	0
...CAGAAAGTTGATGGTGGTAC...	20	0	1	6.00	6	0	1	4	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
...CGGTGAACCACATCAATTTTCTCC...	25	3	1	6.00	6	4	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
...CGGTGAACCACATCAATTTTCC...	24	2	1	6.00	6	4	0	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
...AGGTTGATGGTGGTACACAGCT...	21	0	1	5.00	5	1	3	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
...CAGAAAGTTGATGGTGGTACACA...	24	0	1	5.00	5	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
...CAGAAAGTTGATGGTGGTACAC...	22	0	1	5.00	5	1	1	1	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	0	0	0	0
...AAAGTTGATGGTGGTACACAG...	24	1	1	5.00	5	1	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	0	0	0
...TAATTGAGTTTCTAAATGCA...	20	0	1	5.00	5	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	0	0	0	0	0	0
...CGGTGAACCACATCAATTTTCT...	22	1	1	4.00	4	2	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
...GAAAGTTGATGGTGGTACA...	19	0	1	4.00	4	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	0	0	0	0
...GAAAGTTGATGGTGGTACACAGCT...	24	0	1	4.00	4	1	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
...ACCGGTGAACCACATCAATTTTC...	24	1	1	3.00	3	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	0	0	0	0	0	0	0	0
...CAGAAAGTTGATGGTGGTACA...	23	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...TAATTGAGTTTCTAAATGCAGAATT...	27	3	1	3.00	3	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	0	0	0	0	0	0
...CGGTGAACCACATCAATTTTCT...	22	1	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	0	0	0	0	0	0	0	0
...TGAGTTTCTAAATGCAGAAGTTG...	25	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
...GGTGAACCACATCAATTTTCT...	23	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	0	0	0	0	0	0	0	0
...CGGTGAACCACATCAATTTTCTTC...	26	3	1	3.00	3	0	0	0	1	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
...AAAGTTGATGGTGGTACAA...	19	1	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
...GAAAGTTGATGGTGGTACACAG...	22	0	1	3.00	3	0	2	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
...CAGAAAGTTGATGGTGGTA...	20	1	1	3.00	3	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
...TAGTGCTGTCTAGACTCAG...	19	0	1	3.00	3	0	1	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
...CGGTGAACCACATCAATT...	18	1	1	3.00	3	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
...CGGTGAACCACATCAATTTTCT...	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
...AAAGTTGATGGTGGTACACAG...	22	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...AAAGTTGATGGTGGTACAGC...	22	2	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
...CGGTGAACCACATCAATTTTCTCC...	24	2	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
...AACCACATCAATTTTAATT...	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...CGGTGAACCACATCAATTT...	19	0	1	2.00	2	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
...AAAGTTGATGGTGGTACA...	18	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...AAAGTTGATGGTGGTACAG...	18	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...CGGTGAACCACATCAATTTCTCC...	22	3	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
...CGGTGAACCACATCAATTTCTTAA...	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
...AAAGTTGATGGTGGTACAGA...	21	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
...AGTTGATGGTGGTACACAGCTAA...	23	0	1	2.00	2	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	0	0	0	0
...AAAGTTGATGGTGGTACACA...	23	1	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
...AAAGTTGATGGTGGTACAGC...	23	1	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
...TCTAAATGCAGAAGTTGATGGT...	23	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
...AAAGTTGATGGTGGTACACAGC...	25	2	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
...TTGAGTTTCTAAATGCAGAAGA...	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
...GGTGAACCACATCAATTTTCT...	21	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	0	0
...AAGTTGATGGTGGTACAGCTAA...	23	0	1	1.00	1	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	0	0	0	0
...AAAGTTGATG

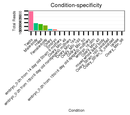
ID	Coordinate	Confidence	Class	Genomic Locale	
dvi_27	**scaffold_12928:2858493-2858550 +**	**confident**	**Canonical miRNA**	**intron**	View on UCSC Genome Browser (Crated Mirror)

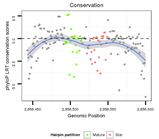
Legend: Stem 5p Terminal Loop 3p Stem Mismatch

Predicted structure









Show Alternative Folds

Flybase annotation

none (0 miRNA/hairpin)

Repeatable elements

Name	Class	Family	Strand
FlyTe	Transposon	mariner	+

Sense Strand Reads

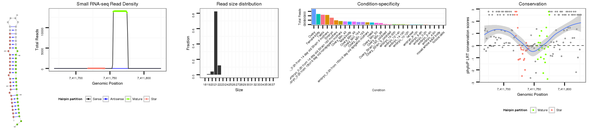
Hide 5p reads show mid mismatch reads

| Seq | 5' Iso | 3' Iso | Total | Total Seq | Arguelles_female_total | wu2e_Pu107_testes_total | Argo9_testes_total | T_testes_total | Pu107_testes_total | Pu107_female_carcasses_total | MEX1 | embryo_female_carcasses_total | 105wt_testes_total | 105_testes_total | 105wt_female_carcasses_total | 105_female_carcasses_total | Bubg_testes_total | 9_males_carcasses_total | 105wt_males_carcasses_total | 105_males_carcasses_total | 105wt_ovaries_total | 105_ovaries_total | Argentina_ovaries_total | 9_ovaries_total | wu2e_Pu107_ovaries_total | Bubg_ovaries_total | 105wt_ovaries_total | Pu107_ovaries_total | Argo9_ovaries_total | 105_ovaries_total | SRR2294033 day old adult whole body | SRR2294035 day old adult whole body | SRR2294036 day old adult whole body | SRR2294037 day old adult whole body | SRR2294038 day old adult whole body | SRR2294039 day old adult whole body | SRR2294040 day old adult whole body | SRR2294041 day old adult whole body | SRR2294042 day old adult whole body | SRR2294043 day old adult whole body | SRR2294044 day old adult whole body | SRR2294045 day old adult whole body | SRR2294046 day old adult whole body | SRR2294047 day old adult whole body | SRR2294048 day old adult whole body | SRR2294049 day old adult whole body | SRR2294050 day old adult whole body | SRR2294051 day old adult whole body | SRR2294052 day old adult whole body | SRR2294053 day old adult whole body | SRR2294054 day old adult whole body | SRR2294055 day old adult whole body | SRR2294056 day old adult whole body | SRR2294057 day old adult whole body | SRR2294058 day old adult whole body | SRR2294059 day old adult whole body | SRR2294060 day old adult whole body | SRR2294061 day old adult whole body | SRR2294062 day old adult whole body | SRR2294063 day old adult whole body | SRR2294064 day old adult whole body | SRR2294065 day old adult whole body | SRR2294066 day old adult whole body | SRR2294067 day old adult whole body | SRR2294068 day old adult whole body | SRR2294069 day old adult whole body | SRR2294070 day old adult whole body | SRR2294071 day old adult whole body | SRR2294072 day old adult whole body | SRR2294073 day old adult whole body | SRR2294074 day old adult whole body | SRR2294075 day old adult whole body | SRR2294076 day old adult whole body | SRR2294077 day old adult whole body | SRR2294078 day old adult whole body | SRR2294079 day old adult whole body | SRR2294080 day old adult whole body | SRR2294081 day old adult whole body | SRR2294082 day old adult whole body | SRR2294083 day old adult whole body | SRR2294084 day old adult whole body | SRR2294085 day old adult whole body | SRR2294086 day old adult whole body | SRR2294087 day old adult whole body | SRR2294088 day old adult whole body | SRR2294089 day old adult whole body | SRR2294090 day old adult whole body | SRR2294091 day old adult whole body | SRR2294092 day old adult whole body | SRR2294093 day old adult whole body | SRR2294094 day old adult whole body | SRR2294095 day old adult whole body | SRR2294096 day old adult whole body | SRR2294097 day old adult whole body | SRR2294098 day old adult whole body | SRR2294099 day old adult whole body | SRR2294100 day old adult whole body | SRR2294101 day old adult whole body | SRR2294102 day old adult whole body | SRR2294103 day old adult whole body | SRR2294104 day old adult whole body | SRR2294105 day old adult whole body | SRR2294106 day old adult whole body | SRR2294107 day old adult whole body | SRR2294108 day old adult whole body |
|---|---|---|---|---|---

ID	Coordinate	Coordinate	Class	Genome Locus
dvi_46 / scaffold_12928:7411718-7411775 +	**rnaMaker**	**Mature**	**intron**	(View on UCSC Genome Browser (Cane&Ribbon))

Legend: Stem Loop Mature Star Hairpin Arm Sequence

Predicted structure



Show Alignment Table

Fiches automatiques

Mirna:[Dvi-miR7976-mat],CSS:[Dvi-miR7976-mat],CSS:[Dvi-miR7976-star]

No Repeatable stacks found

Sense Strand Reads

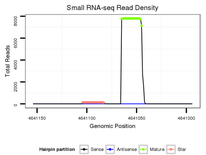
Hide Tip Tails Show Hid mismatch reads

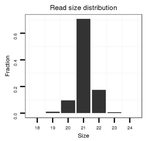
| Tip Tail | Hid Mismatch | Read ID | Strand | Start | End | Total | Sample | Sample | Sample

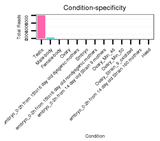
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_61	**scaffold_12723:4641044-4641104 -**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Control/Mirror)]

Legend: Genes TE Mismatch to dm3 reads* mismatch to hairpin

Predicted structure







No conservation details.

Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

nearest	star
5 dvi_63 scaffold_12723:4641063-4641063...	5 dvi_63 scaffold_12723:4641063-4641063...
3 dvi_60 scaffold_12723:4641036-4641056...	3 dvi_60 scaffold_12723:4641036-4641056...

Sense Strand Reads

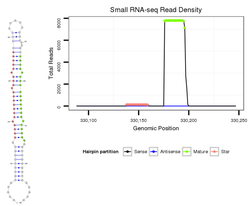
hide 3p reads show mid mismatch reads

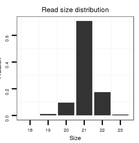
| ACTTGAAA

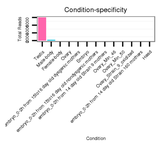
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_60	**scaffold_12963:330138-330197 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: genes TE mismatch to alignment mismatch to hairpin

Predicted structure







No conservation details.

Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

matures	star
1. dvi_61 scaffold_12723:464:883:464:883...	1. dvi_61 scaffold_12723:464:883:464:883...
2. dvi_60 scaffold_2963:330136:330198:+	2. dvi_60 scaffold_2963:330136:330198:+

Sense Strand Reads

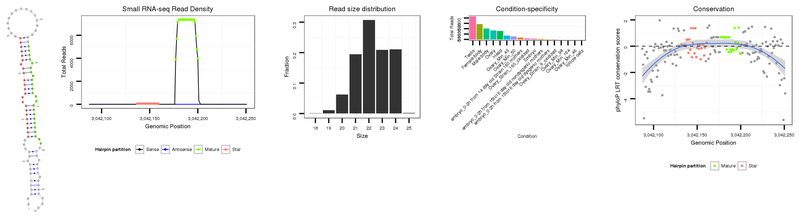
Hide 3p reads Show red mismatch reads

| ACTTGAAAAAAAACAAAAAAAAATATACATACTATATATATTTCAATC | ACTGACTAGATTTATCAGATTTTTTCATTTTTAC | GATATATAT

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_229	**scaffold_12970:3042137-3042201 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Cow4 Mmu)]

Legend: Genes 5p 3p mismatch to dvi_229 mismatch to mm

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatible elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	Alignment	Size	5p Mismatch	Count	Hit Total	Total Body	M047 Female Arpg8_testes_total	SRR040681	SRR040679	140x9_testes_total	SRR040689	V116 male head	V053 male body	SRR040688	W028 Ovary_Mix_43	SRR2096055	SRR2096057	SRR040687	140_females_carcasses_total	140_testes_total	SRR040683	SRR040648	140x8_males_carcasses_total	W027 male	SRR040672	9x140_females_carcasses_total	SRR040674	SRR040677	SRR040688	140_ovaries_total	SRR2096050 embryo_0-2h from 14 day old mothers	SRR040675	140x9_ovaries_total	SRR040674	9x140_ovaries_total	SRR2096014 Ovary_Strain_140_unidimed	SRR040656	9x140_ovaries_total	SRR040666	140_males_carcasses_total	SRR040654	140x9_ovaries_total	SRR2096041 embryo_0-2h from 14 day old mothers	SRR040669	140x9_females_carcasses_total	W041	SRR2096080 embryo_0-2h from 15to16 day old mothers	SRR2096081 embryo_0-2h from 15to16 day old mothers	SRR2096072 embryo_0-2h from 15to16 day old mothers	SRR2096079 embryo_0-2h from 15to16 day old mothers	SRR040659 Argentina_testes_total	SRR2096013 Ovary_Strain_9_unidimed	SRR040657 140_testes_total	SRR040686 Arpg8_0-2h_embryos_total	SRR2096058 Ovary_Mix_88	SRR040660 Argentina_ovaries_total	SRR040658 140_ovaries_total	SRR2096059 Ovary_Mix_144	GSM1528803 follicle	SRR040655 9x140_testes_total	SRR040684 140x8_0-2h_embryos_total	SRR040673 9_ovaries_total	SRR2096056 Ovary_Mix_68	SRR2096024 embryo_0-2h from 14 day old mothers
24	....TTTTCGCACATCTGTTAATTGAT....	0	1	1414.00	1414	137	152		125		44	34	40	39	108	83	37		24	23				23	25		55	56	60		34	50		40		30		28		10		39		11	9		18	7	6	3	2	0	1																			
22	....TTTTCGCACATCTGTTAATTGAT....	0	1	1124.00	1124	149	154		121		87	59	58	54	98	68	35		18	28				40	22		20	15	7		23	11		4		18		9		14		7		19		8	7	4	3	3	4	5		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	....TTTTCGCACATCTGTTAATTGAT....	0	1	1037.00	1037	102	109		100		45	31	47	38	60	51	44		24	34				30	34		27	30	17		31	31		21		16		21		14		14		24		10		5	1	5	2	4	5	2		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	....TTTTCGCACATCTGTTAATTGA....	0	1	1011.00	1011	222	95		103		173	145	43	56	0	1	20		46	20				12	8		3	4	1		0	2		2		2		3		13		5		0		2		2	1	2	2	3		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	....TTTTCGCACATCTGTTAATTGAA....	0	1	840.00	840	131	96		120		82	57	30	30	29		31		36		6	27		11	9		17	7	11		9	13		9		16		3		8		1		4		6		5	7	3	2	3	2	4		4		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	....TTTTCGCACATCTGTTAATTGA....	0	1	401.00	401	26	72		82	18	17	26		13	18	14	12		9	8		3	14		15	12		15	12	11		6	9		18		15		9		6		12		2		1		0	0	1	0	1		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	....TTTTCGCACATCTGTTAATTGA....	0	1	221.00	221	42	52		19		12	10	11	4	4	12	9		3	14		2	6		3	4		2	4	1		5	5		4		8		1		3		3		3		1		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
20	....TTTTCGCACATCTGTTAATTG....	0	1	184.00	184	14	14		7		9	16	13	5	0	0	3		1	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
20	....TTTTCGCACATCTGTTAATTG....	0	1	164.00	164	36	12		11		20	20	17	5	0	0	3		14	10		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	0	0	0	0	0	0	0	0	0	0	0	0	0
21	....TTTTCGCACATCTGTTAATTGA....	0	1	144.00	144	17	27		24		17	5	13	4	4	1	9		5	2		2	5		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	0	0	0
24	....TTTTCGCACATCTGTTAATTGAATTT....	0	1	131.00	131	5	12		13		2	0	5	5	15	16	5		5	2		2	5		8	4		2	6	4		6	6		1		0		0		2		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
23	....TTTCGCACATCTGTTAATTGAATT....	0	1	102.00	102	20	13		6	13	12	6		0	0	1	5		2	2		1	1		0	2		1	1	0		1	0		0		0		0		0		0		2		2		0	0	1	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	....TTTCGCACATCTGTTAATTGAATTT....	0	1	85.00	85	10	11		15	10	3	3		6	3	3	2		2	1		2	1		2	1		1	2	2		1	1		0		0		0		0		0		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	....TTTCGCACATCTGTTAATTGA....	0	1	56.00	56	7	4		1	6	3	3		6	6	2	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	....TTTCGCACATCTGTTAATTGA....	0	1	40.00	40	18	4		4	1	3	2		2	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	....TCATTTCTTATGTCCAAAAT....	0	1	39.00	39	2	1		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	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
19	....TTTTCGCACATCTGTTAATTG....	0	1	34.00	34	3	1		3		2	10	2	2	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	....TTTTCGCACATCTGTTAATTGAATTT....	0	1	27.00	27	2	1		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	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	....TTTTCGCACATCTGTTAATTGAATTT....	0	1	21.00	21	2	1		1	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	....TTTTCGCACATCTGTTAATTGA....	0	1	21.00	21	3	2		1	0	1	1		10	0	0	0		0	0		0	0		0	0		0	0	0		0	0		0		0		0		0		0		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	....TTTTCGCACATCTGTTAATTGAATTT....	0	1	19.00	19	1	0		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	0	0	0	0	0	0	0	0	0	0
23	....TTTTCGCACATCTGTTAATTGA....	0	1	18.00	18	1	0		2	1	1	0		0	0	1	1		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	0
24	....TTTTCGCACATCTGTTAATTGAATTT....	0	1	18.00	18	2	1		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	0	0	0	0	0	0	0	0
25	....TTTTCGCACATCTGTTAATTGAATTT....	0	1	18.00	18	1	1		2	1	0	1		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	0	0	0	0	0	0	0	0
24	....TTTTCGCACATCTGTTAATTGA....	0	1	16.00	16	1	1		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	0	0	0	0	0
19	....TTTTCGCACATCTGTTAATTG....	0	1	15.00	15	4	1		0	3	0	0		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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	....TTTTCGCACATCTGTTAATTGAATTT....	0	1	14.00	14	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	0	0	0	0	0	0	0
24	....TTTTCGCACATCTGTTAATTGA....	0	1	10.00	10	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	0	0	0	0	0	0	0
20	....TTTTCGCACATCTGTTAATTG....	0	1	10.00	10	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	....TCATTTCTTATGTCCAAAA....	0	1	9.00	9	4	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	0	0	0	0	0	0
22	....TTTTCGCACATCTGTTAATTGA....	0	1	9.00	9	3	2		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	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	....TCATTTCTTATGTCCAAAA....	0	1	8.00	8	4	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	0	0	0	0	0	0
22	....TTTTCGCACATCTGTTAATTGA....	0	1	7.00	7	0	2		0	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	....TTTTCGCACATCTGTTAATTGAA....	0	1	7.00	7	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	0	0	0	0	0
25	....TTTTCGCACATCTGTTAATTGAATT....	0	1	7.00	7	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	0	0	0	0	0
22	....TTTTCGCACATCTGTTAATTGA....	0	1	6.00	6	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	0	0	0	0	0	0	0
22	....TTTTCGCACATCTGTTAATTGA....	0	1	6.00	6	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	0	0	0	0	0	0	0
18	....TTTTCGCACATCTGTTAA....	0	1	4.00	4	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	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
22	....TTTTCGCACATCTGTTAATTGA....	0	1	4.00	4	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	0	0	0	0
19	....TTTCGCACATCTGTTAATTG....	0	1	4.00	4	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	0	0	0	0	0	0	0
20	....TTTCGCACATCTGTTAATTGA....	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		0		0		0		0		0		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	....CATTTCTTATGTCCAA....	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	0	0	0	0	0	0	0	0
19	....TTTTCGCACATCTGTTAATTG....	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	0	0	0	0
21	....TTTTCGCACATCTGTTAATTGAATTT....	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	0	0	0	0
21	....TTTTCGCACATCTGTTAATTGA....	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	0	0	0	0
21	....TTTTCGCACATCTGTTAATTGA....	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	0	0	0	0
24	....TTTTCGCACATCTGTTAATTGAATTT....	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		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	....TTTTCGCACATCTGTTAATTGA....	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		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	....TTTTCGCACATCTGTTAATTGAATTT....	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		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	....TTTTCGCACATCTGTTAATTGA....	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		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
24	....TTTTCGCACATCTGTTAATTGAATTT....	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		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	....TTTTCGCACATCTGTTAATTGA....	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		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
23	....TTTTCGCACATCTGTTAATTGAATTT....	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		0		0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
25	....TTTTCGCACATCTGTTAATTGAATTT....	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	0	0	0	0	0	0	0	0
25	....TTTTCGCACATCTGTTAATTGAATTT....	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	0	0	0	0	0	0	0	0

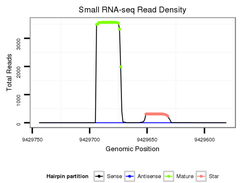
Anti-sense strand reads

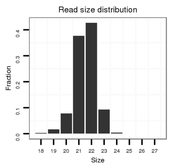
| Read # | Alignment | Size | 5p Mismatch | Count | Hit Total | Total | SRR040681 Arpg8_testes_total | SRR040682 9x140_0-2h_embryos_total | SRR040686 Arpg8_0-2h_embryos_total | SRR040684 140x9_0-2h_embryos_total | W028 head | SRR040660

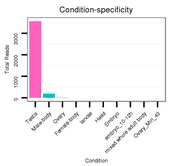
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_66	**scaffold_12970:9429631-9429694 -**	**confident**	**Testes-restricted**	**antisense_to_intron**	[View on UCSC Genome Browser (Comfl Mirror)]

Legend: sense star mismatch in alignment mismatch in star

Predicted structure







No conservation details.

Show Alternate Folds

Flybase annotation

Antisense to intron [Dvir(GI19449-in]

No Repeatable elements found

Sense Strand Reads

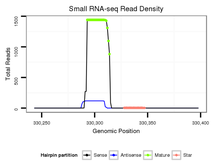
hide 3p reads show mid mismatch reads

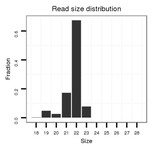
AGTTGATTTAACCCAGTTATTTTATAAGCTTAGTTTGAGTCACATGTGC	Read # size	Hit	Total Norm	Total	SRR060681 Arga9_testes_total	SRR060678 9x140_testes_total	SRR060689 160x9_testes_total	SRR060683 140_testes_total	V116 male body	SRR060659 Argentina_testes_total	SRR060670 9_testes_total	SRR060679 140x9_testes_total	SRR060680 Â 9xArg_testes_total	M027 male body	SRR060655 9x160_testes_total	SRR060657 140_testes_total	M047 female body	SRR060677 Arga9_ovaries_total	SRR2096060 Ovary_Min_193	SRR1106728 larvae	SRR060656 9x160_ovaries_total	SRR060658 140_ovaries_total	SRR1106727 larvae	SRR1106729 mixed whole adult body	V053 head	SRR060676 9xArg_ovaries_total	SRR060686 Arga9_0-2h_embryos_total	SRR2096014 Ovary_Strain_160_oxidized	SRR2096055 Ovary_Min_43	SRR2096059 Ovary_Min_164	SRR060654 160x9_ovaries_total	SRR060667 160_females_carcasses_total	SRR060668 160x9_males_carcasses_total	SRR060673 9_ovaries_total	SRR1106721 embryo_10-12h	SRR1106730 embryo_16-30h	SRR2096013 Ovary_Strain_9_oxidized	SRR2096056 Ovary_Min_46	SRR2096080 embryo_0-2h from 13to14 W147 day old nondyspanic mothers	SRR060462 9x140_0-2h_embryos_total	SRR2096050 embryo_0-2h from 14 day old Strain 160 mothers
**********	Size	Mismatch	Count																																						
.....TTTGCACAGCGGTCTTTTTAA.....	23	0	1	1577.00	1209	0	110	92	56	54	0	0	0	0	0	0	0	1	0	1	0	0	0	1	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTTGCACAGCGGTCTTTTTAA.....	21	0	1	1326.00	1326	1014	0	99	100	59	50	0	0	0	1	0	0	0	2	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTTGCACAGCGGTCTTTTTAAT.....	23	1	1	1003.00	1003	480	0	161	99	121	22	0	0	0	0	0	0	4	0	0	1	0	0	1	2	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0
.....TTTGCACAGCGGTCTTTTTAATG.....	23	0	1	338.00	338	149	0	45	9	29	88	0	0	0	0	0	0	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
.....TTTGCACAGCGGTCTTTTTA.....	20	0	1	207.00	207	160	0	19	19	11	8	7	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
.....TTTGCACAGCGGTCTTTTTAA.....	22	1	1	191.00	191	136	0	16	9	14	13	0	0	0	0	0	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
.....TTTGCACAGCGGTCTTTTTAAT..... TAAAAGCACCGCCCGCACAAT.....	23	1	1	76.00	76	58	0	3	1	5	2	0	1	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
.....TTTGCACAGCGGTCTTTTTAAT..... TAAAAGCACCGCCCGCACAA.....	23	1	1	52.00	52	39	0	0	2	4	3	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
.....TTTGCACAGCGGTCTTTTTAATGG..... TAAAAGCACCGCCCGCACA.....	20	0	1	49.00	49	33	0	2	3	3	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
.....TTTGCACAGCGGTCTTTTTAATGG.....	24	2	1	46.00	46	34	0	4	4	5	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
.....TTTGCACAGCGGTCTTTTTAA..... TAAAAGCACCGCCCGCACAA.....	21	0	1	45.00	45	34	0	2	0	1	1	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
.....TTTGCACAGCGGTCTTTTTAATGG.....	24	2	1	34.00	34	21	0	0	1	4	4	0	0	0	3	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
.....TTTGCACAGCGGTCTTTTT.....	19	0	1	28.00	28	20	0	2	4	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
.....TGCACAGCGGTCTTTTTAATG.....	21	0	1	25.00	25	16	0	2	0	1	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
.....TTTGCACAGCGGTCTTTTTAAT.....	23	2	1	21.00	21	16	0	0	2	1	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
.....TAAAAGCACCGCCCGCACAC.....	20	0	1	21.00	21	13	2	1	0	0	2	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
.....TAAAAGCACCGCCCGCACAAT.....	23	0	1	15.00	15	11	3	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
.....TAAAAGCACCGCCCGCACAA.....	22	0	1	15.00	15	10	1	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	0	0
.....TAAAAGCACCGCCCGCACA.....	21	0	1	14.00	14	10	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	0	0	0	0	0	0
.....TAAAAGCACCGCCCGCAC.....	19	0	1	13.00	13	11	1	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
.....TTTGCACAGCGGTCTTTTTAA.....	22	1	1	12.00	12	7	0	1	0	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
.....TTTGCACAGCGGTCTTTTTAAT.....	23	1	1	12.00	12	6	0	2	0	0	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
.....TAAAAGCACCGCCCGCACAAT.....	23	1	1	11.00	11	6	1	2	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
.....TAAAAGCACCGCCCGCACA.....	19	0	1	11.00	11	8	1	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
.....TTTGCACAGCGGTCTTTTT.....	20	0	1	11.00	11	7	0	3	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
.....TTTGCACAGCGGTCTTTTTAATG.....	24	2	1	10.00	10	8	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	0	0	0	0	0	0	0	0	0
.....TGCACAGCGGTCTTTTTAATGTGG.....	24	0	1	10.00	10	7	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	0	0	0	0	0	0
.....TGCACAGCGGTCTTTTTAATGTG.....	23	0	1	9.00	9	6	0	1	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
.....TTTGCACAGCGGTCTTTTTAATGGG.....	25	3	1	8.00	8	4	0	3	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
.....TTTGCACAGCGGTCTTTTTAATCCG.....	25	3	1	8.00	8	7	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	1
.....TTTGCACAGCGGTCTTTTTAA.....	21	2	1	7.00	7	6	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
.....TTTGCACAGCGGTCTTTTT.....	18	0	1	6.00	6	4	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
.....TTTGCACAGCGGTCTTTTTAAT.....	21	0	1	6.00	6	2	0	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
.....TGCACAGCGGTCTTTTTAATGT.....	22	0	1	6.00	6	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
.....TTGCACAGCGGTCTTTTTAA.....	20	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TAAAAGCACCGCCCGCACAAT.....	23	1	1	5.00	5	5	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
.....TTTTTAATGTGGTTGTTTTGAGA.....	24	0	1	5.00	5	3	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
.....CTTTAAAAGCACCGCCCGCACA.....	23	0	1	5.00	5	1	2	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	0	0	0	0	0	0
.....TTTGCACAGCGGTCTTTTTAATGTGG.....	22	0	1	5.00	5	3	0	0	0	1	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
.....CTTTAAAAGCACCGCCCGCA.....	19	0	1	5.00	5	3	0	0	0	1	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
.....TTTGCACAGCGGTCTTTTTAA.....	24	0	1	4.00	4	3	0	0	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
.....ATCTTTAAAAGCACCGCCGCG.....	21	0	1	4.00	4	2	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	0
.....TTTGCACAGCGGTCTTTTTAAT.....	20	0	1	4.00	4	3	0	0	0	0	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
.....TCTTTAAAAGCACCGCCGCG.....	20	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	0	0	0	0	0	0	0	0
.....TGCACAGCGGTCTTTTTAAT.....	21	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTTGCACAGCGGTCTTTTTAA.....	22	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TAAAAGCACCGCCCGCACG.....	20	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TAAAAGCACCGCCCGCACAAT.....	23	0	1	4.00	4	3	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
.....TTTGCACAGCGGTCTTTTT.....	21	0	1	4.00	4	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	0	0	0
.....TTTGCACAGCGGTCTTTTTAAT.....	22	1	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	0	0	0	0	0	0	0	0
.....TTTGCACAGCGGTCTTTTTAA.....	22	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
.....TTTGCACAGCGGTCTTTTTAA.....	18	0	1	4.00	4	1	0	0	0	0	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	0	0	0	0	0	0
.....TTTGCACAGCGGTCTTTTTAA.....	21	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
.....TTTGCACAGCGGTCTTTTTAAAG.....	24	3	2	4.00	8	5	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	1
.....ATCTTTAAAAGCACCGCCGC.....	22	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	0	0	0	0	0	0	0	0	0	0	0	0
.....TTTGCACAGCGGTCTTTTTAAT.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTTGCACAGCGGTCTTTTTG.....	20	1	1	3.00	3	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
.....TTTGCACAGCGGTCTTTTTAAGG.....	22	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCACAGCGGTCTTTTTAATGTGG.....	26	1	1	3.00	3	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
.....TTTGCACAGCGGTCTTTTTG.....	21	1	1	3.00	3	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
.....TAAAAGCACCGCCCGCACAA.....	21	1	2	2.00	2	2	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
.....TTTGCACAGCGGTCTTTTTA.....	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	0	0	0	0	0	0
.....AAAAGCACCGCCCGCACAAT.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CTTTAAAACACCGCCGCCA.....	21	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
.....TCATGGGACTTAGCTTAAACATT.....	24	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
.....AAAAGCACCGCCCGCACAAT.....	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
.....TTTGCACAGCGGTCTTTTTAAG.....	22	2	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	0	0	0	0	0	0
.....TTTGCACAGCGGTCTTTTTAA.....	21	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
.....CTTTAAAAGCACCGCCCGCAC.....	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	0	0	0	0	0	0	0	0	0	0	0	0
.....TCATGGGACTTAGCTTAAACG.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATCTTTAAAAGCACCGCCGC.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTTTAAGCACCGCCCGCACG.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCATGGGACTTAGCTTAAACA.....	21	0	1	1.00	1	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
.....TCATGGGACTTAGCTTAAAC.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTTAATGTGGTTGTTTTGAGA.....	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

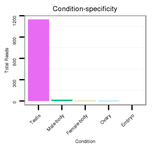
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_104	**scaffold_12963:330293-330348 +**	**confident**	**Testes-restricted**	**intergenic**	View on UCSC Genome Browser (Cornell Mirror)

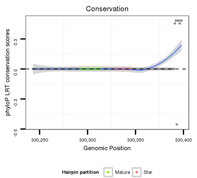
Legend: **hairpin** **star** **mature 5 (5' arm)** **mature 3 (3' arm)**

Predicted structure









Show Alternate Folds

FlyBase annotation

intergenic

No Repeatible elements found

nearest	star
1. dvi_71 scaffold_12723:6464907-6465984 ;	
2. dvi_104 scaffold_12963:330293-330318 +	

Sense Strand Reads

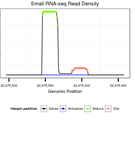
Hide 3p reads show mid mismatch reads

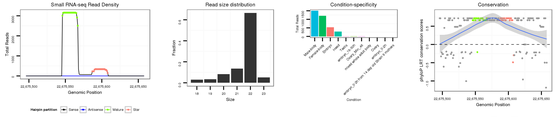
| GACTATTAAACGATAACAAGTGACGATGGGAATAAACCTTATCTAATTTAGACACGATCAACATTTAATTCTCTTCACATTTATTAAACCTTGGTGCACCCTCTAATTATTAGGACCTTATCGATTCCGTTCCGATTATCTTCGGCAAACAA | Read # | Hit | Total | SRR060678 | SRR060681 | SRR060679 | SRR060670 | SRR060680 | SRR060689 | SRR060683 | SRR060655 | Y116 | SRR060657 | SRR060659 | M047 | M027 | SRR060674 | SRR060656 | SRR060676 | SRR060677 | SRR060688 | SRR2096013 | SRR060658 | SRR060671 | SRR060682 | SRR060684 | SRR2096059 | Y047 | SRR060666 | SRR060672 | SRR060673 | SRR060675 | SRR060685 | SRR060686 | SRR11104728 | SRR2096056 | SRR2096081 embryo_0-2h from 15x16 day old nondiapausing mothers |
|---|---|---|---|---|---

ID	Coordinate	Confidence	Class	Genome Locale
dvi_17	**scaffold_13049:22675546-22675698 +**	**confident**	**Canonical miRNA**	**intergenic**

Score: **[redacted]**

Predicted structure





Show Alternate Fields

Flybase annotation

intergenic

No Repeatmk classes found

Sense Strand Reads

Sorts by reads | show red mismatch reads

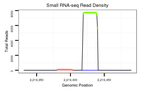
| Seq | Reads | Mismatch | Count | Mean | Total | MEL8 | YV32 | DMR00454 | DMR00455 | DMR00456 | DMR00457 | DMR00458 | DMR00459 | DMR00460 | DMR00461 | DMR00462 | DMR00463 | DMR00464 | DMR00465 | DMR00466 | DMR00467 | DMR00468 | DMR00469 | DMR00470 | DMR00471 | DMR00472 | DMR00473 |

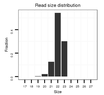
ID	Coordinate	Confidence	Size	Strands Locus
dvi_70_scaffold_13049:2219381-2219440 +		**confident**	**Mature**	**intron**

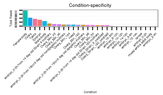
[View miRDeep Manual] [Email Mirco]

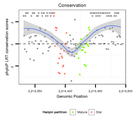
Legend: Mature Star Precursor Loop Conserved Mature

Predicted structure









Show Alternate Fold

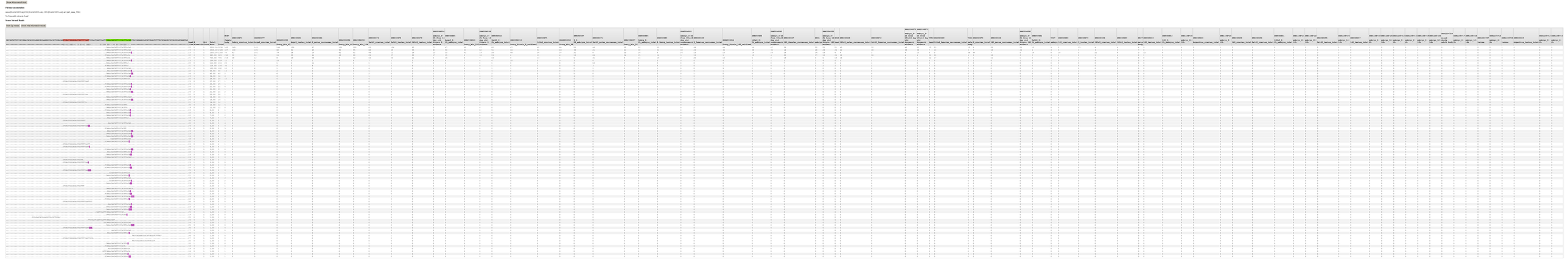
Flybase annotation

dmel:[Dmel2R3:dp] CR9:[Dmel2CR9:ccdp] CR9:[Dmel2CR9:ccdp] ref:[ref_nosq_FB6]

No Ryanodin clients found

Some Read Reads

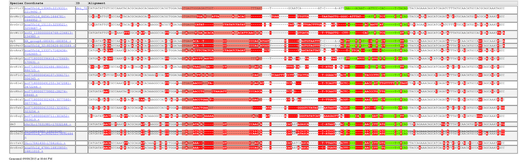
Hide Tip Reads Show Not Mismatch Reads



Antisense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

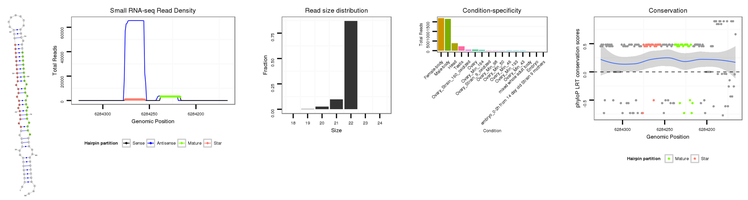


Generated MSAs (Fast & Slow Pw)

ID:	Coordinate:		Confidence:	Class:	Genomic Locale:	
dvi_37	**scaffold_12855:6284216-6284276 -**		**confident**	**Testes-restricted**	**intron**	[View on UCSC Genome Browser (GenoBrowser)]

Legend: exons pre mature 5 arm loop 3' mismatch/error

Predicted structure



Show Alternate Fields

FlyBase annotation

mir-2(FBGE0[illegible])

No Repeatible elements found

Sense Strand Reads

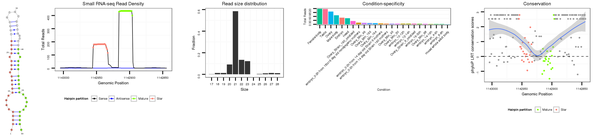
Hide 3p reads show red mismatch reads

| CACTTTGCAGCACTGGCACGCTTTTTCTGCAGAATCTAGCTTGATGCC | ACCACAATCAATAACAATC | TTTCTAAGCTAACAATAC | ATTTCTTATTTTTTTATCCTCA | TCAGAAATTTGACTCCTGGCATCGGACAGCAGTGAGCTCTGCTGTTTCTTCGCACAC | Read # | Bit size | Mismatch | Total Count | Total Reads | MG47 V116 male body | V053 male body | SRR2096072 head | Rel40_females_carcasses_total | SRR2096065 | SRR2096067 | 3_females_carcasses_total | SRR2096071 | Rel40_males_carcasses_total | SRR2096064 | 3_males_carcasses_total | SRR2096066 | 140_males_carcasses_total | MG28 head | SRR2096054 | 140w8_males_carcasses_total | SRR2096068 | 140w8_testes_total | SRR2096089 | Arge8_testes_total | SRR2096081 | 140w8_females_carcasses_total | SRR2096069 | 140w8_females_carcasses_total | SRR2096079 | 140w8_testes_total | SRR2096059 male body | Rel40_testes_total | MG27 male body | SRR2096078 | 140_testes_total | SRR2096083 | Rel40_testes_total | SRR2096055 | 3_testes_total | SRR2096070 | Rel40_overies_total | SRR2096090 | Rel40_ovaries_total | SRR2096013 | SRR2096058 | SRR2096057 | Rebrg_overies_total | SRR2096074 | Rel40_overies_total | SRR2096076 | Arge8_overies_total | SRR2096077 | 140_testes_total | SRR2096056 | 140_overies_total | SRR2096073 | SRR2096059 | Argentina_testes_total | SRR2096075 | 140w8_overies_total | SRR2096058 | 140_overies_total | SRR2096053 | SRR2096060 | 140_overies_total | SRR2096089 | 140w8_overies_total | SRR2096054 | 140w8_overies_total | SRR2096056 | SRR2096038 embryos_0-2h from 14.15hr16 day old embryos | SRR2096081 embryos_0-2h from 14.15hr16 day old embryos | SRR1106729 mixed whole adult body | MG47 V116 male body | SRR2096062 Rel40_0-2h_embryos_total | SRR2096063 140_0-2h_embryos_total |
|---|---|---|---|---|---|---

ID	Coordinate	Confidence	Class	Genome Locale
chr1_57 / scaffold_13246:1142894-1142955	**+:conflicts**	**Mirtron**	**intron**	Click on UCSC Genome Browser (Crash?Bites!)

Strand: **+** **-** Pairing: **Perfect** **Mismatch** **Bulge/Loop**

Predicted structure



Show Alternative Folds

Flybase annotation

dmel:[Dm6:0:0:0:0] sp:[TB:[Dm6:0:0:0:0:0:1:1:0]] CSR:[Dm6:0:0:0:0:1:1]

No Alignable Genes Found

Some Strand Reads

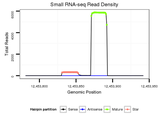
Hide Sp Reads | Show PRE-MAPMER Reads

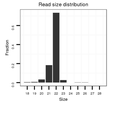
| | | |

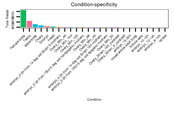
ID	Coordinate	Confidence	Class	Genome Locale
dvi_16654	**scaffold_13047:12453831-12453892 +**	confident	Mirtron	[View on UCSC Genome Browser, [GeneRil, Mirtrons]

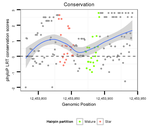
Legend: Stem 5p Terminal Loop Stem 3p

Predicted structure









Show Alternate Folds

Flybase annotation

exon:[Fmr1(CG11148):exon(12411-ub)] CDS:[Fmr1(CG11148)]

No Repeats clients found

Some Strand Reads

hide 3p reads | show mid mismatch reads

| Seq | Pos | Total | MEF2 Dmel Body | SRR2556451 Adult_Ovries_total | SRR2556478 Testis_Ovries_total | SRR2556479 Adult_Testes_total | SRR2556444 Adult_Ovries_total | SRR2556472 Testis_Testes_carcasses_total | SRR2556471 Testis_Ovries_carcasses_total | SRR2556480 Testis_Testes_total | SRR2556445 Adult_Testes_carcasses_total | SRR2556468 Testis_Ovries_carcasses_total | SRR2556447 Adult_Ovries_total | SRR2556476 Testis_Testes_carcasses_total | SRR2556477 Testis_Ovries_total | MCH SRR2556469 Testis_Testes_carcasses_total | YY22 SRR2556474 Testis_Ovries_total | MOG1 Dmel Ovries | SRR2556232 Dmel_Mix_OR | SRR2556446 Adult_Testes_carcasses_total | SRR2556462 Dmel_Mix_OR_adenylos_total | SRR2556233 Dmel_Mix_OR | SRR2556475 Testis_Ovries_total | SRR2556234 Dmel_Mix_OR | SRR2556235 Dmel_Mix_OR | SRR2556463 Dmel_Mix_OR | SRR2556464 Dmel_Mix_OR | SRR2556465 Dmel_Mix_OR | SRR2556466 Dmel_Mix_OR | SRR2556467 Dmel_Mix_OR | SRR2556473 Testis_Testes_carcasses_total | SRR2556236 Dmel_Mix_OR | SRR2556237 Dmel_Mix_OR | SRR2556238 Dmel_Mix_OR | SRR2556239 Dmel_Mix_OR | SRR2556240 Dmel_Mix_OR | SRR2556241 Dmel_Mix_OR | SRR2556242 Dmel_Mix_OR | SRR2556243 Dmel_Mix_OR | SRR2556244 Dmel_Mix_OR | SRR2556245 Dmel_Mix_OR | SRR2556246 Dmel_Mix_OR | SRR2556247 Dmel_Mix_OR | SRR2556248 Dmel_Mix_OR | SRR2556249 Dmel_Mix_OR | SRR2556250 Dmel_Mix_OR | SRR2556251 Dmel_Mix_OR | SRR2556252 Dmel_Mix_OR | SRR2556253 Dmel_Mix_OR | SRR2556254 Dmel_Mix_OR | SRR2556255 Dmel_Mix_OR | SRR2556256 Dmel_Mix_OR | SRR2556257 Dmel_Mix_OR | SRR2556258 Dmel_Mix_OR | SRR2556259 Dmel_Mix_OR | SRR2556260 Dmel_Mix_OR | SRR2556261 Dmel_Mix_OR | SRR2556262 Dmel_Mix_OR | SRR2556263 Dmel_Mix_OR | SRR2556264 Dmel_Mix_OR | SRR2556265 Dmel_Mix_OR | SRR2556266 Dmel_Mix_OR | SRR2556267 Dmel_Mix_OR | SRR2556268 Dmel_Mix_OR | SRR2556269 Dmel_Mix_OR | SRR2556270 Dmel_Mix_OR | SRR2556271 Dmel_Mix_OR | SRR2556272 Dmel_Mix_OR | SRR2556273 Dmel_Mix_OR | SRR2556274 Dmel_Mix_OR | SRR2556275 Dmel_Mix_OR | SRR2556276 Dmel_Mix_OR | SRR2556277 Dmel_Mix_OR | SRR2556278 Dmel_Mix_OR | SRR2556279 Dmel_Mix_OR | SRR2556280 Dmel_Mix_OR | SRR2556281 Dmel_Mix_OR | SRR2556282 Dmel_Mix_OR | SRR2556283 Dmel_Mix_OR | SRR2556284 Dmel_Mix_OR | SRR2556285 Dmel_Mix_OR | SRR2556286 Dmel_Mix_OR | SRR2556287 Dmel_Mix_OR | SRR2556288 Dmel_Mix_OR | SRR2556289 Dmel_Mix_OR | SRR2556290 Dmel_Mix_OR | SRR2556291 Dmel_Mix_OR | SRR2556292 Dmel_Mix_OR | SRR2556293 Dmel_Mix_OR | SRR2556294 Dmel_Mix_OR | SRR2556295 Dmel_Mix_OR | SRR2556296 Dmel_Mix_OR | SRR2556297 Dmel_Mix_OR | SRR2556298 Dmel_Mix_OR | SRR2556299 Dmel_Mix_OR | SRR2556300 Dmel_Mix_OR | SRR2556301 Dmel_Mix_OR | SRR2556302 Dmel_Mix_OR | SRR2556303 Dmel_Mix_OR | SRR2556304 Dmel_Mix_OR | SRR2556305 Dmel_Mix_OR | SRR2556306 Dmel_Mix_OR | SRR2556307 Dmel_Mix_OR | SRR2556308 Dmel_Mix_OR | SRR2556309 Dmel_Mix_OR | SRR2556310 Dmel_Mix_OR | SRR2556311 Dmel_Mix_OR | SRR2556312 Dmel_Mix_OR | SRR2556313 Dmel_Mix_OR | SRR2556314 Dmel_Mix_OR | SRR2556315 Dmel_Mix_OR | SRR2556316 Dmel_Mix_OR | 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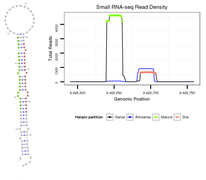
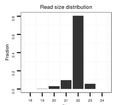
|---|---|---|---|---

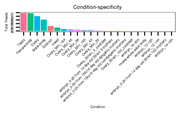
ID	Coordinate	Confidence	Class	Genome Locale
dvi_51	**scaffold_12970:9426640-9426709 +**	**confident**	**Textiso-rest/strict**	**intron**

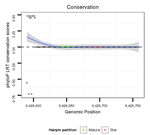
Length: **69 nt** (**Textiso-rest/strict**, **intronic**)

Predicted structure









Show Alternate Folds

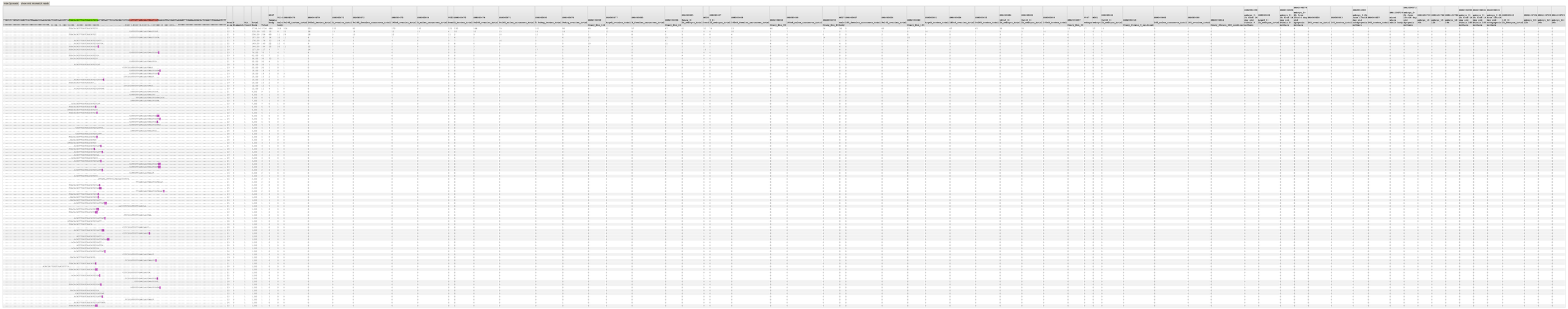
Flybase annotation

mapa:(Dmel)FBM0-mg

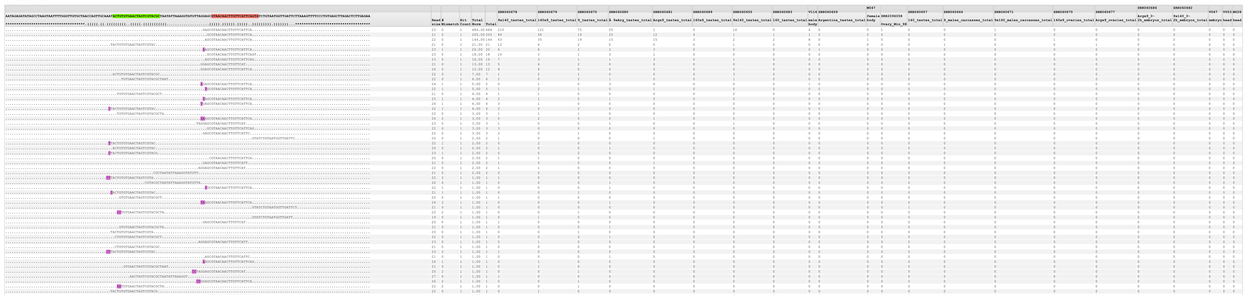
No flyanadb clusters found

Same Strand Reads

Scale: Zp reads | show mid mismatch reads



Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthology

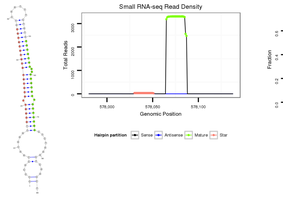
Species	Coordinate	ID	Alignment
[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]

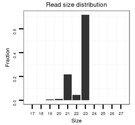
Generated 2026-02-24 at 00:21 PM

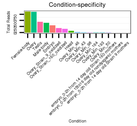
ID:	Coordinate:	Confidence:	Class:	Genome Locale:
dvi_237	**scaffold_12928:578030-578088 +**	**confident**	**Canonical miRNA**	**intron**
				[View on UCSC Genome Browser (Cured3 Mmu1)]

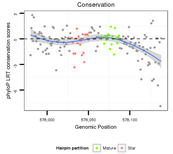
Legend: Loop 5p 3p Mismatch in alignment Mismatch in hairpin

Predicted structure









Show Alternate Folds

Flybase annotation

intron:Dvir5.0:7376-up

Repeatable elements

None	Class	Family	Name
BOX: 1mq13.TE	Pan	1-	

Sense Strand Reads

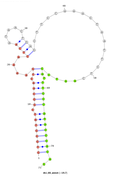
Hide 3p reads | Show mid-mismatch reads

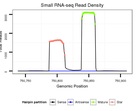
| Seq | Read # | Size | M.mismatch | NUL Count | Total Nuclm | Total | WD47 Female body | SRR040474 fedwg_ovarian_total | SRR040477 hrpp5_ovarian_total | SRR039513 Ovary_Strain_9_unidiscd | SRR040464 hrpp5_carcasses_total | SRR040474 Nc160_ovarian_total | SRR039514 Ovary_Strain_160_unidiscd | SRR040467 hrpp5_female_carcasses_total | SRR040475 14Daf8_ovarian_total | SRR040481 hrpp5_testes_total | SRR040478 Nc160_testes_total | SRR040472 Nc160_female_carcasses_total | SRR040479 14Daf8_testes_total | SRR040465 hrpp5_female_carcasses_total | SRR040485 fedwg_0-2h_embryos_total | SRR040468 14Daf8_male_carcasses_total | VG53 Nc160_0-2h_embryos_total | SRR040482 hrpp5_male_carcasses_total | SRR040469 14Daf8_female_carcasses_total | SRR040466 140_male_carcasses_total | SRR040486 hrpp5_0-2h_embryos_total | SRR040484 14Daf8_0-2h_embryos_total | SRR040471 Nc160_male_carcasses_total | SRR040487 Nc160_0-2h_embryos_total | SRR040480 fedwg_testes_total | SRR039056 Ovary_Mix_4 | SRR039058 Ovary_Mix_8 | SRR039055 Ovary_Mix_43 | SRR039059 Ovary_Mix_164 | SRR040473 3_ovarian_total | SRR040489 14Daf8_testes_total | SRR040488 140_ovarian_total | SRR040456 Nc160_ovarian_total | SRR039061 Ovary_Mix_193 | SRR040454 14Daf8_ovarian_total | SRR040483 140_testes_total | V047 ambryo | M041 ambryo | SRR039057 Ovary_Mix_50 | M028 head_3_testes_total | SRR039041 embryo_0-2h from 14.9716 day old Strain 18 male mothers | SRR040455 Nc160_male carcasses_total | SRR039038 embryo_0-2h from 14 day old Strain 9 mothers | SRR039080 embryo_0-2h from 15hr14 day old Strain 18 mothers | SRR039081 embryo_0-2h from 15hr14 day old Strain 9 mothers | SRR039024 embryo_0-2h from 14 day old Strain 18 mothers | SRR040462 Nc160_0-2h embryos_total | SRR039036 embryo_0-2h from 14 day old Strain 9 mothers |
|---|---|---|---|---

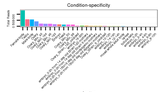
ID	Coordinate	Confidence	Class	Genome Locale
dv1_68_scaffold_13047:759788-759860 +		coeliacus	Mirtrons	intron

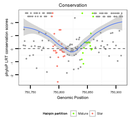
Legend: DICER MATURE 5-PRIME MATURE 3-PRIME MATURE

Predicted structure









Show Alternate Folds

Flybase annotation

intron:[759182759440-.sg:CR0:(2R+0)]759440-.sg:CR0:(2R+0)[759440-.sg]

1x Exonate closest hit

Sense Strand Reads

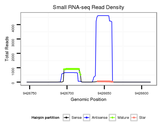
Hide 3p reads | Show mid mismatch reads

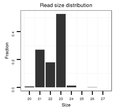
| | | |

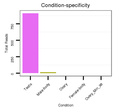
ID	Coordinate	Confidence	Class	Genome Locale	
dvi_328	**scaffold_12970:9426638-9426704 -**	**confident**	**Testes+restricted**	**antisense_to_intron**	Click on UCSC Genome Browser (Cartoll Mirror)

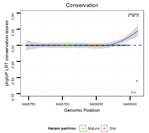
Length: **66bp** (**G:** 0.000 **A:** 0.000 **T:** 0.000 **C:** 0.000 **N:** 0.000)

Predicted structure









Show Alternate Folds

Flybase annotation

Nearest to intro [FBGN0259671:ej]

No Repeats (Genome Scan)

Some Sense Reads

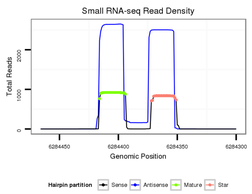
Scale 5p reads | show mid mismatch reads

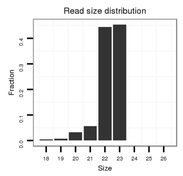
| TTCTCAAATTCAAATTCTCCTTTTAAACTTCTTAATTCTTAATTCTTAATCTTTAATTCTTAATCTTTAATTCTTAATCT

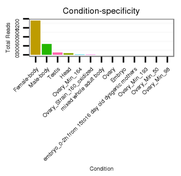
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_79	**scaffold_12855:6284350-6284416 -**	**confident**	**Testes-restricted**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

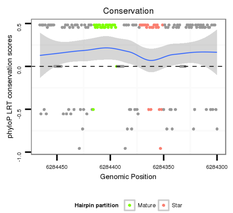
Legend: sense 5p 3p mismatch in alignment mismatch in miRNA

Predicted structure









Show Alternate Folds

Flybase annotation

intron [Dv-nGI H228-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AATGTGTGTATTTATGTTATCTGAAATGTTGTTTTGGCTGTAGACTTAG-CTGTGTACCACCATCAACTTTCTGCATTTAGAAACTCAATTAA-AAAATTGATGTGGTTCACCGCGCAGTCTAGACAGCACTACTACGAACACTTTACAACACTGGCACGCTTTTTG					M047 female body	SRR060672 9x160_females_carcasses_total	SRR060671 9x160_males_carcasses_total	SRR060665 9_females_carcasses_total	SRR060667 160_females_carcasses_total	V116 male body	V053 head	SRR060664 9_males_carcasses_total	SRR060669 160x9_females_carcasses_total	SRR060668 160x9_males_carcasses_total	SRR060666 160_males_carcasses_total	SRR060681 Argx9_testes_total	SRR060679 140x9_testes_total	M027 male body	M028 head	SRR2096059 9x140_testes_total	SRR060678 Ä 9xArg_testes_total	SRR060680 140_testes_total	SRR2096014 Ovary_Strain_160_oxidised	SRR060655 9x160_testes_total	SRR060676 9xArg_ovaries_total	SRR1106729 mixed whole adult body	SRR060659 Argentina_testes_total	SRR060689 160x9_testes_total	M041 embryo Ovary_Min_50	SRR2096057 140_testes_total	SRR060657 9_testes_total	SRR060670 160_testes_total	SRR060683	SRR2096058 Ovary_Min_98	SRR2096040 Ovary_Min_193	SRR2096079 embryo_0-2h from 15x16 day old dysgenic mothers
**********	(((	((((((((((.	(((((.	(((((.	((((.	((.	(((.	((.	((.	((.	))).	))))).	)))))))))).	))))))))))).	))))))))))).	))))).	))).	**********																		
.....	.....	.....	.....	.....	.....	23 0	1	718.00 718	454 38	46	35	16	22 16 21	16	15	16	10	9	13 6 3	6	5	0	2	3	3	0	0	0	0	1	1	0	1	0
.....	.....	.....	.....	.....	.....	22 0	1	604.00 604	137 93	68	51	70	37 18 25	25	29	18	12	10	1 1 0	2	2	0	0	0	1	2	0	0	0	1	0	1	0	0
.....	.....	.....	.....	.....	.....	22 0	1	103.00 103	85 1	5	4	1	0 3 2	0	1	0	0	0	1 1 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	22 0	1	85.00 85	10 17	4	7	2	13 11 6	3	2	2	2	2	0 0 0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	21 0	1	50.00 50	30 1	4	1	4	0 2 0	0	0	3	1	0	1 1 0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	20 0	1	44.00 44	15 3	1	4	4	5 2 0	1	1	0	2	1	0 0 0	0	1	0	0	0	0	1	0	0	1	0	0	0	1	0
.....	.....	.....	.....	.....	.....	23 0	1	38.00 38	13 2	1	2	1	1 0 2	1	2	0	0	0	4 3 4	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	24 1	1	36.00 36	22 2	2	2	2	1 1 0	2	1	0	0	1	1 0 0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	22 0	1	29.00 29	10 2	4	2	0	3 2 0	0	0	0	3	2	1 0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	23 1	1	28.00 28	3 5	4	4	1	5 1 3	1	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	13.00 13	3 0	1	0	2	2 0 1	1	0	0	1	0	0 0 2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	21 0	1	13.00 13	11 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
.....	.....	.....	.....	.....	.....	21 1	1	9.00 9	9 0	0	0	0	0 0 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 1	1	9.00 9	0 4	0	1	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
.....	.....	.....	.....	.....	.....	21 1	1	6.00 6	4 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
.....	.....	.....	.....	.....	.....	20 0	1	5.00 5	2 1	0	0	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
.....	.....	.....	.....	.....	.....	21 1	1	5.00 5	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
.....	.....	.....	.....	.....	.....	19 0	1	5.00 5	3 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
.....	.....	.....	.....	.....	.....	18 0	1	4.00 4	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	0	0
.....	.....	.....	.....	.....	.....	19 0	1	4.00 4	1 1	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
.....	.....	.....	.....	.....	.....	22 1	1	3.00 3	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
.....	.....	.....	.....	.....	.....	21 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
.....	.....	.....	.....	.....	.....	22 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	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	21 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	0	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	23 1	1	3.00 3	1 0	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	0	0	0
.....	.....	.....	.....	.....	.....	18 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	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	21 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
.....	.....	.....	.....	.....	.....	22 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	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	22 1	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	0
.....	.....	.....	.....	.....	.....	21 0	1	2.00 2	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
.....	.....	.....	.....	.....	.....	19 0	1	2.00 2	0 0	0	0	0	0 0 0	0	0	0	0	0	0 2 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	21 0	1	2.00 2	0 0	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
.....	.....	.....	.....	.....	.....	22 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
.....	.....	.....	.....	.....	.....	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	0	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	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	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	25 3	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
.....	.....	.....	.....	.....	.....	25 2	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
.....	.....	.....	.....	.....	.....	22 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
.....	.....	.....	.....	.....	.....	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	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	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	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	24 2	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
.....	.....	.....	.....	.....	.....	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	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	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	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
.....	.....	.....	.....	.....	.....	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	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	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	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	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	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	22 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
.....	.....	.....	.....	.....	.....	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	0	0	0	0	0	0	0	0	0	0	0

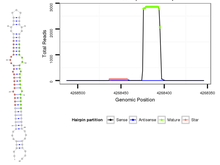
Anti-sense strand reads

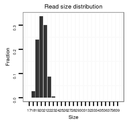
TTAACAACATAAAATACAATAGACTTTACAACAAAACGGACATCTGAATC-GACACATGGTGGTGATTGAAAGA-GCATAAACTTTCAGTTAATT-TTTTAACTACACCAAGTGGCGA-TCAGATCTGTCGTGATGATGCTTGTGAAATGTTGTGACCGTGCGAAAAAC						SRR060681 Argx9_testes_total	SRR060678 9x140_testes_total	SRR060679 140x9_testes_total	SRR060680 9xArg_testes_total	SRR060657 140_testes_total	M027 male body	SRR060670 9_testes_total	M047 female body	SRR060659 Argentina_testes_total	SRR060689 160x9_testes_total	SRR060655 9x160_testes_total	SRR060683 160_testes_total	SRR2096055 Ovary_Min_43	M041 embryo Ovary_Min_50	SRR2096057 male body	V116 Ovary_Strain_160_oxidised	SRR2096014	SRR2096056 Ovary_Min_46	M028 head	SRR060684 140x9_0-2h_embryos_total	SRR2096058 Ovary_Min_98	SRR2096059 Ovary_Min_144	SRR060658 140_ovaries_total	SRR060644 9_males_carcasses_total	SRR060674 9x140_ovaries_total	SRR1106729 mixed whole adult body	SRR1106730 embryo_0-2h from 14 day old 30h	SRR2096026 embryo_0-2h from 15x16 day old Strain 9 mothers	SRR060666 160_males_carcasses_total	V053 head	SRR060665 9_females_carcasses_total	SRR060686 2h_embryos_total	SRR060663 160_0-2h_embryos_total
**********	(((	((((((((((.	(((((.	(((((.	((((.	((.	(((.	((.	((.	((.	))).	))))).	)))))))))).	))))))))))).	))))))))))).	))))).	))).	**********																		
.....	.....	.....	.....	.....	.....	22 0	1	2244.00 2244	779	712	469	245	1	1 6	6 0	9	7	2	0	0 0	5	0	0 0	0	0	0	1	0	1	0	0	0	0	0
.....	.....	.....	.....	.....	.....	21 0	1	1869.00 1869	420	534	387	151	126	114 27	19 28	15	9	2	5	1 0	0	3	2 1	1	1	1	0	0	1	0	0	0	0	0
.....	.....	.....	.....	.....	.....	23 1	1	337.00 337	113	110	65	37	0	0 2	4 0	1	4	0	0	1 0	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	20 0	1	252.00 252	62	62	52	13	20	5 10	4 13	4	3	2	0	0 0	1	0	0 0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	20 0	1	212.00 212	52	68	51	18	13	2 1	4 0	1	1	0	0	1 0	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	24 2	1	169.00 169	68	38	34	24	0	0 1	3 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	147.00 147	61	28	36	21	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
.....	.....	.....	.....	.....	.....	21 0	1	145.00 145	34	42	26	8	0	0 10	0 0	16	5	3	0	0 0	1	0	0 0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	19 0	1	90.00 90	17	24	21	5	8	5 1	2 2	0	1	1	0	0 0	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	22 0	1	82.00 82	19	23	16	6	5	4 1	2 0	1	1	0	0	1 0	0	1	0 0	0	0	0	0	0	1	0	0	0	0	0
.....	.....	.....	.....	.....	.....	23 0	1	53.00 53	19	17	10	7	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
.....	.....	.....	.....	.....	.....	22 1	1	35.00 35	8	10	7	4	4	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
.....	.....	.....	.....	.....	.....	18 0	1	33.00 33	8	5	8	3	6	0 1	1 1	0	0	0	0	0 0	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	21 0	1	31.00 31	8	14	6	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
.....	.....	.....	.....	.....	.....	21 0	1	30.00 30	10	7	7	4	4	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
.....	.....	.....	.....	.....	.....	24 1	1	21.00 21	7	2	3	3	3	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
.....	.....	.....	.....	.....	.....	20 0	1	19.00 19	7	5	3	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
.....	.....	.....	.....	.....	.....	23 0	1	18.00 18	6	3	5	3	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	16.00 16	5	6	2	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
.....	.....	.....	.....	.....	.....	24 1	1	16.00 16	12	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
.....	.....	.....	.....	.....	.....	22 1	1	15.00 15	7	4	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
.....	.....	.....	.....	.....	.....	20 1	1	14.00 14	3	2	3	4	0	0 0	1 0	0	1	0	0	0 0	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	23 2	1	12.00 12	5	4	1	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
.....	.....	.....	.....	.....	.....	23 3	1	12.00 12	1	4	2	2	0	0 0	3 0	0	0	0	0	0 0	1	0	0 0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	.....	.....	.....	.....	22 0	1	12.00 12	5	3	3	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
.....	.....	.....	.....	.....	.....	22 1	1	11.00 11	5	2	1	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
.....	.....	.....	.....	.....	.....	19 1	1	10.00 10	1	6	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
.....	.....	.....	.....	.....	.....	20 0	1	10.00 10	3	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
.....	.....	.....	.....	.....	.....	20 0	1	9.00 9	3	1	1	0	0	0 1	3 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	9.00 9	0	0	0	0	0	0 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	9.00 9	5	1	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
.....	.....	.....	.....	.....	.....	23 0	1	8.00 8	4	2	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	0	0	0
.....	.....	.....	.....	.....	.....	20 0	1	8.00 8	1	2	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
.....	.....	.....	.....	.....	.....	21 1	1	7.00 7	2	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
.....	.....	.....	.....	.....	.....	22 0	1	7.00 7	4	3	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
.....	.....	.....	.....	.....	.....	22 0	1	7.00 7	3	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
.....	.....	.....	.....	.....	.....	20 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
.....	.....	.....	.....	.....	.....	25 3	1	6.00 6	4	0	2	0	0	0 0	0 0	0	0	0	0	0 0	0	0	0 0	0	0	0	0	0

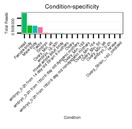
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_251	**scaffold_12928:4268404-4268463 -**	**confident**	**Canonical miRNA**	**intergenic**
				[View on UCSC Genome Browser (GenbrEMbrace)]

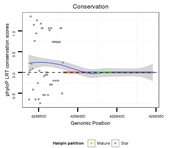
Legend: [illegible] [illegible] [illegible]

Predicted structure









...

Show Alternate Folds

Flybase annotation

intergenic

No Repeatible elements found

Sense Strand Reads

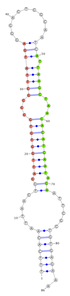
Hide 3p reads | show mid-mismatch reads

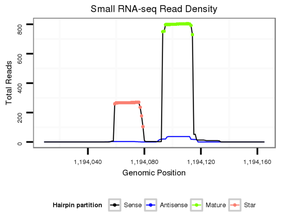
| | | | |

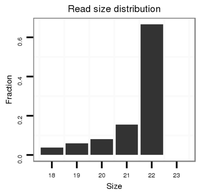
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_253	**scaffold_13047:1194059-1194115 +**	**confident**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser (Comell Mirror)]

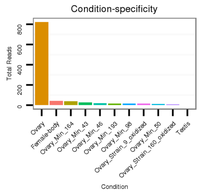
Legend: mature star mismatch in alignment mismatch in read

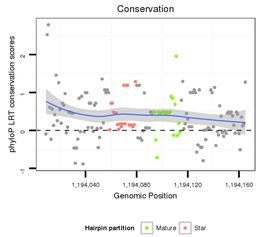
Predicted structure











Show Alternate Folds

Flybase annotation

Antisense to intron [Dvir:GI235540-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CGTGGTGGTGTCTTGCCAATGCACTTGGTACGGCATTTCACAATTAACTGCATTGGTGTGCCCGCTTATGAGGGACTCCGACATCATTAAGCTAACACATCAATACAATTCGCTGTGAGAAAAAGTACAAGTGATACAAAAAGTCTACGTTCCAGCG	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060677 9xkrg_ovaries_total	SRR060676 9xkrg_ovaries_total	SRR060674 9x140_ovaries_total	SRR060675 140x9_ovaries_total	SRR2096059 Ovary_Min_164	M047 female body	SRR2096055 Ovary_Min_43	SRR2096056 Ovary_Min_46	SRR2096058 Ovary_Min_98	SRR2096060 Ovary_Min_193	SRR2096013 Ovary_Strain_9_oxidised	SRR2096014 Ovary_Strain_160_oxidised	SRR2096057 Ovary_Min_50	SRR060658 140_ovaries_total	SRR060688 160_ovaries_total	SRR060673 9_ovaries_total	SRR060660 Argentina_ovaries_total	SRR060654 160x9_ovaries_total	SRR060656 9x160_ovaries_total	SRR060670 9_testes_total	GSM1528803 follicle cells	SRR060671 9x160_males_carcasses_total	SRR060672 9x160_females_carcasses_total
**********	22	0	1	675.00	675	287	217	58	38	2	11	6	6	1	1	12	7	2	0	8	6	2	7	3	1	0	0	0
..CATTGGTGTGCCCGCTTATGA..	21	0	1	91.00	91	10	21	7	8	8	7	4	4	4	7	1	1	0	4	7	0	1	4	0	0	0	0	0
..CATTGGTGTGCCCGCTTATG..	20	0	1	68.00	68	5	12	4	2	6	12	9	1	5	4	2	0	3	2	0	0	1	0	0	0	0	0	0
..ATTAAGCTAACACATCAATAC..	21	0	1	62.00	62	24	18	9	5	1	0	0	2	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0
..CATTGGTGTGCCCGCTTAT..	19	0	1	54.00	54	7	12	2	4	10	3	5	3	1	3	0	0	3	1	0	0	0	0	0	0	0	0	0
..TAAGCTAACACATCAATACAAT..	22	0	1	40.00	40	20	9	4	2	3	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
..CATTGGTGTGCCCGCTTA..	18	0	1	34.00	34	6	2	1	0	10	0	2	2	5	3	0	0	3	0	0	0	0	0	0	0	0	0	0
..ATTAAGCTAACACATCAATACAA..	22	1	1	18.00	18	0	2	1	1	0	0	0	11	1	0	0	2	0	1	0	0	0	0	0	0	0	0	0
..CATTGGTGTGCCCGCTTATGT..	21	1	1	12.00	12	3	2	1	1	0	0	0	2	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0
..ATTAAGCTAACACATCAATA..	20	0	1	10.00	10	3	2	2	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..CATTGGTGTGCCCGCTTATGAG..	22	0	1	6.00	6	1	0	0	1	0	0	3	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
..CATTGGTGTGCCCGCTTATGAT..	22	1	1	5.00	5	1	1	0	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
..ATTAAGCTAACACATCAATACAT..	23	1	1	5.00	5	2	0	1	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0
..CATTGGTGTGCCCGCTTATGAGA..	23	2	1	4.00	4	0	0	0	0	0	3	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..TTCGCTGTGAGAAAAAAG..	18	0	1	4.00	4	0	0	0	0	1	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
..TGCATTGGTGTGCCCGCTTATG..	22	0	1	4.00	4	0	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..ATTGGTGTGCCCGCTTAT..	18	0	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
..TTAAGCTAACACATCAATACA..	21	0	1	3.00	3	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..CATTGGTGTGCCCGCTTATG..	20	1	1	3.00	3	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
..ATTGGTGTGCCCGCTTATGA..	20	0	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
..ATTCGCTGTGAGAAAAAG..	19	0	1	2.00	2	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
..CATTGGTGTGCCCGCTTATA..	19	1	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	0	0
..TTTAGGGACTCCGCAATC..	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
..TAAGCTAACACATCAATACA..	20	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
..TAAGCTAACACATCAATACAA..	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
..TCGATTGTGTAGTTATTTAA..	22	0	1	2.00	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..ATTAAGCTAACACATCAATAC..	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	0	0
..CATTGGTGTGCCCGCTTATGAG..	23	2	1	2.00	2	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..CATCAATACAATTCGCTGT..	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
..TTCGCTGTGAGAAAAAAG..	18	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
..ATTCGCTGTGAGAAAAAG..	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
..ATACAATTCGCTGTGAGAAAAAG..	24	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
..CATTGGTGTGCCCGCTTATGAT..	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
..CATTGGTGTGCCCGCTTATGAT..	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	0	0

Anti-sense strand reads

GCACCACCACAGAACGGTTACGTGAACCATGCCGTAAAGTGTTAATTGACGTAACCACACGGGCGAATACCCTGAGCGTTAGTAATTCGATTGTGTAGTTATGTCTAAGCGACACTCTTTTTTCATGTTCACTATGTTTTCAGATGCAAGGTCGC	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR2096038 M047 female body	SRR2096038 embryo_0-2h from 14 day old Strain 9 mothers	SRR060660 Argentina_ovaries_total	SRR060681 Arg9_testes_total	SRR2096080 embryo_0-2h from 15to16 day old nondyspenic mothers	SRR060674 9x140_ovaries_total	SRR060678 9x140_testes_total	SRR060680 9xkrg_testes_total	SRR060685 9xkrg_0-2h_embryos_total	SRR2096014 Ovary_Strain_160_oxidised	SRR060682 9x140_0-2h_embryos_total	M061 embryo	SRR060656 9x160_ovaries_total	SRR060664 9_males_carcasses_total	SRR060665 9_females_carcasses_total	SRR060670 9_testes_total	SRR060672 9x160_females_carcasses_total	SRR060676 9xkrg_ovaries_total	SRR060677 Arg9_ovaries_total	SRR060679 140x9_testes_total	SRR060686 Arg9_0-2h_embryos_total	SRR060687 9_0-2h_embryos_total	SRR1106713 embryo_0-2h	SRR1106724 embryo_12-14h	SRR2094026 embryo_0-2h from 14 day old Strain 9 mothers	SRR2094050 embryo_0-2h from 14 day old Strain 160 mothers	SRR2096055 Ovary_Min_43	SRR2096060 Ovary_Min_193	V116 male body	V053 head
**********	22	0	1	14.014	14	0	0	0	0	0	2	1	1	0	0	0	1	1	0	0	0	1	0	0	0	0	0	1	0	1	1	1	1	0	0
..TAGTAATTCGATTGTGTAGTTAT..	23	0	1	9.00	9	1	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	1	0
..AGTAATTCGATTGTGTAGTTAT..	22	0	1	6.00	6	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
..TCGATTGTGTAGTTATTTAA..	22	0	1	3.00	3	1	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
..TTAGTAATTCGATTGTGTAGTTAT..	24	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	0	0	0	0	0	0	0	0	0	0
..GTAATTCGATTGTGTAGTTAT..	21	0	1	2.00	2	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
..AAATAGTAATTCGATTGTGTAGTTAT..	24	3	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
..AATAGTAATTCGATTGTGTAGTTAT..	25	2	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
..TAATTCGATTGTGTAGTTATATT..	22	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
..AATTGACGTAACCACACGGGCG..	22	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
..TGACGTAACCACACGGGCGAA..	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
..ACGTAACCACACGGGCGAATA..	21	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

Show Alignment With Reads

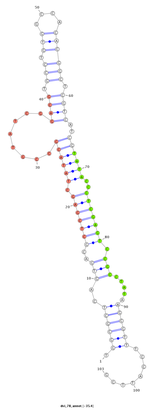
Re-alignment of all predicted orthologs

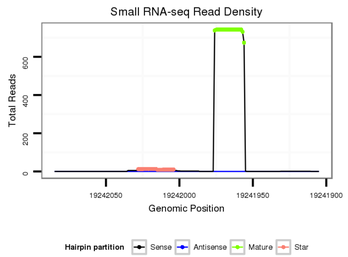
Species	Coordinate	ID	Alignment
droVir3	scaffold_13047:1194059-1194165 +	dvi_253	C--------GTGGTGG--TGTCTTGCCAATGCACTTGGTACGGCATTT-CAC---------AATTA----------ACTCGATTGGTGTGCCCGCTTATGAGGGACTCCGACATCATTAAGCTAACACA----------CCAATACA----TT----------C----------G---C----------TGTGAGAAAAAGTACAAGTGATACAAAAAGTCT-A-CGT-TCCAGCG
droMoj3	dmo_303	dmo_303	C--------GTGGTGG--TGTCTTGCCAATGCTCGCGTGGCATTT-CAC---------AATTA----------ACTCGATGGTGTGCCCGCTTATGAGGGACTCCGCAATTATCAAGCTAACACA----------TCAACACA----TT----------C----------G---C----------TGTGAGAGATGTCAAGTGTCT-A-TGT-TCAGCG
droGri2	scaffold_14926:5073568-5073639 +		C--------GTGGTGG--TGTCTTGCGTA----------GGCATTT-CAC---------AATTA----------ACTCGATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGC----CAACACA TCA---TATCGTATGT----T-G----------CTAATTTGT----C----------TGTGAGAAATATCAGTGCATGTCAAAAAAT-A-TATCGTATGT
droWil2	Ref_1000000004902:74697-74550 +		A--------GTGAAATGTAA----------AA----------CAA--------------------

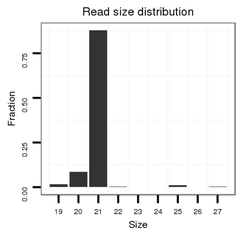
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_78	**scaffold_12875:19241955-19242035 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

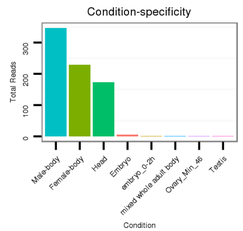
Legend: mature star mismatch in alignment mismatch in read

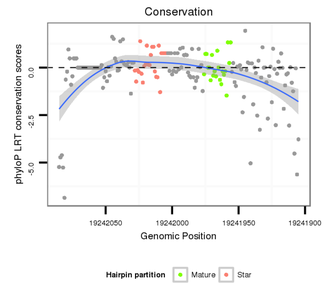
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TCGGATCTGGCGCCAGGCAATAAAATGTCCGATGGCGGCTGCTGGCGCTCAGTGACGCTCGAGCTATACGCCGTATCGGACGTGCCTGTGGCCACACGGCTCGTCATCGTATACCCTCGAGTCCGCCTATAAAGCGTTTCCATTCGTGTACTATATACATATACACACACTCGTCTACCTCA	Read size	# Mismatch	Hit Count	Total Norm	Total	V053 head	SRR060664 9_males_carcasses_total	SRR060671 9x160_males_carcasses_total	SRR060668 160x9_males_carcasses_total	SRR060672 9x160_females_carcasses_total	SRR060665 9_females_carcasses_total	M047 female body	SRR060667 160_females_carcasses_total	SRR060669 160x9_females_carcasses_total	M028 head	V116 male body	SRR060666 160_males_carcasses_total	M061 embryo	V047 embryo	SRR060680 9xArg_testes_total	M027 male body	SRR1106712 embryo_0-2h	SRR1106729 mixed whole adult body	SRR2096056 Ovary_Min_46	SRR060676 9xArg_ovaries_total	SRR1106720 embryo_8-10h
********** (((((((..((((..(((((((.(((((((.....((((.((((.((((....)))))).))))).))))))).))))))).))))).))))).))).))))).))).....)))))).....																										
.....TATACCCTCGAGTCCGCCTAT.....	21	0	1	666.00	666	137	105	101	86	52	53	40	34	22	4	12	11	2	2	1	1	1	1	1	0	0
.....TATACCCTCGAGTCCGCCTA.....	20	0	1	57.00	57	17	12	3	2	2	6	3	3	4	1	1	2	0	1	0	0	0	0	0	0	0
.....TATACCCTCGAGTCCGCCT.....	19	0	1	12.00	12	1	3	2	2	1	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0
.....TATACCCTCGAGTCCGCCTAT.T.....	22	1	1	10.00	10	0	4	3	0	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
.....CTCGAGCTATACGCCGTATCGGACGG.....	25	0	1	5.00	5	0	0	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0	0	0
.....TATACCCTCGAGTCCGCCTATA.....	20	0	1	4.00	4	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TACCCTCGAGTCCGCCTAT.....	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
.....AGTGACGCTCGAGCTATAC.T.....	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
.....GTATACCCTCGAGTCCGCCTAT.....	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
.....AGCTATACGCCGTATCGGACGTGCC.....	25	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0
.....TATACCCTCGAGTCCGCCT.T.....	20	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
.....TATACCCTCGAGTCCGCCTAT.T.....	22	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
.....AGTGACGCTCGAGCTATACGCCGT.....	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
.....TACATATACACACACTCGTCT.....	21	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
.....ACACTCGTCTACCTT.	15	1	5	0.20	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
.....TATACCCTCGAGTCCTTA.....	18	3	20	0.05	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

AGCCTAGACCGCGGTCCGTTATTTTACAGGCTACCGCCGACGACCGCGATCACTGCCAGCTCGATATGCGGCATAGCCTGCACGGACACCGGTGTGCCGAGCAGTAGCATATGGGAGCTCAGGCGGATATTCGCAAAGGTAAGCACATGATATATGTATATGTGTGTGAGCAGATGGAGT	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060672 9x160_females_carcasses_total	M047 female body	SRR060666 160_males_carcasses_total	M028 head	SRR060681 9xArg9_testes_total	SRR060686 9xArg9_0-2h_embryos_total
********** (((((((..((((..(((((((.(((((((.....((((.((((.((((....)))))).))))).))))))).))))))).))))).))))).))).))))).))).....)))))).....											

Show Alignment With Reads

Re-alignment of all predicted orthologs

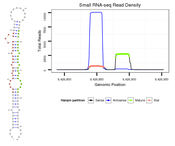
Species	Coordinate	ID	Alignment
droVir3	scaffold_12875:19241905-19242085 -	dvi_78	TCGGATCT----------GGCGCCAGGCAATAAAATGTCCGATGGCGGCTGCTGGCGCT--------CAGTGACGTCGAGCTATACGCCGTATCGGACGTGCCTGTGGCCACACG----------GCTCGTCAT----------CCTATACCCTCGA-GTCCGCCTATAAGCGTTTCCATTCGTGTACTAT----------AT--------ACA----TATACACACACTCGTCTA----------CC----TCA
droMoj3	scaffold_6496:12927574-12927766 -		TCGG----------GGGCAATGCTGGCGCT--------CAGTGCGATAGGAACATAGGCGCAATAGCGCGAATAGCGCGAATAGCGCG

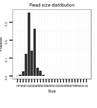
ID	Coordinate	Strand	Genomic Locus
dv1_56_scaffold_12970:9426038-9426903 +	**coeliakor**	**Tetoxo-rvetrcwd**	**intron**

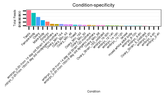
View on UCSC Genome Browser (Grand Mirror)

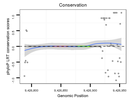
Legend: Stem Loop Terminal Loop Internal Loop

Predicted structure









Show Alignment Table

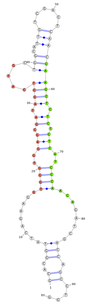
Fichier automatise

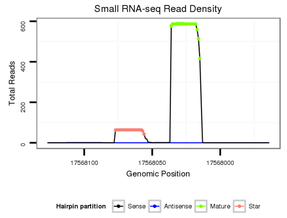
dev1c@ln102:/home/dev1c/mirdeep2/mirdeep_runs/run_2019_03_27_17_11_11_dv1_56/dv1_56_mature.fa -g - -t Human -v -y -n -k -l -m -p /home/dev1c/mirdeep2/genomes/human_hg19_bowtie_index/hg19 -f /home/dev1c/mirdeep2/mirdeep_runs/run_2019_03_27_17_11_11_dv1_56/dv1_56_reads.fa -s /home/dev1c/mirdeep2/mirdeep_runs/run_2019_03_27_17_11_11_dv1_56/dv1_56_mature.fa -d -h -i -t hsa -P /home/dev1c/mirdeep2/genomes/human_hg19_bowtie_index/hg19_hairpin.fa -a /home/dev1c/mirdeep2/genomes/human_hg19_bowtie_index/hg19.fa -r /home/dev1c/mirdeep2/mirdeep_runs/run_2019_03_27_17_11_11_dv1_56/dv1_56_reads_collapsed.fa -c /home/dev1c/mirdeep2/mirdeep_runs/run_2019_03_27_17_11_11_dv1_56/dv1_56_reads_collapsed_vs_genome.arf -o 1 -v -y -n -k -l -m -p /home/dev1c/mirdeep2/genomes/human_hg19_bowtie_index/hg19 -f /home/dev1c/mirdeep2/mirdeep_runs/run_2019_03_27_17_11_11_dv1_56/dv1_56_reads_collapsed_vs_genome.fa -s /home/dev1c/mirdeep2/mirdeep_runs/run_2019_03_27_17_11_11_dv1_56/dv1_56_mature_vs_genome.arf -d -h -i -t hsa -P /home/dev1c/mirdeep2/genomes/human_hg19_bowtie_index/hg19_hairpin.fa -a /home/dev1c/mirdeep2/genomes/human_hg19_bowtie_index/hg19.fa -r

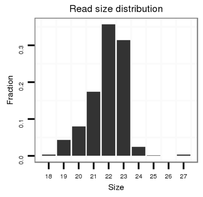
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_86	**scaffold_13049:17568014-17568077 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

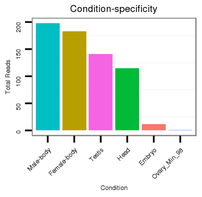
Legend: mature star mismatch in alignment or mismatch in read

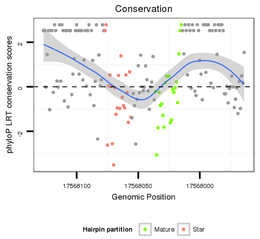
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DvirGJ11624-in]; CDS [DvirGJ11624-cds]; CDS [DvirGJ11624-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CCCACACCATGCCACACACCTCCTTCCAGCCCACGGCACGGTATCAGAAGGTGGGTGGAGCGATAGCTCATGCTGGCATTGTCGACTCAACCAAGCTCTCTCTCATCCCAACAGATCGACCAGCCTGGCGAAAAAGACCAGATGAAGTTCTCAACGCAACGCAA	Read #	Mismatch	Hit Count	Total Norm	Total	SRR060664 9_males_carcasses_total	V053 female head	M047 female body	SRR060665 9_females_carcasses_total	SRR060679 140x9_testes_total	SRR060671 9x160_males_carcasses_total	SRR060668 160x9_males_carcasses_total	SRR060672 9x160_females_carcasses_total	SRR060681 Argx9_testes_total	SRR060680 9xArg_testes_total	SRR060669 160x9_females_carcasses_total	M028 head	SRR060678 9x140_testes_total	M061 embryo male body	V116	SRR060657 140_testes_total	SRR060659 Argentina_testes_total	SRR060670 9_testes_total	V047 embryo	SRR060655 9x160_testes_total	M027 male body	SRR060662 9x160_0-2h_embryos_total	SRR060686 Arg x9_0-2h_embryos_total	SRR060687 9_0-2h_embryos_total	SRR060689 160x9_testes_total	SRR1106727 larvae	SRR2096058 Ovary_Min_98	SRR2096080 embryo_0-2h from 15to16 day old nondrgenic mothers	SRR2096079 embryo_0-2h from 15to16 day old drgenic mothers
**********	size						head	body									head		embryo					embryo		male								
..CAAGCTCTCTCTCATCCCAACA	22	0	1	206.00	206	37		42	33	22	10	12	13	9	7	3	7	2	3	4	1	0	1	0	0	0	0	0	0	0	0	0	0	0
..CAAGCTCTCTCTCATCCCAACAG	23	0	1	199.00	199	48		13	22	14	16	9	10	9	9	19	11	7	5	10	0	2	0	0	1	0	0	0	1	1	0	0	0	1
..CAAGCTCTCTCTCATCCCAAC	21	0	1	96.00	96	20		11	7	9	8	9	8	4	1	2	4	1	5	2	2	2	0	0	0	2	0	0	0	0	0	0	0	0
..CAAGCTCTCTCTCATCCCA	20	0	1	44.00	44	7		11	4	4	1	3	3	3	3	1	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
..CAAGCTCTCTCTCATCCCA	19	0	1	26.00	26	3		10	3	3	0	4	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..GTGGGTGGAGCGATAGCTCATG	22	0	1	22.00	22	0		2	0	0	3	0	0	0	0	0	1	2	0	0	4	5	3	1	0	1	0	0	0	0	0	0	0	0
..GTGGGTGGAGCGATAGCTCATGCT	24	0	1	16.00	16	0		3	1	1	1	0	0	0	0	0	0	0	1	4	1	1	1	0	1	0	0	0	0	0	0	0	0	0
..GTGGGTGGAGCGATAGCTCAT	21	0	1	14.00	14	0		4	0	0	3	0	0	0	1	1	1	0	0	0	2	0	1	1	0	1	0	0	0	0	0	0	0	0
..CAAGCTCTCTCTCATCCCAACAG	24	1	1	11.00	11	1		0	1	1	3	1	0	1	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..GTGGGTGGAGCGATAGCTCA	20	0	1	6.00	6	0		0	0	0	2	0	0	0	0	1	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0
..AAGCTCTCTCTCATCCCAACAG	22	0	1	4.00	4	0		0	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
..AAGCTCTCTCTCATCCCAACA	21	0	1	3.00	3	0		1	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
..CCAAGCTCTCTCTCATCCCAACA	23	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
..CAAGCTCTCTCTCATCCCAACAGA	24	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	0	0	0	0	0	0	0
..GTGGGTGGAGCGATAGCTCATG	22	1	1	2.00	2	0		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
..GTGGGTGGAGCGATAGCTCATGC	23	0	1	2.00	2	0		0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..GTGGGTGGAGCGATAGCTCATGCTGGC	27	0	1	2.00	2	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
..CAAGCTCTCTCTCATCCCAACAG	22	1	1	1.00	1	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
..CTCTCTCTCATCCCAACAG	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
..CAAGCTCTCTCTCATCCCAACAG	23	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
..CAAGCTCTCTCTCATCCCAACAG	23	2	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	0	0	0	0
..CAAGCTCTCTCTCATCCCAACAG	24	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	0	0	0	0	0	0	0	0
..AAGCTCTCTCTCATCCCAAC	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
..CAAGCTCTCTCTCATCCCAAG	21	1	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
..CAAGCTCTCTCTCATCCC	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	0	0	0	0	0	0	0	0	0
..AGCTCTCTCTCATCCCAACAG	22	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
..TGGGTGGAGCGATAGCTCAT	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
..GTGGGTGGAGCGATAGCTCATGCTG	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	0	0	0	0
..GTGGGTGGAGCGATAGCTCATGC	24	1	1	1.00	1	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
..TTGTCGACTCAACCAAGCTCTCT	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	0	0	0	0	0	0	0
..CAAGCTCTCTCTCATCCCAA	20	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
..AAGCTCTCTCTCATCCCAA	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
..GTGGGTGGAGCGATAGCTCATGCTGG	26	2	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
..AAGCTCTCTCTCATCCCA	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	0	0

Anti-sense strand reads

GGGTGTGGTACGGTGTGTGGAGGAAGGTCGGGTGCCGTGCCATAGTCTTCACCCACCTCGCTATCGAGTAGGACCGTAACAGCTGAGTTGTTCGAGAGAGAGTAGGGTTGCTAGCTGGTCGGACCGCTTTTTCTGGTCTACTTCAAGAGTTGCGTTGCGTT	Read #	Mismatch	Hit Count	Total Norm	Total	V116 male head body	V053 embryo	V047	SRR060689 160x9_testes_total
**********	size								
..GTGTGGAGGAAGGTCGGGTGCCGTGCC	27	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

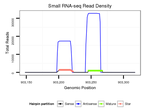
Species	Coordinate	ID	Alignment
droVir3	scaffold_13049:17567864-17568127 -	dvi_86	CCCACACCATGCCACACACCTCCTTCCAGCCC---ACGGCACGGTATCAGAAGGTGGGTGG----------AG-------CGGA==TAGC----TCATG-TGGCATTG-T-CG--------ACT---C---AA----------C-----A-AG-TCCTC-TCT---CATCCCAACG-ATCGACCAGCCTGGCGAAAAAGACCAGATGAAGTTCTCAACGCAACGCAA
droMo3	scaffold_6683:22608040-22608498 -		CCCGCACCTCATGCCACACCTCCTCCAGCCC---ACGGCACGGTATCAGAAGGTAATA----------AGA----GAATA----CATGTCTGCTGCTCTTGCTGCTCTTTTTCTTTTT

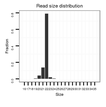
ID	Coordinate	Confidence	Class	Genome Locus
dvi_82 | scaffold_13042:903198-903268 +		**confident**	**Trna-rsrnr/crnl**	**intergenic**

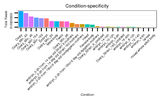
[View on UCSC Genome Browser (Crabb Mirror)]

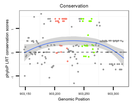
Legend: Stem Hairpin Terminal Loop Internal Loop

Predicted structure









Show Alternate Folds

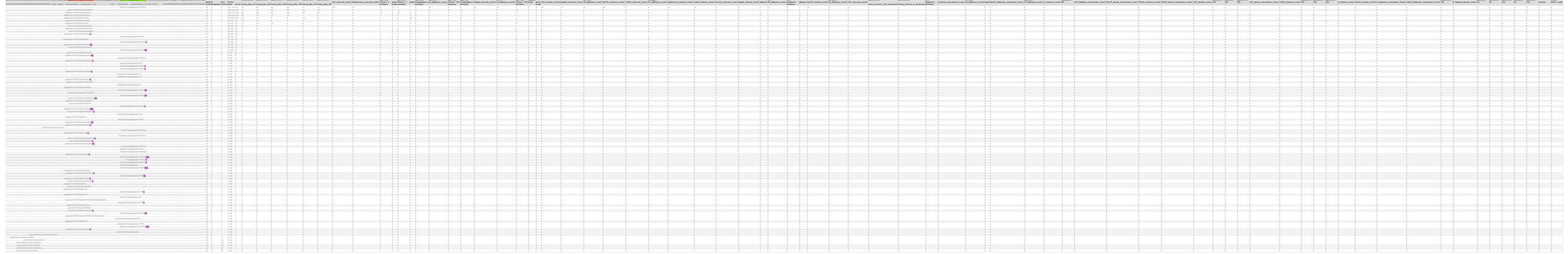
Flybase annotation

dmel-all

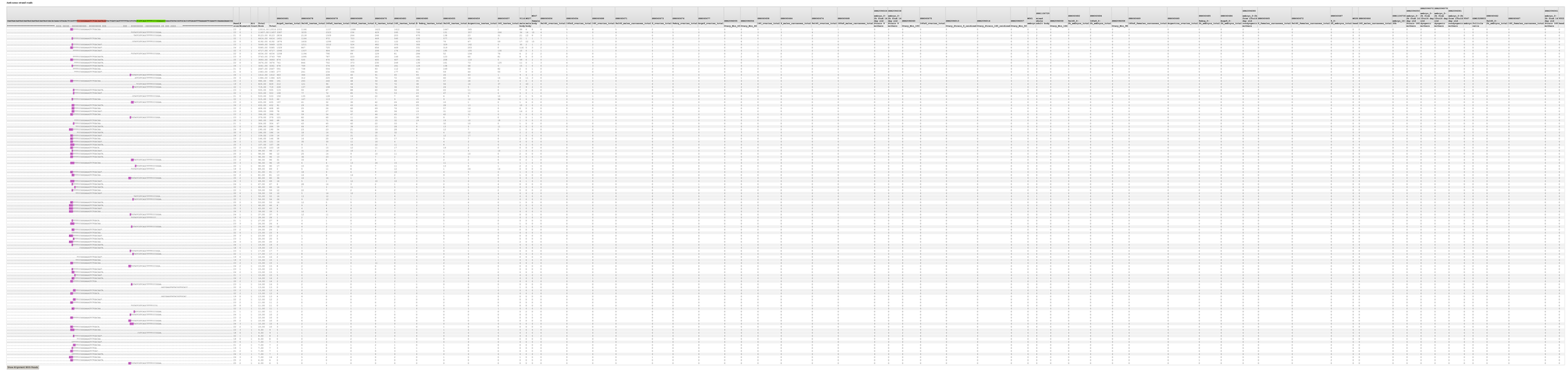
No Reportable Ortologs Found

Some Strand Reads

Sort By reads | Show mid mismatch reads

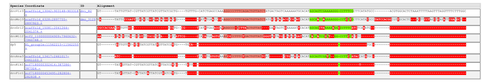


All-same strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

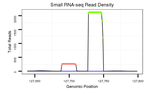


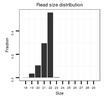
Created 2026-03-21 at 04:04 PM

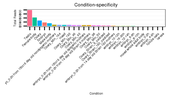
ID	Coordinate	Confidence	Class	Genome Locus
dvi_4667	**scaffold_12875:127689-127749 +**	**confident**	**Mirtron**	**intron**

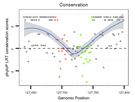
Legend: **Dicer** **Ago** **Dicer & Ago** **miRNA/miRNA***

Predicted structure









Show Alternate Folds

Flybase annotation

dmel:Dicer2:CR40486 (28.2)[ref:GD1]:CR40486-RA[1:1]:Dicer2:CR40486-ra[1

No Repeats records found

Some Strand Reads

Sort By reads Show PAS alignment reads

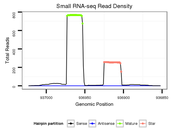
| | | |

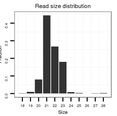
ID	Coordinate	Confidence	Class	Genomic Locale
dvi_125	**scaffold_13047:936902-936973 -**	**confident**	**Canonical miRNA**	**intron**

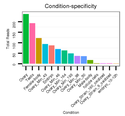
View on UCSC Genome Browser [Grch38/hg38]

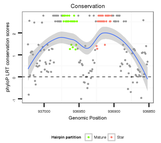
Layer: Sense Antisense Mature Star

Predicted structure









Show Alternate Folds

Flybase annotation

intro:(FlyBase:FBtr0346144)

No Repeatmasker elements found

Sense Strand Reads

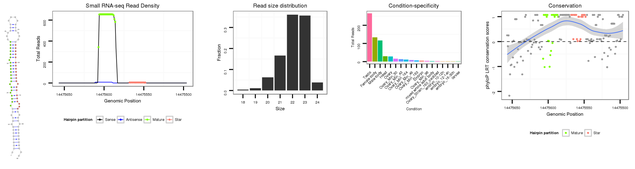
hide 3p reads show red mismatch reads

| Read 5' seq | Mismatch | Count | Mismatch Rate | Total | DM0200055 Female body | DM0200077 Argo4_ovarian_total | DM0200074 Baby_ovarian_total | DM0200056 Dvary_Mix_40 | DM0200059 Dvary_Mix_104 | DM0200060 Dvary_Mix_105 | DM0200081 Argo4_testes_total | DM0200079 18to5_testes_total | DM0200078 9to14_testes_total | DM0200058 Dvary_Mix_98 | DM0200057 Dvary_Mix_20 | DM0200072 9to14_females_carcasses_total | DM0200075 18to5_ovarian_total | DM0200076 9to14_ovarian_total | DM0200085 Dh_embryo_total | DM0200080 3_9day_testes_total | DM0200086 Argo4_0-2hr_embryo_total | DM0200087 Argo4_2-4hr_embryo_total | DM0200083 Argo4ovarian_ovarian_total | DM0200058 10_ovarian_total | M041 embryo_9_testes_total | DM0200070 18to5_0-2hr_embryo_total | DM0200084 9to14_0-2hr_embryo_total | DM0200082 Dh_embryo_total | DM0200056 9to14_ovarian_total | DM0200083 10_testes_total | V047 embryo_male | M027 Y116.DM0200059 Argo4testes_testes_total body_body | DM0200113 Follicle cells | DM0200053 Dvary_Strain_9 | DM0200114 Dvary_Strain_180 | DM0200045 9_females_carcasses_total | DM0200067 10_females_carcasses_total | DM0200088 10to5_ovarian_total | DM0200089 9to14_ovarian_total | DM0200055 10to5_testes_total | DM0200068 9to14_testes_total | DM0200073 10to5_females_carcasses_total | DM0200069 10to5_males_carcasses_total | DM0200057 10_testes_total | DM0200064 9_males_carcasses_total | DM0200066 10_males_carcasses_total | DM0200054 10to5_ovarian_total | DM0200071 9to14_males_carcasses_total | DM0200042 Dh_embryo_total | DM0110070 Dh_embryo_total | DM0200063 12h | DM0110072 embryo_0-2hr_embryo_total | DM0200044 Dg_ovd Strain 9 mothers |
|---|---|---|---|---

ID	Coordinate	Confidence	Class	Genome Locale	
dvi_111	**scaffold_13049:14475546-14475607 -**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Crossb3 Mirror)]

Legend: Mature Star Arabarna (5' Arm) Arabarna (3' Arm)

Predicted structure



Show Alternate Folds

Flybase annotation

intron:[Dvir(GI):TM-ns]

No Repeatable element found

Sense Strand Reads

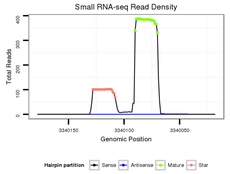
Hide 3p reads show mid mismatch reads

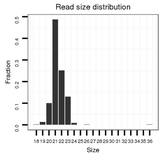
| Read sequence | Read # | Mismatch | Mid Mismatch | Count | Norm | Total | Total Norm | SRR3045861 Angel_testes_total | SRR3045879 10%A_testes_total | SRR3045878 2%G_testes_total | SRR3045860 3%Acg_testes_total | SRR3045872 9%10_Females_carcasses_total | SRR3045864 3%Acg_males_carcasses_total | SRR3045859 Argentina_testes_total | SRR3045869 10%A_testes_total | SRR3045865 3%Acg_testes_total | SRR3045863 A_Females_carcasses_total | SRR3045867 10_testes_total | SRR3045868 10_Females_carcasses_total | SRR3045871 9%10_males_carcasses_total | SRR3045866 10_testes_total | SRR3045870 10_Females_carcasses_total | SRR3045869 10%A_Females_carcasses_total | SRR3045862 Dvwy_Mix_10 | SRR3045876 3%Acg_testes_total | SRR3045855 3%10_testes_total | SRR3045854 3%Acg_Females_carcasses_total | SRR3045877 3%Acg_males_carcasses_total | SRR3045852 Dvwy_Mix_10 | SRR3045853 Dvwy_Mix_10 | SRR3045857 Dvwy_Mix_10 | WGS YES SRR3045873 head | WGS YES SRR3045872 head | WGS Sample Body | SRR3045874 3%10_testes_total | SRR3045858 Dvwy_Mix_10 | YIL4 SRR3045857 male | SRR3045875 10%A_testes_total | SRR3045856 10%A_testes_total | SRR3045854 3%10_testes_total | SRR3045846 Angel_testes_total | SRR3045850 10_testes_total | SRR3045851 Dvwy_Strain_B_wolbiad | SRR3045814 Dvwy_Strain_B_wolbiad | SRR3045840 Argentina_testes_total | SRR3045845 Dvwy_B-_testes_total | SRR3045842 Dvwy_B-_testes_total | SRR3045844 14%A_B-_testes_total | SRR3045838 10_testes_total | SRR3045837 10_testes_total | SRR3104729 mixed whole adult | SRR3045842 Dvwy_B-_testes_total | SRR3045843 10_B-_testes_total | SRR3104731 SRR3104732 SRR3104730 SRR3104733 dmbrpy_T- dmbrpy_T-_2h dmbrpy_2-_2h dmbrpy_2-_2h 2h from 14 2h from 15 from 2 from 2 day old day old day old day old | SRR3045850 SRR3045841 SRR3045840 dmbrpy_10 dmbrpy_10-dmbrpy_10- 10 10 lerves | SRR3104727 SRR3104728 dmbrpy_T- dmbrpy_T- | SRR3045839 Felicia | SRR3045839 Dvwy |
|---|---|---|---|---|---

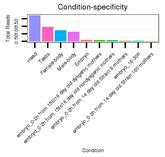
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_55	**scaffold_12970:3340068-3340128 -**	**confident**	**Canonical miRNA**	**intergenic**
				[View on UCSC Genome Browser (Cornell Mirror)]

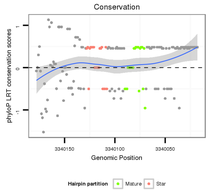
Legend: **mature** **star** **sub-mature in its arm** **mismatch in mature**

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

No Repeatmbk elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

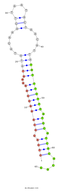
| TAGTGCTCGACATTCGGACCCCTTCTGGCTCGCCCGTTATTTCGAATGC-CAGGAATTCACCAGGACTCAG-TTCTCATGTGTCACTG | Read # size | Mismatch | Count | Total Norm | Total | head | head 9_males_carcasses_total | 9x160_females_carcasses_total | 160_females_carcasses_total | 160_males_carcasses_total | 9_females_carcasses_total | body | 160x9_males_carcasses_total | female body | 160x9_females_carcasses_total | Arga9_testes_total | embryo 160_males_carcasses_total | M061 | male body | 160x9_females_carcasses_total | 9x160_testes_total | 9_testes_total | male body | 160x9_testes_total | 30h | embryo_14-male body | 9x160_testes_total | Ã | 9akrg_testes_total | 1 embryo_0-2h mothers | 1 embryo_0-2h day old | 1 embryo_0-2h from nondygenic mothers | 1 embryo_0-2h from dygenic mothers | 1 day old | 1 mixed whole adult body | 1 embryo_0-2h day old Strain 9 mothers | 1 embryo_0-2h from dygenic mothers | 1 | 1 | 1

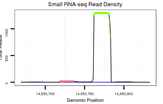
ID	Coordinate	Confidence	Class	Genome Locale
dvi_358	**scaffold_12963:14650719-14650783 +**	**confident**	**Mirtron**	**intron**

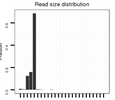
[View on UCSC Genome Browser (Cured Mirny)]

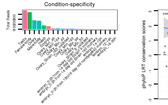
Legend: Stem 5p Terminal Loop Stem 3p

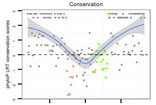
Predicted structure











Show Alternate Folds

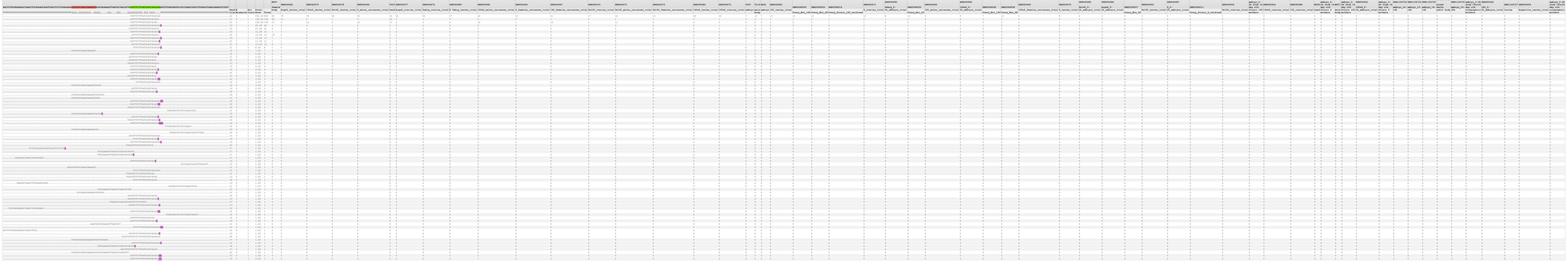
Flybase annotation

mir-2b-stel(CT754-aq) CDS [Dvir(GCT754-aq)]

No flypatch clones found

Sense Strand Reads

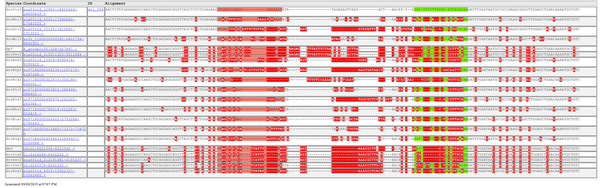
Sort by reads show red mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

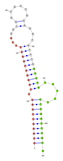


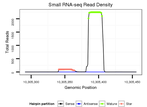
Generated 09/08/2015 at 07:07 PM

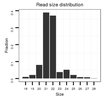
ID	Coordinate	Confidence	Class	Genome Locus
dvi_R3_scaffold_13849:10305341-10305486 +	**cosHdar**	**Mirtron**	**novel**	[View on UCSC Genome Browser (Local Mirror)]

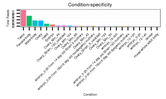
Length: **146** | Strand: **+** | Genome: **cosHdar** | Assembly: **dvi_R3**

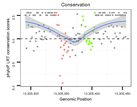
Predicted structure











Show Alternate Folds

Flybase annotation

mmu:Dicer1(3745-aj) CR6:(Dicer01)3745-obj:CR6:(Dicer01)3745-obj; ad1[ad1_sense_4.5Kb] ad1[ad1_sense_4.5Kb]

No Reporter clones found

Some Strand Reads

Scale 3p reads | show 5PE/3PE/5Ph/3Ph reads

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

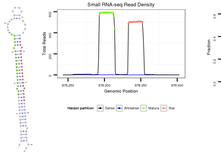
Generated 09/08/2015 at 07:07 PM

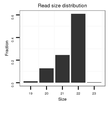
ID	Coordinate	Confidence	Class	Genomic Locus
chi_1188	**scaffold_12932:878293-878353 +**	**confident**	**Canonical miRNA**	**intergenic**

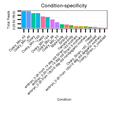
View on UCSC Genome Browser (Grand Mesa)

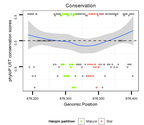
Legend: DICER DROSHA 5' Arm 3' Arm

Predicted structures









Show Alternate Fields

Fitchen annotation

miscgenic

No Repeatdb element found

Same Strand Reads

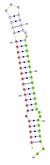
Hide 2p reads | show mid mismatch reads

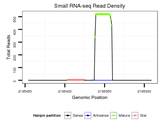
| Read ID | Strand | Hits | Total Score | chi_1188_mature_carcasses_total | chi_1188_mature_ovaries_total | chi_1188_mature_testes_total | chi_1188_mature_total | chi_1188_mature_RPM | chi_1188_mature_ovaries_total | chi_1188_mature_testes_total | chi_1188_mature_total | chi_1188_mature_RPM | chi_1188_star_carcasses_total | chi_1188_star_ovaries_total | chi_1188_star_testes_total | chi_1188_star_total | chi_1188_star_RPM | chi_1188_star_ovaries_total | chi_1188_star_testes_total | chi_1188_star_total | chi_1188_star_RPM | chi_1188_mature_carcasses_total | chi_1188_mature_ovaries_total | chi_1188_mature_testes_total | chi_1188_mature_total | chi_1188_mature_RPM | chi_1188_star_carcasses_total

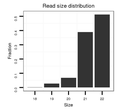
ID	Coordinate	Confidence	Class	Genome Locus
chr_250	**scaffold_12875:2195341-2195396 -**	**confident**	**Mirtron**	**intron**

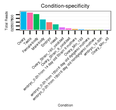
Legend: **RNA-seq** **Predicted structure** **conservation**

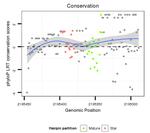
Predicted structure











Show Alternate Folds

Flybase annotation

mmu:(Dicer1)CG26-aj, CG6:(Dicer2)CG5246-aj; ncCart_plus_r6:79

No Repeatmk elements found

Genome Locus
+ scaffold_12875:2195341-2195396 -

Sense Strand Reads

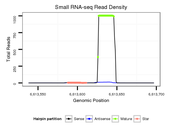
Hide 2p reads | Show red mismatch reads

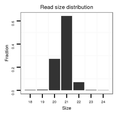
| Alignment | | |

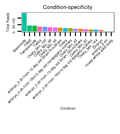
ID	Coordinate	Confidence	Class	Genome Locale	
dvi_354	**scaffold_12875:6613588-6613647 +**	**confident-exception**	**Canonical miRNA**	**antisense_to_CDS**	[View on UCSC Genome Browser (Canid Mirror)]

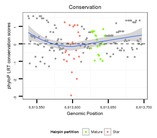
Seed: **GGA** Mature: **UCUCCAGCUGUGCAUGUGCUU** Antisense: **AAGCACAUGCAGCUGGAGAGA**

Predicted structure









Show Alternative Folds

Flybase annotation

Antisense to CDS:[FAM120C*99-exk]

No flyanalifs element found

Score Strand Reads

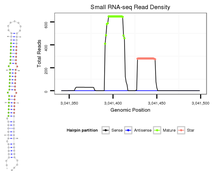
Hide Tp reads | show red mismatch reads

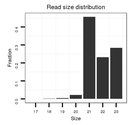
| Read ID | Alignments | Mismatch | Count | Score | MIR | MIR2 | mdrosophila_2: 5p_arm | mdrosophila_2: 3p_arm | mdrosophila_2: Flank | mdrosophila_2: Loop

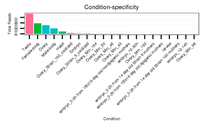
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_240	**scaffold_12970:3041391-3041449 +**	**confident**	**Testes-restricted**	**intergenic**
[View on UCSC Genome Browser (Crosed5.Mimic)]				

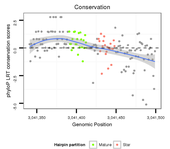
Legend: Loop, 5p, Mismatch, 3p, Flank, Mismatch Loop

Predicted structure









Show Alternate Folds

FlyBase annotation

ovcpsn

Repeatable elements

Name	Class	Family	Strand
L1-I-3Tom	Tom_ncpsn	Tom_ncpsn	+

mature

	Star
1 dvi_240 scaffold_12970:3041391-3041411 +	
2 scaffold_12970:3041428-3041449 +	

Sense Strand Reads

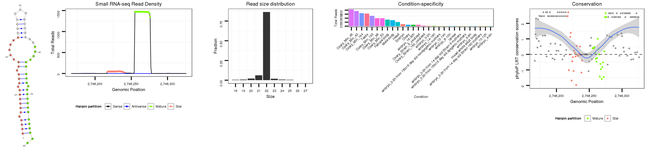
Hide 3p reads | show mid mismatch reads

| Read # | M/A Mismatch | Total Count | Reads | MG47 Testes Body | SRR040681 Arge9_testes_total | SRR040679 Ub5a8_testes_total | V116_SRR040676 male Bubsy_ovarian_total | SRR040677 Arge9_ovarian_total | SRR040678 Ub5a8_testes_total | V053_SRR040680 Bubsy_testes_total | SRR040689 Ub5a8_testes_total | SRR298014 Ovary_Strain_105_mel(female) | SRR040672 Ub105_female_carcassess_total | SRR040674 Ub105_ovarian_total | SRR040668 Ub5a8_malesc_carcassess_total | SRR040667 Ub105_female_carcassess_total | SRR040675 Ub5a8_ovarian_total | SRR298013 Ovary_Strain_8_mel(female) | SRR040665 8_female_carcassess_total | SRR040664 8_malesc_carcassess_total | SRR040654 Ub5a8_ovarian_total | SRR040666 Ub105_malesc_carcassess_total | SRR040669 Ub5a8_female_carcassess_total | V047 | SRR040688 | SRR040683 Ub105_ovarian_total | SRR040655 Ub105_testes_total | SRR040673 8_ovarian_total | SRR040656 Ub105_ovarian_total | SRR298057 Ovary_Mix_30 | SRR040671 Ub105_malesc_carcassess_total | SRR298059 8_testes_total | SRR040670 | M41 | SRR298058 Ovary_Mix_60 | SRR298040 Ovary_Mix_120 | SRR298055 | SRR040658 105_ovarian_total | SRR040660 Argentina_ovarian_total | SRR040657 105_testes_total | SRR298051 SRR298050 embryo_0-2h embryo_2-4h embryo_4-6h embryo_6-8h embryo_8-10h day old day old day old day old Strain 105 Strain 8 Argentina_testes_total | SRR040659 20h | SRR298041 SRR298038 embryo_0- embryo_0- mothers mothers | SRR040643 embryo_8- mothers | SRR115670 SRR115672 SRR115673 SRR115674 embryo_10- embryo_12- embryo_14- embryo_16- day old day old day old day old Strain 105 Strain 8 mothers mothers | SRR040684 8h fixed dpsquelch mutant head | SRR040682 Ub5a8_0- 2h_embryo_total larvae embryo_12- embryo_14- embryo_16- Ovary_Mix_7h |
|---|---|---|---|---

ID	Coordinate	Confidence	Class	Genome Locale	
dvi_22389	**scaffold_13324:2748217-2748276 +**	**confident**	**Mirtron**	**intron**	View on UCSC Genome Browser (Linear View)

Legend: Stem 5p Terminal loop Stem 3p Mismatch

Predicted structure



Show Alternate Forms

Flybase annotation

dmel:[Dmel]CTTTcAgCCDG:[Dmel]CPTTcAcgCCDG [Dmel]CPTTcAcgC

No Exposable intersections found

Sense Strand Reads

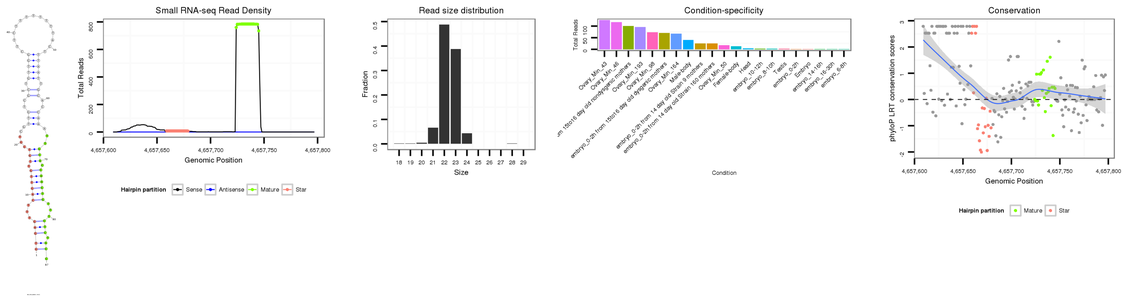
Hide 3p reads show mid mismatch reads

| Read # | Strand | Total | 5p Total | Loop Total | 3p Total | Mismatch Total | Mismatch Count | Mean Length | Mean Loop | Mean 5p | Mean 3p | 2R0170054 | 2R0170055 | 2R0170056 | 2R0170057 | 2R0245670 | 3R0E8:3R0G5670 | 2R0G5670 | 2R0G5687 | 2R0G5681 | 2R0G5684 | MW47 Cmax | MW47 Cmin | 2R0110730 body | 2R0245672 | 2R0G5672 | 2R0G5673 | 2R0G5674 | 2R0G5675 | 2R0G5676 | 2R0G5677 | 2R0G5678 | 2R0G5679 | 2R0G5680 | 2R0G5683 | 2R0G5685 | 2R0G5686 | 2R0G5687 | 2R0G5688 | 2R0G5689 | 2R0G5690 | 2R0G5691 | 2R0110715 body | 2R0110716 | 2R0110717 | 2R0110718 | 2R0110719 | 2R0110720 | 2R0110721 | 2R0110722 | 2R0110723 | 2R0110724 | 2R0170052 mated with body | 2R0170053 Dpnpep:1 mutbase | 2R0170058 dm_fish:14:15:cut:1 mutbase | 2R0170059 dm_fish:14:15:cut:1 mutbase | 2R0170060 dm_fish:14:15:cut:1 mutbase | 2R0170061 Dpnpep:1 mutbase | 2R0170062 mutbase | 2R0170063 mutbase | 2R0170064 mutbase | 2R0170065 mutbase | 2R0170066 mutbase | 2R0170067 mutbase | 2R0170068 mutbase | 2R0170069 mutbase | 2R0170070 mutbase | 2R0170071 mutbase | 2R0170072 mutbase | 2R0170073 mutbase | 2R0170074 mutbase | 2R0170075 mutbase | 2R0170076 mutbase | 2R0170077 mutbase | 2R0170078 mutbase | 2R0170079 mutbase | 2R0170080 mutbase | 2R0170081 mutbase | 2R0170082 mutbase | 2R0170083 mutbase | 2R0170084 mutbase | 2R0170085 mutbase | 2R0170086 mutbase | 2R0170087 mutbase | 2R0170088 mutbase | 2R0170089 mutbase | 2R0170090 mutbase | 2R0170091 mutbase | 2R0170092 mutbase | 2R0170093 mutbase | 2R0170094 mutbase | 2R0170095 mutbase | 2R0170096 mutbase | 2R0170097 mutbase | 2R0170098 mutbase | 2R0170099 mutbase | 2R0170100 mutbase | 2R0170101 mutbase | 2R0170102 mutbase | 2R0170103 mutbase | 2R0170104 mutbase | 2R0170105 mutbase | 2R0170106 mutbase | 2R0170107 mutbase | 2R0170108 mutbase | 2R0170109 mutbase | 2R0170110 mutbase | 2R0170111 mutbase | 2R0170112 mutbase | 2R0170113 mutbase | 2R0170114 mutbase | 2R0170115 mutbase | 2R0170116 mutbase | 2R0170117 mutbase | 2R0170118 mutbase | 2R0170119 mutbase | 2R0170120 mutbase | 2R0170121 mutbase | 2R0170122 mutbase | 2R0170123 mutbase | 2R0170124 mutbase | 2R0170125 mutbase | 2R0170126 mutbase | 2R0170127 mutbase | 2R0170128 mutbase | 2R0170129 mutbase | 2R0170130 mutbase | 2R0170131 mutbase | 2R0170132 mutbase | 2R0170133 mutbase | 2R0170134 mutbase | 2R0170135 mutbase | 2R0170136 mutbase | 2R0170137 mutbase | 2R0170138 mutbase | 2R0170139 mutbase | 2R0170140 mutbase | 2R0170141 mutbase | 2R0170142 mutbase | 2R0170143 mutbase | 2R0170144 mutbase | 2R0170145 mutbase | 2R0170146 mutbase | 2R0170147 mutbase | 2R0170148 mutbase | 2R0170149 mutbase | 2R0170150 mutbase | 2R0170151 mutbase | 2R0170152 mutbase | 2R0170153 mutbase | 2R0170154 mutbase | 2R0170155 mutbase | 2R0170156 mutbase | 2R0170157 mutbase | 2R0170158 mutbase | 2R0170159 mutbase | 2R0170160 mutbase | 2R0170161 mutbase | 2R0170162 mutbase | 2R0170163 mutbase | 2R0170164 mutbase | 2R0170165 mutbase | 2R0170166 mutbase | 2R0170167 mutbase | 2R0170168 mutbase | 2R0170169 mutbase | 2R0170170 mutbase | 2R0170171 mutbase | 2R0170172 mutbase | 2R0170173 mutbase | 2R0170174 mutbase | 2R0170175 mutbase | 2R0170176 mutbase | 2R0170177 mutbase | 2R0170178 mutbase | 2R0170179 mutbase | 2R0170180 mutbase | 2R0170181 mutbase | 2R0170182 mutbase | 2R0170183 mutbase | 2R0170184 mutbase | 2R0170185 mutbase | 2R0170186 mutbase | 2R0170187 mutbase | 2R0170188 mutbase | 2R0170189 mutbase | 2R0170190 mutbase | 2R0170191 mutbase | 2R0170192 mutbase | 2R0170193 mutbase | 2R0170194 mutbase | 2R0170195 mutbase | 2R0170196 mutbase | 2R0170197 mutbase | 2R0170198 mutbase | 2R0170199 mutbase | 2R0170200 mutbase | 2R0170201 mutbase | 2R0170202 mutbase | 2R0170203 mutbase | 2R0170204 mutbase | 2R0170205 mutbase | 2R0170206 mutbase | 2R0170207 mutbase | 2R0170208 mutbase | 2R0170209 mutbase | 2R0170210 mutbase | 2R0170211 mutbase | 2R0170212 mutbase | 2R0170213 mutbase | 2R0170214 mutbase | 2R0170215 mutbase | 2R0170216 mutbase | 2R0170217 mutbase | 2R0170218 mutbase | 2R0170219 mutbase | 2R0170220 mutbase | 2R0170221 mutbase | 2R0170222 mutbase | 2R0170223 mutbase | 2R0170224 mutbase | 2R0170225 mutbase | 2R0170226 mutbase | 2R0170227 mutbase | 2R0170228 mutbase | 2R0170229 mutbase | 2R0170230 mutbase | 2R0170231 mutbase | 2R0170232 mutbase | 2R0170233 mutbase | 2R0170234 mutbase | 2R0170235 mutbase | 2R0170236 mutbase | 2R0170237 mutbase | 2R0170238 mutbase | 2R0170239 mutbase | 2R0170240 mutbase | 2R0170241 mutbase | 2R0170242 mutbase | 2R0170243 mutbase | 2R0170244 mutbase | 2R0170245 mutbase | 2R0170246 mutbase | 2R0170247 mutbase | 2R0170248 mutbase | 2R0170249 mutbase | 2R0170250 mutbase | 2R0170251 mutbase | 2R0170252 mutbase | 2R0170253 mutbase | 2R0170254 mutbase | 2R0170255 mutbase | 2R0170256 mutbase | 2R0170257 mutbase | 2R0170258 mutbase | 2R0170259 mutbase | 2R0170260 mutbase | 2R0170261 mutbase | 2R0170262 mutbase | 2R0170263 mutbase | 2R0170264 mutbase | 2R0170265 mutbase | 2R0170266 mutbase | 2R0170267 mutbase | 2R0170268 mutbase | 2R0170269 mutbase | 2R0170270 mutbase | 2R0170271 mutbase | 2R0170272 mutbase | 2R0170273 mutbase | 2R0170274 mutbase | 2R0170275 mutbase | 2R0170276 mutbase | 2R0170277 mutbase | 2R0170278 mutbase | 2R0170279 mutbase | 2R0170280 mutbase | 2R0170281 mutbase | 2R0170282 mutbase | 2R0170283 mutbase | 2R0170284 mutbase | 2R0170285 mutbase | 2R0170286 mutbase | 2R0170287 mutbase | 2R0170288 mutbase | 2R0170289 mutbase | 2R0170290 mutbase | 2R0170291 mutbase | 2R0170292 mutbase | 2R0170293 mutbase | 2R0170294 mutbase | 2R0170295 mutbase | 2R0170296 mutbase | 2R0170297 mutbase | 2R0170298 mutbase | 2R0170299 mutbase | 2R0170300 mutbase | 2R0170301 mutbase | 2R0170302 mutbase | 2R0170303 mutbase | 2R0170304 mutbase | 2R0170305 mutbase | 2R0170306 mutbase | 2R0170307 mutbase | 2R0170308 mutbase | 2R0170309 mutbase | 2R0170310 mutbase | 2R0170311 mutbase | 2R0170312 mutbase | 2R0170313 mutbase | 2R0170314 mutbase | 2R0170315 mutbase | 2R0170316 mutbase | 2R0170317 mutbase | 2R0170318 mutbase | 2R0170319 mutbase | 2R0170320 mutbase | 2R0170321 mutbase | 2R0170322 mutbase | 2R0170323 mutbase | 2R0170324 mutbase | 2R0170325 mutbase | 2R0170326 mutbase | 2R0170327 mutbase | 2R0170328 mutbase | 2R0170329 mutbase | 2R0170330 mutbase | 2R0170331 mutbase | 2R0170332 mutbase | 2R0170333 mutbase | 2R0170334 mutbase | 2R0170335 mutbase | 2R0170336 mutbase | 2R0170337 mutbase | 2R0170338 mutbase | 2R0170339 mutbase | 2R0170340 mutbase | 2R0170341 mutbase | 2R0170342 mutbase | 2R0170343 mutbase | 2R0170344 mutbase | 2R0170345 mutbase | 2R0170346 mutbase | 2R0170347 mutbase | 2R0170348 mutbase | 2R0170349 mutbase | 2R0170350 mutbase | 2R0170351 mutbase | 2R0170352 mutbase | 2R0170353 mutbase | 2R0170354 mutbase | 2R0170355 mutbase | 2R0170356 mutbase | 2R0170357 mutbase | 2R0170358 mutbase | 2R0170359 mutbase | 2R0170360 mutbase | 2R0170361 mutbase | 2R0170362 mutbase | 2R0170363 mutbase | 2R0170364 mutbase | 2R0170365 mutbase | 2R0170366 mutbase | 2R0170367 mutbase | 2R0170368 mutbase | 2R0170369 mutbase | 2R0170370 mutbase | 2R0170371 mutbase | 2R0170372 mutbase | 2R0170373 mutbase | 2R0170374 mutbase | 2R0170375 mutbase | 2R0170376 mutbase | 2R0170377 mutbase | 2R0170378 mutbase | 2R0170379 mutbase | 2R0170380 mutbase | 2R0170381 mutbase | 2R0170382 mutbase | 2R0170383 mutbase | 2R0170384 mutbase | 2R0170385 mutbase | 2R0170386 mutbase | 2R0170387 mutbase | 2R0170388 mutbase | 2R0170389 mutbase | 2R0170390 mutbase | 2R0170391 mutbase | 2R0170392 mutbase | 2R0170393 mutbase | 2R0170394 mutbase | 2R0170395 mutbase | 2R0170396 mutbase | 2R0170397 mutbase | 2R0170398 mutbase | 2R0170399 mutbase | 2R0170400 mutbase | 2R0170401 mutbase | 2R0170402 mutbase | 2R0170403 mutbase | 2R0170404 mutbase | 2R0170405 mutbase | 2R0170406 mutbase | 2R0170407 mutbase | 2R0170408 mutbase | 2R0170409 mutbase | 2R0170410 mutbase | 2R0170411 mutbase | 2R0170412 mutbase | 2R0170413 mutbase | 2R0170414 mutbase | 2R0170415 mutbase | 2R0170416 mutbase | 2R0170417 mutbase | 2R0170418 mutbase | 2R0170419 mutbase | 2R0170420 mutbase | 2R0170421 mutbase | 2R0170422 mutbase | 2R0170423 mutbase | 2R0170424 mutbase | 2R0170425 mutbase | 2R0170426 mutbase | 2R0170427 mutbase | 2R0170428 mutbase | 2R0170429 mutbase | 2R0170430 mutbase | 2R0170431 mutbase | 2R0170432 mutbase | 2R0170433 mutbase | 2R0170434 mutbase | 2R0170435 mutbase | 2R0170436 mutbase | 2R0170437 mutbase | 2R0170438 mutbase | 2R0170439 mutbase | 2R0170440 mutbase | 2R0170441 mutbase | 2R0170442 mutbase | 2R0170443 mutbase | 2R0170444 mutbase | 2R0170445 mutbase | 2R0170446 mutbase | 2R0170447 mutbase | 2R0170448 mutbase | 2R0170449 mutbase | 2R0170450 mutbase | 2R0170451 mutbase | 2R0170452 mutbase | 2R0170453 mutbase | 2R0170454 mutbase | 2R0170455 mutbase | 2R0170456 mutbase | 2R0170457 mutbase | 2R0170458 mutbase | 2R0170459 mutbase | 2R0170460 mutbase | 2R0170461 mutbase | 2R0170462 mutbase | 2R0170463 mutbase | 2R0170464 mutbase | 2R0170465 mutbase | 2R0170466 mutbase | 2R0170467 mutbase | 2R0170468 mutbase | 2R0170469 mutbase | 2R0170470 mutbase | 2R0170471 mutbase | 2R0170472 mutbase | 2R0170473 mutbase | 2R0170474 mutbase | 2R0170475 mutbase | 2R0170476 mutbase | 2R0170477 mutbase | 2R0170478 mutbase | 2R0170479 mutbase | 2R0170480 mutbase | 2R0170481 mutbase | 2R0170482 mutbase | 2R0170483 mutbase | 2R0170484 mutbase | 2R0170485 mutbase | 2R0170486 mutbase | 2R0170487 mutbase | 2R0170488 mutbase | 2R0170489 mutbase | 2R0170490 mutbase | 2R0170491 mutbase | 2R0170492 mutbase | 2R0170493 mutbase | 2R0170494 mutbase | 2R0170495 mutbase | 2R0170496 mutbase | 2R0170497 mutbase | 2R0170498 mutbase | 2R0170499 mutbase | 2R0170500 mutbase | 2R0170501 mutbase | 2R0170502 mutbase | 2R0170503 mutbase | 2R0170504 mutbase | 2R0170505 mutbase | 2R0170506 mutbase | 2R0170507 mutbase | 2R0170508 mutbase | 2R0170509 mutbase | 2R0170510 mutbase | 2R0170511 mutbase | 2R0170512 mutbase | 2R0170513 mutbase | 2R0170514 mutbase | 2R0170515 mutbase | 2R0170516 mutbase | 2R0170517 mutbase | 2R0170518 mutbase | 2R0170519 mutbase | 2R0170520 mutbase | 2R0170521 mutbase | 2R0170522 mutbase | 2R0170523 mutbase | 2R0170524 mutbase | 2R0170525 mutbase | 2R0170526 mutbase | 2R0170527 mutbase | 2R0170528 mutbase | 2R0170529 mutbase | 2R0170530 mutbase | 2R0170531 mutbase | 2R0170532 mutbase | 2R0170533 mutbase | 2R0170534 mutbase | 2R0170535 mutbase | 2R0170536 mutbase | 2R0170537 mutbase | 2R0170538 mutbase | 2R0170539 mutbase | 2R0170540 mutbase | 2R0170541 mutbase | 2R0170542 mutbase | 2R0170543 mutbase | 2R0170544 mutbase | 2R0170545 mutbase | 2R0170546 mutbase | 2R0170547 mutbase | 2R0170548 mutbase | 2R0170549 mutbase | 2R0170550 mutbase | 2R0170551 mutbase | 2R0170552 mutbase | 2R0170553 mutbase | 2R0170554 mutbase | 2R0170555 mutbase | 2R0170556 mutbase | 2R0170557 mutbase | 2R0170558 mutbase | 2R0170559 mutbase | 2R0170560 mutbase | 2R0170561 mutbase | 2R0170562 mutbase | 2R0170563 mutbase | 2R0170564 mutbase | 2R0170565 mutbase | 2R0170566 mutbase | 2R0170567 mutbase | 2R0170568 mutbase | 2R0170569 mutbase | 2R0170570 mutbase | 2R0170571 mutbase | 2R0170572 mutbase | 2R0170573 mutbase | 2R0170574 mutbase | 2R0170575 mutbase | 2R0170576 mutbase | 2R0170577 mutbase | 2R0170578 mutbase | 2R0170579 mutbase | 2R0170580 mutbase | 2R0170581 mutbase | 2R0170582 mutbase | 2R0170583 mutbase | 2R0170584 mutbase | 2R0170585 mutbase | 2R0170586 mutbase | 2R0170587 mutbase | 2R0170588 mutbase | 2R0170589 mutbase | 2R0170590 mutbase | 2R0170591 mutbase | 2R0170592 mutbase | 2R0170593 mutbase | 2R0170594 mutbase | 2R0170595 mutbase | 2R0170596 mutbase | 2R0170597 mutbase | 2R0170598 mutbase | 2R0170599 mutbase | 2R0170600 mutbase | 2R0170601 mutbase | 2R0170602 mutbase | 2R0170603 mutbase | 2R0170604 mutbase | 2R0170605 mutbase | 2R0170606 mutbase | 2R0170607 mutbase | 2R0170608 mutbase | 2R0170609 mutbase | 2R0170610 mutbase | 2R0170611 mutbase | 2R0170612 mutbase | 2R0170613 mutbase | 2R0170614 mutbase | 2R0170615 mutbase | 2R0170616 mutbase | 2R0170617 mutbase | 2R0170618 mutbase | 2R0170619 mutbase | 2R0170620 mutbase | 2R0170621 mutbase | 2R0170622 mutbase | 2R0170623 mutbase | 2R0170624 mutbase | 2R0170625 mutbase | 2R0170626 mutbase | 2R0170627 mutbase | 2R0170628 mutbase | 2R0170629 mutbase | 2R0170630 mutbase | 2R0170631 mutbase | 2R0170632 mutbase | 2R0170633 mutbase | 2R0170634 mutbase | 2R0170635 mutbase | 2R0170636 mutbase | 2R0170637 mutbase | 2R0170638 mutbase | 2R0170639 mutbase | 2R0170640 mutbase | 2R0170641 mutbase | 2R0170642 mutbase | 2R0170643 mutbase | 2R0170644 mutbase | 2R0170645 mutbase | 2R0170646 mutbase | 2R0170647 mutbase | 2R0170648 mutbase | 2R0170649 mutbase | 2R0170650 mutbase | 2R0170651 mutbase | 2R0170652 mutbase | 2R0170653 mutbase | 2R0170654 mutbase | 2R0170655 mutbase | 2R0170656 mutbase | 2R0170657 mutbase | 2R0170658 mutbase | 2R0170659 mutbase | 2R0170660 mutbase | 2R0170661 mutbase | 2R0170662 mutbase | 2R0170663 mutbase | 2R0170664 mutbase | 2R0170665 mutbase | 2R0170666 mutbase | 2R0170667 mutbase | 2R0170668 mutbase | 2R0170669 mutbase | 2R0170670 mutbase | 2R0170671 mutbase | 2R0170672 mutbase | 2R0170673 mutbase | 2R0170674 mutbase | 2R0170675 mutbase | 2R0170676 mutbase | 2R0170677 mutbase | 2R0170678 mutbase | 2R0170679 mutbase | 2R0170680 mutbase | 2R0170681 mutbase | 2R0170682 mutbase | 2R0170683 mutbase | 2R0170684 mutbase | 2R0170685 mutbase | 2R0170686 mutbase | 2R0170687 mutbase | 2R0170688 mutbase | 2R0170689 mutbase | 2R0170690 mutbase | 2R0170691 mutbase | 2R0170692 mutbase | 2R0170693 mutbase | 2R0170694 mutbase | 2R0170695 mutbase | 2R0170696 mutbase | 2R0170697 mutbase | 2R0170698 mutbase | 2R0170699 mutbase | 2R0170700 mutbase | 2R0170701 mutbase | 2R0170702 mutbase | 2R0170703 mutbase | 2R0170704 mutbase | 2R0170705 mutbase | 2R0170706 mutbase | 2R0170707 mutbase | 2R0170708 mutbase | 2R0170709 mutbase | 2R0170710 mutbase | 2R0170711 mutbase | 2R0170712 mutbase | 2R0170713 mutbase | 2R0170714 mutbase | 2R0170715 mutbase | 2R0170716 mutbase | 2R0170717 mutbase | 2R0170718 mutbase | 2R0170719 mutbase | 2R0170720 mutbase | 2R0170721 mutbase | 2R0170722 mutbase | 2R0170723 mutbase | 2R0170724 mutbase |
|---|---|---|---|---|---

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_116	**scaffold_13042:4657659-4657747 +**	**confident**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star non-mature h-le s/bg non-st mismatch in read

Predicted structure



Show Alternate Folds

Flybase annnotation

intron [DvirGI16022-mI], CDS [DvirGI16022-cds]

Repeatable elements

Name	Class	Family	Strand
CT-rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	Alignment
22	....TTGCACCAACTGTTTCTCTACC.....
21	....TTGCACCAACTGTTTCCTCTACCT.....
21	....TTGCACCAACTGTTTCCTCTAC.....
24	....TTGCACCAACTGTTTCCTCTACCTT.....
23	....TTGCACCAACTGTTTCCTCTACC[G].....
22	....TTGCACCAACTGTTTCCTCTA[G].....
22	....TGCACCAACTGTTTCCTCTACCT.....
22	....TTGCACCAACTGTTTCCTCTAC[C].....
20	....ATTGTGGAGCTCAATCTTGA.....
21	....TGCACCAACTGTTTCCTCTACC.....
21	....TGCACCAACTGTTTCCTCTACCT.....
23	....GGCATTGTGGAGCTCAATCTTGA.....
21	....ATCGCGTTCATCATATCGGGC.....
22	....TGCACCAACTGTTTCCTCTAC[G].....
19	....ATCGGGCATTGTGGAGCT.....
20	....ATCGGGCATTGTGGAGCTGTGAGTTTCAGTTGTTGTCGTCGTTGTC
23	....TTGCACCAACTGTTTCCTCTAC[T].....
19	....ATCATATCGGGCATTGTGGAGCTCAAT.....
19	....GTTCATCATATCGGGCATT.....
20	....TTGCACCAACTGTTTCCTCTAC.....
25	....TTGCACCAACTGTTTCCTCTACAAA.....
23	....ATCATATCGGGCATTGTGGAGCT.....
18	....ATCGGGCATTGTGGAGCT.....
28	....GTGAGTTTCAGTTGTTGTCGTCGTTGTC
19	....GTGAGCTCAATCTTGA[G].....
21	....CATATCGGGCATTGTGGAGCT.....
18	....ATCGCGTTCATCATATCG.....
19	....CGGCATCGGGTTCAGTATTGGAGCT.....
21	....ATCATATCGGGCATTGTGGA.....
20	....TTCATCATATCGGGCATT.....
24	....TTGCACCAACTGTTTCCTCTACAA
21	....TGAGCTCAATCTTGA[G].....
19	....CATCATATCGGGCATTGTG.....
26	....GGGCATTGTGGAGCTCAATCTTGA[G].....
21	....ATCATATCGGGCATTGTGGAG.....
22	....TTGCACCAACTGTTTCCTCTACAA
19	....CATATCGGGCATTGTGGAG.....
25	....CATATCGGGCATTGTGGAGCTCAAT.....
18	....CGTTCATCATATCGGGCA.....
19	....CATCATATCGGGCATTGTGGA.....
23	....TCATCATATCGGGCATTGTGGAGCTCA.....
23	....TTGCACCAACTGTTTCCTCTAC.....
19	....GGCGTTCATCATATCGGGC.....
22	....TTGCACCAACTGTTTCCTCTACAA
18	....CGTTCATCATATCGGGCA.....
21	....CGTTCATCATATCGGGCAT.....
18	....ATCATATCGGGCATTGTGGA.....
23	....ATCATATCGGGCATTGTGGAGCTCAT.....
18	....ATCGCGTTCATCATATCGGGCA.....
22	....TTGCACCAACTGTTTCCTCTAC.....
20	....ATCATATCGGGCATTGTGGAGCT.....
23	....ATCGCGTTCATCATATCGGGCAT.....
19	....GTTGTGTCGTTGTCGT.....

Anti-sense strand reads

Read #	Alignment
18	....TATAAAGAATGGTTGGAGCTCAATCTTGA.....
18	....CAACAGCAGCACACGGA.....

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID
dvi	scaffold_13042:4657659-4657747 +	dvi_116
dsimW3	scaffold_6328:3921973-3922137 +	
dsecGrig	scaffold_15051:2843588-2844806 +	
dmel12	arf2_1000000004909:1186483-1188504 +	
dyak	chr_group14:6314674-6317035 +	
dsecPre2	scaffold_25:253476-253640 +	
dsimNat	scaffold_14:1710230-1712414 +	
dsecBip2	arf7180000398412:629330-629488 +	
dsecFri1	arf7180000202517:158008-159152 +	
dsecFle1	arf7180000453901:697920-698091 +	
dsecMel1	arf7180000493018:293573-293830 +	
dsecNok1	arf7180000079314:363596-363864 +	
dsecBla1	arf7180000302421:254533-254692 +	
dsecTak1	arf7180000415248:570039-570206 +	
dsecEug1	arf7180000405553:2192B-22084 +	
dm3	chr4:1731462-1731613 +	
dsimM2	s21663221-2663638 +	
dsecMer2	scaffold_6423532:2316102 +	
dsecYak1	s14643436-4643604 +	
dsecEre2	scaffold_6690:1155462-1155598 +	

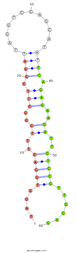
Generated: 09/06/2015 at 07:30 PM

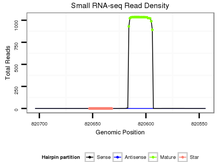
	PASSFAIL
crit.star	1
crit.loop	0
crit.mism	0
crit.half	0
crit.score	0
crit.pairing	1
crit.gap1	0
crit.gap1	0
crit.u1	0
crit.mfe	1
rescue.star	0
rescue.dominant	0
rescue.mature	0
rescue.confident	0
rescue.candidate	0

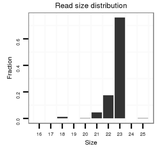
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_2375	**scaffold_12822:820594-820654 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

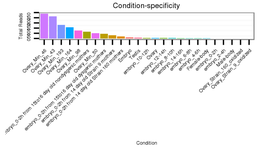
Legend: **Intron** **exon** **Mismatch in siblings or mismatch in seed**

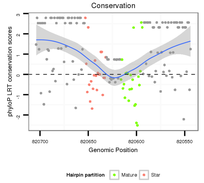
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dvir(GI1821-in], CDS [Dvir(GI1821-cds], CDS [Dvir(GI1821-cds]

No Repeatmiler elements found

Sense Strand Reads

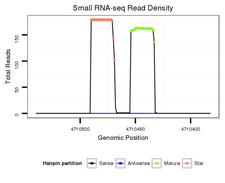
hide 3p reads show mid mismatch reads

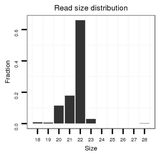
| | | |

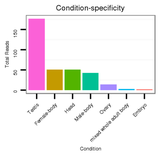
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_263	**scaffold_13042:4710432-4710490 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

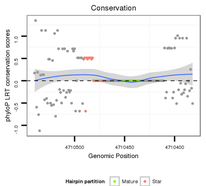
Legend: sense 5p 3p mismatch to alignment mismatch to star

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

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ATATTAATTTTACAATGAGTGTTGATTAAGTGTATGTCACTTAGTTA	TGTGAATGATTCATGTGCTTATA	TGAATATAAGCTT	GAGTGCTTGTCTTATTCACAGC	CACTTTTGACATTGGGCTGCAATTTCTTGCTATGATTGTTCATTCGTTTCT	Read Size	# Mismatch	Hit Count	Total Norm	Total	Arga9_testes_total	14E0_testes_total	14Ex9_testes_total	8_males_carcasses_total	14G_females_carcasses_total	14Ex8_males_carcasses_total	14Ex9_females_carcasses_total	9_females_carcasses_total	14G2_females_carcasses_total	9a14G_males_carcasses_total	14Ex9_females_carcasses_total	9_testes_total	14E_males_carcasses_total	14Ex9_testes_total	14Ex8_males_carcasses_total	female body	14Ex9_ovaries_total	9a14G_testes_total	9aArg_ovaries_total	Arga9_ovaries_total	mixed whole adult body	14G_testes_total	9a14G_ovaries_total	Ovary_Mix_43	embryo male body	2h_embryo_total	14Ex2_0-2h_embryo_total	14Ex9_ovaries_total	Argentina_testes_total	9_ovaries_total	14G_testes_total	14Ex2_0-2h_embryo_total	Arga9_0-2h_embryo_total	embryo_4-8h	male body	Ovary_Strain_14G_unidissed body
.....	TGTGAATGATTCATGTGCTTAT	.....	.....	.....	22	0	1	133.00	133	22	7	2	2	2	5	0	0	0	3	0	1	0	2	0	2	0	2	0	0	0	0	0	1	0	1	0	0	0	0	0	0
.....	TGTGAATGATTCATGTGCTTAT	.....	.....	.....	22	0	1	92.00	92	7	10	8	6	4	4	4	2	0	0	0	1	3	0	0	1	2	2	1	0	0	0	0	1	0	0	0	0	0	0	0	0
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.....	TGTGAATGATTCATGTGCTTT	.....	.....	.....	20	0	1	35.00	35	4	1	4	17	1	0	0	0	0	1	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
.....	TGTGAATGATTCATGTGCTTATG	.....	.....	.....	23	1	1	33.00	33	4	0	14	4	0	0	0	0	0	1	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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.....	TGTGAATGATTCATGTGCTTATGTA	.....	.....	.....	25	3	1	4.00	4	1	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
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.....	TGTGAATGATTCATGTGCTTATGTA	.....	.....	.....	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
.....	TGTGAATGATTCATGTGCTTATAG	.....	.....	.....	25	2	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
.....	TGTGAATGATTCATGTGCTTATGCAGTCA	.....	.....	.....	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
.....	TGTGAATGATTCATGTGCTTATGCAGCT	.....	.....	.....	23	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
.....	TGTGAATGATTCATGTGCTTATG	.....	.....	.....	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
.....	TGTGAATGATTCATGTGCTTATGCAGCA	.....	.....	.....	25	3	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	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

					SRR060686	GSM1528803	M027
TATAAATTAATAAATGTTCACTCACAACTAATTCACATACAGTGAATCAATGACACTTACTATAAGTACACGAATA	TCACGAACAGAATAATGTTA	ACTTATATTCGA	CTTACGAACAGAATAATGTTA	CTGAAAACTGTAACCCGACGTTAAAGAACGATACTAACAAGTAACGAAGA	Read Size	# Mismatch	Hit Count	Total Norm	Total	Arga9_0-2h_embryo_total	follicle cells	male body
.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dsim(+)	scaffold_14054:1152824-1152882(+)	dvi_263	ATATTAAT-ATTTACAATGAGTGTTGATTAAGTGTATGTCACTTAGTTA-TGTGAATGATTCATGTGCTTATATG-TGAATATAAGCTT-GAGTGCTTGTCTTATTCACAGC-ACTTTTGACATTGGGCTGCAATTTCTTGCT--ATGATTGTTCATTCGTTTCT
dmel(+)	scaffold_X:8861288833-8861288891(+)		ATATTAAT-ATTTACAATGAGTGTTGATTAAGTGTATGTCACTTAGTTA-TGTGAATGATTCATGTGCTTATATG-TGAATATAAGCTT-GAGTGCTTGTCTTATTCACAGC-ACTTTTGACATTGGGCTGCAATTTCTTGCT--ATGATTGTTCATTCGTTTCT
dvir(+)	scaffold_15245:1033183-1033241(+)		ATATTAAT-ATTTACAATGAGTGTTGATTAAGTGTATGTCACTTAGTTA-TGTGAATGATTCATGTGCTTATATG-TGAATATAAGCTT-GAGTGCTTGTCTTATTCACAGC-ACTTTTGACATTGGGCTGCAATTTCTTGCT--ATGATTGTTCATTCGTTTCT
dyak	fu_scaffold_1568398:3265821-0		ATATTAAT-ATTTACAATGAGTGTTGATTAAGTGTATGTCACTTAGTTA-TGTGAATGATTCATGTGCTTATATG-TGAATATAAGCTT-GAGTGCTTGTCTTATTCACAGC-ACTTTTGACATTGGGCTGCAATTTCTTGCT--ATGATTGTTCATTCGTTTCT
dvir(F1c1)	scf7180000543787:1058341-1058383(+)		ATATTAAT-ATTTACAATGAGTGTTGATTAAGTGTATGTCACTTAGTTA-TGTGAATGATTCATGTGCTTATATG-TGAATATAAGCTT-GAGTGCTTGTCTTATTCACAGC-ACTTTTGACATTGGGCTGCAATTTCTTGCT--ATGATTGTTCATTCGTTTCT

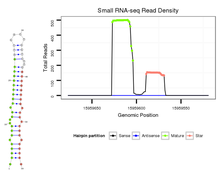
Generated on 2025-07-22 at 08:07 PM

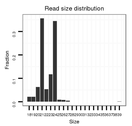
PHASTCONS	
vertebrate	-
mammal	-
primate	-
vertebrate	-
mammal	-
primate	-
PHYLOP	
vertebrate	-
mammal	-
primate	-
vertebrate	-
mammal	-
primate	-

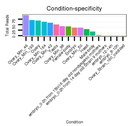
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_12155	**scaffold_12963:15959569-15959627 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser (GenoBrowse)]

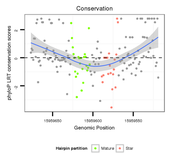
Legend: Sense Antisense 5' Arm Loop 3' Arm Mismatch Bulge

Predicted structure









Show Alternate Folds

FlyBase annotation

intron [FlyeGG2M03-ub], CDS [FlyeGG2M03-ub], CDS [FlyeGG2M03-ub]

Repeatable elements

Name	Class	Family	Detail
G-rich	Simple_repeat	Simple_repeat	

Sense Strand Reads

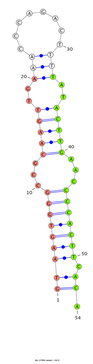
Hide 3p reads show mid mismatch reads

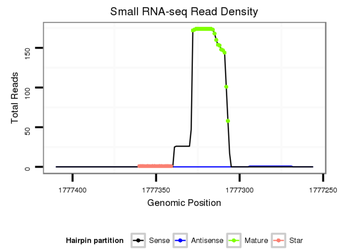
| | | |

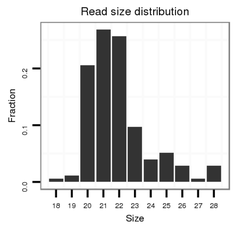
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_17904	**scaffold_13049:1777306-1777360 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

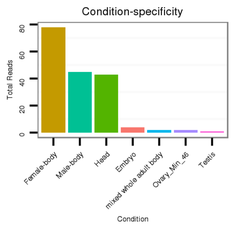
Legend: mature star mismatch in alignment mismatch in read

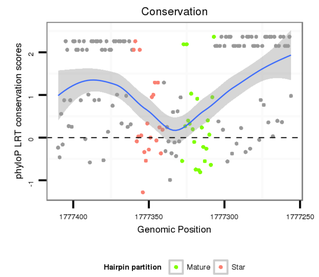
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DvirGJ12590-in]; CDS [DvirGJ12590-cds]; CDS [DvirGJ12590-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GCCGCTGCCAAAGGACGAGCACAACTACACCGAGCCCAAATACTATCTGGGTAAGTGGGCCGCAAGTTGAAACCCAGACTTTTATACTTGAACCCCACTTCACAGGCGACCTAATACCGGGCACCTATTGCTCGCGCATCTTCAGCGATTGCGAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M047 female body	M028 head	SRR060664 9_males_carcasses_total	SRR060665 9_females_carcasses_total	V053 head	SRR060671 9x160_males_carcasses_total	SRR060668 160x9_males_carcasses_total	SRR060667 160_females_carcasses_total	SRR060669 160x9_females_carcasses_total	M027 male body	SRR060672 9x160_females_carcasses_total	M061 embryo	SRR060666 160_males_carcasses_total	SRR1106729 mixed whole adult body	SRR2096056 Ovary_Min_46	SRR060679 140x9_testes_total	SRR2096026 embryo_0-2h from 14 day old Strain 9 mothers	SRR060677 Argx9_ovaries_total	SRR060658 140_ovaries_total	SRR060684 140x9_0-2h_embryos_total	SRR060686 Argx9_0-2h_embryos_total	SRR060673 9_ovaries_total
..TATACTTGAACCCCACTTCACA	22	0	1	38.00	38	10	1	8	5	3	2	2	2	2	0	2	0	0	0	0	1	0	0	0	0	0	0
..TATACTTGAACCCCACTTCAC	21	0	1	36.00	36	8	4	6	7	0	3	2	1	1	1	1	2	0	0	0	0	0	0	0	0	0	0
..TATACTTGAACCCCACTTCA	20	0	1	34.00	34	15	3	2	1	7	2	1	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0
..TATACTTGAACCCCACTTCACAG	23	0	1	14.00	14	5	0	3	2	0	0	1	1	0	0	0	1	1	0	0	0	0	0	0	0	0	0
..TTATACTTGAACCCCACTTCA	21	0	1	9.00	9	1	2	1	2	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..TATACTTGAACCCCACTTCACAG	24	1	1	8.00	8	0	2	2	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
..ACCCAGACTTTTATACTTGAACCCC	25	0	1	8.00	8	0	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..TTATACTTGAACCCCACTTCAC	22	0	1	7.00	7	1	0	0	1	0	1	0	2	0	0	0	1	0	1	0	0	0	0	0	0	0	0
..ACCCAGACTTTTATACTTGAACC	24	0	1	5.00	5	0	3	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
..ACCCAGACTTTTATACTTGAACCCC	26	0	1	5.00	5	0	3	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
..ACCCAGACTTTTATACTTGAACCCC	28	0	1	5.00	5	0	4	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
..TTATACTTGAACCCCACTTCACA	23	0	1	2.00	2	0	0	0	1	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0
..TTATACTTGAACCCCACTTCACAG	24	0	1	2.00	2	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
..TATACTTGAACCCCACTTC	19	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	0	0
..TTATACTTGAACCCCACTTC	20	0	1	1.00	1	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..ACCCAGACTTTTATACTTGAACC	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
..TATACTTGAACCCCACTTT	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
..ATACTTGAACCCCACTTCACA	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	0	0	0
..TTATACTTGAACCCCACTTCACA	24	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
..ACCCAGACTTTTATACTTGAACCCAC	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	0	0	0
..ATACTTGAACCCCACTTCACAG	23	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	0	0
..GTAAGTGGGCCGCAAGTTGA	20	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
..TATACTTGAACCCCACTTCA	20	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	0	0
..TTATACTTGAACCCCACTTC	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
..CCCAGACTTTTATACTTGAACCCCA	25	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
..TACTTGAACCCCACTTCACAG	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	0	0

Anti-sense strand reads

CGGCGACGGTTTCCTGCTCGTGTTGATGTGGCTCGGGTTTATGATAGACCCATTCACCCGGGCGTTCAACTTTGGGTCTGAAAATATGAACTTGGGGTGAAGTGTCCGCTGGATTATGGCCCGTGGATAACGAGCGCGTAGAAGTCGCTAACGCTG	Read size	# Mismatch	Hit Count	Total Norm	Total	M047 female body	SRR060664 9_males_carcasses_total	SRR060678 9x140_testes_total	V053 head	SRR060671 9x160_males_carcasses_total	V047 embryo	V116 male body
..GGCCCGTGGATAACGAGCGCGTAGAA	26	0	1	1.00	1	1	0	0	0	0	0	0

Show Alignment With Reads

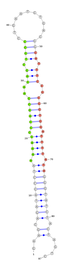
Re-alignment of all predicted orthologs

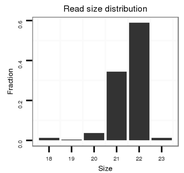
Species	Coordinate	ID	Alignment
droVir3	scaffold_13049:1777256-1777410 -	dvi_17904	GCCGCTGCCAAAGGACGAGCACAACTACACCGAGCCCAAATACTATCTGGGTAAGTGGGCCGCAAGTTGAAACCCAGACTTTTATACTTGAACCCCACTTCACAGGCGACCTAATACCGGGCACCTATTGCTCGCGCATCTTCAGCGATTGCGAC
droMoj3	scaffold_6654:2055092-2055252 +		GCCGCTGCCAAGGACGAGCACAACTACACCGAACCCAAATACTATCTGGGTAAGCGGCAAGTTGAAACCCAGACTTTTATACTTGAACCCCACTTCACAGGCGACCTAATACCGGCACCTATTGCTCGCGCATCTTCAGCGAGTGCGAC
droGri2	scaffold_15110:2847861-2847917 -		GCCGCTGCCAAGGACGAGCACAACTACACCGAACCCAAATACTATCTGGGTGGCGACAAGTTGAAACCCAGACTTTTATACTTGAACCCCACTTCACAGGCGACCTAATACCGGGCACCTATTGCTCGCGCATCTTCAGCGATTGCGAC
droWil2	scf2_1100000004762:15597924-15598085 +		A-TATGATGAAGGATGATATGATGTACACCGACGAACCGAAATATATGTGGGTAAGCTCGAAA

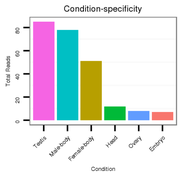
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_376	**scaffold_13049:363372-363430 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cons8 Mmu1]]

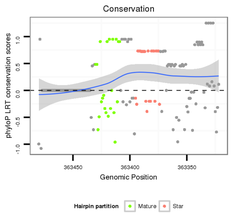
Legend: mature star hairpin arm (can match 5 or 3) one of mismatch in star

Predicted structure









Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GACTATGCAGATACCCTAGGGTTAACTGTGTCTACGAAGCAGATACCCTAAAAGCCCAGCGAAGAGCTGCCCTGAATCTGACGCGCATTTCCGGCCTGGATTTTATAGGGTATCTACTAGTCGAGCACGTTCCCTTTGTACACACGTATAAACAAGAGT	Read #	Hit	Total		V114 female body	M047 male body	SRR060659 Argentina_testes_total	SRR060672 9x160_females_carcasses_total	SRR060683 160_testes_total	SRR060655 head 9x160_testes_total	SRR060667 160_females_carcasses_total	SRR060657 140_testes_total	SRR060671 9x160_males_carcasses_total	SRR060679 140x9_testes_total	SRR060689 160x9_testes_total	SRR060678 9x140_testes_total	SRR060681 Arg9_testes_total	SRR060668 160x9_males_carcasses_total	SRR060669 160x9_females_carcasses_total	W041 embryo	SRR060658 140_ovaries_total	V147 embryo	SRR060660 Argentina_ovaries_total	SRR060666 140_males_carcasses_total	M027 male body	SRR060676 9xArg_ovaries_total	SRR060680 9xArg_testes_total	M028 head	SRR060656 9x160_ovaries_total	SRR060675 140x9_ovaries_total	SRR1106730 embryo_16-30h	SRR060670 9_testes_total	SRR1106724 embryo_12-14h	SRR1106728 larvae	SRR060665 9_females_carcasses_total
********************************..((.((((((((((.((((.((((((.....((.((((.....)))).))).....)))))).))))))))).))....	size	Mismatch	Count	Norm	Total																													
..AAAAGCCCAGCGAAGAGCTGCC	22	0	1	138.00	138	38	15	10	3			11		8	6		7			5	5		3		3	0		1		1	0		1		0	0	0	0	0
..AAAAGCCCAGCGAAGAGCTGCC	22	0	1	81.00	81	21	3	6	6			2		3	6		5			4	4		3		1	1		2		0	2		1		0	0	1	0	0
..AAAAGCCCAGCGAAGAGCTGC	22	0	1	8.00	8	1	0	0	0			0		1	0		0			0	1		0		2	0		0		0	2		0		0	0	0	0	0
..AAAAGCCCAGCGAAGAGCTG	20	0	1	8.00	8	1	0	2	0			0		0	0		0			0	0		0		0	0		1		1	0		0		1	0	0	0	0
..AAAAGCCCAGCGAAGAGCTGCC	23	1	1	6.00	6	2	2	0	1			0		0	0		0			0	0		1		0	0		0		0	0		0		0	0	0	0	0
..AAAAGCCCAGCGAAGAGCTGCC	23	0	1	4.00	4	0	0	1	1			0		0	0		0			1	0		0		0	0		1		0	0		0		0	0	0	0	0
..AAAAGCCCAGCGAAGAGCTGCC	22	0	1	4.00	4	0	1	0	0			0		0	0		1			0	1		0		0	0		0		0	0		0		0	0	0	0	0
..AAAAGCCCAGCGAAGAGCT	18	0	1	3.00	3	0	0	0	0			1		0	0		0			1	0		0		0	0		0		0	0		0		1	0	0	0	0
..AAAAGCCCAGCGAAGAGCTG	21	0	1	2.00	2	0	0	0	1			0		0	0		0			0	0		0		0	0		0		1	0		0		0	0	0	0	0
..AAAAGCCCAGCGAAGAGCTGCC	23	0	1	2.00	2	0	0	0	0			0		0	0		0			1	0		0		0	0		1		0	0		0		0	0	0	0	0
..AAGCCCAGCGAAGAGCTGCC	21	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
..AAAGCCCAGCGAAGAGCTGCC	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
..AAAAGCCCAGCGAAGAGCT	20	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
..AAAAGCCCAGCGAAGAGCTG	21	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
..AAAAGCCCAGCGAAGAGCTGC	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
..AAAAGCCCAGCGAAGAGCTGC	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
..AAAAGCCCAGCGAAGAGCT	20	1	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
..ATTTCGGGCTGGATTTTATAG	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	0
..AAAGCCCAGCGAAGAGCTGCC	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	0	0

Anti-sense strand reads

CTGATACGTCTATGGGATCCCAATTGACACAGATGCTTCGTCTATGGGATTTTCGGGTCGCTTCTCGACGGGACTTAGACTGCCGTAAAAGGCGCGACCTAAAATATCCCATAGATGATCAGCTCGTGCAAGGGAAACATGTGTCATATTTGTTCTCA	Read #	Hit	Total		SRR060659 Argentina_testes_total	SRR060681 Arg9_testes_total	SRR2096081 V116 from 15to16 day old male nondygenic body mothers	SRR2096555 male nondygenic mothers	SRR2096080 M027 from 15to16 day old male nondygenic body mothers	Ovary_Min_43
********************************..((.((((((((((.((((.((((((.....)))).))).....)))))).))))))))).))....	size	Mismatch	Count	Norm	Total					
..CCGTAAAAGGCGCGACCTAAAAT	22	0	1	2.00	2	1	0	1	0	0
..CCCATAGATGATCAGCTCGT	20	0	11	8.18	2	0	0	0	2	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_13049:363372-363480	dvi_376	GACTATGCAGATACCCTAGGGTTAACTGTGTCTACGAAGCAGATACCCTAAAAGCCCAGCGAAGAGCTGCC-TGAATC-------TGACGCGCATTTCCGGCCTGGATTTTATAGGGTATCTACTAGTCGAGCACGTTCCCTTTGTACACACGTATAAACAAGAGT
droMoj3	scaffold_6473:12117732-12117808..		G-G----------T-G-ACG-T-G-A-G-A-AG-AGCTGAA-G-TCTAAGC-GCTATT----------TTACC-T-CCGTCAC-G-CTTG-G-G-UACACG-GTG-GCG-G-AAC
droWil2	Scf0_1500000045851:1488492-1488521..		G----------T-G-CCG-G-UACACAC-G-AAACAA-AAA
droAna3	scaffold_13165:584292-584305		G----------T-----------TATAAAG-G-AGT
droHel1	scf7180000762911:14262-14821		G-G----------T-G-A-G-AAG-AG-G-G-G-G--------TCCCA-CTTTCCCAA-AA-GTT-CTATT-G-TTA----------

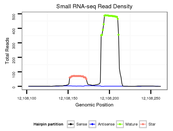
Generated: [illegible]15 at 09:02 PM

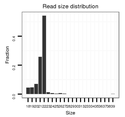
	PASSFAIL
cyt.dup	0
cyt.mapq	0
cyt.frac	0
cyt.pval	0
cyt.partial	1
cyt.mg3	1
cyt.mm3	0
cyt.ar	1
cyt.back	1
rescue.dup	0
rescue.dominant	0
rescue.known	0
rescue.novel	0
rescue.candidate	0

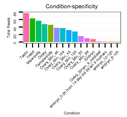
ID	Coordinate	Confidence	Class	Genomic Locale
dvi_322	**scaffold_12875:12108152-12108212 +**	**confident**	**Canonical miRNA**	**intergenic**
				Click on UCSC Genome Browser (Control/Meta+C)

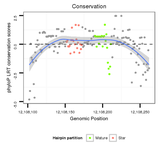
Legend: Arm 5p Loop Arm 3p Mature 5p Mature 3p

Predicted structure









Show Alternate Folds

Flybase annotation

miscpro

No Repeatble elements found

Sense Strand Reads

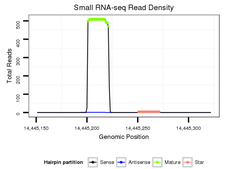
Hide 3p reads | show mismatch reads

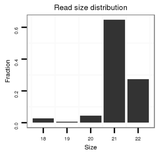
| Read # | Dri | Total | MC28 | | | |

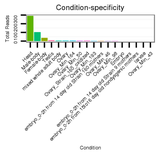
ID:	Coordinate:	Confidence:	Class:	Genome Locale:
dvi_65	**scaffold_13049:14445201-14445272 +**	**confident**	**Canonical miRNA**	**intergenic**
				[View on UCSC Genome Browser (Cornell Mirror)]

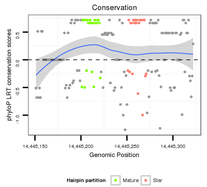
Legend: Sense Star 5nt mismatch in alignment mismatch in star

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

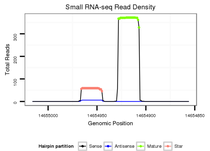
hide 3p reads show mid mismatch reads

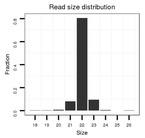
| | | | |

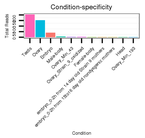
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_257	**scaffold_12875:14654906-14654966 -**	**confident**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser (Cotted Mature)]

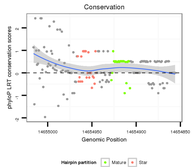
Legend: mature star mismatch in all reads mismatch in star

Predicted structure









Show Alternate Folds

FlyBase annotation

CDS (FlyBase2025-rel6)

No Repeatable elements found

Sense Strand Reads

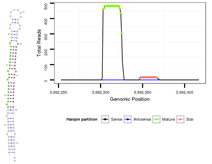
hide 3p reads show mid mismatch reads

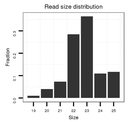
Read #	Size	Mismatch	Count	Total Norm	SRR040678 Ovary_Strain_9_unfixed	SRR040681 Argo9_testes_total	SRR040679 Ovary_Strain_9_unfixed	SRR040676 Ovary_ovarian_total	SRR040673 Ovary_Strain_9_unfixed	SRR040677 Argo9_ovarian_total	SRR040658 Ovary_Strain_9_unfixed	SRR040668 Ovary_ovarian_total	SRR040680 Argo9_testes_total	SRR040674 Ovary_Strain_9_unfixed	SRR040675 Ovary_ovarian_total	SRR040669 Ovary_Strain_9_unfixed	SRR040654 Ovary_ovarian_total	SRR040655 Ovary_Strain_9_unfixed	SRR040673 Ovary_ovarian_total	SRR040654 Ovary_ovarian_total	SRR040685 Dnha_0-3h_embryos_total	SRR040687 D_0-3h_embryos_total	MO41 embryo_total	SRR040657 Ovary_Strain_9_unfixed	SRR040682 Ovary_ovarian_total	SRR040684 Ovary_ovarian_total	SRR209013 Ovary_Strain_9_unfixed	SRR040659 Argentina_testes_total	MO47 female body	SRR040660 Argentina_ovarian_total	SRR209055 Ovary_Mix_43	SRR040686 Argo9_0-3h_embryos_total	SRR040671 Ovary_Strain_9_unfixed	SRR040664 Ovary_Strain_9_unfixed	SRR040663 Ovary_Strain_9_unfixed	SRR040683 Ovary_Strain_9_unfixed	SRR040643 Ovary_Strain_9_unfixed	SRR209014 Ovary_Strain_140_unfixed	SRR209040 embryo_0-2h from 14 Strain 9 mothers	SRR209041 embryo_0-2h from 14 Strain 9 mothers	SRR209042 embryo_0-2h from 14 Strain 9 mothers	SRR040662 male M02 body	SRR040642 Argo2_0-3h_embryos_total	SRR040688 Ovary_Strain_9_unfixed	SRR209060 Ovary_Mix_193	VG3 head	SRR209059 Ovary_Mix_164	SRR040666 L2_male_carcass_total	VG47 embryo
TGTGTTGAATGTATACTTTCCTGATGTGCAGGAATTGCAATTTCCTTGCTTAAGGCTAAAAGTGCTCAGGCTCTAAAACTTATAAATAAACACTTGAGCAGTTTTTGCGCTTGAACAATGAATTGTATAACAGCATTTGATGTGTCAGCAGACAGACGUTATA																																																	
********************************((((((.(((((((((((.(((((((((.(((((.....))))).))))))))))).))))))).))))))..))))))))))

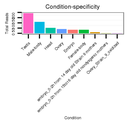
ID:	Coordinate:	Confidence:	Class:	Genome Locale:	
dvi_91	**scaffold_13042:3992303-3992367 +**	**confident**	**Canonical miRNA**	**intergenic**	View on UCSC Genome Browser: [Cured/Mature]

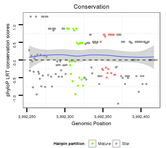
Legend: Loop 5p Mature 3p Star Mismatch Seed

Predicted structure









...

Show Alternate Folds

Flybase annotation

intergenic

No Repeatible elements found

Sense Strand Reads

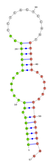
hide 5p reads | show mid mismatch reads

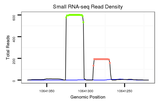
| | | |

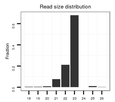
ID	Coordinate	Confidence	Class	Genome Locus
chr_1129	**scaffold_12875:10641269-10641325 -**	**confident**	**Microrna**	**intron**

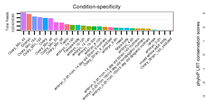
Length: **57** Strand: **Minus** Structure: **AUGUGUGAUGUGUGCAUGCAUGCAU**

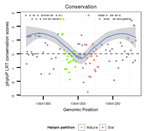
Predicted structures











Show Alternate Folds

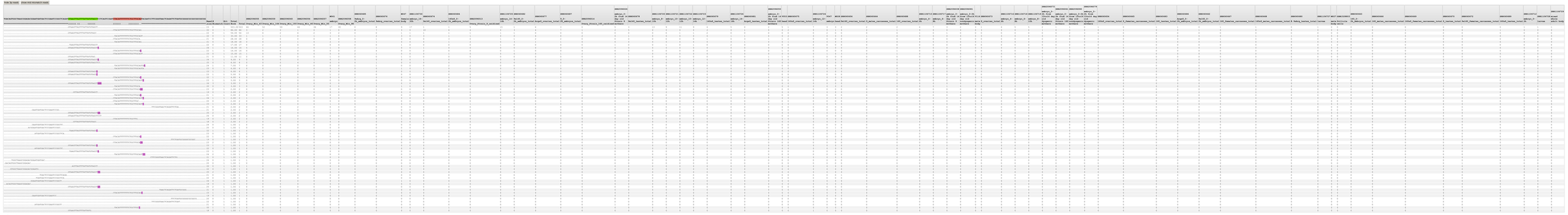
Flybase annotation

dmel:2L(+):2574:5-142:CR9120(+):ub(-):CR9120(+):ub(-):CR9120(+):ub(-)

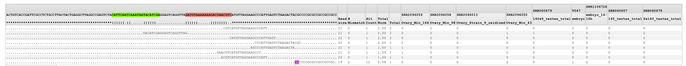
No Ensembl chrome hsalt

Some Strand Reads

Sort Tp reads show mid mismatch reads



Antisense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

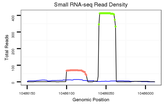
Generated 2009/28/10 at PTim PM

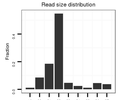
ID	Confidence	Confidence	Class	Genome Locus
dvi_102	**scaffold_13049:10486038-10486100 -**	**confident**	**Mirtron**	**CDS**

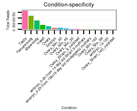
[View on UCSC Genome Browser (Grandi Mirs)]

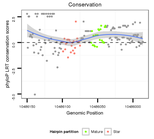
Legend: Mature Star Hairpin arm Alternative

Predicted structure









Show Alternate Forms

Flybase annotation

CDS (FlyBase:FBgn0[illegible])

No Repeatmasker elements found

Sense Strand Reads

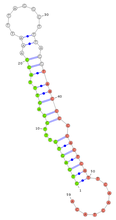
Hide 2p reads show red mismatch reads

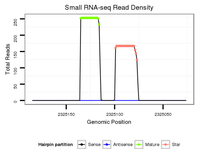
| Read Seq | Length | Mismatch | Total Count | Total Norm | Total | 2R0400678 hsd-1 | 2R0400681 hsd-1 | 2R0400679 hsd-1 | 2R0400684 hsd-1 | 2R0400667 hsd-1 | 2R0400672 hsd-1 | 2R0400680 hsd-1 | 2R0400665 hsd-1 | 2R0400668 hsd-1 | 2R0400666 hsd-1 | 2R0400674 hsd-1 | 2R0400677 hsd-1 | 2R0400673 hsd-1 | 2R0400671 hsd-1 | 2R0400689 hsd-1 | 2R0400669 hsd-1 | 2R0400686 hsd-1 | 2R0400683 hsd-1 | 2R0400682 hsd-1 | 2R0400687 hsd-1 | 2R0400688 hsd-1 | 2R0400675 hsd-1 | 2R0400676 hsd-1 | 2R0400670 hsd-1 | 2R0400685 hsd-1

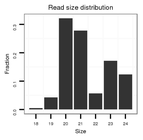
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_92	**scaffold_13047:2325076-2325135 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

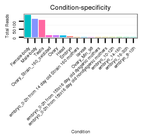
Legend: [redacted] [redacted] [redacted] [redacted]

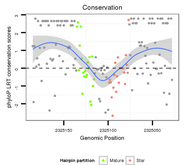
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dvir(GI13467-u)], CDS [Dvir(GI13467-u)], CDS [Dvir(GI13467-u)]

No Repeatable elements found

Sense Strand Reads

Hide 3p reads | Show mid mismatch reads

GACATAATCCACCTTTACCCTCTGTAATGTACAATGAGAATCCACCACC	GTGAGTGTTTGGATTTAG	AAATTTAGCCTTTAG	GAACCCCACTCATTCACTCA	GATTGATGCCACATCTGCGTTGAGGGATGTGCTCAAGACCTCGGACCTGAA
**********	(((((((.(...(((.(((.(((.(.....).))))))).))))))).)))))))	.....	**********	**********

	Read B ases	Mis Match	Uni Count	Mult Count	Total Reads	W047 female body	Y114 male Argentina_testes_total	SRR060681 Arps4_testes_total	SRR2096014 Ovary_Strain_160_unfilled	SRR060679 140x9_testes_total	SRR060664 9_males_carcasses_total	SRR060672 9x160_females_carcasses_total	SRR060678 9x140_testes_total	Y053 head	SRR060657 140_testes_total	SRR060665 9_females_carcasses_total	SRR060655 9x140_testes_total	SRR060667 140_females_carcasses_total	SRR060669 140x9_females_carcasses_total	SRR060670 9_testes_total	SRR060663 140_2-embryos_total	SRR060666 25_embryos_total	SRR060680 140_males_carcasses_total	SRR060689 9xkrg_testes_total	SRR060668 140x9_testes_total	Y047 140x9_males_carcasses_total	SRR060656 embryo	SRR060660 9x140_ovaries_total	SRR060661 140x9_0-25_embryos_total	SRR060675 Argentina_ovaries_total	SRR060674 140x9_ovaries_total	SRR060683 9xkrg_ovaries_total	SRR060688 140_ovaries_total	W041 embryo	SRR060671 9x160_males_carcasses_total	SRR1104727 larvae	SRR2096055 embryo_0-25_fruit 14 day old mothers	SRR2096058 Strain 160 mothers	W037 male head	W029 140x9_ovaries_total	SRR060654 140_ovaries_total	SRR060658 Arps4_ovaries_total	SRR060677 embryo_8-12h	SRR1104723 embryo_10-12h	SRR1104721 embryo_14-16h	SRR1104725 embryo_16-18h	SRR1104729 mixed whole adult body	SRR1104730 embryo_0-25 fruit 15x16 day old dynamic mothers	SRR2096079 embryo_0-25 fruit 15x16 day old nondynamic mothers	SRR2096080 embryo_0-25 fruit 15x16 day old mothers
.....GTGAGTGTTTGGATTTAG.....	20	0	1	122.00 122	0	12	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTACA.....	21	0	1	158.00 158	0	36	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TAACCCCACTCATTCACTCA.....	21	0	1	41.00 41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TAACCCCACTCATTCACTACA.....	24	0	1	32.00 32	37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TAACCCCACTCATTCACTAC.....	22	0	1	19.00 19	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTAC.....	24	0	1	18.00 18	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	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTACG.....	23	0	1	15.00 15	0	6	1	0	2	0	1	0	0	0	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TAACCCCACTCATTCAAA.....	20	0	1	13.00 13	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	0	0	0	0	0	0
.....TAACCCCACTCATTCACTA.....	21	0	1	7.00 7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTACAAA.....	24	0	1	5.00 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTA.....	24	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	0	0	0	0	0	0	0
.....AACCCCACTCATTCACTACA.....	20	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	0	0	0	0	0	0	0
.....AACCCCACTCATTCACTACG.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAACCCACTCATTCACTA.....	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	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTA.....	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	0	0	0	0	0	0	0
.....TAACCCCACTCATTCACATG.....	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	0	0	0	0	0	0	0
.....AACCCCACTCATTCACTAC.....	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	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTACA.....	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	0	0	0	0	0	0	0
.....AACCCCACTCATTCACTCA.....	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	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTAG.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTACAAA.....	23	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTACG.....	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	0	0	0	0	0	0	0
.....GTAACCCCACTCATTCACTC.....	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	0	0	0	0	0	0	0
.....TAACCCCACTCATTCACTCA.....	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	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTACG.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

CTGTATTACGTCCTGGAAGTGGGACAGTACATGTTACTCTTACGGTGGTCC	GACTCACAAACCTCAAATCT	TTTAAATCCGAAATCCT	ATTGGGGTGATTAATTGATCT	TAACTACCGTTGTAGACGCACTCCTACACGATTCTGGACCTCGACTT
**********	(((((((.(...(((.(((.(((.(.....).))))))).))))))).)))))))	.....	**********	**********

	Read B ases	Mis Match	Uni Count	Mult Count	Total Reads	W047 embryo	Y114 male body	SRR060689 140xk_0-25_embryo_total	SRR060684 140x9_testes_total	SRR060682 25_embryo_total	SRR060662 9x140_0-25_embryo_total
.....GTGAGTGTTTGGATTTACG.....	21	0	1	122.00 122	0	12	12	0	0	0	0
.....GTGAGTGTTTGGATTTACA.....	21	0	1	158.00 158	0	36	12	0	0	0	0
.....TAACCCCACTCATTCACTCA.....	21	0	1	41.00 41	0	0	0	0	0	0	0
.....TAACCCCACTCATTCACTACA.....	24	0	1	32.00 32	37	0	0	0	0	0	0
.....TAACCCCACTCATTCACTAC.....	22	0	1	19.00 19	7	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTAC.....	24	0	1	18.00 18	3	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTACG.....	23	0	1	15.00 15	0	6	1	0	2	0	1
.....TAACCCCACTCATTCAAA.....	20	0	1	13.00 13	2	0	0	0	0	0	0
.....TAACCCCACTCATTCACTA.....	21	0	1	7.00 7	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTACAAA.....	24	0	1	5.00 5	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTA.....	24	0	1	4.00 4	0	0	0	0	0	0	0
.....AACCCCACTCATTCACTACA.....	20	0	1	4.00 4	0	0	1	0	0	0	0
.....AACCCCACTCATTCACTACG.....	23	0	1	2.00 2	2	0	0	0	0	0	0
.....GTAACCCACTCATTCACTA.....	22	0	1	2.00 2	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTA.....	18	0	1	2.00 2	0	0	0	0	0	0	0
.....TAACCCCACTCATTCACATG.....	21	0	1	1.00 1	0	0	0	0	0	0	0
.....AACCCCACTCATTCACTAC.....	21	0	1	1.00 1	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTAG.....	19	0	1	1.00 1	0	0	0	0	1	0	0
.....AACCCCACTCATTCACTCA.....	20	0	1	1.00 1	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTACAAA.....	23	0	1	1.00 1	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTACG.....	21	0	1	1.00 1	0	0	0	0	0	0	0
.....GTAACCCCACTCATTCACTC.....	21	0	1	1.00 1	1	0	0	0	0	0	0
.....TAACCCCACTCATTCACTCA.....	24	0	1	1.00 1	0	0	0	0	0	0	0
.....GTGAGTGTTTGGATTTACG.....	23	0	1	1.00 1	0	0	0	0	0	0	0

Re-alignment of all predicted orthologs

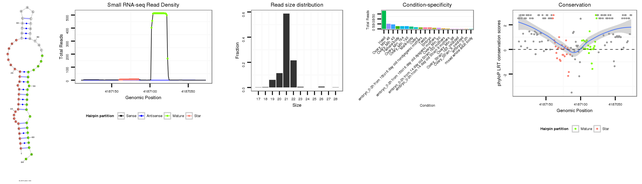
Species	Coordinate	ID	Alignment
dvir(+)	scaffold_13047:2325076-2325135 -	dvi_92	GCATTATCCACCTTTACCCTCTGTAATGTACAATGAGAATCCACCACCGTGAGTGTTTGGATTTAGAAATTTAGCCTTTAGGAACCCCACTCATTCACTCAGATTGATGCCACATCTGCGTTGAGGGATGTGCTCAAGACCTCGGACCTGAA
dsimw(+)	scaffold_6500:1533545-1533616 -		--
dsim(+)	scaffold_6:1513-1585:+		--
dsim2(+)	scaffold_20000:2040-2112:+		--
dyak	scaffold_14:4-76:+		--
dsecw(+)	scaffold_4:1360-1432:+		--
dsec(+)	scaffold_4:1341-1413:+		--
dmel(+)	scaffold_2L:1000-1072:+		--
dmelh(+)	scaffold_2000:1998-2070:+		--
dmeln(+)	scaffold_2000:1998-2070:+		--
dmoj(+)	scaffold_2:1000-1072:+		--
dmojw(+)	scaffold_2:1000-1072:+		--
dere(+)	scaffold_2:1000-1072:+		--
derew(+)	scaffold_2:1000-1072:+		--
dyak	scaffold_2:1000-1072:+		--
dsim	scaffold_2:1000-1072:+		--
dsim2	scaffold_2:1000-1072:+		--
dsim2	scaffold_2:1000-1072:+		--
dsim2	scaffold_2:1000-1072:+		--
dsim2	scaffold_2:1000-1072:+		--
dsim2	scaffold_2:1000-1072:+		--
dsim2	scaffold_2:1000-1072:+		--

Generated 09/08/2015 at 07:03 PM

ID	Coordinate	Confidence	Class	Genome Locale
dvi_18274	**scaffold_13049:4187077-4187140 -**	**confident-exception**	**Mirtron**	**intron**

Legend: **Hits to Dmel** | **Hits to Dmel - alternative**

Predicted structure



Show Alternate Folds

FlyBase annotation

mmu:Dmel:CG31712-mQ:CR:chr4:CG31712-mQ:CDS:[2nd:CG31712-mQ]

No Repeats-masked elements found

Some Strand Reads

Hide Tip reads | Show Hit mismatch reads

| Read # | Hits to Dmel | Hits to Dmel - alternative | Total Reads | MC01 head | 20MD250005 head | 20MD250006 head | 20MD250008 head | 20MD250009 head | 20MD250010 head | 20MD250011 wdmyo_0-2h Stress 9 arthsmo | 20MD250012 wdmyo_0-2h Stress 10 arthsmo | 20MD250013 wdmyo_0-2h Stress 11 arthsmo | 20MD250014 wdmyo_0-2h Stress 12 arthsmo | 20MD250015 wdmyo_0-2h Stress 13 arthsmo | 20MD250016 wdmyo_0-2h Stress 14 arthsmo | 20MD250017 wdmyo_0-2h Stress 15 arthsmo | 20MD250018 wdmyo_0-2h Stress 16 arthsmo | 20MD250019 wdmyo_0-2h Stress 17 arthsmo | 20MD250020 wdmyo_0-2h Stress 18 arthsmo | 20MD250021 wdmyo_0-2h Stress 19 arthsmo | 20MD250022 wdmyo_0-2h Stress 20 arthsmo | 20MD250023 wdmyo_0-2h Stress 21 arthsmo | 20MD250024 wdmyo_0-2h Stress 22 arthsmo | 20MD250025 wdmyo_0-2h Stress 23 arthsmo | 20MD250026 wdmyo_0-2h Stress 24 arthsmo | 20MD250027 wdmyo_0-2h Stress 25 arthsmo | 20MD250028 wdmyo_0-2h Stress 26 arthsmo | 20MD250029 wdmyo_0-2h Stress 27 arthsmo | 20MD250030 wdmyo_0-2h Stress 28 arthsmo | 20MD250031 wdmyo_0-2h Stress 29 arthsmo | 20MD250032 wdmyo_0-2h Stress 30 arthsmo | 20MD250033 wdmyo_0-2h Stress 31 arthsmo | 20MD250034 wdmyo_0-2h Stress 32 arthsmo | 20MD250035 wdmyo_0-2h Stress 33 arthsmo | 20MD250036 wdmyo_0-2h Stress 34 arthsmo | 20MD250037 wdmyo_0-2h Stress 35 arthsmo | 20MD250038 wdmyo_0-2h Stress 36 arthsmo | 20MD250039 wdmyo_0-2h Stress 37 arthsmo | 20MD250040 wdmyo_0-2h Stress 38 arthsmo | 20MD250041 wdmyo_0-2h Stress 39 arthsmo | 20MD250042 wdmyo_0-2h Stress 40 arthsmo | 20MD250043 wdmyo_0-2h Stress 41 arthsmo | 20MD250044 wdmyo_0-2h Stress 42 arthsmo | 20MD250045 wdmyo_0-2h Stress 43 arthsmo | 20MD250046 wdmyo_0-2h Stress 44 arthsmo | 20MD250047 wdmyo_0-2h Stress 45 arthsmo | 20MD250048 wdmyo_0-2h Stress 46 arthsmo | 20MD250049 wdmyo_0-2h Stress 47 arthsmo | 20MD250050 wdmyo_0-2h Stress 48 arthsmo | 20MD250051 wdmyo_0-2h Stress 49 arthsmo | 20MD250052 wdmyo_0-2h Stress 50 arthsmo | 20MD250053 wdmyo_0-2h Stress 51 arthsmo | 20MD250054 wdmyo_0-2h Stress 52 arthsmo | 20MD250055 wdmyo_0-2h Stress 53 arthsmo | 20MD250056 wdmyo_0-2h Stress 54 arthsmo | 20MD250057 wdmyo_0-2h Stress 55 arthsmo | 20MD250058 wdmyo_0-2h Stress 56 arthsmo | 20MD250059 wdmyo_0-2h Stress 57 arthsmo | 20MD250060 wdmyo_0-2h Stress 58 arthsmo | 20MD250061 wdmyo_0-2h Stress 59 arthsmo | 20MD250062 wdmyo_0-2h Stress 60 arthsmo | 20MD250063 wdmyo_0-2h Stress 61 arthsmo | 20MD250064 wdmyo_0-2h Stress 62 arthsmo | 20MD250065 wdmyo_0-2h Stress 63 arthsmo | 20MD250066 infant_0- day old | 20MD250067 infant_0- day old | 20MD250068 infant_0- day old | 20MD250069 infant_0- day old | 20MD250070 wdmyo_0- 2h fluo | 20MD250071 wdmyo_0- 2h fluo | 20MD250072 wdmyo_0- 2h fluo | 20MD250073 wdmyo_0- 2h fluo | 20MD250074 wdmyo_0- 2h fluo | 20MD250075 wdmyo_0- 2h fluo | 20MD250076 wdmyo_0- 2h fluo | 20MD250077 wdmyo_0- 2h fluo | 20MD250078 wdmyo_0- 2h fluo | 20MD250079 wdmyo_0- 2h fluo | 20MD250080 wdmyo_0- 2h fluo | 20MD250081 wdmyo_0- 2h fluo | 20MD250082 wdmyo_0- 2h fluo | 20MD250083 wdmyo_0- 2h fluo | 20MD250084 wdmyo_0- 2h fluo | 20MD250085 wdmyo_0- 2h fluo | 20MD250086 wdmyo_0- 2h fluo | 20MD250087 wdmyo_0- 2h fluo | 20MD250088 wdmyo_0- 2h fluo | 20MD250089 wdmyo_0- 2h fluo | 20MD250090 wdmyo_0- 2h fluo | 20MD250091 wdmyo_0- 2h fluo | 20MD250092 wdmyo_0- 2h fluo | 20MD250093 wdmyo_0- 2h fluo | 20MD250094 wdmyo_0- 2h fluo | 20MD250095 wdmyo_0- 2h fluo | 20MD250096 wdmyo_0- 2h fluo | 20MD250097 wdmyo_0- 2h fluo | 20MD250098 wdmyo_0- 2h fluo | 20MD250099 wdmyo_0- 2h fluo | 20MD250100 wdmyo_0- 2h fluo | 20MD250101 wdmyo_0- 2h fluo | 20MD250102 wdmyo_0- 2h fluo | 20MD250103 wdmyo_0- 2h fluo | 20MD250104 wdmyo_0- 2h fluo | 20MD250105 wdmyo_0- 2h fluo | 20MD250106 wdmyo_0- 2h fluo | 20MD250107 wdmyo_0- 2h fluo | 20MD250108 wdmyo_0- 2h fluo | 20MD250109 wdmyo_0- 2h fluo | 20MD250110 wdmyo_0- 2h fluo | 20MD250111 wdmyo_0- 2h fluo | 20MD250112 wdmyo_0- 2h fluo | 20MD250113 wdmyo_0- 2h fluo | 20MD250114 wdmyo_0- 2h fluo | 20MD250115 wdmyo_0- 2h fluo | 20MD250116 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fluo | 20MD250483 wdmyo_0- 2h fluo | 20MD250484 wdmyo_0- 2h fluo | 20MD250485 wdmyo_0- 2h fluo | 20MD250486 wdmyo_0- 2h fluo | 20MD250487 wdmyo_0- 2h fluo | 20MD250488 wdmyo_0- 2h fluo | 20MD250489 wdmyo_0- 2h fluo | 20MD250490 wdmyo_0- 2h fluo | 20MD250491 wdmyo_0- 2h fluo | 20MD250492 wdmyo_0- 2h fluo | 20MD250493 wdmyo_0- 2h fluo | 20MD250494 wdmyo_0- 2h fluo | 20MD250495 wdmyo_0- 2h fluo | 20MD250496 wdmyo_0- 2h fluo | 20MD250497 wdmyo_0- 2h fluo | 20MD250498 wdmyo_0- 2h fluo | 20MD250499 wdmyo_0- 2h fluo | 20MD250500 wdmyo_0- 2h fluo | 20MD250501 wdmyo_0- 2h fluo | 20MD250502 wdmyo_0- 2h fluo | 20MD250503 wdmyo_0- 2h fluo | 20MD250504 wdmyo_0- 2h fluo | 20MD250505 wdmyo_0- 2h fluo | 20MD250506 wdmyo_0- 2h fluo | 20MD250507 wdmyo_0- 2h fluo | 20MD250508 wdmyo_0- 2h fluo | 20MD250509 wdmyo_0- 2h fluo | 20MD250510 wdmyo_0- 2h fluo | 20MD250511 wdmyo_0- 2h fluo | 20MD250512 wdmyo_0- 2h fluo | 20MD250513 wdmyo_0- 2h fluo | 20MD250514 wdmyo_0- 2h fluo | 20MD250515 wdmyo_0- 2h fluo | 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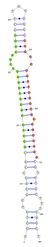
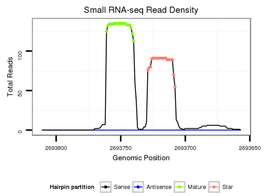
wdmyo_0- 2h fluo | 20MD250550 wdmyo_0- 2h fluo | 20MD250551 wdmyo_0- 2h fluo | 20MD250552 wdmyo_0- 2h fluo | 20MD250553 wdmyo_0- 2h fluo | 20MD250554 wdmyo_0- 2h fluo | 20MD250555 wdmyo_0- 2h fluo | 20MD250556 wdmyo_0- 2h fluo | 20MD250557 wdmyo_0- 2h fluo | 20MD250558 wdmyo_0- 2h fluo | 20MD250559 wdmyo_0- 2h fluo | 20MD250560 wdmyo_0- 2h fluo | 20MD250561 wdmyo_0- 2h fluo | 20MD250562 wdmyo_0- 2h fluo | 20MD250563 wdmyo_0- 2h fluo | 20MD250564 wdmyo_0- 2h fluo | 20MD250565 wdmyo_0- 2h fluo | 20MD250566 wdmyo_0- 2h fluo | 20MD250567 wdmyo_0- 2h fluo | 20MD250568 wdmyo_0- 2h fluo | 20MD250569 wdmyo_0- 2h fluo | 20MD250570 wdmyo_0- 2h fluo | 20MD250571 wdmyo_0- 2h fluo | 20MD250572 wdmyo_0- 2h fluo | 20MD250573 wdmyo_0- 2h fluo | 20MD250574 wdmyo_0- 2h fluo | 20MD250575 wdmyo_0- 2h fluo | 20MD250576 wdmyo_0- 2h fluo | 20MD250577 wdmyo_0- 2h fluo | 20MD250578 wdmyo_0- 2h fluo | 20MD250579 wdmyo_0- 2h fluo | 20MD250580 wdmyo_0- 2h fluo | 20MD250581 wdmyo_0- 2h fluo | 20MD250582 wdmyo_0- 2h fluo | 20MD250583 wdmyo_0- 2h fluo | 20MD250584 wdmyo_0- 2h fluo | 20MD250585 wdmyo_0- 2h fluo | 20MD250586 wdmyo_0- 2h fluo | 20MD250587 wdmyo_0- 2h fluo | 20MD250588 wdmyo_0- 2h fluo | 20MD250589 wdmyo_0- 2h fluo | 20MD250590 wdmyo_0- 2h fluo | 20MD250591 wdmyo_0- 2h fluo | 20MD250592 wdmyo_0- 2h fluo | 20MD250593 wdmyo_0- 2h fluo | 20MD250594 wdmyo_0- 2h fluo | 20MD250595 wdmyo_0- 2h fluo | 20MD250596 wdmyo_0- 2h fluo | 20MD250597 wdmyo_0- 2h fluo | 20MD250598 wdmyo_0- 2h fluo | 20MD250599 wdmyo_0- 2h fluo | 20MD250600 wdmyo_0- 2h fluo | 20MD250601 wdmyo_0- 2h fluo | 20MD250602 wdmyo_0- 2h fluo | 20MD250603 wdmyo_0- 2h fluo | 20MD250604 wdmyo_0- 2h fluo | 20MD250605 wdmyo_0- 2h fluo | 20MD250606 wdmyo_0- 2h fluo | 20MD250607 wdmyo_0- 2h fluo | 20MD250608 wdmyo_0- 2h fluo | 20MD250609 wdmyo_0- 2h fluo | 20MD250610 wdmyo_0- 2h fluo | 20MD250611 wdmyo_0- 2h fluo | 20MD250612 wdmyo_0- 2h fluo | 20MD250613 wdmyo_0- 2h fluo | 20MD250614 wdmyo_0- 2h fluo | 20MD250615 wdmyo_0- 2h fluo | 20MD250616 wdmyo_0- 2h fluo | 20MD250617 wdmyo_0- 2h fluo | 20MD250618 wdmyo_0- 2h fluo | 20MD250619 wdmyo_0- 2h fluo | 20MD250620 wdmyo_0- 2h fluo | 20MD250621 wdmyo_0- 2h fluo | 20MD250622 wdmyo_0- 2h fluo | 20MD250623 wdmyo_0- 2h fluo | 20MD250624 wdmyo_0- 2h fluo | 20MD250625 wdmyo_0- 2h fluo | 20MD250626 wdmyo_0- 2h fluo | 20MD250627 wdmyo_0- 2h fluo | 20MD250628 wdmyo_0- 2h fluo | 20MD250629 wdmyo_0- 2h fluo | 20MD250630 wdmyo_0- 2h fluo | 20MD250631 wdmyo_0- 2h fluo | 20MD250632 wdmyo_0- 2h fluo | 20MD250633 wdmyo_0- 2h fluo | 20MD250634 wdmyo_0- 2h fluo | 20MD250635 wdmyo_0- 2h fluo | 20MD250636 wdmyo_0- 2h fluo | 20MD250637 wdmyo_0- 2h fluo | 20MD250638 wdmyo_0- 2h fluo | 20MD250639 wdmyo_0- 2h fluo | 20MD250640 wdmyo_0- 2h fluo | 20MD250641 wdmyo_0- 2h fluo | 20MD250642 wdmyo_0- 2h fluo | 20MD250643 wdmyo_0- 2h fluo | 20MD250644 wdmyo_0- 2h fluo | 20MD250645 wdmyo_0- 2h fluo | 20MD250646 wdmyo_0- 2h fluo | 20MD250647 wdmyo_0- 2h fluo | 20MD250648 wdmyo_0- 2h fluo | 20MD250649 wdmyo_0- 2h fluo | 20MD250650 wdmyo_0- 2h fluo | 20MD250651 wdmyo_0- 2h fluo | 20MD250652 wdmyo_0- 2h fluo | 20MD250653 wdmyo_0- 2h fluo | 20MD250654 wdmyo_0- 2h fluo | 20MD250655 wdmyo_0- 2h fluo | 20MD250656 wdmyo_0- 2h fluo | 20MD250657 wdmyo_0- 2h fluo | 20MD250658 wdmyo_0- 2h fluo | 20MD250659 wdmyo_0- 2h fluo | 20MD250660 wdmyo_0- 2h fluo | 20MD250661 wdmyo_0- 2h fluo | 20MD250662 wdmyo_0- 2h fluo | 20MD250663 wdmyo_0- 2h fluo | 20MD250664 wdmyo_0- 2h fluo | 20MD250665 wdmyo_0- 2h fluo | 20MD250666 wdmyo_0- 2h fluo | 20MD250667 wdmyo_0- 2h fluo | 20MD250668 wdmyo_0- 2h fluo | 20MD250669 wdmyo_0- 2h fluo | 20MD250670 wdmyo_0- 2h fluo | 20MD250671 wdmyo_0- 2h fluo | 20MD250672 wdmyo_0- 2h fluo | 20MD250673 wdmyo_0- 2h fluo | 20MD250674 wdmyo_0- 2h fluo | 20MD250675 wdmyo_0- 2h fluo | 20MD250676 wdmyo_0- 2h fluo | 20MD250677 wdmyo_0- 2h fluo | 20MD250678 wdmyo_0- 2h fluo | 20MD250679 wdmyo_0- 2h fluo | 20MD250680 wdmyo_0- 2h fluo | 20MD250681 wdmyo_0- 2h fluo | 20MD250682 wdmyo_0- 2h fluo | 20MD250683 wdmyo_0- 2h fluo | 20MD250684 wdmyo_0- 2h fluo | 20MD250685 wdmyo_0- 2h fluo | 20MD250686 wdmyo_0- 2h fluo | 20MD250687 wdmyo_0- 2h fluo | 20MD250688 wdmyo_0- 2h fluo | 20MD250689 wdmyo_0- 2h fluo | 20MD250690 wdmyo_0- 2h fluo | 20MD250691 wdmyo_0- 2h fluo | 20MD250692 wdmyo_0- 2h fluo | 20MD250693 wdmyo_0- 2h fluo | 20MD250694 wdmyo_0- 2h fluo | 20MD250695 wdmyo_0- 2h fluo | 20MD250696 wdmyo_0- 2h fluo | 20MD250697 wdmyo_0- 2h fluo | 20MD250698 wdmyo_0- 2h fluo |

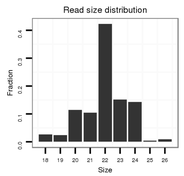
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_106	**scaffold_12855:2693707-2693761 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cons][Mmtr1]]

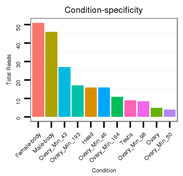
Legend: mature star no-mirb-b-3p alignment mismatch in star

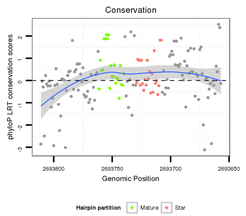
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

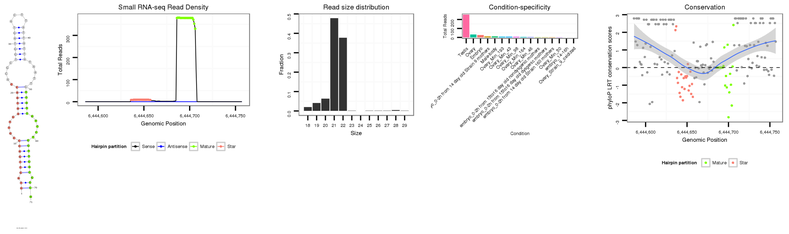
hide 3p reads show mid mismatch reads

						SRR060672	M027			M047		SRR060665	SRR060664	M028	SRR2096059	SRR2096058	SRR060671	V053		V116	SRR060655	SRR060675	SRR060679	SRR060681	SRR060667	M061	SRR060656	SRR060668	SRR060673	SRR060676	SRR060689	SRR060657	SRR060654	SRR060669	SRR060670	SRR060683	SRR2096050	SRR060688
ACAACAGCAATTACATTGCATTCGCAGTCGCTGTCGCAGTCGCAGCTGCTGTCGCAGTCGCAGCGACAGCGCTCGCGCTGTCGCAGTCGCAGCGACAGCGCTTGCGGCGCTGCCCGCTGCTTTCAGCTGCAACGGCCAACGTCGTCAGTCGCCAGTCGTCAGTT	Read Size	# Mismatch	Hit Count	Total Norm	Total	9x160_females_carcasses_total	male body	Ovary_Min_43	Ovary_Min_193	female body	Ovary_Min_46	9_females_carcasses_total	9_males_carcasses_total	head body	Ovary_Min_164	Ovary_Min_98	9x160_males_carcasses_total	head body	Ovary_Min_50	male body	9x160_testes_total	160x9_ovaries_total	160x9_testes_total	160_females_carcasses_total	embryo	9x160_ovaries_total	160x9_males_carcasses_total	9_ovaries_total	9xkrg_ovaries_total	160x9_testes_total	160_testes_total	160x9_ovaries_total	160x9_females_carcasses_total	9_testes_total	160_testes_total	embryo_0-2h from 14 day old mothers	160_ovaries_total
..CCCC

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_261	**scaffold_12970:6444636-6444707 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cosmid Mirror)]

Legend: [illegible] [illegible] [illegible]

Predicted structure



Show Alternate Folds

Flybase annotation

intron [DroVGI19515-aj], CDS [DroVGI19515-aj], CDS [DroVGI19515-ab]

No Repeatmasker elements found

Sense Strand Reads

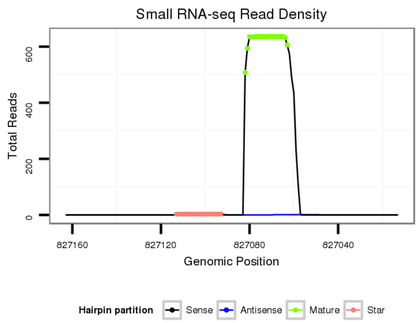
hide 3p reads | show mid mismatch reads

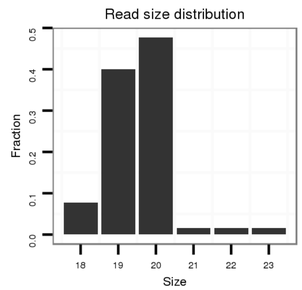
| AGATGATACCCTGAGAACCCTCTTTCGGCAGGACACAGACAATAAATCAA | GTAGTTGACCCGTTGAATAACC | ACGCTGGTGATACTTATTATTATTATTTTTATTGATTTTCTGGTTGACGGCG | A | | |

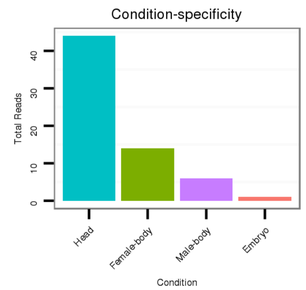
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_452	**scaffold_13042:827063-827113 -**	**confident**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

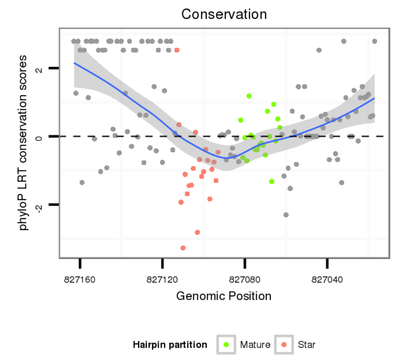
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annnotation

intron [Dvir\GJ15757-in]; CDS [Dvir\GJ15757-cds]; CDS [Dvir\GJ15757-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CCGTACACGCAAATCACAGGCTATCTCTGCGTCGGCCTGCAGTATGACAAGTGAGTGCCCATTCATTCAAATGAAAATCCATTTGATGCATGCGACACTCATCTTTCAGGCACAACAGCAACAGCGGCGAGAACGAGGAGGAGGAGCAGCT **********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060664 9_males_carcasses_total	SRR060671 9x160_males_carcasses_total	SRR060672 9x160_females_carcasses_total	SRR060667 160_females_carcasses_total	V053 head	SRR060668 160x9_males_carcasses_total	M028 head	SRR060665 9_females_carcasses_total	SRR060669 160x9_females_carcasses_total	M047 female body	SRR060666 160_males_carcasses_total	V116 male body	M027 male body	M061 embryo	V047 embryo
.....TTTGATGCATGCGACACTCATCT.....	23	0	1	172.00	172	29	32	27	16	13	19	4	13	12	5	2	0	0	0	0
.....TTTGATGCATGCGACACTCATCTT.....	24	0	1	85.00	85	15	12	13	13	3	9	0	11	5	2	2	0	0	0	0
.....TTTGATGCATGCGACACTCAT.....	21	0	1	84.00	84	5	20	7	14	11	8	0	5	5	5	3	1	0	0	0
.....TTTGATGCATGCGACACTCATCTTT.....	25	0	1	55.00	55	12	9	11	7	1	2	0	4	6	0	3	0	0	0	0
.....TTTGATGCATGCGACACTCATC.....	22	0	1	52.00	52	9	6	3	8	1	5	6	4	4	4	1	0	1	0	0
.....TTTGATGCATGCGACACTCA.....	20	0	1	31.00	31	0	3	2	1	6	1	9	0	2	6	0	0	0	0	1
.....TTGATGCATGCGACACTCATCTTT.....	24	0	1	29.00	29	7	3	4	8	0	4	0	2	1	0	0	0	0	0	0
.....TTGATGCATGCGACACTCATCT.....	22	0	1	26.00	26	4	1	4	3	1	1	0	4	5	1	1	1	0	0	0
.....TTGATGCATGCGACACTCATCTT.....	23	0	1	26.00	26	7	4	5	2	4	0	0	2	0	0	2	0	0	0	0
.....TTTGATGCATGCGACACTC.....	19	0	1	25.00	25	0	1	0	0	2	0	21	0	1	0	0	0	0	0	0
.....TGATGCATGCGACACTCATCTTT.....	23	0	1	18.00	18	5	7	2	1	0	1	0	1	0	0	0	0	0	1	0
.....TGATGCATGCGACACTCATCTT.....	22	0	1	15.00	15	3	4	2	3	1	1	0	0	0	1	0	0	0	0	0
.....TGATGCATGCGACACTCATCT.....	21	0	1	6.00	6	1	0	0	1	2	0	0	1	0	0	1	0	0	0	0
.....TTTGATGCATGCGACACT.....	18	0	1	4.00	4	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0
.....TTGATGCATGCGACACTCATC.....	21	0	1	2.00	2	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0
.....TTTGATGCATGCGACACTCATCTTTT.....	26	1	1	2.00	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGCCCATTCATTCAAA.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
.....TTGATGCATGCGACACTCA.....	19	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
.....TTGATGCATGCGACACTCATCTTTT.....	25	1	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
.....TTGATGCATGCGACACTC.....	18	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....TTGATGCATGCGACACTCAT.....	20	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCATGCGACACTCATCT.....	18	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
.....TGATGCATGCGACACTCATCTTTC.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTTGATGCATGCGACACTCATT.....	22	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGCCCATTCATTCAAATG.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTGCCCATTCATTCAAAT.....	22	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
.....TGATGCATGCGACACTCATC.....	20	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
.....TTTGATGCATGCGACACC.....	18	1	2	0.50	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0

Anti-sense strand reads

GGCATGTGCGTTTAGTGTCCGATAGAGACGCAGCCGGACGTCATACTGTTCACTCACGGGTAAGTAAGTTTACTTTTAGGTAAACTACGTACGCTGTGAGTAGAAAGTCCGTGTTGTCGTTGTCGCCGCTCTTGCTCCTCCTCCTCGTCGA **********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060659 Argentina_testes_total	V116 male body	M047 female body	SRR060684 140x9_0-2h_embryos_total	SRR060686 Argx9_0-2h_embryos_total	SRR060682 9x140_0-2h_embryos_total	SRR060681 Argx9_testes_total	SRR060687 9_0-2h_embryos_total	SRR2096056 Ovary_Min_46	SRR060685 9xArg_0-2h_embryos_total
.....TGTGAGTAGAAAGTCCGTGTT.....	21	0	1	1.00	1	1	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_13042:827013-827159 -	dvi_452	ACACGCAAATCACAGGCTATCTCTGCGTCGGCCTGCAGTATGACAAGTGAGTGCCC---ATT----------CATTCAAA----------TGA-AAATCCAT----------TTGATGC----------ATGCGACACTCAT-------CTT------TCAGGCACAACAGCAACAGCGGCGAGAACGAGGAGGAGGAGCAGCT
droMoj3	scaffold_6328:2823950-2824072 -		ACACACAAATCACGGCTATCTCTGCGTTGGCCTGCAGTTGAGAAGTAGTGACG---A--------**--AAGTCAGATTGGGT**-------A-CCC-------**TGAAGTGAAATT**------**----------C**----------**-------TTT**------TTGGGTTATTCA-----GCA-------CAGT--GAGGAGCAGTT
droGri2	scaffold_15081:1214840-1214992 -		ACACCAAATCACGGCTACCTCTGCGTTGGCCTGCAGTTGAGAAGTAGTTT---ACCTT----------**-CATCGTCTTCGCAG**--------**TCCA**T-------**-CAAAATTGTTTA**-------**-ACTT**--------**AT**----------**TCCGTCACTT**TCACGCGTCACAGGAACA-----GCAGCT-TCCGAGC--GAGGAGCAGCT
droWil2	scf2_1100000004963:1363215-1363344 +		ATACAAAATACCGGATATCTCTGTGGCCTCAATATGAAAGTAGTCGG----CTC----------**-TCTCTCTTTCTCTTT**--------C--**-------CTTTCTGTATAAA**------**----------TGTT**----------**-TC--A-CTT**------CGTTAACATCA-----GCT------ACC--ACCACGGTTT
dp5	XL_group1a:5997115-5997240 -		ACACCCACATCACGGATATCTCTGCATTGGCCTGCATATGACAAGTAGCAAGA----TTCC----------**-CC**------C--------C--------**CCAAT**---**-**------TC----------**CCA**CTGGAACTCATTCCC--**----------**------TTTTTG----CTTCAGAACA-----GCAT------CAGC--AGCTTGGGCAT
droPer2	scaffold_25:1376863-1376985 +		ACACCCACATCACGGATATCTCTGCATTGGCCTGCATATGACAAGTAGCAAGA----TT----------**------C--**C--------**CCAAT**---**-**------TC----------**CCA**CTGGAACTCATTCCC--**----------**------TTTTTG----CTTCAGAACA-----GCAT------CAGC--AGCTTGGGCAT
droAna3	scaffold_13335:883496-883618 -		ACACTCACATTAGCGGTATCTCTGCGTCGGATTGCATTATGAAAGTAGTCGTT----**---**----------**-GAAA**TATGTTTCAGTT--------CCTTC--------TTGTATTTATCCT------**----------T**--**----------**-------TA**-------TTTGAAGGAACT-----GCAT------CAGC--ACGGAGGCAT
droBip1	scf7180000396006:137975-138098 -		ACACTCACATCACAGGATATCTCTGCGTCGGCCTGCACTAGACAAGTAGTCGTT----**---**----------**-TGGA**TATGTACAAGTT--------CCTGC--------TGGTATTTATCCA------**----------T**--**----------**-------TC**-------TTCGAAGGAACT-----GCAT------CAGC--ACGGAGGCAT
droKik1	scf7180000302696:857048-857183 -		ACACCCACATCACGGATATCTCTGCGTCGGCCTGCACTATGACAAGTAGCAGT---AGTGT---------**CTTTGGGTGC**----T----------**CCA-TG**GATTT----------TTGAT**TGAGACTTAAAATTAT**----------**-------T**C-------TTGCCAGGAACA-----GCAT------TAGC--AAGGAGGCAT
droFic1	scf7180000454050:1254447-1254581 +		ACACCCACATCACGGATATCTCTGCATTGGCTTGCACTATGACAAGTGGTTT---CCCCC---------**TTTGGGGATA**----------**CTA-TA**GGTAT----------CAAT**CT**----------**AT**TATTTTGTT--------**TTT**------TTCGAAGGAACA-----GCAT------CAGC--AAGGAGGCAT
droEle1	scf7180000491001:1760403-1760532 -		ACACTCACATTAGCGGCTACCTCTGCATTGGCCTCACATACGATAAAGTAGCTAAG----AAACACACCTTT---TTA----ATTTAATT--------A-CC--------**-------**TAAAGA----------**-------**TGTT----------**-GC--ACATT**------CTCAAAGGAACA-----GCAT------TAGC--AAGGAGGCAT
droRho1	scf7180000779333:1058542-1058672 +		ACACTCACATTAGCGGCTACTTGTGGCATTGGCCTCACATACGACAAGTGAGTGT----**---**----------**-AGATGTA**CCGGCTT--ATT-AATGT-------GATAACTTAAATA----------**-------**CCTT----------**-TC--G-ATT**------TGCCAAGAACA-----GCAT------TAGC--AAGGAGGCAT
droBia1	scf7180000298389:1230300-1230438 +		ACACTCACATTAGCGGCTACTTGTGGCATTGGCCTCACATACGACAAGTGAGTGG---TGGCC----------**-GAGGATG**---**CCA**TGCCACAGT--T--------CAGAT------**-T**TCGTATCCTCTTTGCC--**----------A**--**-------TC**------TTCCAAGGAACA-----GCAT------CAGC--AAGGAGGCAT
droTak1	scf7180000414740:58631-58757 +		ACACTCACATTAGCGGTATCTTGTGGCATTGGCCTCATATACGACAAGTGAGTTTGT----CAC----------**-CATGTAAA**----------**CCA-AA**GGATC----------TTTATTGA----------**TCTT**----------**TC**--**-------CC**------TTTCAAGAACA-----GCAT------TAGC--AAGGAGGCAT
droEug1	scf7180000408958:348287-348421 -		ACACTCACATTAGCGGCTATCTATGCGTTGGCCTCATACGACAGTAAGTAAAATGTTTTT----------**-TGATTTTA**----------**AGA**---**-**------TC----------**-CATATTTAACAT**----------**AT**----------**TATTGCACTTG**C------TGTAAAGGAACA-----GCAT------TAGC--AAGGAGGCAT
dm3	chrX:13258860-13258987 +		ACACTCACATTAGCGGCTATCTATGCGTTGGCCTCATACGACAGTAAGTAGTGG---TTTTT----------**-GAA**TTATCTCTATT-------GCTC-------ATAGATTCATAAA----------**TCCA**----------**-T----**---------TACAAAGGATGA-----TAT------TAGC--AAGGAGGCAT
droSim2	xr12603015-12603142 +	dsi_2945	ACACTCACATTAGCGGCTATCTATGCGTTGGCCTCATACGACAGTAAGTAGTGG---TTTCT----------**-GAA**TCATCTCTATT-------GCTC-------AAAGATTCATAAA----------**TCCT**----------**-T----**---------CACATAGGATGA-----GCAT------TAGC--AAGGAGGCAT
droSec2	scaffold_21:1012611-1012738		ACACTCACATTAGCGGCTATCTATGCGTTGGCCTCATACGACAGTAAGTAGTGG---CTTTT----------**-GAA**TCATCTCTATT-------GCTC-------AAAGATTTATAAA----------**TCCT**----------**-T----**---------CACATAGGATGA-----GCAT------TAGC--AAGGAGGCAT
droYak3	X:7539568-7539696 +		ACACGCACATAAGCGGCTATCTATGCGTTGGCCTCATACGACAGTAAGTAGTTG---AGTCAC----------**-CGAA**TATCTCTAAT-------TATT-------GA-TAATCATATA----------**TTCC**----------**-------AT**--------TTCACAGGATGA-----GCAT------TAGC--AAGGAGGCAT
droEre2	scaffold_4690:13610866-13610993 -		ACACGCACATAAGCGGCTATCTATGCGTTGGCCTCATACGACAGTAAGTAGTTG---TCTTT----------**-GAA**TCATCTCCATT-------ATTT-------GAAATTTCACAAT----------**TCCC**----------**-T----**---------TAAACAGATGA-----GCAT------TAGC--AAGGAGGCAT

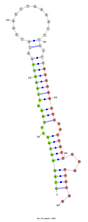
Generated: 09/08/2015 at 07:06 PM

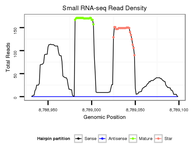
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

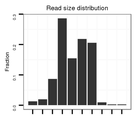
ID:	Coordinate:	Confidence:	Class:	Genome Locale:
dvi_271	**scaffold_13049:8788981-8789049 +**	**confident**	**Mirtron**	**3pUTR**
				[View on UCSC Genome Browser (Cuttle5Mbits)]

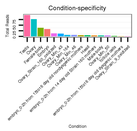
Legend: [redacted] [redacted] [redacted] [redacted]

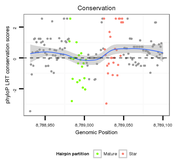
Predicted structure











Show Alternate Folds

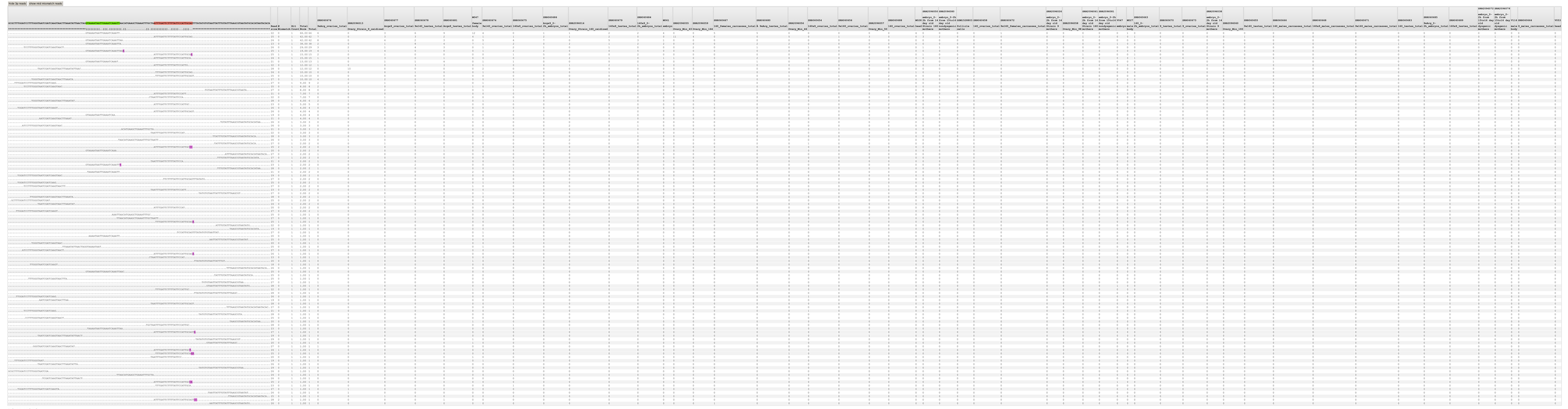
FlyBase annotation

nt1:247_nmo_444(2)

No Repeatite elements found

Sense Strand Reads

Hide 3p reads | show mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

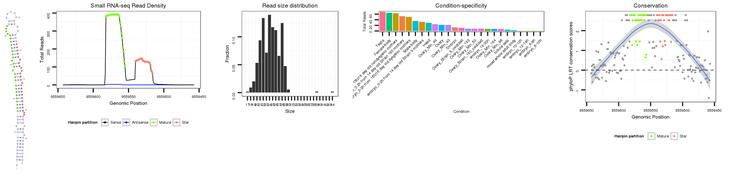
Re-alignment of all predicted orthologs

Generated: 09/06/2025 at 07:01 PM

ID	Coordinate	Confidence	Class	Genomic Locus
dvi_24635	**scaffold_13047:9559507-9559593 -**	**confident**	**Canonical miRNA**	**intergenic**
				View on UCSC Genome Browser (Cactus/TBlastx)

Legend: Stem 5p Terminal loop 3p Flanking

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatible elements found

Sense Strand Reads

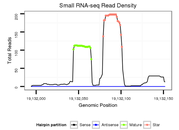
Hide Sp reads | Show mid mismatch reads

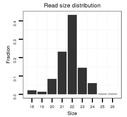
| Read # | Size | Total | 28822194081 webrys_0-2k MGT from iTrack webrys_0-2k_Core 2k webrpeaks body | 28822194072 webrys_0 webrys_0-2k webrys_0-4 iTrack dmy_Ch_Core 14.2k_Core 2k Dmyr_Strain 100 Dmyr_100 mothers | 28822194041 28822194050 webrys_0 webrys_0-2k webrys_0-4 iTrack dmy_Ch_Core 14.2k_Core 2k Dmyr_Strain 100 Dmyr_100 mothers | 28822194090 webrys_0-2k webrys_0-4 iTrack WS10 28826540 webrpeaks 2k-webrpeaks head Argot_testes_testes | 28822194024 webrys_0 2k_Core 14.2k 28826540 Dmyr_Strain 0 fs141_testes_testes mothers | 28822194138 webrys_0 webrys_0-2k webrys_0-4 iTrack 28826540 Dmyr_Strain 7 14fs4_testes_testes mothers | 28822194079 webrys_0 webrys_0-2k webrys_0-4 iTrack dmy 28826545 dynamic mothers | WS10 28826544 | 28826513 webrys_0 webrys_0-2k webrys_0-4 | 28826480 webrys_0 webrys_0-2k webrpeaks 2k-webrpeaks head Argot_testes_testes | 28825540114 webrys_0 webrys_0-2k webrpeaks 2k-webrpeaks head Argot_testes_testes | 28826540171 webrys_0 webrys_0-2k webrpeaks 2k-webrpeaks head Argot_testes_testes | 28826540172 webrys_0 webrys_0-2k webrpeaks 2k-webrpeaks head Argot_testes_testes | 28811104720 dmel_Ch_Core 14.2k_Core 2k Dmyr_Strain 0 fs141_testes_testes mothers | 28825294513 WS41 follicle cells | 28826540468 webrys 14fs4_testes_testes | 28825294577 Dmyr_Mic_50 | 28825294553 Dmyr_Mic_148 | 28826540469 webrys 14fs4_testes_testes | 28825294558 Dmyr_Mic_96 | 28826540467 webrys 141_female_testes_testes | 28826540475 webrys 14fs4_ovarian_total | 28826540474 fs4_ovarian_total | 28826540456 fs4_ovarian_total | 28826540470 fs4_testes_total | 28811104724 mixed whole body | 28826540466 webrys fs141_testes_total | 28826540477 Argot_ovarian_total | 28826540469 14fs4_testes_total | 28826540482 male 2k_embryos_total | 28826540481 webrys fs141_testes_total | 28826540484 fs141_testes_total | 28826540454 14fs4_ovarian_total | 28826540463 2k_embryos_total | 28826540473 fs_ovarian_total | 28826540483 141_testes_total | 28826540464 2k_embryos_total | 28826540465 2k_embryos_total | 28811104717 fs | 28811104714 | 28811104722 | 28811104723 |
|---|---|---|---|---

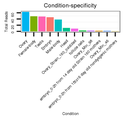
ID	Coordinate	Confidence	Class	Genome Locale
dvi_275	**scaffold_13047:19132044-19132102 +**	**confident**	**Canonical miRNA**	**intergenic**
				[View on UCSC Genome Browser (Crosse0.5dmel)]

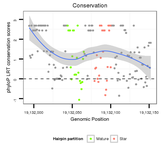
Legend: Arm 5p 3p Loop Mature Star Mismatch

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

No Repeatile element found

Sense Strand Reads

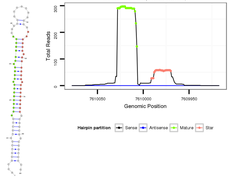
Note 3p reads show mid mismatch reads

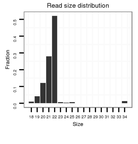
| Read # | Arm | Mismatch | Count | Mism | Total | MI47 Y147 Female male body | MI61 Female male body | SRR040658 adult_ovarian_total | SRR040661 Angat5_testes_total | SRR040672 Angat5_ovarian_total | SRR040667 Female_carcasses_total | SRR040679 L10_testes_total | SRR040656 Fb_embryos_total | SRR040657 Hs10_ovarian_total | SRR040674 Dmbcg_ovarian_total | SRR040686 Angat2_ovarian_total | SRR040689 Hs10_testes_total | SRR2396014 Ovary_Strain_100_residual | SRR040665 Argentina_ovarian_total | SRR040676 Hs10_testes_total | V312 SRR040665 head_Female_carcasses_total | GSM1528863 SRR040677 Fu11cin cells | SRR040664 Angat_ovarian_total | SRR040668 Female_carcasses_total | MI28 SRR040662 Hs10_2- Fb_embryos_total | SRR040688 L10_ovarian_total | SRR040663 Hs10_testes_total | SRR040666 Hs10_2- Angat_ovarian_total | SRR040671 Hs10_ovarian_total | SRR040674 Hs10_testes_total | SRR040675 L10ak_2- Fb_embryos_total | SRR040684 L10ak_ovarian_total | SRR040687 L10_testes_total | SRR2396058 Ovary_Mos_48 | SRR040680 Dmbcg_testes_total | SRR040682 Hs10_2- Fb_embryos_total | SRR040654 L10ak_ovarian_total | SRR040683 L10_testes_total | SRR2396056 Ovary_Mos_60 | SRR2396059 Ovary_Mos_144 | SRR040659 Argentina_testes_total | SRR040681 L10ak_2- Fb_embryos_total | SRR040669 L10ak_female_carcasses_total | SRR040673 L10ak_ovarian_total | SRR2396072 webcyc_2- 2h from 12hrs day mothers | MGT7 webcyc_2- body | SRR040672 webcyc_2- 2h from 14.2h from 14 days mothers | SRR2396024 webcyc_2- 2h from 14.2h from 14 days mothers | SRR2396050 Ovary_Mos_63 mothers | SRR2396081 webcyc_2- 2h from 14 days mothers | SRR2396085 webcyc_2- 2h from 12hrs mothers | SRR2396091 Ovary_Strain_8_residual |
|---|---|---|---|---

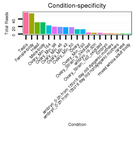
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_377	**scaffold_12875:7609967-7610028 -**	**confident**	**Canonical miRNA**	**CDS** [View on UCSC Genome Browser (Cured5 Mints1)]

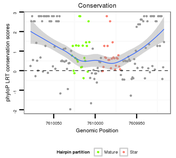
Legend: [illegible] [illegible] [illegible]

Predicted structure









Show Alternate Folds

FlyBase annotation

CDS [FlyEnz(2879)-cds]

No Repeatitle elements found

Sense Strand Reads

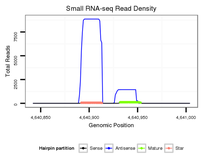
Hide 3p reads Show mid mismatch reads

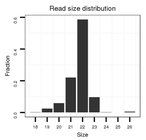
| | | |

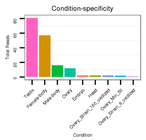
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_265	**scaffold_12723:4640892–4640954 +**	**confident**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

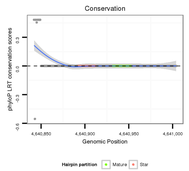
Legend: hairpin stem mismatch 1 to 4bp mismatch 5 to 10bp mismatch 11 to 15bp

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

number	star
1. dvi_265 scaffold_12723:4640892–4640953 +	
2. dvi_265 scaffold_12963:330298–330359 +	

Sense Strand Reads

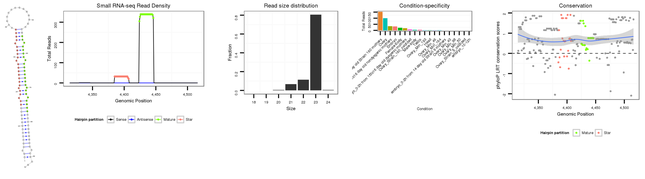
hide 3p reads show mid mismatch reads

| | | |

ID	Coordinate	Confidence	Class	Genome Locale	
dvi_353	**scaffold_9572:4364-4466 +**	**confident**	**Canonical miRNA**	**intergenic**	View on UCSC Genome Browser (Grand Mirror)

Target: Gene Repeat Pseudogene Antisense

Predicted structure



Show Alternate Forms

Flybase annotation

intergenic

No flyanalide chrom fread

Genes	Star
1 dvi_256 scaffold_17:2424-732 , 2 dvi_33 scaffold_9572:4364-4466 ,	1 dvi_256 scaffold_17:2424-732 , 2 scaffold_7836:2236-2236 , 3 scaffold_7836:2385-2385 , 4 scaffold_9572:4364-4466 , 5 scaffold_9572:4365-4465 , 6 scaffold_9572:4366-4464 , 7 scaffold_9572:4367-4463 , 8 scaffold_1287:41179-41196:41400 , 9 scaffold_1287:41179-41196:41400 , 10 scaffold_4294:1025945:1025928 , 11 scaffold_4294:1025945:1025928 , 12 scaffold_4294:1025946:1025928 , 13 dvi_2988 scaffold_2870:92969:92 4296:61 , 14 scaffold_2326:2808:2808 , 15 scaffold_2326:2808:2808:2 ,

Sense-strand Reads

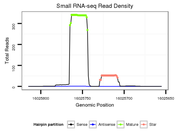
Hide by reads | show red mismatch reads

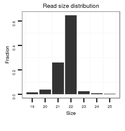
Read #	Mismatch	Count	Strm	Total	2R2:29435553	2R2:29436041	2R2:29436081	2R2:29436272	2R2:29436350	2R2:29436479	2R2:29436481	2R2:29436487	2R2:29436493	2R2:29436502	2R2:29436477	2R2:29436489	2R2:29436463	2R2:29436460	2R2:29436484	2R2:29436474	2R2:29436467	2R2:29436462	2R2:29436470	2R2:29436475	2R2:29436471	2R2:29436236	2R2:29436473	2R2:29436455	2R2:29436457	2R2:29436479	2R2:29436447	2R2:29436444	2R2:29436458	2R2:29436469	2R2:29436464	2R2:29436463	2R2:29436478	2R2:29436236	2R2:29436235	2R2:29436408	2R6:1167572
					29 from 18:2k from 14	29435553	29436041	29436081	29436272	29436350	29436479	29436481	29436487	29436493	29436502	29436477	29436489	29436463	29436460	29436484	29436474	29436467	29436462	29436470	29436475	29436471	29436236	29436473	29436455	29436457	29436479	29436447	29436444	29436458	29436469	29436464	29436463	29436478	29436236	29436235	29436408	2R6:1167572
					29 from 18:2k from 14																																			

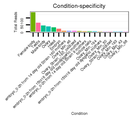
ID	Coordinate	Confidence	Class	Genome Locale	
dvi_173	**scaffold_12875:16025705-16025765 -**	**confident**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser (Cured Mites)]

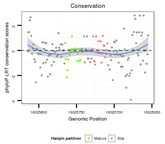
Legend: Arm: 5p 3p Loop: Mismatch: Unpaired:

Predicted structure









Show Alternate Folds

Flybase annotation

Antisense to intron [Dvir4GI2299-mk], Antisense to CDS [Dvir4GI2299-mk], Antisense to CDS [Dvir4GI2299-mk]

No Repeatitis strands found

Sense Strand Reads

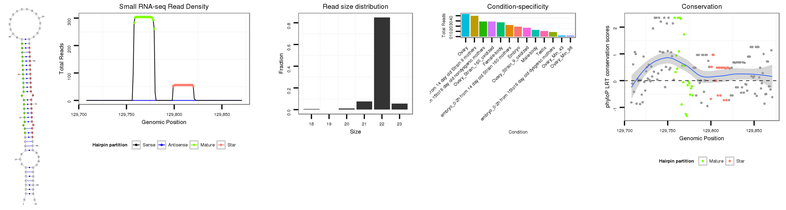
Hide 3p reads show mid mismatch reads

| Read # | Size | Mismatch | Count | Note | Total | MI7 Female body | MI5 2R6D6C72 | 2R6D6D78 | 2R6D6D79 | 2R6D6D7A | MI7 2R6D6D67 | MI1 2R6D6D68 | 2R6D6D6B | 2R6D6D6D | 2R6D6D6E | 2R6D6D6F | 2R6D6D70 | 2R6D6D71 | 2R6D6D75 | 2R6D6D81 | 2R6D6D84 | 2R6D6D74 | 2R6D6D76 | 2R6D6D79 | V114 male body | MI28 2R6D6D69 | 2R6D6D84 | 14wd_3- 2R_embryos_total | 2R6D2H04 | 2R6D2H14 | 2R6D2H55 | 2R6D2H29 | 2R6D2H58 | 2R6D2H63 | 2R6D2H65 | 2R6D2H50 | 2R6D2H51 | 2R6D2H61 | 2R6D2H62 | 3DMC52H03 | 2R6D2H64 | 2R6D2H70 | 2R6D2H80 | 2R6D2H87 | 2R6D2H88 | 2R6D2H24 | 2R6D2H25 | 2R6D2H26 | 2R6D2H27 | 2R6D2H79 | 2R6D2H57 | 2R6D2H13 | 2R6D2H54 | 2R6D2H55 | 2R6D2H59 | 2R6D2H63 | 14_2- 2R_embryos_total | 2R6D2H77 | 2R6D2H95 | 2R6D2H96 | 2R6D2H28 | 2R6D2H30 | 2R6D2H41 | 2R6D2H65 | 2R6D2H73 | 2R6D2H74 | 2R6D2H75 |
|---|---|---|---|---|---

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_283	**scaffold_13049:129758-129821 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Core48 Mmu12)]

Legend: mature star mismatch in alignment mismatch in star

Predicted structure



Show Alternate Folds

Flybase annotation

intron:2R:6427272-wp

No Repeatable elements found

Sense Strand Reads

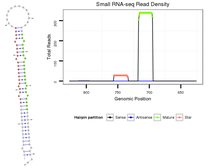
hide 3p reads show red mismatch reads

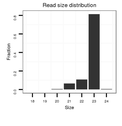
```
                                                
```

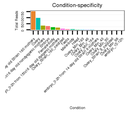
ID	Coordinate	Confidence	Class	Genome Locale
dvi_356	**scaffold_171:675-777 -**	**confident**	**Canonical miRNA**	**Intergenic**
				[View on UCSC Genome Browser (Local Mirror)]

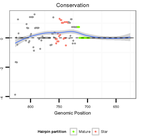
Legend: Mature Star Loop Passenger strand Alternative

Predicted structure









Show Alternate Forms

Flybase annotation

intergenic

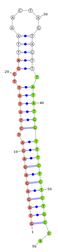
No Repeatmk element found

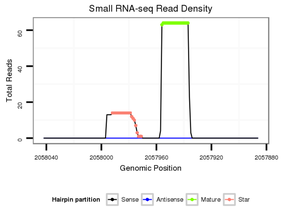
mature	star
1 dvi_356 scaffold_171:675-777 - 2 dvi_23 scaffold_317:9124-9206 +	1 dvi_356 scaffold_171:736-756 - 2 scaffold_7:9412:9-2125 + 3 scaffold_3:2125:2141 + 4 scaffold_3:2125:2141 + 5 scaffold_3:2125:2141 + 6 scaffold_3:2125:2141 + 7 scaffold_3:2125:2141 + 8 dvi_23 scaffold_317:8183:8207 + 9 scaffold_1:2672:2688:-:8:7:0:0 + 10 scaffold_1:2672:2688:-:8:7:0:0 + 11 scaffold_1:2963:2325:2341 + 12 scaffold_1:2963:2325:2341 + 13 scaffold_1:2963:2325:2341 + 14 dvi_2:9:7:0:0:0

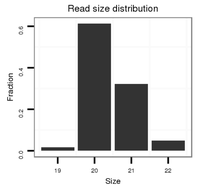
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_400	**scaffold_13049:2057936-2057992 -**	**candidate-rescued**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Comell Mirror)]

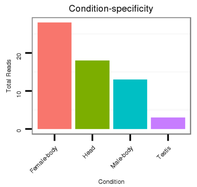
Legend: mature star mismatch in alignment mismatch in star

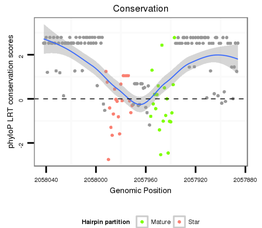
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DviGI12573-in]; CDS [DviGI12573-cds]; CDS [DviGI12573-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
GCACCTGGAGCTCCTGTCGCGAGGGCTGCACCTCATCACTCACCAAGTAAGTAGAGAGAGATCTATATTCGATTAAACTAGTAGTTTATATGGTTTCTCTCTGCCAGGTGCCATCAGCTGTTTGTCAACTATACGCGCATACCCTACAGCGAATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
**********(((((((((.(((((.(((((.(((((.....))))).))))))))))))))).**********
```

Read #	Hit Count	Total Norm	Total	SRR060672 9x160_females_carcasses_total	V053 head	SRR060664 9_males_carcasses_total	SRR060667 160_females_carcasses_total	SRR060668 160x9_males_carcasses_total	M028 head	SRR060671 9x160_males_carcasses_total	SRR060665 9_females_carcasses_total	M047 female body	SRR060666 160_males_carcasses_total	SRR060669 160x9_females_carcasses_total	SRR060655 9x160_testes_total	SRR060681 Argx9_testes_total	SRR2096014 Ovary_Strain_160_oxidised	SRR2096056 Ovary_Min_46	M061 embryo	SRR060679 160x9_testes_total	SRR060678 9x160_testes_total	SRR060680 Â 9xArg_testes_total	SRR060670 9_testes_total	SRR060659 Argentina_testes_total	SRR060673 9_ovaries_total	SRR060683 160_testes_total	SRR060689 160x9_testes_total	V116 male body	V047 embryo	SRR2096038 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096081 embryo_0-2h from 15to16 day old nondygenic mothers
22	1	1	272.00	272 59	40 31	28	21	11 13	21	5 16	6	0	0	3	3	3	0	2 2	1	1	1	1	1	0	1	1	0	0	1	0	0
22	1	1	40.00	40 3	4 7	3	2	2	1	4 6	2	0	0	0	0	0	0	2 1	1	0	1	0	0	0	0	0	0	0	0	0	0
20	0	1	38.00	38 1	4 2	4	1	11 6	0	7 0	0	0	0	1	0	0	0	0 0	0	0	0	1	0	0	0	0	0	0	0	0	0
21	0	1	18.00	18 5	0 3	0	1	0	0	6 0	0	0	0	0	0	0	0	0 0	1	0	0	0	0	0	0	0	0	0	0	0	0
22	0	1	4.00	4 1	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
21	0	1	3.00	3 1	0 0	0	0	0	0	0 1	0	0	0	0	0	0	0	0 0	0	0	0	0	1	0	0	0	0	0	0	0	0
22	0	1	3.00	3 0	1 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
21	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	0	0	0	0	0	0	0	0	0	0	0
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	0	0	0	0	0	0	0	0	0	0
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	0	0	0	0	0	0	0
18	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	0
23	0	1	2.00	2 0	0 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
22	2	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
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
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
23	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	0	0	0	0	0	0	0	0	0	0
22	2	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
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	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	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	1	0	0	0	0	0	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

```
CGTGGACCTCGAGGACAGCGCTCCCGACGTGGAGTAGTGAGTGGTTCATTCATCTCTCTAGATATAAGCTAATTTGATCATCAAATATACCAAAGAGAGACGGTCCACGGTAGTCGACAAACAGTTGATATGCGCGTATGGGATGTCGCTTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
**********(((((((((.(((((.(((((.(((((.....))))).))))))))))))))).**********
```

Read #	Hit Count	Total Norm	Total	M028 head	M027 male body	V116 male body	SRR060687 9_0-2h_embryos_total	SRR060673 9_ovaries_total	SRR2096080 embryo_0-2h from 15to16 day old nondygenic mothers	SRR2096081 embryo_0-2h from 15to16 day old nondygenic mothers	V053 head	M047 female body
22	1	1	272.00	272	59	40	31	28	21	11	13	21
22	1	1	40.00	40	3	4	7	3	2	2	1	1
20	0	1	38.00	38	1	4	2	4	1	11	6	0
21	0	1	18.00	18	5	0	3	0	1	0	0	0
22	0	1	4.00	4	1	1	0	0	0	0	0	1
21	0	1	3.00	3	1	0	0	0	0	0	0	0
22	0	1	3.00	3	0	1	0	0	0	0	0	0
21	0	1	2.00	2	0	0	1	1	0	0	0	0
22	0	1	2.00	2	2	0	0	0	0	0	0	0
22	1	1	2.00	2	0	0	0	0	0	0	0	0
18	0	1	2.00	2	2	0	0	0	0	0	0	0
23	0	1	2.00	2	0	0	1	0	0	0	0	0
22	2	1	1.00	1	0	0	1	0	0	0	0	0
20	1	1	1.00	1	1	0	0	0	0	0	0	0
22	0	1	1.00	1	0	1	0	0	0	0	0	0
23	2	1	1.00	1	0	1	0	0	0	0	0	0
22	2	1	1.00	1	1	0	0	0	0	0	0	0
20	0	1	1.00	1	0	0	0	0	0	0	0	0
19	0	1	1.00	1	0	0	0	0	0	0	0	0
19	0	1	1.00	1	0	0	0	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

```
Species  Coordinate                                ID      Alignment
dsvVir3  Scaffold_13049:2057886-2058642 -         dvi_400 GCACCTGGAGCTCCTGTCGCGAGGGCTGCACCTCATCACTCACCAAGTAAGTAGAGAGAGATCTATATTCGATTAAACTA-----------------------GT-----------------------------AGTTGGGGGTATA----TGGG-----------------------------TGGGGTGCCATCAGCTGTTTGTCAACTATACGCGCATACCCTACAGCGAATGGG
drsMoj3  Scaffold_6654:1793561-1793700 -          |       GCAGCTGGAGCTCCTGTCGCGAGGGCTGCACCTCATCACTCACCAAGTAAGTAGAGAGAGATCTATATTCGATTAAACTA-----------------------GT-----------------------------AGTTGGGGGTATACATATATTTGATTCTTGAT-GA-------AA-------G-GT-----TC-AT-------GA-AGGGTGCCATCAGTGTTTGTCAACTATACGCGCATACCCTACAGCGAATGGG
droGri2  Scaffold_15110:310633-310834 -           |       GCAGCTGGAGCTCCTGTCGCGAGGGCTGCACCTCATCACTCACCAAGTAAGTAGAGAGAGATCTATATTCGATTAAACTA-----------------------GT-----------------------------TTTACCAAATCATTAAATGAGATTC-AATAAATCCATCACGAATCATTTAAATGAAATTACC----------AC-G-----AATCCCAATAAC-----------------------------G-----------------------------GA-------GAA-AGGTGCCATCAGTGTTTGTCAACTATACGCGCATACCCTACAGCGAATGGG
droWil2  Scaffold_1100000024782:3924722-3924886 -  |       GCAGCTGGAGCTCCTGTCGCGAGGGCTGCACCTCATCACTCACCAAGTAAGTAGAGAGAGATCTATATTCGATTAAACTA-----------------------GT-----------------------------ACGGATAACGATATCTGTCTATATTA-----------------------------CTGGGC-GC-----------------------AC-------G-GT-----------G-AGGGTGTTGGGTGCCATCAGTGTTTGTCAACTATACGCGCATACCCTACAGCGAATGGG
dp5      Ch_dsim8:8346781-8346943 -                |       GCAGCTGGAGCTCCTGTCGCGAGGGCTGCACCTCATCACTCACCAAGTAAGTAGAGAGAGATCTATATTCGATTAAACTA-----------------------GT-----------------------------AT-----------G-GT-----TAATCCAATCGATTCTGATTCCATATC-GA-------G-A-------G-----------A-------GA-AGGGTGCCATCAGTGTTTGTCAACTATACGCGCATACCCTACAGCGAATGGG
droPer2  Scaffold_40:538384-538443 -               |       GCAGCTGGAGCTCCTGTCGCGAGGGCTGCACCTCATCACTCACCAAGTAAGTAGAGAGAGATCTATATTCGATTAAACTA-----------------------GT-----------------------------AT-----------G-GT-----------G-----------G-----------A-------GA-AGGGTGCCATCAGTGTTTGTCAACTATACGCGCATACCCTACAGCGAATGGG
droAna   Scaffold_13337:14602329-14602478 -        |       GCAGCTGGAGCTCCTGTCGCGAGGGCTGCACCTCATCACTCACCAAGTAAGTCTCTTGCAGA----G-------------------GA-----------------------------TA--ATAAG----------A-CG-----------------CTGAAACT-GA-AAC-------G-A-------G-AA-------A-ATT-GGGTGCCATCAGTGTTTGTCAACTATACGCGCATACCCTACAGCGAATGGG
droBip1  Scaffold_20000039644:1708947-1709386 -    |       GCAGCTGGAGCTCCTGTCGCGAGGGCTGCACCTCATCACTCACCAAGTAAGTATGCAATGCAA----G-------------------GA-----------------------------TA---ATATG----------A-CG-----------------CTGAAA-------GCAAGC-A-------G-AA-------A-ATT-GGGTGCCATCAGTGTTTGTCAACTATACGCGCATACCCTACAGCGAATGGG
droKik1  Scaffold_20000039238:1565501-1565659 -    |       GCAGCTGGAGCTCCTGTCGCGAGGGCTGCACCTCATCACTCACCAAGTAAGTAGAGAGAGAC-ATTGTAA-----TATATA-T----------                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
droEre   Scaffold_4784:1681643-1691845 -          |       GCAGCTGGAGCTCCTGTCGCGAGGGCTGCACCTCATCACTCACCAAGTAAGTAGAGAGAGATCTATATTCGATTAAACTA-----------------------GT-----------------------------AT-----------G-GT-----------G-----------G-----------A-------GA-AGGGTGCCATCAGTGTTTGTCAACTATACGCGCATACCCTACAGCGAATGGG
```

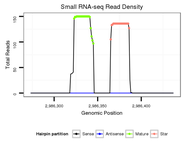
Generated: 09/08/2015 at 07:17 PM

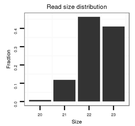
	PASSFAIL
crit.star	0
crit.seqp	0
crit.hairp	0
crit.half	0
crit.loner	1
crit.mism	0
crit.bp3	1
crit.gmap1	1
crit.bp5	1
crit.back	1
rescue.total	0
rescue.mature	0
rescue.known	0
rescue.confident	0
rescue.candidate	1

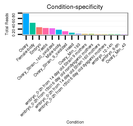
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_276	**scaffold_12928:2986323-2986387 +**	**confident**	**Canonical miRNA**	**intergenic**
				View on UCSC Genome Browser (Loaded Mines)

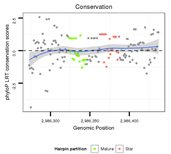
Legend: Loop 5p 3p Mature 5p Mature 3p Mismatch Mismatch

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

No Repeatible elements found

Sense Strand Reads

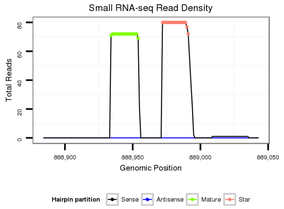
Hide 3p reads show mid mismatch reads

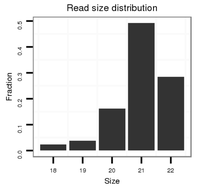
| | | | |

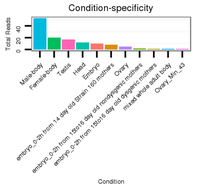
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_101	**scaffold_12723:888934-888993 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

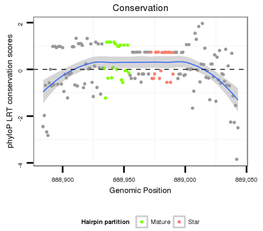
Legend: mature star sub-match in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annotation

intron [DviGI18158-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CAAGGTGTAGTGCAAGCTATTGGGAAATATTTGTTAAATGTTGAACGAGTTGTCTAACAGAGCAAGTCATAGTGCAACTGGAAAACATGGGCTTGGGCATGTTGGGGATGTCGTAATATTTGATTATCAAATGGATAAGAGCTTGCTAAGCTGAGGTCG																																													
**********	size	Mismatch	Count	Norm	Total	male body	V116 V053	female body	M047	SRR2094050 embryo_0-2h from 14 day old Strain 160 mothers	SRR060667 160_females_carcasses_total	SRR060683 160_testes_total	SRR2096061 embryo_0-2h from 14 day old Strain 160 mothers	SRR060672 9x160_females_carcasses_total	SRR060655 9x160_testes_total	SRR060661 160x9_0-2h_embryos_total	SRR060668 160x9_males_carcasses_total	SRR060689 160x9_testes_total	SRR060666 160_males_carcasses_total	SRR060688 160_ovaries_total	M061 embryo	SRR060656 9x160_ovaries_total	SRR060663 160_0-2h_embryos_total	SRR060671 9x160_males_carcasses_total	SRR2096080 embryo_0-2h from 15to16 day old nondygenic mothers	V047 embryo	M027 male body	M028 head	SRR060669 160x9_females_carcasses_total	SRR2096072 embryo_0-2h from 15to16 day old dygenic mothers	SRR2096081 embryo_0-2h from 15to16 day old nondygenic mothers	SRR1106729 mixed whole adult body	SRR060654 160x9_ovaries_total	SRR2096055 Ovary_Min_43	SRR2096059 Ovary_Min_164	SRR060670 9_testes_total	SRR060486 Arga9_0-2h_embryos_total	SRR060487 9_0-2h_embryos_total
.....TGTCTAACAGAGCAAGTCATA.....	21	0	1	47.00	47	14	5	0	2	5	0	1	0	2	1	2	2	0	0	0	3	0	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
.....TGTCTAACAGAGCAAGTCCATA.....	22	0	1	21.00	21	9	0	1	0	2	2	0	0	0	1	0	1	0	0	0	1	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
.....TGGGCTTGGGCATGTTGGGCATG.....	23	0	1	20.00	20	5	3	2	0	3	0	0	2	1	1	0	0	0	0	0	1	1	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
.....TGGGCTTGGGCATGTTGGGCA.....	20	0	1	17.00	17	4	2	3	1	0	0	0	1	0	2	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
.....TGGGCTTGGGCATGTTGGGCA.....	21	0	1	17.00	17	9	2	1	0	0	2	0	0	0	0	1	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	0	0	0	0	0
.....TGGGCTTGGGCATGTTGGGCAT.....	22	0	1	16.00	16	5	0	1	3	2	0	0	1	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
.....TGGGCTTGGGCATGTTGGG.....	19	0	1	5.00	5	2	1	0	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	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGGGCTTGGGCATGTTGGGCATT.....	23	1	1	4.00	4	1	0	0	1	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	0	0	0
.....TGTCTAACAGAGCAAGTCCA.....	20	0	1	3.00	3	0	0	1	0	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
.....TGGGCTTGGGCATGTTGG.....	18	0	1	3.00	3	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	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGTCTAACAGAGCAAGTCCATAA.....	24	1	1	3.00	3	0	0	0	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	0	0	0	0	0
.....TGGGCTTGGGCATGTTGGGCATGT.....	24	1	1	2.00	2	0	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	0
.....TGGGCTTGGGCATGTTGGGCAT.....	22	1	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	0	0	0	0	0
.....TGGGCTTGGGCATGTTGGGCATGT.....	24	0	1	2.00	2	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	0	0	0	0	0	0	0
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.....TGGGCTTGGGCATGTTGGGCATA.....	24	2	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	0	0	0
.....TGTCTAACAGAGCAAGTCCATAAA.....	25	3	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	0	0	0
.....TGGGCTTGGGCATGTTGGGCATGTT.....	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	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGGGCTTGGGCATGTTGGGCATT.....	23	2	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	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGGGCTTGGGCATGTTGGGCATGTAAA.....	27	3	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	0	0	0	0	0
.....TATCAAATGGATAAGAGCTTGCTAAGC.....	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	1	0	0	0	0	0	0
.....TGGGCTTGGGCATGTTGGGCA.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTGGGCATGTTGGGCATT.....	18	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	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGGGCTTGGGCATGTTGGGAAA.....	21	3	13	0.08	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	0	0	0	0	0

Anti-sense strand reads

GTTCCACATCACGTTCGATAACCCTTTATAAACAATTTACAACTTGCTCACAGATTGTCTCGTTCAGGTATCACGTTGACCTTTTGTACCCGAACCCGTACAACCCGTACAGCATTATAAACTAATAGTTTACCTATTCTCGAACGATTCGACTCCAGC																																													
**********	size	Mismatch	Count	Norm	Total	male body	M027	M028 head	M047 female body	SRR060666 160_males_carcasses_total	M061 embryo	SRR060684 160x9_0-2h_embryos_total	SRR060663 160_0-2h_embryos_total	SRR060682 9x140_0-2h_embryos_total	V116	SRR060667 160_females_carcasses_total	SRR060672 9x160_females_carcasses_total	V053	SRR060665 9_females_carcasses_total
..(((((((..(((((..(((((((((...(((((((((..((.(.....)))))))))))....))))))))..)))))))))).**********																																													

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12723:888884-889043 +	dvi_101	CAAGGT--GTAGTGCAAGCTATTG-GGAAATATTTGTTAAATGTTGAACGAGTTGTCTAACAGAGCAAGTCCAAGTGCAACTGGAAAACATGGGCTTGGGCATGTTGGGGATGTCGTAATA--TTTGATTATCAA-ATGGAT-AAGAGCTTGCTAAGCTGAGGTCG
droMoj3	scaffold_6496:3974600-3974693 -		CAA--T--
droGri2	scaffold_15203:129755-129798 -		TTATT--
droWil2	scf_1000000047762:3994353-3994394 +		AT-T--
droPer2	scaffold_1101:86474-86517 +		AT-T--
droAna3	scaffold_13036:116006-116063 -		TC-T--
droBip	scf1800003951423131-53224 -		A-TACTT--
droKik1	scf1800003037071324193-3042371 -		-T-A-T--A-T-TGCAA-T-TGT-T-AAATATTTG-T-T--
droFic1	scf180002653840192485-92526 -		CATATCTT-----------A--
droTel1	scf1800004912141304092-1304142 -		GTCAC-T-------------T-AAAATTTGTATA-T-TGATA-T-GAGTTGTTA-T-A--
droRho1	scf1800007791571418739-18820 -		GG-A-TTT-------------T-CT-T-A-T--
droBia1	scf1800003014101938310027 -		GTT-A-T--
droTak1	scf1800026415389:829215-829285 -		CA-TCA--A-T-A-T-A-TT-TTG-T-TTA-T-TTTGTAAAATGTATATGTTTGTCTAACAGAGCAAGTCCTCGCA--
droEug1	scf1800004097101364889-34533 -		CA-T-TCCT-------------AAG-T-T-T--
droYak3	2_chrUn_4389:123521-123560 -		A-TTT-T--

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

	PASSFAIL
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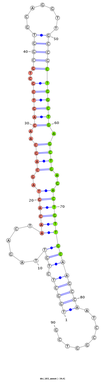
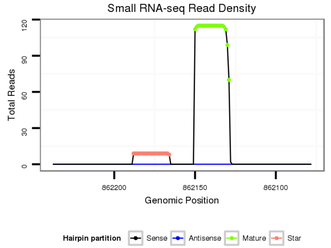
crit.loop	0
crit.hairp	1
crit.half	0
crit.total	1
crit.mism	0
crit.bug1	1
crit.bmp3	1
crit.bmp4	1
crit.dark	1
rescue.total	0
rescue.mature	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

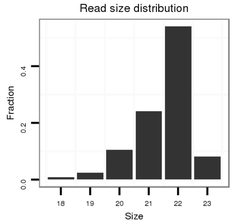
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_103	**scaffold_12726:862128-862188 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

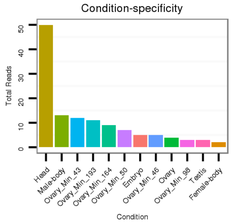
Legend: mature star **mismatch in alignment** mismatch in read

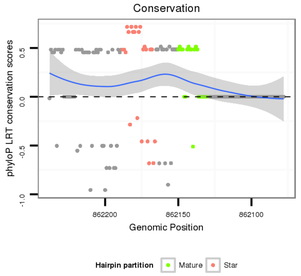
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

Hide 3p reads show mid mismatch reads

AACGTATTGTACAAAAGATTATAGCCGCCTGCTGTTGGCTCTGTTAGACT	Read size	# Mismatch	Hit Count	Total Norm	Total	M028 head	SRR2096055 Ovary_Min_43	SRR2096060 Ovary_Min_193	V053 head	M027 male body	SRR2096059 Ovary_Min_164	SRR2096056 Ovary_Min_46	M061 embryo	SRR2096057 Ovary_Min_50	M047 female body	V116 male body	V047 embryo	SRR2096058 Ovary_Min_98	SRR060660 Argentina_ovaries_total	SRR060673 9_ovaries_total	SRR060659 Argentina_testes_total	SRR060664 9_males_carcasses_total	SRR060670 9_testes_total	SRR060671 9x160_males_carcasses_total	SRR060677 Argx9_ovaries_total	SRR060678 9x140_testes_total	SRR2096079 embryo_0-2h from 15to16 day old dysgenic mothers	SRR060658 140_ovaries_total	SRR060686 Argx9_0-2h_embryos_total	GSM1528803 follicle cells	SRR1106729 mixed whole adult body	SRR2096014 Ovary_Strain_160_oxidized
**********																																
CTGGCTGAGCTGAGACTGTTGC	22	0	1	66.00	66	25	6	5	3	5	2	2	4	0	2	3	3	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTGGCTGAGCTGAGACTGTTG	21	0	1	29.00	29	9	1	3	3	3	1	1	0	3	1	0	0	0	2	0	0	0	1	0	0	1	0	0	0	0	0	0
CTGGCTGAGCTGAGACTGTTT	20	0	1	12.00	12	3	4	1	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
AACAGTAGCAGCAACAGTCGCTG	23	0	1	8.00	8	1	1	0	0	0	2	2	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
CTGGCTGAGCTGAGACTGTTGG	22	1	1	4.00	4	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTGGCTGAGCTGAGACTGTTGT	22	1	1	4.00	4	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
CTGGCTGAGCTGAGACTGT	19	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	0	0	0	0	0	0	0
CTGGCTGAGCTGAGACTGTTGCA	23	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	0	0	0	0	0	0
TGGCTGAGCTGAGACTGTTGT	21	1	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	0	0	0	0	0	0
CTGGCTGAGCTGAGACTGTTGG	23	1	1	2.00	2	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
AACAGTAGCAGCAACAGTCGCT	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	0	0	0	0	0	0
GGCTGAGCTGAGACTGTTGC	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
TGGCTGAGCTGAGACTGTT	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	0
CTGGCTGAGCTGAGACTG	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	0	0	0	0	0	0	0
TGGCTGAGCTGAGACTGTTGC	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	0
CTGGCTGAGCTGAGACTGTTT	21	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
CTGGCTGAGCTGAGACTGTTGG	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	0	0	0
TGAGCTGAGACTGTTGC	18	1	2	1.00	2	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

TTGCATAACATGTTTCTAATATCGGCGGACGACAACCGAGACAATCTGA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060673 9_ovaries_total	SRR060670 9_testes_total
**********							

Show Alignment With Reads

Re-alignment of all predicted orthologs

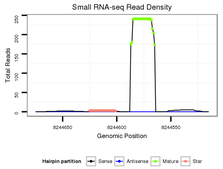
Species	Coordinate	ID	Alignment
droVir3	scaffold_12726:862078-862218 -	dvi_103	AACGTATTGTACAAAAGATTATAGCCG-CCTGCTGTTGGCTCTGTTAGACT--AACAGTAGCAGCAACAGTCGCTG-CGGTGCAGGTTGCCGCTGGCTGAGACTGTTGCAAGCCAATCCGGTCGGAATCCAGAGGGAAACTCTATGGCATTGTTCTGATC
droMoj3	scaffold_6473:9344396-9344453 +		AACGTGTTGT--------TAGCGCGCAGCGCCTGTTAAGCTGATGCACTGTAACAGCAGCAA
droGri2	scaffold_14853:4662150-4662197 -		C-----------------------T-----------------------T--AAGCAGGAGCAGCACAGCGAGCGCTGCGCGCCCTGCAGCAGGCAGCA
droKik1	scf7180000297778:18859-18859 -		A-----------------------T-----------------------T-------------------

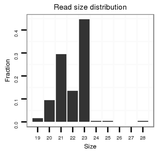
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_16006	**scaffold_13047:8244565-8244625 -**	**confident**	**Mirtron**	**intron**

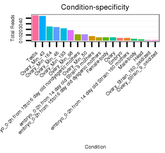
[View on UCSC Genome Browser (Cornell Mirror)]

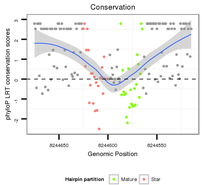
Legend: Sense Star Sub-match in stem or mismatch in star

Predicted structure









Show Alternate Folds

Flybase annotation

intron [DvirGZ23168-aj], CDS [DvirGZ23168-cdc], CDS [DvirGZ23168-cdc]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read Seq	Read #	Size	Mismatch	Hit Count	Total Norm	Total Raw	SRR2096055 Ovary_Mix_43	SRR2096059 Ovary_Mix_164	SRR2096060 Ovary_Mix_193	SRR2096061 Ovary_Mix_46	SRR040681 Arga9_testes_total	SRR2096058 Ovary_Mix_88	SRR2096057 Ovary_Mix_50	SRR2096080 embryo_0-2h from 15to16.2h from 14 mothers	SRR2096039 embryo_0- 2h from 15to16 day Strain 9 mothers	SRR040678 9a160_testes_total	SRR2096081 embryo_0-2h from 15to16 day nondygenic mothers	SRR040679 140a9_testes_total	M047 female body	SRR2096079 embryo_0- 2h from 15to16 day dygenic mothers	SRR040675 140a9_ovaries_total	SRR040680 A	SRR2096024 embryo_0- 2h from 14 mothers	SRR2094041 embryo_0- 2h from 14 Strain 160 mothers	SRR040655 9a160_testes_total	SRR040683 160_testes_total	SRR040685 2h_embryos_total	SRR2096013 Ovary_Strain_9_unidissed	SRR2096072 embryo_0- 2h from 15to16 day nondygenic mothers	SRR2096050 embryo_0- 2h from 15to16 day dygenic mothers	SRR040676 9a9_ovaries_total	M027 male body	M028 female body	SRR040670 9_testes_total	SRR040677 Arga9_ovaries_total	SRR1106730 embryo_16-30h	SRR040657 160_testes_total	SRR040667 160_females_carcasses_total	SRR040671 9a160_males_carcasses_total	SRR040673 9_ovaries_total	SRR040684 2h_embryos_total	SRR040687 2h_embryos_total	SRR1106724 16h	SRR2096014 embryo_12-24h Strain 160_unidissed	V047 male	V116 Argentina_testes_total	SRR040659 9a160_0-2h embryos_total	SRR040662 2h_embryos_total	SRR040666 160_males_carcasses_total	M061 embryo
TCCTTTACGCGACCGCCGTGGCAAGTCGTTGTGGGCCGTCCACCTACACACTCAACACACCCGCCAGGTGGATGTCGTCCCAGCCTACCAGCAATAAATAAATGCTTTGTTACGTCCTCAGCGCTCTTCAGATCACATTCCTGTTCCCGTCGACGCGCCTGCTGTATGTGG																																																	
((((((.((.(((.(((.(((((((.....))))))).))))).))))).)).))).....	read #	size	Mismatch	Hit Count	Total Norm	Total Raw								embryo_0-2h from 15to16.2h from 14 mothers	embryo_0- 2h from 15to16 day nondygenic mothers		embryo_0-2h from 15to16 day nondygenic mothers	140a9_testes_total		embryo_0-2h from 15to16 day dygenic mothers	140a9_ovaries_total	A	embryo_0- 2h from 14 mothers	embryo_0- 2h from 14 Strain 160 mothers	9a160_testes_total	160_testes_total	2h_embryos_total	Ovary_Strain_9_unidissed	embryo_0- 2h from 15to16 day nondygenic mothers	embryo_0- 2h from 15to16 day dygenic mothers	9a9_ovaries_total	male body	female body	9_testes_total	Arga9_ovaries_total	embryo_16-30h	160_testes_total	160_females_carcasses_total	9a160_males_carcasses_total	9_ovaries_total	2h_embryos_total	2h_embryos_total	16h	embryo_12-24h Strain 160_unidissed	male	Argentina_testes_total	9a160_0-2h embryos_total	2h_embryos_total	160_males_carcasses_total	embryo
.....TATGCCTTTGTTACGCTCTCGAG.....	23	0	1	109.00	109	27	15	6	13	6	14	5	1	2	2	1	1	3	0	2	1	1	0	0	0	3	1	0	0	0	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
.....TATGCCTTTGTTACGCTCTCGCAG.....	24	0	1	95.00	95	11	4	11	6	5	4	6	2	1	0	1	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	0	0
.....TATGCCTTTGTTACGCTCTCGCA.....	22	0	1	29.00	29	6	4	3	4	1	0	0	0	1	0	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
.....TATGCCTTTGTTACGCTCTCG.....	23	0	1	22.00	22	0	0	0	0	10	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	0	0
.....TATGCCTTTGTTACGCTCTCAG.....	23	1	1	21.00	21	4	1	1	0	0	0	0	0	4	2	0	3	0	0	1	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATGCCTTTGTTACGCTCTCGC.....	24	1	1	11.00	11	0	0	0	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	0	0	0
.....TATGCCTTTGTTACGCTCTCGCAG.....	24	1	1	5.00	5	0	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATGCCTTTGTTACGCTCTCGCAG.....	24	1	1	6.00	6	0	2	0	0	0	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	0
.....TATGCCTTTGTTACGCTCTCGCAG.....	24	1	1	4.00	4	0	0	0	0	1	0	0	0	0	1	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
.....TATGCCTTTGTTACGCTCTCGCAAG.....	24	1	1	3.00	3	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	0	0	0	0	0	0	0
.....TGCCTTTGTTACGCTCTCGCA.....	22	1	1	3.00	3	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	0
.....TGCCTTTGTTACGCTCTCG.....	23	1	1	2.00	2	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	0	0	0	0	0	0	0
.....TATGCCTTTGTTACGCTCTCG.....	21	1	1	2.00	2	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	0	0	0	0	0	0	0
.....TCACATTCCTGTTCCCGTCGACGGCC.....	24	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	0	0	0	0	0	0	0
.....TATGCCTTTGTTACGCTCTCGCAAT.....	25	3	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	0	0	0	0	0	0	0
.....TCCTTTTCCCCTCGACGGCCTCCCTT.....	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	0	0
.....GTGAGTGCCTGTCACAATTGTATAT.....	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	0	0
.....GTGAGTGCCTGTCACAATTGTATA.....	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	0	0
.....TATGCCTTTGTTACGCTCTCG.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCCCCTCGACGGCCTCCCT.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TATGCCTTTGTTACGCTCTCGCAG.....	24	1	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	0	0	0	0	0	0	0
.....GACCGCGCGTGGCAATGTTGTGGGC.....	28	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	0	0	0	0	0	0	0
.....TATGCCTTTGTTACGCTCTCG.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GCCTTTGTTACGCTCTCGAG.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATGCCTTTGTTACGCTCTCGA.....	23	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	0	0	0	0	0	0	0	0	0	0
.....TCACATTCCTGTTCCCGTCGACGGCC.....	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	0	0
.....TATGCCTTTGTTACGCTCTCGCAG.....	24	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	0	0	0	0	0	0	0

Anti-sense strand reads

Read Seq	Read #	Size	Mismatch	Hit Count	Total Norm	Total Raw	V053 head	GSM152803 follicle cells	SRR040661 140a9_0-2h_embryos_total	M041 embryo	SRR040663 140_0-2h_embryos_total	SRR040684 male body	V116 140a9_0-2h_embryos_total	V047 embryo	SRR2096057 Ovary_Mix_50	SRR2096081 embryo_0-2h from 15to16 day nondygenic mothers
AGGAAATGCCCTGGCGCGCACCCTTACCAACACCCGCGCAGGTGGATGTCGTCACTCACGCGCGCAGGTGGATGTCGTCACTCACAGTTTTTACATATATACTATCTTTATTTTTACGCGAAACAATGCGAGACGTCCGAGAAGTACTAGTGTGAGGACAAGGCACGCTGCCGCGACGACATACC															
((((((.((.(((.(((.(((((((.....))))))).))))).))))).)).)))....	read #	size	Mismatch	Hit Count	Total Norm	Total Raw										

Show Alignment With Reads

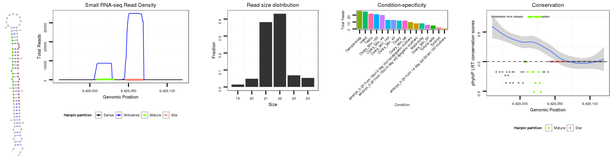
Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dvir(r1)	scaffold_2:8847-8847511:-	Dvir_16006	TCCTTTACGCGACCGCCGTGGCAAGTCGTTGTGGGCCGCCGTCCACCTACACGTGGATGTCGTCGCGCGTCCACCTACACGTGGATGTCGTCGCGCGTCCACCTACACGTGGATGTCGTCGCG

ID	Coordinate	Confidence	Class	Genome Locus
dvi_172	**scaffold_12970:9429010-9429070** +	**confident**	**Testes-restricted**	**intron**

Legend: **Mature** **Star** **Mature and Star** **Alternative**

Predicted structure



Show Alternate Folds

Flybase annotation

intron (Dvir v2.0 FlyBase 5.xx)

No Repeats-Masker found

Some Strand Reads

Sort by reads | show mid mismatch reads

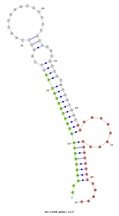
| | | |

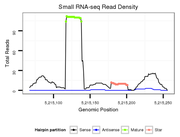
ID:	Coordinate:	Confidence:	Class:	Genome Locale:
dvi_13168	**scaffold_12970:5215117-5215206** +	**confident**	**Mirtron**	**intron**

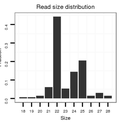
[View on UCSC Genome Browser (Control Mitter)]

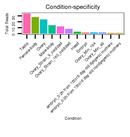
Legend: Loop Sense/5-Arm Antisense/3-Arm Mismatch/Error

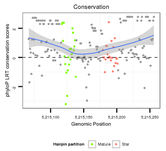
Predicted structure











Show Alternate Folds

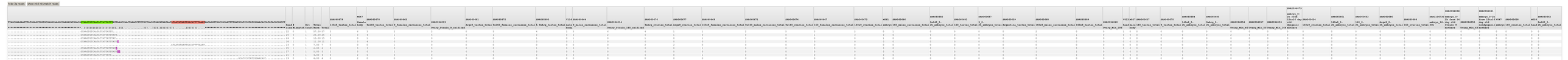
Flybase annotation

mirc:[Dvir]GF19262-aj;CDS:[Dvir]GF19262-cds;CDS:[Dvir]GF19262-cds;

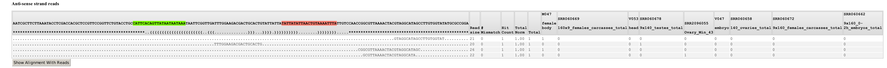
No Repeatitic elements found

Sense Strand Reads

Hide 3p reads show mid mismatch reads



Anti-sense strand reads



Show Alignment With Reads

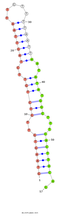
Re-alignment of all predicted orthologs

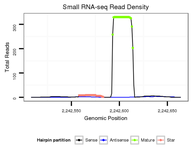
Generated 09/08/2017 at 07:01 PM

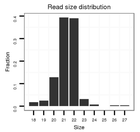
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_22275	**scaffold_13246:2242558-2242614 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cons8.Mmm)]

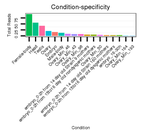
Legend: miRNA pre-miRNA Mature & Star/Loop miRNA Seed

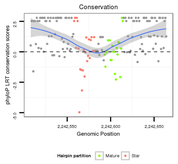
Predicted structure











Show Alternate Folds

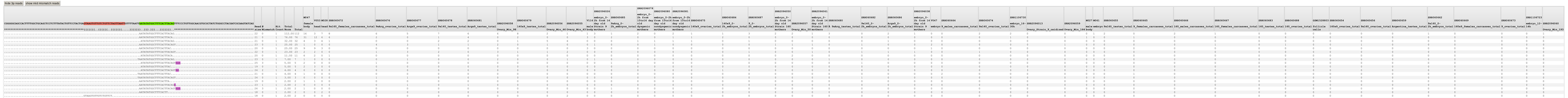
Flybase annotation

intron:[FlyEB:FBGN:46,CDS:[FlyeGEN:CR]+sub],CDS:[FlyeGEN:CR]+sub]

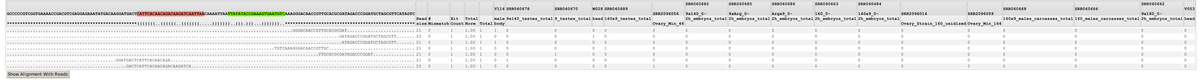
No Repeatable elements found

Sense Strand Reads

Hide 3p reads show red mismatch reads



Anti-sense strand reads



Show Alignment With Reads

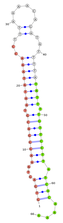
Re-alignment of all predicted orthologs

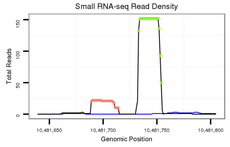
Generated 09/08/2025 at 5:09 PM

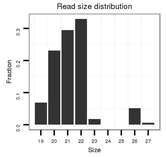
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_19388	**scaffold_13049:10481689-10481755 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Genef) Mirtor1]

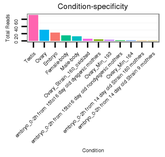
Legend: **mature** **star** **sub-mature** **in hairpin arm** **mismatch in seed**

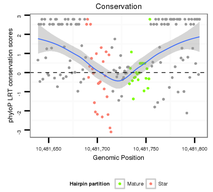
Predicted structure











Show Alternate Folds

Flybase annotation

intron [DvuGI13361-td], CDS [DvuGI13361-cds], CDS [DvuGI13361-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GGCAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAA	CGAGTAAAGGGACGTAATATAAACCTTTAAAACCAATATTTTA	TATTTTGTTCCTTATCACAAAA	CACCGACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA																																															
**********	((((.(((((((((.(((((((.((.(.....).).))))))).))))))))).))))))	**********																																																						
				Read # size	Mismatch	Hit Count	Total Norm	Total	SRR060681 Arge9_testes_total	SRR060678 9x140_testes_total	SRR060679 140x9_testes_total	SRR060676 9xArg_ovaries_total	SRR060674 9x140_ovaries_total	SRR060677 Arge9_ovaries_total	SRR060684 140x9 0-2h_embryos_total	SRR060680 Arge9_testes_total	M047 À 9xArg_testes_total	SRR2096014 body Ovary_Strain_140_oxidized	SRR060664 female 9_males_carcasses_total	SRR060685 9xArg 0-2h_embryos_total	SRR060675 140x9_ovaries_total	SRR060667 140_females_carcasses_total	SRR060682 9x140 0-2h_embryos_total	SRR060686 Arge9 0-2h_embryos_total	SRR2096123 Ovary_Strain_9_oxidized	M041 embryo_9_females_carcasses_total	SRR060665 9_males_carcasses_total	SRR060666 140_males_carcasses_total	SRR060671 9x140_males_carcasses_total	SRR2096050 embryo_0-2h from 14 Strain 140 mothers	SRR2096045 embryo_0-2h from 15x14 day Ovary_Min_19	SRR2096079 SRR060672 9x140_females_carcasses_total	SRR060687 9_0- 2h_embryos_total	SRR2096056	SRR2096059 Ovary_Min_64	Ovary_Min_144	SRR2096080 embryo_0-2h from 15x14 Strain 9 mothers	SRR2096026 embryo_0-2h from 14 Strain 9 mothers	SRR060683 140_testes_total	SRR1106718 embryo_0-2h from 15x14 Strain 140 mothers	SRR2096072 SRR2096081 embryo_0-2h from 15x14 day V059 embryo_0-2h from 15x14 V047	SRR060663 140_0- 2h_embryos_total
.....	.....	TATTTTGTTCCTTATCACAAAA		22	0	1	37.00 37	9	2	3	4	3	2	2	3	0	0	0	3	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
.....	.....	TATTTTGTTCCTTATCACAAA		21	0	1	34.00 34	3	5	4	1	2	3	3	2	1	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	0	0
.....	.....	TATTTTGTTCCTTATCACAA		20	0	1	31.00 31	3	3	2	0	1	3	3	3	1	0	0	2	1	0	0	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
.....	.....	TATTTTGTTCCTTATCACAAAG		23	0	1	15.00 15	2	2	2	2	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	TATTTTGTTCCTTATCAC		19	0	1	10.00 10	2	3	1	0	0	0	0	0	1	0	0	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
.....	.....	TATTTTGTTCCTTATCAAA		26	0	1	9.00 9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	ATTTTGTTCCTTATCAAA		20	0	1	7.00 7	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	0	0	0	0
.....	GTGAGTAAAGGGACGTAATATAAACC	.....		22	0	1	6.00 6	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	0
.....	GTGAGTAAAGGGACGTAATATA	.....		22	0	1	6.00 6	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	0
.....	.....	TATTTTGTTCCTTATCACA		22	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	0
.....	.....	TATTTTGTTCCTTATCAC		21	0	1	5.00 5	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	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	ATTTTGTTCCTTATCAAAAA		22	0	1	5.00 5	2	0	0	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	0	0	0	0	0	0	0	0	0	0
.....	.....	ATTTTGTTCCTTATCAAAA		21	0	1	4.00 4	1	0	0	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	0	0	0	0	0	0	0	0	0	0
.....	.....	ATTTTGTTCCTTATCACAA		21	0	1	4.00 4	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	0	0	0	0	0	0	0	0	0	0
.....	.....	ATTTTGTTCCTTATCAAAA		23	0	1	3.00 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	0	0	0	0	0	0	0	0	0
.....	.....	ATTTTGTTCCTTATCACAAAA		22	1	1	3.00 3	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	0	0	0	0	0	0	0	0	0	0
.....	.....	TATTTTGTTCCTTATCACAA		21	1	1	2.00 2	0	0	0	0	0	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	0	0
.....	.....	ATTTTGTTCCTTATCAC		19	1	1	2.00 2	0	0	0	0	0	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	0	0
.....	.....	ATTTTGTTCCTTATCAAAG		22	1	1	2.00 2	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	0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	ATTTTGTTCCTTATCAAA		21	1	1	2.00 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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	.....	ATTTTGTTCCTTATCAAAAA		22	1	1	2.00 2	0	0	0	0	0	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	0	0
.....	GTGAGTAAAGGGACGTAATAT	.....		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	0	0	0	0	0
.....	CCAAACAAGTGATTAAAG	.....		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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	TGAGTAAAGGGACGTAATATA	.....		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	0	0	0	0	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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.....	CCGTGTGCACGTTTCGGCCA	.....		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	0	0	0	0	0
.....	GCCGTGTGCACGTTTCGGCC	.....		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	0	0	0	0	0
.....	TGAGTAAAGGGACGTAATATAA	.....		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	0	0	0	0	0
.....	.....	ATATTTGTTCCTTATCACAAAA		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	0	0	0	0	0
.....	.....	ATTTTGTTCCTTATCACAA		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	0	0	0	0	0
.....	.....	ATTTTGTTCCTTATCACAAA		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	0	0	0	0	0	0	0	0
.....	.....	ATTTTGTTCCTTATCACAA		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	0	0	0	0	0	0	0	0
.....	.....	ATTTTGTTCCTTATCAAAAA		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	0	0	0	0	0	0	0	0	0	0	0
.....	.....	ATTTTGTTCCTTATCACAAAG		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	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	GTGAGTAAAGGGACGTAATA	.....		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	0	0	0	0	0	0	0	0
.....	.....	TTTTGTTCCTTATCACAAAGG		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	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

CCGCTTCTTGACGTCCGATAACGCGCACACGTAGCAAAGCCGGTTTGTTTCACTCATTTCCCTGCATTATATATTTGGAAATTTTGTCTATAAAATATAAAACAAGGAATAGTGTTTTCTGGCTGATGTCACGTAGCAAAGTAACATTTACCATGTTAGCTCCTTTTAA																																																						
**********	((((.(((((((((.(((((((.((.(.....).).))))))).))))))))).))))))	**********																																																						
				Read # size	Mismatch	Hit Count	Total Norm	Total	SRR060673 9_ovaries_total	SRR060676 9xArg_ovaries_total	SRR060683 140_testes_total	SRR1106718 embryo_6-8h	GSM1528803 mixed 140_0-2h_embryos_total	SRR1106729 whole adult body	SRR060682 9x140_0-2h_embryos_total	SRR060667 140_females_carcasses_total	M028 head	SRR060671 9x140_males_carcasses_total	male body
.....	.....	TGATGTTTTCTGGCTGATGTCACG		24	0	1	1.00 1	0	0	0	0	1	0	0	0	0	0	0	0	0
.....	.....	TGACGTAGCAAAGTAACATTTACCA		24	0	1	1.00 1	0	0	0	0	1	0	0	0	0	0	0	0	0
.....	GCACACGTAGCAAAGCCGGTT	.....		21	0	1	1.00 1	0	1	0	0	0	0	0	0	0	0	0	0	0
.....	.....	TAACATGTTAGCTCCTTTTAA		21	0	1	1.00 1	0	0	0	1	0	0	0	0	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

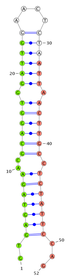
Species	Coordinate	ID	Alignment
dvrVI17	scaffold_13049:10481639-10481815:	dvi_19388	GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA----------TAAACCTTTAAA---ACAGATA-TT-------TTTTGTTCCTTATCACAAAACACCGACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrMr53	scaffold_6680:10298293-10298366:		-GCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrCo12	scaffold_1311:8747417-8747490:		-GCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrM112	scf7_1100000004511:3486465-3486538:		GCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dp3	GL_8400:8135261:8202417:+		GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrFe2	scaffold_2122:2138-2222:		GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrAn9	scaffold_1337:2015343:		GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrDp1	scf1800000386703:617624-617718:		GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrFi31	scf1800000132214:436712-436814:		GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrFi43	scf1800000483929:1415570-1415682:		GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrFi41	scf1800000283193:921767-921879:		GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrMo51	scf1800000778251:21335-21188:		GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrHi41	scf1800000302193:712843-712955:		GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrFa51	scf1800000419839:819-93355:		GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrFv41	scf1800000468464:3542831-3542944:		GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dm3	chr3R:4414764-4417933:		GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrCr12	scf1800000114763:688178-6		GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrGr2	scaffold_2141:1308-1215683:		GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrVa43	scf1800000418464:6-6		GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA
dvrGr42	scaffold_4768:8864302-8867351:		GGCGAAGAACTGCAGGCTATTGGCCGTGTGCATCCTTTCGGCCAACAAACGAGTAAAGGGACGTAATA-TTTGTTGTTCCTTATCACAAAACCCCAGTACTACAGTGCATCGTTTCATTGTTAAATGTGTACAATCGACGAAAATA

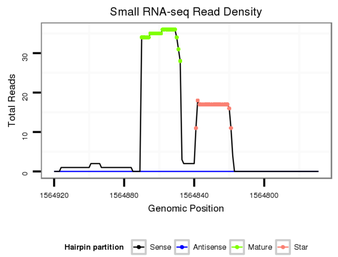
Generated: 09/08/2015 at 07:06 PM

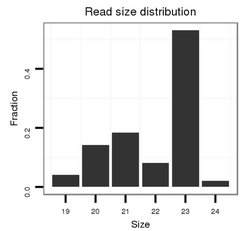
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_112	**scaffold_12875:1564819-1564870 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

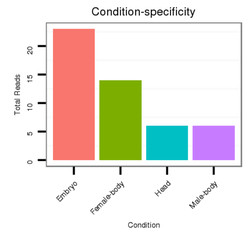
Legend: mature star mismatch in alignment mismatch in read

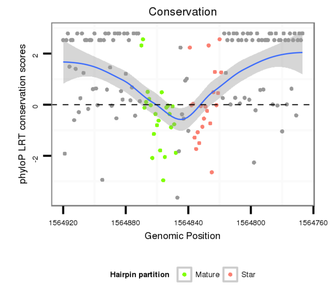
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DvirGJ21070-in]; CDS [DvirGJ21070-cds]; CDS [DvirGJ21070-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GGGATCCCAATCTGGGCGGCAGTGGCGTCTATGTGAATCTGACACTTAAAGTGAGTAGAACGCAGGTGGATTGGAACTCTAATTAACTTGCCTCTATTCCAGCTGGATGAGAGTGTGGAAACACTGCGTCCCAATCTGCGCAGCGATGTGCA	Read size	# Mismatch	Hit Count	Total Norm	Total	M061 embryo	V047 embryo	M047 female body	M028 head	SRR2096059 Ovary_Min_164	V116 male body	SRR2096060 Ovary_Min_193	V053 head	SRR2096055 Ovary_Min_43	SRR2096056 Ovary_Min_46	M027 male body	SRR060663 160_0-2h_embryos_total	SRR060674 9x140_ovaries_total	SRR060679 140x9_testes_total	SRR060660 Argentina_ovaries_total	SRR060664 9_males_carcasses_total	SRR060669 160x9_females_carcasses_total	SRR060672 9x160_females_carcasses_total	SRR060676 9xArg_ovaries_total	SRR060678 9x140_testes_total	SRR060686 Argx9_0-2h_embryos_total	SRR060687 9_0-2h_embryos_total	SRR2096050 embryo_0-2h from 14 day old Strain 160 mothers	SRR2096057 Ovary_Min_50	SRR2096058 Ovary_Min_98	SRR2096026 embryo_0-2h from 14 day old Strain 9 mothers
**********..((((((((..((((((.(((((((....)))))))..)))))))..))))))).)))))))....																															
.....GTGAGTAGAACGCAGGTGGATTG.....	23	0	1	25.00	25	1	16	1	4	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTAACTTGCCTCTATTCCAGC.....	21	1	1	23.00	23	11	2	2	0	0	0	0	0	0	0	0	2	0	0	0	0	0	1	0	1	1	1	0	0	0	0
.....ATTAACTTGCCTCTATTCCAGC.....	22	1	1	16.00	16	6	1	7	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ATTAACTTGCCTCTATTCCAG.....	21	0	1	5.00	5	0	0	3	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
.....GTGAGTAGAACGCAGGTGGATT.....	22	0	1	3.00	3	1	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
.....ATTAACTTGCCTCTATTCCA.....	20	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	0	0	0	0	0
.....GTGAGTAGAACGCAGGTGGAT.....	21	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	0	0
.....TTAACTTGCCTCTATTCCAGC.....	21	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	0	0	0	0	0
.....TTAACTTGCCTCTATTCCAG.....	19	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
.....GTGAGTAGAACGCAGGTGGA.....	20	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
.....TTAACTTGCCTCTATTCCAG.....	20	0	1	2.00	2	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	0
.....ATTAACTTGCCTCTATTCCAG.....	22	1	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
.....GTGAGTAGAACGCAGGTGGATTGG.....	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
.....GTGGCGTCTATGTGAATCTGACAC.....	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
.....TAACTTGCCTCTATTCCAGCG.....	21	2	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
.....ATTAACTTGCCTCTATTCCAGC.....	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	0	0
.....CAGGTGGATTGGAACTCTAAT.....	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
.....TAGAACGCAGGTGGATTGGAAC.....	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
....TCCCAATCTGGGCGGCAGTGGCG.....	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	0	0	0	0	0
.....TTAACTTGCCTCTATTCCAGAA.....	22	2	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
.....TCTAATTAACTTGCCTCTATTCC.....	23	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
.....GTGAGTAGAACGCAGGCAAA.....	19	3	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	1

Anti-sense strand reads

CCCTAGGGTAGACCGCCGTCACCGCAGATACACTTAGACTGTGAATTTCACTCATCTTGCGTCCACCTAACCTTGAGATTAATTGAACGGAGATAAGGTCGACCTACTCTCACACCTTTGTGACGCAGGGTTAGACGCGTCGCTACACGT	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060677 Argx9_ovaries_total	SRR2096081 M027 male body	SRR2096081 embryo_0-2h from 15to16 day old mothers	SRR060657 140_testes_total	SRR060669 160x9_females_carcasses_total
**********..((((((((..((((((.(((((((....)))))))..)))))))..))))))).)))))))....										

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12875:1564767-1564920 -	dvi_112	GGGATCCCAATCTGGGCGGCAGTGGCGTCTATGTGAATCTGACACTTAAAGTGAGTAGAACGCAGG---TG----------G---A---------TTGGAACTC-------TAATTAACTTGCCTC-TATTCCAGCTGGATGAGAGTGTGGAAACACTGCGTCCCAATCTGCGCAGCGATGTGCAGA
droMoj3	scaffold_6496:4673079-4673239 -		-GGATCCCAACCTGGGCGGCAGTGGCGTCTATGTGAATCTGACGTGTGAGTGAAGTCAAGCA----A----------T---C-AGGTCATAAAATTAG--------TAACTGTGCGTCCCGCAACTCGGAGAGAGCTGCGCCCCAATCTGCGCAGCGATGTGCAGA
droGri2	scaffold_15245:9436956-9437147 +		-GGATCCCAATCTGGGCGGCAAGCGCGTCTATGTGAATCTGACACTTAAAGTGAGTAGCAATAAA----C----------AAACTG---A-----ACTT---TCAG----TAA--TGCGAACCATCGCAATTTGAACTGGATGAGAGCTGGGACCACTGCGTCCCAATCTGCGCAGCGATGTGCAGA
droWil2	scaff_1100000004513:2829609-2829710 +		-AGATCCCCAATGGGCGGCAAGCGCGTCTATGTGAATCTGACTCTAAGTGAGTAG----------T---C----------T---T--------T--------T--------T-------------T-------ATTGGATGAGAGTGTGGAAACTTGCAGCCCCAATCTGCGCAGCGATGTGCAGA
dsp5	11:1455451-1455605 +		-AGATCCCAATCTGGGCGGCAAGCGCGTCTAGTGAATCTGAGATGTGAGTGAAGTCTTCAA----A-C----------CCAATG---G-A-----AT-------A-CTATTCAT-----TATTGATTCCCGTGAGAGCTGGGACTGCGTCGCCCCAATCTGCGCAGCGATGTGCAGA
droPer2	scaffold_21628703-1628857 +		-AGATCCCAATCTGGGCGGCAAGCGCGTCTAGTGAATCTGAGATGTGAGTGAAGTCTTCAA----A-C----------CCAATG---G-A-----AT-------A-CTATTCAT-----TATTGATTCCCGTGAGAGCTGGGACTGCGTCGCCCCAATCTGCGCAGCGATGTGCAGA
droAna3	scaffold_13266:3398875-3399033 +		-AGATCCCAACTTGGGCGGCAGTGGCGTCTTGTGAATCTGAGATGTGAGTGAATAAGCAGTCTCCAGG----AA----------T---C-ACCAA-AGAGCGCTAACTGCGTTTGTGGATGAGAGTGTGGACTGCTGCACCAATCTGCGCAGCGATGTGCAGA
droBip1	scf718000039642 7:1865564-1865723 +		-AGATCCAAACTTGGGCGGCAGTGGCGTCTTGTGAATCTGAGATGTAAAGCAGTCCGCCAAG----A----------T---C-ACTAAAAGACGCGAAGA----TAACCCCGCTTACC-TGCTTGAGTGGATGAGAGTGTGGACTGCTGCACCAATCTGCGCAGCGATGTGCAGA
droKik1	scf718000030264 0:291731-291930 +		-GGATCCCAATCTGGGCGGCAAGCGCGTCTATGTGAATCTGAGATGTGAGTGAGTCAGTCCATAGGGAGTAAACAGTCCAT-----CAAAAATCGCCCCAAGTGGATGAGCGTGCGCCCCAATCTGGCGAGCGATGTGCAGA
droPic1	scf718000045395 5:84089-84249 -		-GGATCCCAATCTGGGCGGCAAGCGCGTCTATGTGAATCTGAGATGTGAGTGAATTATCTCGCAAA----A----------C---T-CGTGGAGAAACCAGTG--------TATTCGTTGTCGC-TATCCAAGTGGATGAGAGTGTGGACTGCGTCCCAATCTGCGCAAGCGATGTGCAGA
droEle1	scf718000049126 5:329969-330129 +		-GGATCCCAACTTGGGCGGCAAGCGGCGTCTATGTGAATCTGAGATGTGAGTGAATATCTTAAGG----A----------T---C-CCTTAAAAAACATTG--------ACATTTTCCCTATCC-TGATCCAAGTGGATGAGAGTGTGGACTGCGTCCCAAGTGCGCAGCGATGTGCAGA
droRho1	scf718000075814 4:6129-6288 +		-GGATCCCAACTTGGGCGGCAGTGGCGTCTATGTGAATCTGAGATGTAGTGAATCTATAGG----A----------T---C-CCTAAAAAACTAAG--------TATTCAGCTTACC-TGATCCAGTGGATGAGAGTGTGGACTGCGTCCCAAGTGCGCAGCGATGTGCAGA
droBia1	scf718000030229 2:963233-963393 -		-GGATCCCAACTTGGGCGGCAGTGGCGTCTATGTGAATCTGAGATGTAGTGTGCGAT----A----------T---A-TCCAAAAAAAACCTG--------TATTCCAATTTGCC-TATCCAAGTGGATGAGAGTGTGGACTGCGTCCCAAGTGCGCAGCGATGTGCAGA
droTak1	scf718000041585 6:59027-59187 -		-GGATCCCAACTTGGGCGGCAGGGCGTCTATGTGAATCTGAGATGTAGAGTATCCGCTAT----A----------T---T-TTCCCAGAAACTCG--------TATCGCTAGTTGTCC-TGCTCCAGTGGATGAGAGTGTGGACACTCGCCCCAATCTGCGCAGCGATGTGCAGA
droEug1	scf718000040967 2:5196219-5196378 +		-GGATCCCAACTTGGGCGGCAAGCGCGTCTATGTGAATCTGAGATGTAGAGTATCCGCTCC----A----------T---C-TTTAAAAAACTCCAG--------TATTCTCTTGTCC-TGCTCCAGTGGATGAGAGTGTGGACACTCGCCCCAATCTGCGCAGCGATGTGCAGA
dsm3	chr28:3186213-3186373 +		-GGATCCCAATCTGGGCGGCAAGCGGCGTCTATGTGAATCTGAGATGTGAGTGAATATCTCTCAA----CA----------T---T-GCTAATGGAACGCGAAG--------TATTATCTTGTCC-TGCTCCAGTGGATGAGTGTGAAACATGCGCCCCAATCTGCGCAGCGATGTGCAGA
droSim2	Zr:4011733-4011893 +		-GGATCCCAATCTGGGCGGCAAGCGGCGTCTATGTGAATCTGAGATGTGAGTGAATATCTCTCAA----CA----------T---T-GCTAATGGAACGCGAAG--------TATTATCTTGTCC-TGCTCCAGTGGATGAGTGTGGAAACATGCGCCCCAATCTGCGCAGCGATGTGCAGA
droSec2	scaffold_1830119-830279 +		-GGATCCCAATCTGGGCGGCAAGCGGCGTCTATGTGAATCTGAGATGTGAGTGAATATCTCTCAGG----CA----------T---T-GCTAATGGAACGATCG--------TATTATCTTGTCC-TGCTCCAGTGGATGAGTGTGGAAACATGCGCCCCAATCTGCGCAGCGATGTGCAGA
droYak3	Zr:15870543-15870703 +		-GGATCCCAATCTGGGCGGCAAGCGCGTCTATGTGAATCTGAGATGTGAGTGAATATCTCTCAGG----CA----------T---T-GCCCATGGTAACCCG--------TATTCCGTTGTAC-TGCTCCAGTGGATGAGAGTGTGGAAACATGCGCCCCAATCTGCGCAGCGATGTGCAGA
droEre2	scaffold_4929:19407573-19407736 -		-CGGATCCCAATCTGGGCGGCAAGCGGCGTCTATGTGAATCTGAGATGTGAGTGAATGTAGTGATGTCC----------T---C-GC-------A---G--TGATTAAGCGATTAACTTCTGCTCCAGTGGATGAGAGTGTGGAAACATGCGCCCCAATCTGCGCAGCGATGTGCAGA

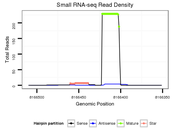
Generated: 09/08/2015 at 07:06 PM

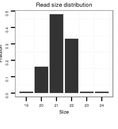
	PASS/FAIL
crit.star	1
crit.mis	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.loop1	1
crit.loop2	1
crit.stem	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.novel	0
rescue.candidate	0

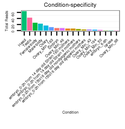
ID	Coordinate	Confidence	Class	Genome Locale	
dvi_378	**scaffold_12963:8166401-8166460 -**	**confident**	**Canonical miRNA**	**intergenic**	Open on UCSC Genome Browser [Grand3.Mmu1]

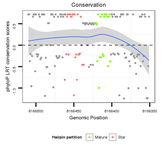
Layout: Arm: 5p 3p Loop: Mismatch:

Predicted structure









Show Alternate Folds

Flybase annotation

miscpsu

No Repeatitis elements found

Sense Small Reads

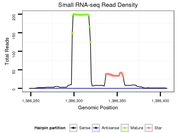
Hide 3p reads show mid mismatch reads

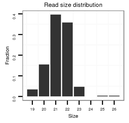
| | | |

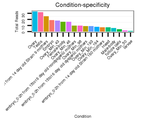
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_281	**scaffold_13246:1386298-1386358 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (GenoBiMine)]

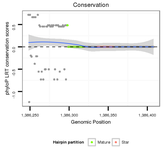
Legend: **Loop** **5p** **Mature-3p (phased)** **mismatch/bulge**

Predicted structure









Show Alternate Folds

FlyBase annotation

intergenic

No Repeatitle elements found

Sense Strand Reads

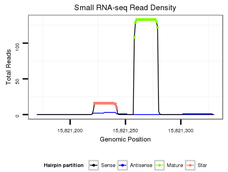
Hide 3p reads show mid mismatch reads

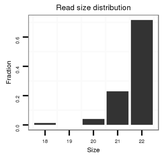
| | | |

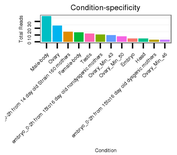
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_161	**scaffold_12963:15821220-15821280 +**	**confident**	**Canonical miRNA**	**intergenic**
				[View on UCSC Genome Browser (CompI-Mimic)]

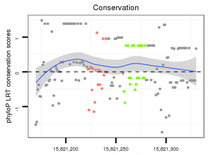
Legend: sense 5p sub-mat/s in alignment mismatch in seed

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
AT_rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read #	Hit	Total	V114 male body	M47 female body	SRR2096050 embryo_0-2h from 14 day old Strain 140 ovaries mothers	SRR2096054	SRR2096055	SRR2096057	SRR2096061 embryo_0-2h from 14 day old Strain 140 nondygenic mothers	SRR2096080 embryo_0-2h from 15to16 day old nondygenic mothers	SRR2096081 embryo_0-2h from 15to16 day old dygenic mothers	SRR2096079 embryo_0-2h from 15to16 day old dygenic mothers	V047	SRR2096072 embryo_0-2h from 15to16 day old dygenic mothers	SRR2096079	SRR2096080	W061	SRR2096075	SRR2096084 140e9_0-2h_embryos	SRR2096056 head	V053	SRR2096058	SRR2096071	SRR2096072	SRR2096078	SRR2096077	SRR2096076	SRR2096655	SRR2096660	SRR2096663 160_0-2h_embryos	SRR2096669	SRR2096670	SRR2096674	SRR2096683	SRR2096688	SRR2096689	SRR2096014	SRR2096681	SRR2096648
	size	Mismatch	Count	male	body	mothers				Strain 140								embryo	140e9_ovaries_total	2h_embryos_total	Ovary_Min_46		140e9_testes_total	head	9ard_testes_total	9_testes_total	9ard_ovaries_total	9ard_testes_total	Argentina_ovaries_total	140e9_females_carcasses_total	9_testes_total	9ard_ovaries_total	160_testes_total	160_ovaries_total	140e9_testes_total	Ovary_Strain_160_unidissed	9ard_ovaries_total	Argw9_testes_total	160e9_males_carcasses_total
.....	22	0	1	169.00	100	12	4	10	3	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
.....TTTTGGGCTCGGCTGTTCTCT.....	22	0	1	18.00	18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTTTGGGCTCGGCTGTTCTCT.....	21	0	1	4.00	4	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
.....AGAGCAGCCAGGCCCAAAATA.....	23	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
.....TTTTGGGCTCGGCTGTTCTCT.....	22	1	1	3.00	3	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
.....AAGAGCAGCCAGGCCCAAAATA.....	22	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
.....AAGAGCAGCCAGGCCCAAAATA.....	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
.....TTTTGGGCTCGGCTGTTCTCT.....	22	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	0	0
.....AGAGCAGCCAGGCCCAAAAT.....	20	0	1	2.00	2	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
.....TTTTGGGCTCGGCTGTTCTCT.....	20	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
.....TTTGGGCTCGGCTGTTCTCTA.....	21	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
.....TTTTGGGCTCGGCTGTTCTCT.....	20	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
.....TTTTGGGCTCGGCTGTTCTCT.....	22	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	0	0
.....AAGAGCAGCCAGGCCCAAAAT.....	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
.....AAAGAGCAGCCAGGCCCAAAATA.....	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	0	0	0	0	0	0	0	0	0	0	0
.....TTTTGGGCTCGGCTGTTCTCT.....	22	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
.....AGAGCAGCCAGGCCCAAAATAT.....	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	0	0	0	0	0	0	0	0	0	0	0
.....AGAGCAGCCAGGCCCAAA.....	18	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
.....TAATAGCCTTGTAGACATTTCTCGGGG..	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
.....TTTTGGGCTCGGCTGTTCTCTA.....	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	0	0	0	0	0	0	0	0	0	0	0
.....TTTGGGCTCGGCTGTTCT.....	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	0	0	0
.....TTTGGGCTCGGCTGTTCTCTAA.....	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

Anti-sense strand reads

	Read #	Hit	Total	SRR2096055 140e9_ovaries_total	SRR060675 9ard_ovaries_total	SRR060674 Â	SRR060680 9ard_testes_total	SRR2096058 Ovary_Min_98	SRR060665 9_females_carcasses_total
	size	Mismatch	Count	Norm	Total	Ovary_Min_43			
.....TCCGGGTTTTATAGAGTGTTT.....	21	0	1	1.00	1	1	0	0	0
.....TTTCTCGTCGGTCCGGGTTTTA.....	22	0	1	1.00	1	0	1	0	0
.....TTCTCGTCGGTCCGGGTTTTA.....	21	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
drosVir3	scaffold_12963:15821220- 15821280.	dvi_161	AAUC--TTTA--TAGTTATTGTATTCCCAT---------ATATATATATTAATTAAATATATTAAAGAGCAGCCAGGCCCAAAATATCTCTACACAAAATATATTTTGGGCTCGGCTGTTCTCTAAATATTTTATTAAG-------CCTATTTAATAGCCTTGTAGACATTTCTCGGGGTC
drosMel3	scaffold_6413:9068537-9068619		---------ATATATATATTAA[illegible]TATTTAA[illegible]GCAGCCAGGCCCAAAATA[illegible]GCGGGTTTAAATATCTCTA[illegible]
droSim12	scaffold_14822:390679-390771		TAC--TTTA--TAGTTATTGTATTCCCAT---------ATATATATATTAATTAAATATATTAAAGAGCAGCCAGGCCCAAATAATTAAAAAGCAATTTATTTCTCGTCGGTCCGGGTTTTAAATAGCCTTGTAGACATTTCTCGGGGTC
droWil12	scaf2_1100000004511:1017231- 1017294:1		TTAAATAC[illegible]TTTTCTCGTCGGTCCGGGTTTTA
droPer2	scaffold_ccc4886:16343-		TAC--TTTA--TAGTTATTGTATTCCCAT---------ATATATATATTAATTAAATATATTAAAGAGCAGCCAGGCCCAAAATATCTCTACACAAAATATATTTTGGGCTCGGCTGTTCTCTAAATATTTTATTAAG-------CCTATTTAATAGCCTTGTAGACATTTCTCGGGGTC
droEre1	scaffold_4929:1941:1939735- 1939795:1		TTAAATAC[illegible]TTTTCTCGTCGGTCCGGGTTTTA
droEre2	scaffold_4929:1941:1654737- 1654794:1		TTAAATAC[illegible]TTTTCTCGTCGGTCCGGGTTTTA
droEre2	scaffold_4929:1941:1654737- 1654794:1		TTAAATAC[illegible]TTTTCTCGTCGGTCCGGGTTTTA

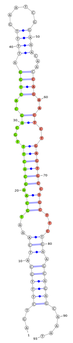
Generated: 09/08/2015 9:09:22 PM

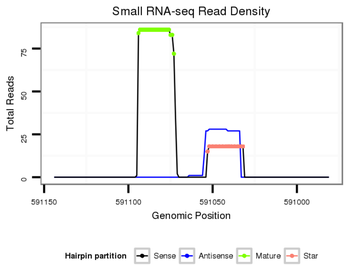
chr.star	1
chr.loop	1
chr.mid	1
chr.hairpin	1
chr.pairing	1
chr.mature	1
chr.star2	1
chr.loop2	1
chr.bach	1
rescue.mature	1
rescue.dominant	1
rescue.known	1
rescue.hairpin	1
rescue.candidate	1

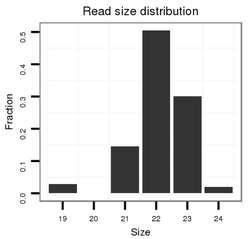
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_128	**scaffold_12928:591031-591094 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

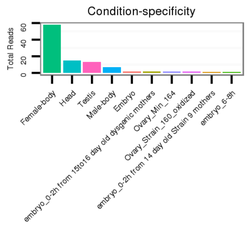
Legend: mature star mismatch in alignment mismatch in read

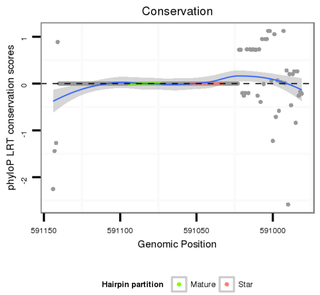
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GGCTAGGAATAAGGTGCTGCTAACATTTATAAATGAGTCTTTGCATCAAATGCAAGCACTTTGCAGCACTGGATTTTGAATCGGAAACAACCAGAACTCTGAGTGCCTGCTTCTGAAGCAGAGCAAATCACTGCTTAATTTTATTGTTTAATCTAACACTTTCC	Read size	# Mismatch	Hit Count	Total Norm	Total	M047 female body	M028 head	SRR060681 Argx9_testes_total	M027 male body	SRR060672 9x160_females_carcasses_total	SRR060679 140x9_testes_total	M061 embryo	SRR060678 9x140_testes_total	SRR2096014 Ovary_Strain_160_oxidized	SRR2096059 Ovary_Min_164	SRR2096081 embryo_0-2h from 15to16 day old nondysgenic mothers	SRR2096079 embryo_0-2h from 15to16 day old dysgenic mothers	SRR060664 9_males_carcasses_total	SRR060666 160_males_carcasses_total	SRR060667 160_females_carcasses_total	SRR060668 160x9_males_carcasses_total	SRR1106717 embryo_6-8h	SRR2096038 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096072 embryo_0-2h from 15to16 day old dysgenic mothers	V053 head	SRR1106730 embryo_16-30h	SRR060673 9_ovaries_total
********************************...((((((.(((....((.(((((.((((.....))))).....))))..))..))))))).))))...))))).))))))).....********************************																											
.....TGCAAGCACTTTGCAGCACTGG.....	22	0	1	36.00	36	26	1	5	0	1	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCAAGCACTTTGCAGCACTGGA.....	23	0	1	31.00	31	18	1	2	0	1	3	0	1	0	0	0	1	1	0	0	1	0	1	1	0	0	0
.....CAGAACTCTGAGTGCCTGCTTC.....	22	0	1	15.00	15	2	7	1	1	1	0	0	0	0	1	0	0	0	1	0	0	0	1	0	0	0	0
.....TGCAAGCACTTTGCAGCACTG.....	21	0	1	11.00	11	3	4	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCAAGCACTTTGCAGCACTGGAA.....	24	1	1	4.00	4	2	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCAAGCACTTTGCAGCAC.....	19	0	1	3.00	3	0	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
.....AGAACTCTGAGTGCCTGCTTC.....	21	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	0	0
.....TGCAAGCACTTTGCAGCACTGGAT.....	24	0	1	2.00	2	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGCAAGCACTTTGCAGCACTGGAT.....	24	1	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
.....TGCAAGCACTTTGCAGCACTGGAAA.....	25	2	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
.....ATGCAAGCACTTTGCAGCACTGG.....	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
.....GCAAGCACTTTGCAGCACTGGA.....	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
.....TGCAAGCACTTTGCAGCACTGGCG.....	24	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	0
.....GCAAGCACTTTGCAGCACTGG.....	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	0	0	0
.....GCAAGCACTTTGCAGCACTGT.....	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
.....TGCAAGCACTTTGCAGCACTGT.....	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	1	0	0

Anti-sense strand reads

CCGATCCTTATTCCACGACGATTGTAAATATTTACTCAGAAACGTAGTTTACGTTCGTGAAACGTCGTGACCTAAAACTTAGCCTTTGTTGGTCTTGAGACTCACGGACGAAGACTTCGTCTCGTTTAGTGACGAATTAAAATAACAAATTAGATTGTGAAAGG	Read size	# Mismatch	Hit Count	Total Norm	Total	V053 head	SRR060672 9x160_females_carcasses_total	V116 male body	M047 female body	SRR060666 160_males_carcasses_total	SRR060668 160x9_males_carcasses_total	SRR060669 160x9_females_carcasses_total	V047 embryo	SRR060664 9_males_carcasses_total	SRR060667 160_females_carcasses_total	SRR060689 160x9_testes_total	SRR060686 Argx9_0-2h_embryos_total	SRR060676 9xArg_ovaries_total	SRR060665 9_females_carcasses_total	SRR060659 Argentina_testes_total	SRR060673 9_ovaries_total
********************************...((((((.((((...((((.((.((((.((((.....))))).....))))..))..))))))).))))...))))).))))))).....********************************																					
.....GGTCTTGAGACTCACGGACGA.....	21	0	1	14.00	14	5	2	2	0	1	1	2	0	0	0	1	0	0	0	0	0
.....TGGTCTTGAGACTCACGGACGA.....	22	0	1	12.00	12	5	1	1	1	1	0	0	1	1	1	0	0	0	0	0	0
.....GCTTGAGACTCACGGACGA.....	19	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGGTCTTGAGACTCACGGACGA.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AGCCTTGTTGGTCTTGAGACTC.....	23	0	1	1.00	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
.....TCTTGAGACTCACGGACGA.....	19	0	1	1.00	1	1	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_12928:590981-591144 -	dvi_128	GGCTAGGAATAAGGTGCTGCTAACATTTATAAATGAGTCTTTGCATCAAATGCAAGCACTTTGCAGCACTGGATTTTGAATCGGAAACAACCAGAACTCTGAGTGCCTGCTTCTGAAGCAGAGCAAATCACTGCTTAATTTTAT---TGTTTAATC------TAACACTTTCC
droMoj3	scaffold_6680:17147976-17148095 -		TCA----------ATTTTA---A-GAGCATC------CC-A-TATTCC
droGri2	scaffold_8094:777-806 +		ATG----------TAATGTAC-C-GTA-C-T------TAACATCTCTT
dp5	XL_group1a:4484982-4484997 -		ATG----------T--------T------T-A-T-T-C-T
droPer2	scaffold_11:1069844-1069856 -		T----------T--------T------TAA-A-T-T-C-T
droEle1	scf7180000490214:1425294-1425344 +		AG----------GCGTGCTGACTGCA-G-A-TTTAT---G-GTTGAATTTTGGTGCCCACTCC-TC

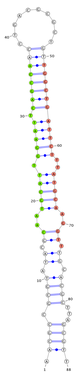
Generated: 09/08/2015 [illegible] PM

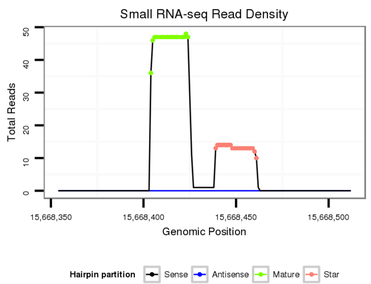
score	**1**
crit.dist	1
crit.loop	0
crit.mor	0
crit.star	1
crit.total	1
crit.pairing	1
crit.top3	1
crit.gtop3	1
crit.uri	0
crit.back	0
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

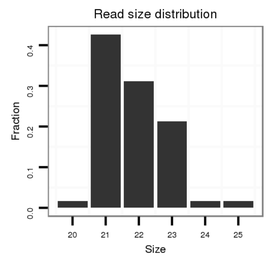
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_407	**scaffold_12963:15668404-15668462 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

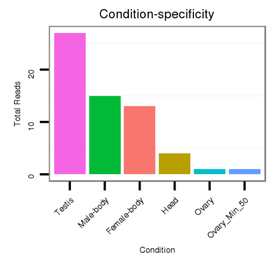
Legend: mature star **mismatch in alignment** mismatch in read

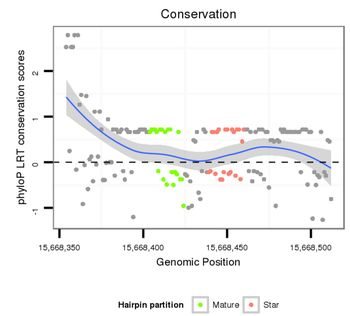
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dvir/GJ17618-in]; CDS [Dvir/GJ17618-cds]; utr5 [utr5_minus_901]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GAGGGTGAGTAAACAAATCAAATACTCAAGTGCACAACGCCGCGTATACGCAATGCATTGGAATTCAGCCAACCTGACGCGCTGTTGGCTGATTCTTTATGCAAGGTTTGCACGCTTAGCGTTTCGAGACACGCCCGCGCATTTTGCCCAAGCCCCAGG	Read size	# Mismatch	Hit Count	Total Norm	Total	M047 female body	SRR060681 Argx9_testes_total	V116 male body	SRR060678 9x140_testes_total	SRR060689 160x9_testes_total	V053 head	SRR060666 160_males_carcasses_total	SRR060679 140x9_testes_total	SRR060680 9xArg_testes_total	SRR060664 9_males_carcasses_total	SRR060668 160x9_males_carcasses_total	SRR060683 160_testes_total	SRR060655 9x160_testes_total	SRR060656 9x160_ovaries_total	SRR060671 9x160_males_carcasses_total	SRR2096057 Ovary_Min_50	V047 embryo	SRR060670 9_testes_total	M027 male body
********************************.((((.((((.((.((...(((((.(((((.((((((((((.....)))))))))))).)))))..)).)).)).))))...)))).********************************.																								
.....CAATGCATTGGAATTCAGCCA.....	21	0	1	18.00	18	3	1	4	3	0	1	1	0	0	2	1	2	0	0	0	0	0	0	0
.....CAATGCATTGGAATTCAGCCAA.....	22	0	1	13.00	13	0	6	3	1	0	0	0	0	1	0	0	0	0	0	1	1	0	0	0
.....TGGCTGATTCTTTATGCAAGGT.....	23	0	1	9.00	9	4	1	0	0	0	0	1	0	1	0	1	0	1	0	0	0	0	0	0
.....AATGCATTGGAATTCAGCCAAC.....	22	0	1	5.00	5	1	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0
.....AATGCATTGGAATTCAGCCAA.....	21	0	1	5.00	5	0	1	0	0	0	2	0	0	1	0	0	0	0	1	0	0	0	0	0
.....CAATGCATTGGAATTCAGCCAAC.....	23	0	1	4.00	4	1	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGGCTGATTCTTTATGCAAGGTT.....	24	1	1	3.00	3	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
.....GGCTGATTCTTTATGCAAGGTT.....	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
.....TGGCTGATTCTTTATGCAAGGT.....	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
.....TGGCTGATTCTTTATGCAAGG.....	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
.....ATGCATTGGAATTCAGCCAAC.....	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
.....CAACCTGACGCGCTGTTGGCTGATT.....	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
.....GGCTGATTCTTTATGCAAGGT.....	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
.....CAATGCATTGGAATTCAGCC.....	20	0	1	1.00	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
.....TGGCTGATTCTTTATGCAAGGTT.....	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
.....TGGCTGATTCTTTATGCAAGGTTT.....	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

Anti-sense strand reads

CTCCCACTCATTTGTTTAGTTTATGAGTTCACGTGTTGCGGCGCATATGCGTTACGTAACCTTAAGTCGGTTGGACTGCGCGACAACCGACTAAGAAATACGTTCCAAACGTGCGAATCGCAAAGCTCTGTGCGGGCGCGTAAAACGGGTTCGGGGTCC	Read size	# Mismatch	Hit Count	Total Norm	Total	M027 male body	SRR2096014 Ovary_Strain_160_oxidized
********************************.((((.((((.((.((...(((((.(((((.((((((((((.....)))))))))))).)))))..)).)).)).))))...)))).********************************.							

Show Alignment With Reads

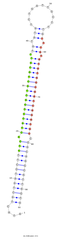
Re-alignment of all predicted orthologs

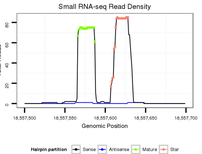
Species	Coordinate	ID	Alignment
droVir3	scaffold_12963:15668354-15668512 +	dvi_407	GAGGGTGAGTAAACAAAT-CAAATACTCAAGTGCACAACGCCGCGTATACGCAATGCATTGGAATTCAGCCAACCTGACGCGCTGTTGGCTGATTCTTT--ATGCAAGGTTT--GCACGCTTAGCGTTTCGAGACACGCCCGCGCATTTTGCCCAAGCCCCAGG
droMoj3	scaffold_6500:18656751-18656904 +		GA[illegible]GGTGAGT[illegible]AAC[illegible]T-CAA------AGTGCACAACG[illegible]GCGTATACGCAATGCATTGGAAT[illegible]TTGT[illegible]AAGACGACTGTTGGC[illegible]GAT[illegible]T[illegible]GGCATGCAA[illegible]GTT--GC[illegible]G[illegible]A[illegible]CG[illegible]TTC[illegible]AGACACGCCCGCGCATTT[illegible]GCGTCCT[illegible]CAAG
droGri2	scaffold_15126:4800945-4801090 -		GAGGGT[illegible]AGTAAA[illegible]AAAT[illegible]CAA-A[illegible]CT--A[illegible]TGCA[illegible]CACGC[illegible]GCGTATACGCAAT[illegible]GA[illegible]C[illegible]A[illegible]ACA[illegible]TTT[illegible]ATA---A[illegible]CT[illegible]GAA[illegible]GCGA[illegible]GCCTTT--[illegible]TG[illegible]AAA-T[illegible]T[illegible]TA-TT[illegible]GCTTA[illegible]G------ACACGCCCGCGC[illegible]TTT[illegible]GC[illegible]A[illegible]CC[illegible]A--C
droWil2	scf2_1100000004585:5528542-5528551 +		GA[illegible]GGT[illegible]AA[illegible]T------------------

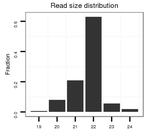
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_24188	**scaffold_13047:18557550-18557649 +**	**Candidate**	**Unknown**	**intergenic**	[View on UCSC Genome Browser (Cerne9.Mmtr1)]

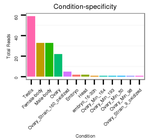
Legend: **miRNA** **Star** **mature(5-arm)** **mature(3-arm)**

Predicted structure









No conservation details.

Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	MC47 female body	SRR060679 140s9_testes_total	SRR060672 3s140_females_carcasses_total	SRR060678 3s140_testes_total	SRR060681 Argo9_testes_total	SRR060684 7_males_carcasses_total	SRR060670 7_testes_total	V116 SRR060673 male 9_ovaries_total body	SRR060665 7_females_carcasses_total	SRR060680 Argo9_testes_total	SRR060671 3s140_males_carcasses_total	SRR296014 Ovary_Strain_140_oxidized	SRR060668 140s9_males_carcasses_total	SRR060674 Argo9_ovaries_total	SRR060683 140_testes_total	SRR060689 140s9_testes_total	SRR296013 Ovary_Strain_9_oxidized	SRR060677 Argo9_ovaries_total	SRR060682 male2_0-20_embryos_total body	MC27 SRR060654 male140s9_ovaries_total body	SRR060674 3s140_ovaries_total	SRR060688 140_ovaries_total	V053 SRR060658 head140_ovaries_total	SRR060647 140_females_carcasses_total	SRR060669 140s9_females_carcasses_total	SRR060675 140s9_ovaries_total	SRR060684 140s9_0-20_embryos_total	SRR060686 Argo9_0-20_embryos_total	SRR110730 embryo_14-20h	SRR296055 Ovary_Mix_43	SRR296056 Ovary_Mix_46	SRR296057 Ovary_Mix_50	SRR296058 Ovary_Mix_88	SRR296059 Ovary_Mix_164	SRR296060 Ovary_Mix_153	SRR110727 Larvae
TTCGAGTTTCGATTTAATTTTTATATATACAAGTTGATTAGACAGCTAATAATACTACTAATGCT+																																									
**********																																										
...CTCATACTCGATTCCTATAT...	22	0	1	50.00 50	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
...TTTATATAGCAATCAGATAG...	22	0	1	16.00 16	1	0	0	0	2	1	0	2	0	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
...CTCATACTCGATTCCTATAT...	21	0	1	11.00 11	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	0	0	0
...TATATGCAATCAGATGCCGC...	22	0	1	10.00 10	1	0	0	0	1	0	0	1	2	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0
...TATATGCAATCAGATGCGCAA...	22	0	1	10.00 10	0	0	0	0	1	0	0	1	1	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
...ATATGCAATCAGATGCGCAAG...	22	1	1	9.00 9	0	0	0	0	1	0	0	1	1	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
...TATATGCAATCAGATGCCGCAA...	22	0	1	8.00 8	0	0	0	0	1	0	0	1	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
...ATATGCAATCAGATGCGCA...	21	0	1	8.00 8	0	0	0	0	1	0	0	1	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
...ATATGCAATCAGATGCGCA...	20	0	1	7.00 7	0	0	0	0	0	0	0	0	2	1	0	1	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
...TCACTATCTGATTCCTATATTT...	22	0	1	6.00 6	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	0	0
...TATATGCAATCAGATGCC...	20	0	1	5.00 5	0	0	0	0	0	0	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
...TATATGCAATCAGATGCAG...	22	0	1	3.00 3	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	0	0	0	0
...TGTCACTATCTGATTCCTATAT...	22	0	1	3.00 3	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
...TATATGCAATCAGATGCC...	23	0	1	2.00 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	0	0	0	0	0	0	0	0	0	0	0	0
...ACTATCTGATTCCTATATTTA...	21	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
...GTCACTATCTGATTCCTATATTT...	23	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
...ATATGCAATCAGATGCGCAA...	23	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
...TATATGCAATCAGATGCCGCA...	23	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
...TATATGCAATCAGATGCGCAG...	23	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
...TATATGCAATCAGATGCGCAC...	23	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
...TAGCGACAAGCATAGTATGC...	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
...TTGCTATTTTATATACTCTA...	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
...ATATGCAATCAGATGCCGCAG...	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	0	0	0	0	0	0	0	0	0	0	0
...TTATATGCAATCAGATGAG...	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
...ATATATCAAGTTGATTAC...	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
...ATTACTATAATGCTTTCTCATC...	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
...TATATGCAATCAGATGCCGC...	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	0	0	0	0	0	0	0	0	0	0	0	0	0
...TATATGCAATCAGATGCCGCA...	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	0
...ATATGCAATCAGATGCCGCAG...	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
...ATATGCAATCAGATGCCGCAA...	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
...ATATGCAATCAGATGCCGCAC...	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	0
...TATATGCAATCAGATGCCGCAG...	25	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	0	0	0	0	0	0	0	0	0
...TATATGCAATCAGATGCCGCAG...	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
...GTCACTATCTGATTCCTATG...	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
...TTATATATAGCAATCAGATA...	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	0	0	0	0
...TAGCAATCAGATGCGCAA...	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
...TAGCAATCAGATGCGCAG...	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
...CTGATTGCGTATTTATATAT...	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
...ATATATACTTACTAATGCTC...	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

Anti-sense strand reads

	Read # size	Mismatch	Hit Count	Total Norm	Total	MC28 head140s9_testes_total	SRR296014 Ovary_Strain_140_oxidized	SRR296058 Ovary_Mix_88 body	V116 V053 SRR060663 140_ovaries_total male head	SRR060685 Argo_0-20_embryos_total	SRR060682 male2_0-20_embryos_total
AAACTCAAAGCTAAATTAAAAATATATGTTCACTATGTTGTTGATTATATGTAGTAATTACGAA+											
**********											
...ACATGATAGACTAACGATATAA...	23	1	1	2.00 2	2	0	0	0	0	0	0
...GACACATGATAGACTAACGATA...	22	0	1	1.00 1	0	0	1	0	0	0	0
...ACACATGATAGACTAACGATA...	22	1	1	1.00 1	0	0	0	1	0	0	0
...CCTGTTTCGTAATGTATGTATGA...	21	0	1	1.00 1	0	0	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species Coordinate	ID	Alignment
Dvirilis(+) scaffold_13047:18557550-18557649	Dvir_24188	TTCGAGTTTCGATTTAATTTTTATATATACAAGTTGATTACACAGCTAATAATACTACTAATGCTCTCACTATCTGATTCCTATATATGTGCTTTTTTATATATACAAGTTGATTAGACAGCTAATAATACTACTTAAAAATCAATATTATTAATAATCTTTTTTTTTTAATTTTTGGGT

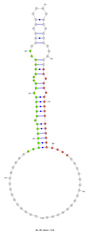
Generated 08Dec2019 miRBAM v1.0

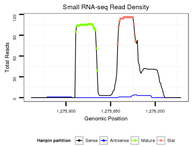
ref_bam	1
ref_fasta	1
ref_gtf	1
ref_bed	1
ref_chrom	1
ref_gff3	1
ref_mature	1
ref_hairpin	1
ref_species	1
ref_genome_build	1
miRBAM_version	1
miRBAM_date	1
miRBAM_time	1
miRBAM_cmdline	1

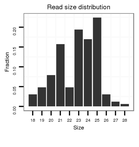
ID	Coordinate	Confidence:	Class:	Genomic Locale:	
dvi_287	**scaffold_12822:1275911-1275979 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (Cosmid Mirror)]

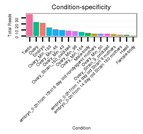
Legend: mature star mismatch in alignment mismatch in loop

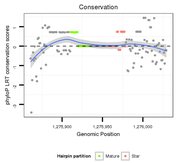
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

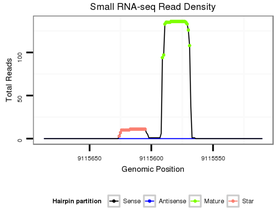
Hide 3p reads Show mid mismatch reads

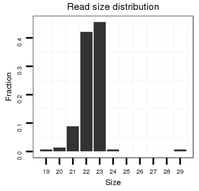
| | Seed 8 size | Mismatch | Count | RUN | Total | SRR2596080 Ovary_Mix_1R3 | SRR2596081 Ovary_Mix_2R3 | SRR2596056 Ovary_Mix_5R | SRR2596057 Ovary_Mix_6R | SRR6006678 5w140_testes_total | SRR2596059 Ovary_Mix_1R4 | SRR2596054 Ovary_Strain_1R5_unidissected | SRR2596030 embryo_2-2h from 14 days old mothers | SRR6006676 Adult_ovaries_total | SRR6006677 18w5_testes_total | SRR6006679 Adult_testes_total | SRR2596080 embryo_0-2h from 15\n14 days old mothers | SRR6006689 14w5_ovaries_total | SRR2596024 embryo_2-2h from 14 days old mothers | SRR2596050 embryo_0-2h from 14 days old mothers | SRR6006656 5w140_ovaries_total | SRR6006670 5w_testes_total | SRR6006682 5w140_0-2h_embryo_total | SRR6006685 3w_testes_total | SRR6006688 14w_ovaries_total | SRR2596041 embryo_0-2h from 14 days old mothers | SRR6006663 3w140_0-2h_embryo_total | SRR6006681 Adult_testes_total | SRR6006661 140w5_0-2h_embryo_total | SRR6006680 Adult_ovaries_total | SRR2596013 Ovary_Strain_9_unidissected | M027 mix body | M041 embryo body | SRR6006674 5w140_ovaries_total | SRR6006683 140_testes_total | SRR1106715 embryo_6-8h | SRR1106716 embryo_8-10h from 15\n14 days old mothers | SRR2596041 embryo_2-2h from 15\n14 days old mothers | M047 male body | M028 female head | SRR6006655 5w140_testes_total | SRR6006657 140_testes_total | SRR6006659 Argentina_testes_total | SRR6006675 18w5_ovaries_total | SRR2596072 embryo_0-2h from 15\n14 days old mothers | SRR2596079 embryo_0-2h from 15\n14 days old mothers | SRR6006684 male head | SRR6006673 140w5_0-2h_embryo_total | SRR6006658 5w140_0-2h_embryo_total | SRR6006662 5w_ovaries_total | SRR1106714 embryo_2-6h | SRR1106713 embryo_4-6h | SRR1106724 mixed stage which body |
|---|---|---|---|---|---

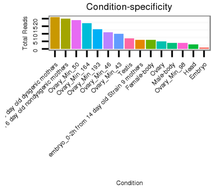
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_23807	**scaffold_12963:9115560-9115637 -**	**Candidate**	**Unknown**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure







No conservation details.

Show Alternate Folds

Flybase annotation

intron [Dvir/GI24548-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

ATTATTAAACTGCATTTGCTTGCAGAAATAATGTGCAAATAATTTAGCATAGATAAAGTACTTATCATATTACTCGAAAGGTTTTTAATCTAGAAACACCGTCGAATAATCTGATAAGTACTTCATCTGAACTGTTCAAGATTTACATTTTAAAAAATGTTTTTAAACAAATAGAAA	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR2096057 Ovary_Min_50	SRR2096059 Ovary_Min_164	SRR2096060 Ovary_Min_193	SRR2096056 Ovary_Min_46	SRR2096079 embryo_0-2h from 15to16 old dygenic mothers	SRR2096081 embryo_0-2h from 15to16 day old nondygenic mothers	SRR2096080 embryo_0-2h from 15to16 day old nondygenic mothers	SRR2096055 Ovary_Min_43	SRR2096072 embryo_0-2h from 15to16 day old dygenic mothers	SRR2096026 embryo_0-2h from 14 day old Strain 9 mothers	M028 female head	M047 embryo_0-2h from 14 day old body	SRR2096038 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096058 Ovary_Min_98	SRR060664 9_males_carcasses_total	SRR060673 9_ovaries_total	M027 male body	SRR060655 9x160_testes_total	SRR060669 160x9_females_carcasses_total	SRR060677 Arg x9_ovaries_total	SRR060674 9x140_ovaries_total	SRR060676 9xArg_ovaries_total	SRR060678 9x140_testes_total	SRR060679 140x9_testes_total	SRR060680 Arg x9_testes_total	SRR060681 Arg x9_testes_total	SRR060687 9_0-2h_embryos_total	SRR060689 160x9_testes_total	SRR1106724 embryo_12-14h	SRR1106730 embryo_14-30h	V047 9xArg_0-2h_embryos_total	SRR060685 embryo
**********	...(((((.(((((((((((.(((((.(((((..(((((((.....)))).))).)))).)))).)))))))))))).)))))....	23	0	1	65.00	65	10	8	4	3	9	4	8	3	7	2	0	0	2	3	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....	.....CACCCGTCGAATAATCTGATAAG.....	22	0	1	33.00	33	5	6	4	2	1	1	1	6	1	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	.....CCCGTCGAATAATCTGATAAGT.....	22	0	1	18.00	18	2	2	3	4	4	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
.....	.....CACCCGTCGAATAATCTGATAA.....	21	0	1	3.00	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
.....	.....TTATCATATTACTCGAAAGGTT.....	21	0	1	3.00	3	0	0	0	1	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
.....	.....CACCCGTCGAATAATCTGATA.....	22	0	1	3.00	3	0	0	0	0	1	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
.....	.....CCCGTCGAATAATCTGATAAG.....	21	0	1	3.00	3	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	.....CCGTCGAATAATCTGATAAGT.....	21	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	0	0	0	0	0	0	0	0	0	0	0
.....	.....ACCCGTCGAATAATCTGATAAG.....	22	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	1	0	0	0	0	0	0	0
.....	.....TATCATATTACTCGAAAGGTTTT.....	23	0	1	2.00	2	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
.....	.....ATCATATTACTCGAAAGGTTTT.....	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	1	0	0	0	0	0	0
.....	.....CACCCGTCGAATAATCTGATAAA.....	23	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
.....	.....ACACCCGTCGAATAATCTGAT.....	21	0	1	2.00	2	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	1	0	0	0	0
.....	.....TATCATATTACTCGAAAGGTT.....	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	0	0	0	0	0	0	0	0	0	0	0	0
.....	.....TATCATATTACTCGAAAGGTTT.....	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	0	0	0	0	0	0	0	0	0	0
.....	.....ATCATATTACTCGAAAGGTTT.....	21	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
.....	.....CCCGTCGAATAATCTGATAAGT.....	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
.....	.....CACCCGTCGAATAATCTGA.....	19	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	1	0	0
.....	.....TACTCGAAAGGTTTTTAATCTAGAAACAC.....	29	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
.....	.....ACCCGTCGAATAATCTGATA.....	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
.....	.....CCGTCGAATAATCTGATAAGTAA.....	24	2	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
.....	.....CACCCGTCGAATAATCTGATAAG.....	24	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	0	0	0	0	0	0	0	0	0	0	0
.....	.....CGAATAATCTGATAAGTACT.....	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	0	0	0	0	0	0	0	0	0	0
.....	.....CACCCGTCGAATAATCTG.....	19	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

Anti-sense strand reads

TAATAATTGACGTAAACGAACGTCTTTATTAACACGTTTATTAAATCGTATCTATTTCATGAATAGTATAATGAGCTTTCCAAAAATTAGATCTTTGTGGGCAGCTTATTAGACTATTCATGAAGTAGACTTGACAAGTTCTAAATGTAAAATTTTTTACAAAAATTTGTTTATCTTT	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR2096014 Ovary_Strain_160_oxidized	V047 embryo 9xArg_ovaries_total	SRR060676	M061 embryo 9_testes_total	SRR060670
**********	...((((((.((((((((((((.((((.((((..((((((.....)))).))).)))).)))).)))))))))))).)))))....	24	0	1	1.00	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species Coordinate	ID	Alignment
StroVir3 scaffold_12963:9115510-9115687	dvi_23807	ATTATTAAACTGCATTTGCTTGCAGAAATAATGTGCAAATAATTTAGCATAGATAAAGTACTTATCATATTACTCGAAAGGTTTTTAATCTAGAAACACCGTCGAATAATCTGATAAGTACTTCATCTGAACTGTTCAAGATTTACATTTTAAAAAATGTTTTTAAACAAATAGAAA

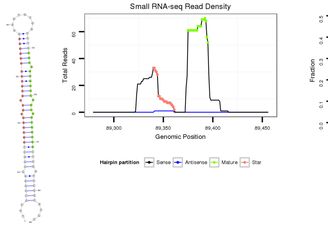
Generated on 2015 at 05:08 PM

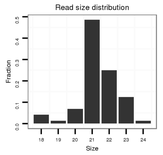
(chrom)	
cnt.star	1
cnt.mid	1
cnt.half	0
cnt.total	1
cnt.spec	1
cnt.top3	1
cnt.spop3	1
cnt.frac	1
cnt.back	1
rescue.total	0
rescue.conserved	0
rescue.known	0
rescue.confident	0
rescue.candidate	0

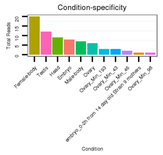
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_23723	**scaffold_12932:89329-89406 +**	**Candidate**	**Unknown**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

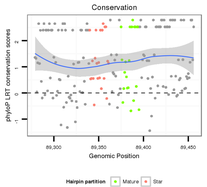
Legend: **intron** **exon** **Mismatch in alignment** **Mismatch in read**

Predicted structure









Show Alternate Folds

Flybase annotation

intron [DroGI16492-ra]

No Repeatable elements found

Sense Strand Reads

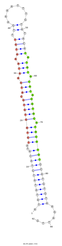
hide 3p reads show mrd mismatch reads

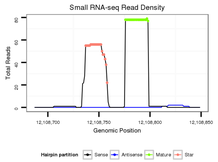
| | | |

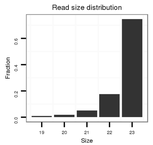
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_455	**scaffold_12875:12108737-12108799 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (ConsMiRNA)]

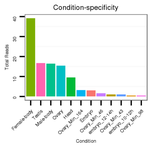
Legend: hairpin 5p 5' mature 5' star 3' mature 3' star mismatch to star

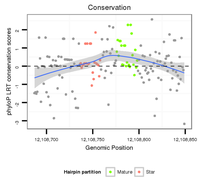
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
CATATA	Simple_repeat	Simple_repeat	+
CATATA	Simple_repeat	Simple_repeat	+
CATATA	Simple_repeat	Simple_repeat	+

number	star
1. dvi_455 scaffold_12875:12108737-12108799 + 2. scaffold_18049:9746848-9974730 -	

Sense Strand Reads

hide 3p reads show mid mismatch reads

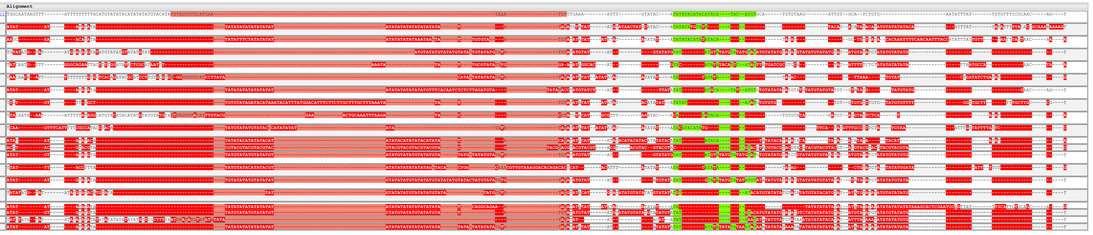
Read #	Hit Count	Total Reads	Total Mismatch	M047 female body	SRR040677 Argor5_ovaries_total	SRR040664 9_males_carcasses_total	SRR040647 160_females_carcasses_total	SRR040681 Argo8_testes_total	V053 head	SRR040669 160a9_females_carcasses_total	SRR040665 9_females_carcasses_total	V047 embryo	SRR040678 9a160_testes_total	M028 head	V116 male body	SRR2096056 Ovary_Mix_44	SRR040672 9a160_females_carcasses_total	SRR040676 Pakrg_ovaries_total	SRR040679 160a9_testes_total	SRR2096059 Ovary_Mix_164	SRR040671 9a160_males_carcasses_total	SRR2096055 Ovary_Mix_43	SRR040666 160_males_carcasses_total	SRR040670 9_testes_total	SRR040674 9a160_ovaries_total	SRR2096058 Ovary_Mix_98	SRR040668 160a9_males_carcasses_total	SRR1106722 embryo_10-12h	SRR040683 160_testes_total	SRR040654 160a9_ovaries_total	SRR040655 9a160_testes_total	SRR040657 140_testes_total	SRR040659 Argentina_testes_total	SRR040673 9_ovaries_total	SRR040675 160a9_ovaries_total	SRR040688 160_ovaries_total	SRR1106723 embryo_12-14h	SRR2096014 Ovary_Strain_160_cuticle	SRR2096057 Ovary_Mix_50	SRR040656 9a160_ovaries_total	SRR040680 Pakrg_testes_total	SRR040682 9a160_0-2h_embryos_total	M041 embryo
TGGCAATAAGTTTATTTTTTTTACATGTATATATATATGTACATA[TATATGTGTCATGTAAATAAATGT]TTGAAAATTTGTATACA[TATATACATACATACATACATGTC]CATGTGTAAGATTTGTGCACTGTGGATATTTATTGTGTGTTTCCGCAACAGT																																												
**********	22	1	15.00	15	1	0	1	0	0	1	0	1	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
..TGTAATGTGCATGAATAATGT..	22	1	7.00	7	1	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	0	0	0	0	0	0	0	0	0	0	0	0	0
..TATATGTGCATGAATAATGT..	21	1	5.00	5	1	0	0	0	0	2	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
..ATGTATGTGCATGAATAAT..	19	1	5.00	5	0	0	0	0	0	2	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
..ATGTATGTGCATGAATAATG..	22	1	4.00	4	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	0	0	0	0	0	0	0	0	0	0	0	0	0
..TTATGTGCATGCATGAAT..	22	1	3.00	3	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	0	0
..ATGTATGTGCATGCATGAA..	23	1	3.00	3	0	0	0	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	0	0	0	0	0
..TGTAATGTGCATGAATAAAT..	20	1	2.00	2	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	0	0	0	0	0
..ATGTAATGTGCATGAATAAAT..	21	1	2.00	2	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	0	0	0	0	0
..TATATACATACATACATACA..	22	6	1.67	10	6	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..ATATATACATACATACATACAT..	23	4	1.33	8	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
..GTGCATGTGTAAGATTGTGC..	20	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
..TGTGCATGAATAATGTTT..	19	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
..TTTTACATGTATATACATATAT..	22	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
..TATGTATGTGCATGAATAA..	20	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
..ATATGTGCATGCATGAATAAGTT..	22	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
..ATGTATGTGCATGAATAAGTA..	22	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
..ATGTATGTGCATGAATAAAT..	23	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
..TATATACATACATACATACGCA..	24	1	0.67	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
..ATGTATATACATATATATGTA..	21	4	0.50	2	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	0
..ACATATACACATATACACACT..	21	20	0.45	9	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
..TATATACATACATACATGT..	22	7	0.29	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	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

Read #	Hit Count	Total Reads	Total Mismatch	V116 male body	M028 head	M028 head	SRR040666 160_males_carcasses_total	SRR040663 160_0-2h_embryos_total	SRR040682 9a160_0-2h_embryos_total	SRR040684 160a9_0-2h_embryos_total	SRR040662 9a160_0-2h_embryos_total	SRR040687 9_0-2h_embryos_total	SRR040668 160a9_males_carcasses_total	SRR2096058 Ovary_Mix_98	SRR2096081 embryo_0-2h male body	SRR2096080 embryo_0-2h female body	SRR040669 160a9_females_carcasses_total	SRR040686 160_females_carcasses_total	SRR040679 160a9_testes_total	SRR2096060 Ovary_Mix_137	SRR040661 160a9_0-2h_embryos_total	SRR2096071 9a160_males_carcasses_total	SRR2096059 Ovary_Mix_164	SRR040667 160_females_carcasses_total	SRR040664 9_males_carcasses_total	SRR040672 9a160_females_carcasses_total	SRR040665 9_females_carcasses_total	SRR2096057 Ovary_Mix_50	SRR040655 Ovary_Mix_43	SRR040659 Argentina_testes_total	SRR2096056 Ovary_Mix_44	SRR040685 160a9_0-2h_embryos_total	M041 embryo	V053 head	SRR2096079 embryo_0-2h from cuticle day 16 dysgenic mothers	SRR040675 160a9_ovaries_total	SRR2096072 embryo_0-2h from cuticle day 16 dysgenic mothers	SRR2096050 embryo_0-2h from cuticle day 16 Strain 160 mothers	SRR040681 Argo8_testes_total	SRR2096038 embryo_0-2h from cuticle day 16 Strain 9 mothers	SRR2096061 embryo_0-2h from cuticle day 16 Strain 160 mothers	V047 embryo	SRR040674 9a160_ovaries_total
ACCGTTATCTAAATAAAAAAAGTCATACATATATGTATATATACATGTA[ACATACACATGCATTATTATACA]ACCTTTAAACATATC[TATATGTATATTTGTATTATACA]CATACACATTCTAACGCTATACACTTATAATAACACAAAGCCTTTGTTCA																																												
**********	22	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
..AGACATTTATAAATAACACAA..	21	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
..ACAGTTGAGACGTTTAAATA..	21	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

Show Alignment With Reads

Re-alignment of all predicted orthologs

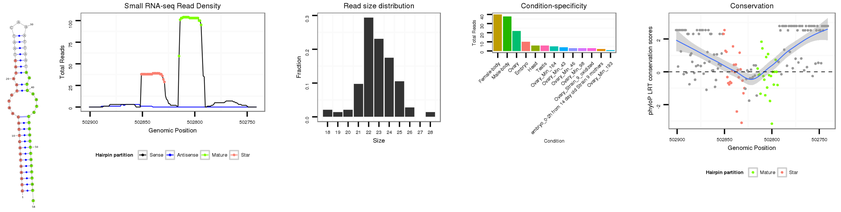


Generated 09/08/2015 at 08:28 PM

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_9593	**scaffold_12936:502791-502851 -**	**confident**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser (Cons8.Mmu)]

Legend: seed no mismatch in alignment mismatch in seed

Predicted structure



Show Alternate Folds

Flybase annotation

intron:[Dvir(GI120-u)], CDS:[Dvir(GI120-ub)], CDS:[Dvir(GI120-ub)]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACG	Read #	Hit	Total	SRR060644 female 9a140_males_carcasses_total	SRR060671 Mate-Tag body	SRR060672 9a140_females_carcasses_total	SRR060676 9a8arg_ovaries_total	SRR060677 Arga9_ovaries_total	SRR060645 9_females_carcasses_total	SRR2096013 Ovary_Strain_9_unidissed	SRR060646 140_males_carcasses_total	SRR060685 9a8arg_0-2h_embryos_total	SRR2096059 head Ovary_Min_164	V053 SRR2096055 head Ovary_Min_43	SRR060654 9a140_ovaries_total	SRR060648 140x9_males_carcasses_total	SRR060679 140x9_testes_total	SRR2096056 Ovary_Min_46	SRR2096057 Ovary_Min_50	SRR2096058 Arga9_0-2h_embryos_total	SRR060686 Ovary_Min_98	M028 head	SRR060649 140x9_females_carcasses_total	SRR060674 9a140_ovaries_total	SRR060678 9a140_testes_total	SRR060681 Arga9_testes_total	9_0-2h_embryos_total	SRR060687 embryo_0-2h_embryos_total	M041 head	140x9_0-2h_embryos_total	SRR2096014 Ovary_Strain_140_unidissed	SRR060659 Argentina_testes_total	9a140_0-2h_embryos_total	SRR060662 140x9_ovaries_total	SRR060675 Strain 9 mothers	SRR060682 embryo_0-2h_embryos_total	SRR2096016 embryo_0-2h from 14 Strain 9 mothers	SRR2096038 embryo_0-2h from 14 Strain 140 mothers	SRR2096060 Ovary_Min_193	SRR2096061 embryo_0-2h from 14 V047 mothers	V116 embryo_male body
**********	23	1	14.00 14	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
.....ATGAATCCTAATTTATTTTAG.....	24	1	20.00 20	2	3	0	2	0	3	1	1	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
.....GTAAATAATTGAAATGTAATT.....	23	1	16.00 16	0	1	0	0	0	2	0	1	0	0	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
.....AATGAATCCTAATTTATTTTAG.....	25	1	14.00 14	1	2	0	0	0	1	0	1	0	0	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
.....ATGAATCCTAATTTATTTTAG.....	23	1	14.00 14	0	2	0	0	0	1	0	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
.....ATGAATCCTAATTTATTTTATT.....	22	1	14.00 14	4	1	1	0	0	0	0	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
.....ATGAATCCTAATTTATTTTAT.....	21	1	5.00 5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAATAATTGAAATGTAAT.....	21	1	4.00 4	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	0
.....GTAAATAATTGAAATGTAATATT.....	24	1	4.00 4	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
.....GTAAATAATTGAAATGTAATATTAA.....	26	1	4.00 4	0	0	0	0	0	0	0	1	0	0	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
.....AATGAATCCTAATTTATTTTAT.....	22	1	4.00 4	0	0	0	0	0	0	0	1	0	0	0	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
.....GTAAATAATTGAAATGTAATA.....	22	1	4.00 4	0	0	0	0	0	0	0	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
.....AATGAATCCTAATTTATTT.....	19	1	2.00 2	0	0	0	0	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	0
.....GTAAATAATTGAAATGTAA.....	20	1	2.00 2	0	0	0	0	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	0
.....AATTGACTTAGAAAAACAACAGC.....	25	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	0	0	0	0
.....GTAAATAATTGAAATGTAATATTA.....	25	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	0	0	0	0
.....CATAAAACCTTATCCGAGAGT.....	22	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	0	0	0	0
.....GTAAATAATTGAAATGT.....	19	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	0	0	0	0
.....AGAAAATCCTAATTTATTTTA.....	25	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
.....ATGAATCCTAATTTATTTTATTTA.....	23	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
.....TTAACCAAATTAATAATGAATGCT.....	24	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	0	0	0	0
.....TGTCATAAAACCTTATCCGAGATCA.....	21	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	0	0	0	0
.....ATTCCGAGATGACATTCACC.....	21	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	0	0	0	0
.....AATGAATCCTAATTTATTTTTTT.....	22	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
.....AATGAATCCTAATTTATTT.....	19	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
.....GTAAATAATTGAAATGTAATAA.....	24	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	0	0	0
.....ATGAATCCTAATTTATTTT.....	20	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
.....AATGAATCCTAATTTATTT.....	19	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
.....GTAAATAATTGAAATGTAATAA.....	24	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	0	0	0
.....ATGAATCCTAATTTATTTT.....	20	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
.....AATGAATCCTAATTTATTTTATT.....	25	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
.....TATTCCGAGATGACATTCAC.....	23	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
.....AATGAATCCTAATTTATTTTTTTA.....	23	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
.....CATAAAACCTTATCCGAGG.....	20	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
.....TCATAAAACCTTATCCGAGATGACA.....	27	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	0	0	0

Anti-sense strand reads

TTATTAATATTGGGAAGTCTTTAACTGAATCTTTTCGTGTCGGCGTGC	Read #	Hit	Total	GSM1520803 female Follicle cells	M028 head	SRR060674 9a140_ovaries_total	SRR060666 140_males_carcasses_total	SRR060684 140x9_0-2h_embryos_total
**********	18	1	2.00 2	0	0	0	0	0
.....TCGTGTCGGCGTGCCATTTATTCAA.....	24	1	1.00 1	0	1	0	0	0
.....GGAAGTCTTTAACTGAATCTT.....	21	1	1.00 1	0	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

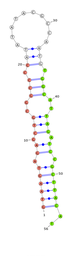
Species	Coordinate	ID	Alignment
dvir(r1)	scaffold_6936:502791-502851	dvi_9593	AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsim(r1)	scaffold_6540:82819-82956:+		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsec(r2)	scaffold_7514:48433-48550:+		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dmel(r6)	scaffold_4000000054931:1984755:- 1984755:-		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
Q5	Scaffold2831:1821835:- 0		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsim(r2)	scaffold_2153403:56823:+ 0		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsim(r3)	scaffold_2153403:56823:+ 56823:+		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsec(r2)	scaffold_2000000038721:1453131- 1453131:-		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsim(r1)	scaffold_2000000032088:1162128- 1162128:0		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsim(r1)	scaffold_2000000046035:761882- 761882:0		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsim(r1)	scaffold_2000000047124:1174270- 1174270:-		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsim(r1)	scaffold_2000000073264:12957-12118		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsim(r1)	scaffold_2000000038134:165678- 165678:0		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsim(r1)	scaffold_2000000039932:33732- 33732:0		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsim	scaffold_2000000041172:1484148- 1484148:0		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsim(r1)	scaffold_2000000039095:66280- 0	dmel_chr3R	AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsim(r1)	scaffold_2000000039095:66280- 0		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsim(r1)	scaffold_2000000041172:1484148- 0		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsim(r1)	scaffold_2000000039095:66280- 0		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA
dsim(r1)	scaffold_2000000039095:66280- 0		AATAATTATAACCCTTCAGAAATTGACTTAGAAAAACAACAGCCGCACGCTAAATAATTGAATGAATCCTAATTTATTTATTAGATTTTTTGCATAAAACCTTATCCGAAGATGACATTCATGCGAATATAA

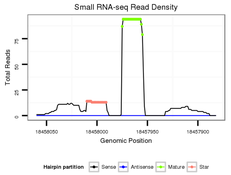
Generated:09/08/2015 at 07:06 PM

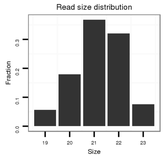
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_17510	**scaffold_13047:18457932-18458010 -**	**confident**	**3p_tailed_mirtron**	**intron**
				[View on UCSC Genome Browser (Cornell Mirror)]

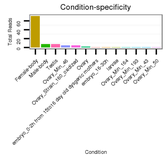
Legend: **seed** **3p** **mismatch in alignment** **mismatch in seed**

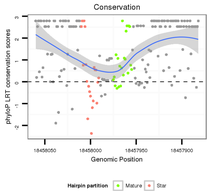
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dvir/GI22586-aj], CDS [Dvir/GI22586-cds], CDS [Dvir/GI22586-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGGATATACTGGAGCAGCCGCATACCGTTGGTCTATCTGCCGCCCGAGATG	Read #	Hit	Total	M047 female body	SRR060681 Argx9_testes_total	SRR060667 160_females_carcasses_total	SRR060678 9x160_testes_total	SRR2096014 Ovary_Strain_160_ovidissed	SRR2096056 Ovary_Min_4h	SRR060672 9x160_females_carcasses_total	SRR060659 Argentina_testes_total	SRR060665 9_females_carcasses_total	SRR060671 9x160_males_carcasses_total	SRR060668 160x9_males_carcasses_total	SRR2096058 Ovary_Min_98	SRR060666 160_males_carcasses_total	SRR060669 160x9_females_carcasses_total	SRR060675 160x9_ovaries_total	SRR060680 9xArg_testes_total	SRR1106727 V047 larvae	SRR2096055 embryo Ovary_Min_43	M027 male body	SRR060660 Argentina_ovaries_total	SRR060664 9_males_carcasses_total	SRR1106723 embryo_12-14h larvae	SRR1106728 embryo_16-30h larvae	SRR1106730 Ovary_Min_50	SRR2096057 Ovary_Min_164	SRR2096059 Ovary_Min_193	SRR2096060 SRR2096079 embryo_0-2h from 15to16 day old dysgenic mothers	SRR060655 9x160_testes_total	SRR060688 160_ovaries_total	SRR060689 160x9_testes_total	V053 head	M061 embryo	SRR060684 160x9_0-2h_embryo_total	SRR1106729 mixed whole adult body
**********	size	Mismatch	Count	Norm	Total																																	
.....	21	0	1	35.00	35	20	4	1	0	0	0	0	3	1	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGGCATTAGATCCCTTACATA.....	22	0	1	30.00	30	18	1	2	0	5	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGGCATTAGATCCCTTACA.....	20	0	1	9.00	9	5	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
.....GTAAGTAGAGCTGCGGCCCC.....	20	0	1	8.00	8	0	0	0	0	0	3	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	1	1	0	1	0	0	0	0	0
.....TGGCATTAGATCCCTTACATAG.....	23	0	1	7.00	7	4	0	0	1	0	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
.....TGGCATTAGATCCCTTAC.....	19	0	1	5.00	5	4	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
.....GATGTATTGGAATACCAAGGAGT.....	23	0	1	4.00	4	0	0	1	0	0	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
.....TACCGTTGGTCTATCTGCCGCC.....	22	0	1	3.00	3	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
.....GTAAGTAGAGCTGCGGCCCCA.....	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
.....GGCATTAGATCCCTTACAT.....	20	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	0	0	0
.....ATATGTCGGATATCTTGTGC.....	21	0	1	2.00	2	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
.....TGGCATTAGATCCCTTACAT	22	1	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	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGTAGAGCTGCGGCCCCAT.....	22	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
.....GGCATTAGATCCCTTACATA.....	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	0	0	0
.....GGCATTAGATCCCTTACATAG.....	22	0	1	2.00	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	0
.....ATACCGTTGGTCTATCTGCCGCCCGAGATG.....	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	0	0	0	0	0	0	0
.....AAGGAGTATATGTCGGATCATC.....	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
.....AGTATATGTCGGATCATCTGG.....	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
.....CTATCTGCCGCCCGAGATG.....	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	0	0	0
.....AGCGCATACCGTTGGTCTATCTGCCGCC.....	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	0	0	0	0	0	0	0	0	0
.....ATGGTAGTAAGCTGCGGCCCCAT.....	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	0	0	0	0	0
.....ACCGTTGGTCTATCTGCCGCCCGAGATG.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GCAGCGCATACCGTTGGTCTC.....	19	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
.....TACCGTTGGTCTATCTGCCGCCC.....	23	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
TGGATATACTGGAGCAGCC.....	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
.....GGCATTAGATCCCTTACA.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GCATACCGTTGGTCTATC.....	18	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
.....ATTGGAATACCAAGGAGTATA.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCTGCGCCCGAGATGGTAAG.....	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
.....CATACCGTTGGTCTATCTGCCGCCC.....	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	0	0	0	0	0
.....GTATTGGAATACCAAGGAGT.....	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	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGGCATTAGATCCCTTACATA.....	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	0	0	0	0	0	0	0	0	0	0	0	0
.....ATTGGAATACCAAGGGTATATGTCGG.....	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	0	0	0	0	0
.....TGGAGCAGCCGCATACCGTTGGTCTATCTT.....	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	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

ACCTATATGGACCTCGTCGCGTATGGCAACCAGATAGACGGCGGGCTCTAC	Read #	Hit	Total	M047 male body	M027 female body	SRR2096055 Ovary_Min_43	SRR060684 160x9_0-2h_embryo_total
**********	size	Mismatch	Count	Norm	Total		
.....	23	0	1	1.00	1	0	0

Show Alignment With Reads

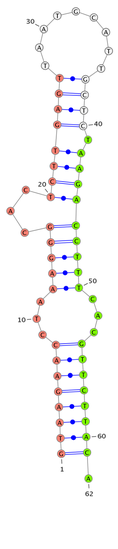
Re-alignment of all predicted orthologs

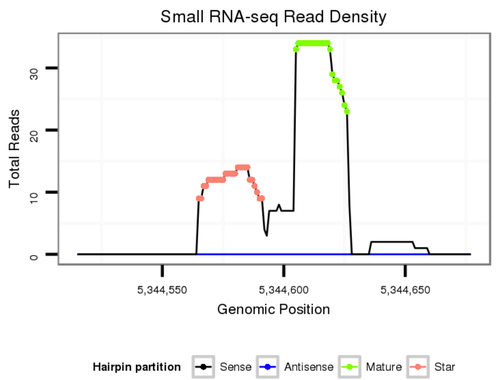
Species	Coordinate	ID	Alignment
drsVir13	scaffold_13047:18457932- 18458010 -	dvi_17510	TGGATATACTGGAGCAGCCGCATACCGTTGGTCTATCTGCCGCCCGAGATGTAAGTAGAGCTGCGGCCCCATATATACGCCAATGGCATTAGATCCCTTACATAGGCCATCATATTGTTTTAAAGATGTATTGGAATACCAAGGAGTATATGTCGGATCATCTGGTGCGGCCCGT-TATGCCCAATGGCATTAGATCCCTTACATATGTATTGGAATACCAAGGAGTATATGTCGGATCATCTGGTGCGGCCCGT
drsMel3	scaffold_6540:12584432- 12584468, -		TGGATATACTGGAGCAGCCGCATACCGTTGGTCTATCTGCCGCCCGAGATGTAAGTAGAGCTGCGGCCCCATATATACGCCAATGGCATTAGATCCCTTACATAGGCCATCATATTGTTTTAAAGATGTATTGGAATACCAAGGAGTATATGTCGGATCATCTGGTGCGGCCCGT-TATGCCCAATGGCATTAGATCCCTTACATATGTATTGGAATACCAAGGAGTATATGTCGGATCATCTGGTGCGGCCCGT
drsVir12	scaffold_1047:6241939- 6241978, +		TGATATACTGGAGCAGCCGCATACCGTTGGTCTATCTGCCGCCCGAGATGTAAGTAGAGCTGCGGCCCCATATATACGCCAATGGCATTAGATCCCTTACATAGGCCATCATATTGTTTTAAAGATGTATTGGAATACCAAGGAGTATATGTCGGATCATCTGGTGCGGCCCGT
drsMel2	scaffold_14000000049313:3335273- 3335341, +		TGGATATACTGGAGCAGCCGCATACCGTTGGTCTATCTGCCGCCCGAGATGAAGCAAGCCTTTGCATATTCTCTTCTTTT

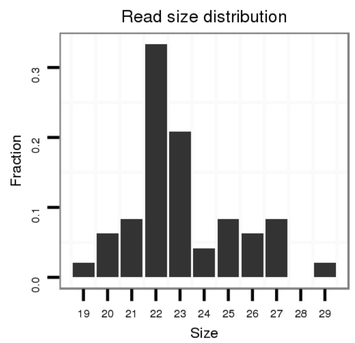
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_5303	**scaffold_12875:5344565-5344627 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

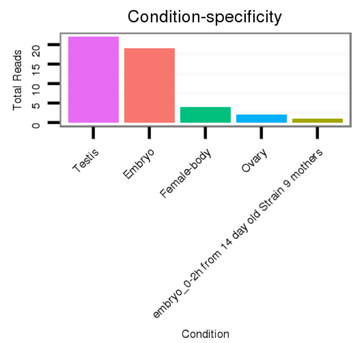
Legend: mature star mismatch in alignment mismatch in read

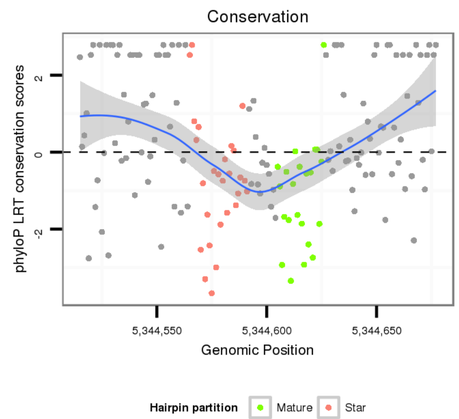
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dvir\GJ21461-in]; CDS [Dvir\GJ21461-cds]; CDS [Dvir\GJ21461-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GACGCGACATTCTGTTTCAAAGTGGACCCTCCCATCCGTGGCTTGTTGATGTAAGAACCTAAAGGGCACTCTTGAGTTAATGCATTGCTCTAAGACCTTTCACGTTCTTACAGTACTACAAGAAGAGCGCCAAGCACCCATTTGCCACAACCTTGGGCGAGGA **********((((((((...((((((...((((((((.....)))).)))))))))...)))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M061 embryo	SRR060678 9x140_testes_total	SRR060679 140x9_testes_total	V047 embryo	M047 female body	SRR060681 Argx9_testes_total	SRR060675 140x9_ovaries_total	SRR060666 160_males_carcasses_total	SRR060680 Â 9xArg_testes_total	SRR2096026 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096081 embryo_0-2h from 15to16 day old nondysgenic mothers	SRR2096072 embryo_0-2h from 15to16 day old dysgenic mothers
.....TAAGACCTTTCACGTTCTTACA.....	22	0	1	14.00	14	0	6	3	0	1	2	2	0	0	0	0	0
.....TAAGACCTTTCACGTTCTTACAG.....	23	0	1	8.00	8	0	4	1	0	1	1	0	0	1	0	0	0
.....GTAAGAACCTAAAGGGCACTCTTGAGT.....	27	0	1	3.00	3	2	0	0	0	0	0	0	0	0	1	0	0
.....ATGCATTGCTCTAAGACCTTTCACGT.....	26	0	1	3.00	3	1	0	0	2	0	0	0	0	0	0	0	0
.....GTAAGAACCTAAAGGGCACTC.....	21	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0	0
.....AAGAACCTAAAGGGCACTCTTGAGT.....	25	0	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0	0
.....TAAGACCTTTCACGTTCTTA.....	20	0	1	2.00	2	0	0	1	0	1	0	0	0	0	0	0	0
.....GTAAGAACCTAAAGGGCACTCTTGA.....	25	0	1	2.00	2	1	0	0	1	0	0	0	0	0	0	0	0
.....TAAGACCTTTCACGTTCTT.....	19	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0
.....GAAGAGCGCCAAGCACCCATTTGC.....	18	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....ATTGCTCTAAGACCTTTCACGT.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGAACCTAAAGGGCACTCTT.....	23	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....GAAGAGCGCCAAGCACCCATTTGC.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....TAAGACCTTTCACGTTCTTAC.....	21	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0
.....AAGACCTTTCACGTTCTTACA.....	21	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0
.....GTTAATGCATTGCTCTAAGACCTTTCACG.....	29	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....AAGGGCACTCTTGAGTTAATGCA.....	23	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0
.....CACTCTTGAGTTAATGCATTGC.....	22	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....TCTAAGACCTTTCACGTTCT.....	20	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....GAACCTAAAGGGCACTCTTGAGTT.....	24	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGAACCTAAAGGGCAGC.....	20	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGAACCTAAAGGGCACTCTTG.....	24	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0
.....ATGCATTGCTCTAAGACCTTTCACGTT.....	27	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0

Anti-sense strand reads

CTGCGCTGTAAGACAAAGTTTCACCTGGGAGGGTAGGCACCGAACAACTACATTCTTGGATTTCCCGTGAGAACTCAATTACGTAACGAGATTCTGGAAAGTGCAAGAATGTCATGATGTTCTTCTCGCGGTTCGTGGGTAAACGGTGTTGGAACCCGCTCCT **********((((((((...(((((...((((((((.....)))))..)))))))))...))))))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060685 9xArg_0-2h_embryos_total	SRR060657 140_testes_total	SRR060687 9_0-2h_embryos_total

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12875:5344515-5344677 +	dvi_5303	GACGCGACATTCTGTTTCAAAGTGGACCCTCCCATCCGTGGCTTGTTGATGTAAGA-------ACCTAAAG--GGCACTCTT-----------GAG----TTAAT----GCAT----TG-----CT-CTAAGACC---------TTTCACGTTCTTACAGTACTACAAGAAGAGCGCCAAGCACCCATTTGCCACAACCTTGGGCGAGGA
droMoj3	scaffold_6496:24751892-24752049 -		GGCGCGAAATTCGTTTTCAAAGTGGTCCCTCCATCCGTGGCTTGTCGAAGTAAGT------TGCTGAGAA-CGCACTCG-----------G---AGAT---------TAAT----------T--A-TAAAATC---------AATTCAATCTTTAAGTACTACAAGAAACAGGCCAAGCATCGCGTTTGCCACATCGTTGGGCGAGGA
droGri2	scaffold_15245:4340537-4340699 -		GACGAGAAATTCGATTTCAGAGTGGTCCCAACCACCATGGCTTGTAAATGTAAGT------TATCTTATT-TTCAATGGC-----------A--T---TT--TTAAT----------CAAT--TAT-AAGCATT---------GTTCATTTAAAACAGTACTACAAGAATATATCAAACACGCTTTCGCCACAACCGTGGCCGAGGA
droWil2	scf2_1100000004510:504347-504504 +		GACGAGAAATTCGTTTCAAAGTGGTCCCAATATCCTGGCTGGTTGATGTAAGT------TACTTTCTT--------AAATATCAATCTAA-----------GG---TTGATT-CAAATT---------GTTTTGCTTTGTAGGCCTATAAGAACAATGCTAGACATGCTTTGCCACACCATTGGCTGAGGA
dp5	3:7434575-7434740 +		GACGCGAGATTCGTTCGAGACTGGACCGAACCATCCGTGGCTTGTAAAGTAAGC-------AAGCCTGAA-GCCGCTGCC-----------A-T---CTGATGCAA----------CGAT--TCT-ATACCACG---------ATTTTCAATTCGAGTACTACAAGAAGAATGCCAAGCATCCATTCGCGACCACCATTGGCTGAGGA
droPer2	scaffold_2:7633242-7633407 +		GACGCGAGATTCGTTCGAGACTGGACCGAATCATCCGTGGCTTGTAAAGTAAGC-------AAGCCTTAA-GCCGCTGCC-----------A-T---CTGATGCAA----------CGAT--TCT-ATACCACG---------ATTTTCAATTCGAGTACTACAAGAAGAATGCCAAGCATCCATTCGCGACCACCATTGGCTGAGGA
droAna3	scaffold_13266:1997718-1997872 -		G---AGAGCTGCTGTTTCAAACTGGACCGAATCACCTTGGCTAGTCGAAGTAAGA-------ATTGTTGAA-ATTGTTTT-----------GAAAT---------CTAT----------T--A-CTTGTTAT---------GCCATTTACGTTCAGCGCCTACAAACAGAATGCCCTACACCCGTTTGCCACAAGGCTGGGTGAGGA
droBip1	scf7180000396730:2983394-2983549 -		G---AGAGCTTCTGTTTCAAACTGGACCGAATCATCCTTGGCTGGTAGAGTAAGA-------GCAACTTACGACTGTTTTA-----------GGGAT---------CTAT----------G--A-ATTGTTAC---------CCGAATTACCTTCAGCGCCTACAAACAGAATGCCTTGCACCCATTCGCCACAAGGCTGGGTGAGGA
droKik1	scf7180000302471:1523635-1523792 +		GACGTGAGCTGCTGTTTTCAGACAGGACCGAATCATCCGTGGCTGGTAGATGTAAGC-------ATACCTTAAAACGATC-T-----------CA--GTCCT---------T---------TT-GT-TAATCCA---------AATTCTCTCAATCAGTACTACAAGATGCATGCAAAGCACCCATTTGGTACCAGAGTGGCCGAAGA
droFic1	scf7180000454066:1866606-1866768 -		GACGCGAAATTATGTTTCAAACAGGACCAAAAATCCTGGCTGGTTAATGTAAGA-------TTTTATAGT-TTTACCTG-----------------TTATATAT----------TTAT--CTA-ATTATTG---------ATTTTTATCTAACAGATATACAAAAAGGCGCCAAGCATTACTTTTGTACCAGAATGGCTGAGGA
droEle1	scf7180000491240:761286-761437 +		--CGTGAGCTACTCTTTCAAACTGGACCGAATCATCCATGGCTAGTAGATGTGAGC-------CCTATAAAGCATTGTCT--------------------CT-CTGCCACA--T-TAAATAAGAA-AACCCTTAGTATTACAAGAGAATGCCAAGCACCCATTTGGTACCAGAGTGGGTGAGGA
droRho1	scf7180000779005:35661-35819 -		GACGTGAGCTACTCTTTCAAACTGGCCCCAACCATCCGTGGCTAGTAGATGTAAGC-------ATGCAAAG-CTTCTCTTT-----------T--TT-AT----------TAGC----------C-T-CTTAAAC---------TTAATTGCTTTGAGTATTACAAGAAGAGTGCCAAGCACCCATTTGCCACCAGAGTGGGCGAGGA
droBia1	scf7180000301754:1670006-1670172 -		GAAGAGAATATTCTGTTTCAAAGTGGTCCAAACCATCCGTGGTTAGTAAAGTACGA-------AAATAAATTAACCTTAT-----------AAT----ATAAA----ATATAAA--T--T--TATT-CAGATTT---------ATCATTTAAAATTAGTATTACAAGCAACATTCAAAGCATCGTTTGCCTTTGAGATTGGCCGAAGA
droTak1	scf7180000415379:114812-114969 +		GACGCGAATTACGTCTTTCAAACTGGACCGAACCATCCGTGGCTAGTAGACGTAAGC-------CCTCTCCAATTTTTTTC----------TTTCCT----------TATT----------T--C-TATGTTAAA---------ATAAATATAGTTTTAGTACTACAAGAAGCACGCCAAACATCCATTCGCCACAACCGTGGGCGAGGA
droEug1	scf7180000409672:5884909-5885066 -		GTGCCGAATATTGTTTCCAAAGTGGACCGAACAATCCTGGCTTGTAGAAGTTAGT-------AGCACTTAACATTCGTTT----------GC-AT----------TATC----------C-T-A-ACTTAA-------GTAA-ACATTACTTTATAGCACTATAAGAAAAGTGCCAAGCATCCATTAGCTACCACCATTGGCTGAGGA
dm3	chr2R:15274387-15274553 +		GACGCGAACTAATGTTCCAATCTGGCCCAAATATCCATGGTTGGTTAAGGTAATA-------ATCCTCTA-GTTACTTAA-----------GAA----ACTAT----CTATATAT--T--CT-AG-CTGTTTC---------AGTGATATCTTCCAGATATATAAGGATGGCGCCAAGCATTATTTCTCCACCACCATTGGCTGAGGA
droSim2	2r:8949312-8949463 +		GACGAGAATATTCGATTCCAGAGTGGTCCAAATATCCCTGGCTAGTAAGGTACTT-------ATAGATATT----------AAACATA----------TAA--TTT-TG-CCTTAT---------AGTGGTTTATTTTAGTATTATAAACAGCATCGAAACATCGCTTTGCCTCTGAGATTGGCTGAAGA
droSec2	scaffold_1:5789636-5789787 +		GACGAGAATATCGTATTCCAGAGTGGTCCAAATATCCCTGGCTAGTGAAGGTACTT-------ATAGATATT----------AAACATA----------TAA--TTT-TG-CCTTAT---------AGTGGTTTATTTTAGTATTATAAACAGCATCGAAACATCGCTTTGCCTCTGAGATTGGCTGAAGA
droYak3	2R:8694577-8694741 -		GACGTGAGCTCTATTCCAGAGTGGACCGAATACTCCTTGGCTGATGAAGGTAATGTCATAGTTGGACCTAAA----------------ACTTA----------TTA--TAT-AT-TCCTTATACCAAGCATCT-ATTGAATATATAGTACTACAGGAGCATGCGAGACATCGTTTGCCACCAGAGCAGCCGAAGA
droEre2	scaffold_4845:17548166-17548317 -		GACGAGAATACGTATTCCAGAGTGGTCCAAATACGCCTGGCTGGTGAAGGTACGT-------AGGAGATAT----------CAACCAA----------CAA--TAT-TG-CAGTGAT---------ATGTGGCTTATTTTAGTATTATAAAGAGCATCGAAAGCATCGTTTGCCTCTGACATTGGCGGAAGA

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

	PASS/FAIL
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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
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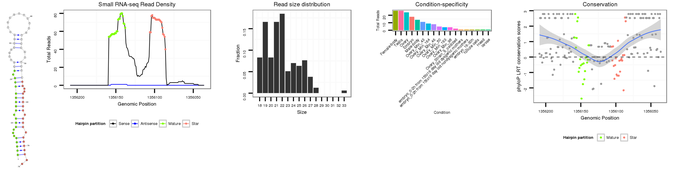
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

ID	Coordinate	Confidence	Class	Genomic Locale	
dvi_8438	**scaffold_12928:1356086-1356159 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser (GenbMinus)]

Legend: Arm 5p Loop Arm 3p Mismatch

Predicted structure



Show Alternate Folds

Flybase annotation

mmu:(Dvir(GW6)-sq:CDS:[Dvir(GW6)-cds]-CDS:[Dvir(GW6)-cds]-mR:[mR_mma_9790]-mT:[mT_mma_9800]

No Repeatable element found

Sense Strand Reads

Hide 2p reads | show mid mismatch reads

GGCGACTCTGTGCCTGTTGCCTGTTGCTACACTGCGACGACTCCAGCGGCGC	CTAGCCTCACCAGCATCCGCA	ACTTCAGCGAACTCCACTCCTTCATTCCGTTCCTC	CCTTCCTCTTCCCTTCACGA	CATTCAGCGAACTCACTCCTCTTCCCGCGCAGCGACTCACTCTGGAC
read #	Hit	Total		
size Mismatch Count Rows	Total			
21	1	44.00 44		
21	1	10.00 10		
21	1	19.00 19		
21	1	15.00 15		
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21	1	10.00 10		
19	1	8.00 8		
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21	1	4.00 4		
22	1	3.50 7		
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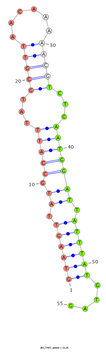
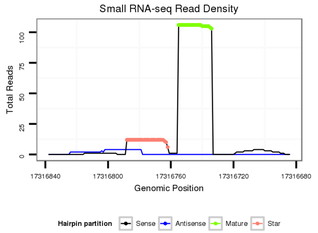
21

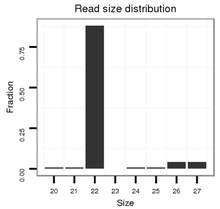
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_7467	**scaffold_12875:17316734-17316788 -**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

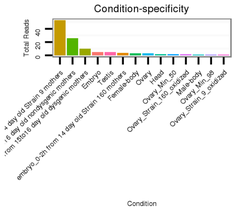
Legend: canon. start/stop match in alignment mismatch in mature

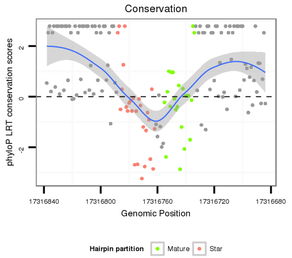
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DviriGI20090-in]; CDS [DviriGI20090-cds]; CDS [DviriGI20090-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GGTGACAATTTTAGACCATCGAGTATATCTTGAGCACATTCCGAAAATGTAAGTTATGCCATTTATGCGTTAACGAAAACCTCTCAATGGATTATTTATGTAGTGCTGCGCTTCGGCAAGGGCTTGGATGTATTCTATGCGAGCCTACGAGCC	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR2096038 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096026 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096081 embryo_0-2h from 15to16 day old nondyegenic mothers	SRR2096080 embryo_0-2h from 15to16 day old nondyegenic mothers	M047 female old body	SRR2096072 embryo_0-2h from 15to16 day old dyegenic mothers	SRR2096079 embryo_0-2h from 15to16 day old dyegenic mothers	SRR2096014 Ovary_Strain_160_oxidized	SRR2096050 embryo_0-2h from 14 day old Strain 160 mothers	SRR2096058 Ovary_Min_98	SRR060663 160_0-2h_embryos_total	SRR060672 9x160_females_carcasses_total	SRR060674 9x140_ovaries_total	SRR060678 9x140_testes_total	SRR060682 9x140_0-2h_embryos_total	SRR060684 140x9_0-2h_embryos_total	SRR2096057 Ovary_Min_50	M028 head	SRR060671 9x160_males_carcasses_total	SRR060677 Argx9_ovaries_total	SRR060679 9x140_testes_total	SRR060680 9xArg_testes_total	SRR060681 Argx9_testes_total	SRR2096013 Ovary_Strain_9_oxidized	V047 embryo	V053 head	V116 male body	SRR060689 160x9_testes_total
**********	(((((.(.(.(((((...(((((.....))))).....))))))).))))))....**********	22	0	1	103.00	103	31	22	14	12	3	5	5	0	4	1	0	0	0	0	2	0	0	0	0	0	1	0	1	1	0	0
.....TCTCAATGGATTATTTATGTAG.....		27	0	1	5.00	5	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	0
.....GTAAGTTATGCCATTTATGCGTTAACA.....		26	0	1	4.00	4	0	0	0	0	0	0	1	0	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGTTATGCCATTTATGCGTTAAC.....		26	3	1	2.00	2	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
.....TATCTTGAGCACATTCCGAAAATGT.....		23	1	2	1.50	3	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
.....TCTCAATGGATTATTTATGTAGA.....		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	0	0	0	0	0	0
.....GTAAGTTATGCCATTTATGCGT.....		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
.....GTAAGTTATGCCATTTATGCGTTA.....		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
.....AGTATATCTTGACACATTCC.....		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
.....TAACAAAAACGTCTCAATGGATTATT.....		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
.....TTGGATGTATTCTATGCGAGCCT.....		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
.....GTAAGTTATGCCATTTATGCGTTAA.....		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
.....GTATTCTATGCGAGCCTACG.....		20	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
.....TCTCAATGGATTATTTATGTA.....		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
.....TCTCAATGGATTATTTATGT.....		20	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
.....AGGGCTTGGATGTATTCT.....		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
.....AAGGGCTTGGATGTATTCTATGCG.....		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

Anti-sense strand reads

CCACCTGTTAAAATTCTGGTAGCTCATATAGAACTCGTGTAAGGCTTTTACATTCAATACGGTAAATACGCAATTGTTTTTGCAGAGTTACCTAATAAATACATCACGACGCGAAGCCGTTCCCGAACCTACATAAGATACGCTCGGATGCTCGG	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR060681 Argx9_testes_total	SRR2096014 Ovary_Strain_160_oxidized	SRR2096056 Ovary_Min_46	SRR060672 9x160_females_carcasses_total	SRR060679 140x9_testes_total	V053 head	SRR060656 9x160_ovaries_total	SRR060675 140x9_ovaries_total
**********	(((((.(.(.(((((...(((((.....))))).....))))))).))))))....**********	24	0	1	2.00	2	1	0	0	1	0	0	0
.....GTGTAAGGCTTTACATTCAATAC.....		21	0	1	2.00	2	0	2	0	0	0	0	0
.....TCTGGTAGCTCATATAGAACT.....		26	0	1	1.00	1	1	0	0	0	0	0	0
.....TCGTGTAAGGCTTTACATTCAATAC.....		26	0	1	1.00	1	1	0	0	0	0	0	0
.....CGTGTAAGGCTTTACATTCAATAC.....		25	0	1	1.00	1	1	0	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12875:17316684-17316838 -	dvi_7467	GGTGGACAATTTTAAGACCATCGAGTATATCTTGAGCACATTCCGAAAATGTAAGTTATGCCATTTATGCGTT-AACGAA-A---A--------------C---CT-----------CTCAATGG---ATTATTTA--TGTAGTGCTGCGCTTCGGCAAGGGCTTGGATGTATTCTATGCGAGCCTACGAGCC
droMoj3	scaffold_6496:10695105-10695257 +		GGTGGACAATTTAAGACATCGAGTATATCTTGAGCACATTCCGAAAATGTAGTTGCTTATTTGCGTTAGCGAAAA-T---T-------------T---TT---ATTGAGA--------T-T-CT---TCGCGTTGCTGCGCTTCGGCAAGGGCTTGGATGTTTCTATGCGAGCCTACGAGCC
droGri2	scaffold_15245:16832366-16832527 -		GGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAAATGTAAGTTATTTGCGATTATTTGCGAAAA-A---A-------------CGATTCC---ATTGAG----ATGGCCCTTA-T-CT---AACGTTATTTGCGATGGCAAGGGCACTTGGATGTATTCTATGCGAGCCTACGAGCC
droWil2	scaff_1100000004558:897710-897876 -		GGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAAATGTAGTTGAAA---------G-TCTTT-T-AAACTATATTTAGAAAATTTATCTAATCTAATGCACC--------T-T--CTAAA-CCCCAATGGTTGCGCTTCGGCAAGGGCTTGGATGTATTCTATGCGTACCTACGAGT
dp5	3:18351989-18352142 +		GGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAATGTAGTTGCATTCAATACGCAATTGCCAT-A-AC-TTGT-T-T---T-------------A---CTA---------CT----AATACTCTGCAATCGCAATTCCATTGGATGTTTCTATTCATTCTCTCATA
droRer2	scaffold_3613626:4-902827 +		GGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAATGTAGTTGCATTCAATACGCAATTGCCAT-A-AC-TTGT-T-T---T-------------A---CTA---------CT----AATACTCTGCAATCGCAATTCCATTGGATGTTTCTATTCATTCTCTCATA
droAna3	scaffold_13266:11846588-11846739 +		GGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAATGTAGTTGCATTCAATACGCAATTGCCAT-A-AC-TTGT-T-T---T-------------A---CTA---------CT----AATACTCTGCAATCGCAATTCCATTGGATGTTTCTATTCATTCTCTCAAGCC
droBip1	scf1800003965547:625110-625272 -		GGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAGCGTAGTTGCATTCAATACGCAATTGCCAT-A-AC-TTGT-T-T---T-------------T---TCC---ATTAAGTTCTCCATCC----ATTATTTCCTCTTAGCGTTTGCGCTTCGGCAAGGGCTTGGATGTTTCTATTCATTCTCTCAAGCC
droKik1	scf1800000302385:1107336-1107488 -		GGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAATGTAGTTGCATTCAATACGCAATTGCCAT-A-AC-TTGT-TAA-GGTTA-T-AATTT-T---T-------------T---TTA---------ACT----AATTCTCTTCCATCCCCAATTCCATTGGATGTTTCTATTCATTCTCTCAAGCC
droFic1	scf1800000453948:1127204-1127355 -		GGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAATGTAGTTGCATTCCTGCACAC-GAG-A-T---T-------------C---CA---------ACT----ATTCCCCCTTCCTCCATCGCTGCGCTTCGGCAAGGGCTTGGATGTATTCTATGCGAGCCTACGAGCC
droEle1	scf1800000491107:881464-881596 -		GGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAATGTAGTTGCATTCCTTCGAACCGGGTTCCTAGTT-T-T---T-------------A---CA---------ACT----TATACCCGGCAATTCCCCCTGCGCTTCGGCAAGGGCTTGGATGTTTCTATGCGCGCTTCGAAGCC
droRho1	scf1800000779911:221067-221219 +		GGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAATGTAGTTGCATTCAATACGCAATTGCCAT-A-AC-TTGT-T-T---T-------------A---CA---------CCT----TATCCCCGCAATCCCCCATTCCATTGGATGTTTCTATGCGCGCTTCGAAGCC
droBia1	scf1800000302292:2051982-2052136 -		GGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAATGTAGTTGCATTCCTGCAACGACGACC-GTAGT-T---A-------------T---CA---------TCT----AATCCCCGCATTCCCCATTCCATTGGATGTTTCCTATGCGCGCTTCGAAGCA
droTak1	scf1800000415795:684937-685087 +		GGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAATGTAGTTGCATTCCTTGCGTCGCAGCAAATCCC-T---T-------------T---CA---------ACT----AATTCTCGCAATCCCCATTCCATTGGATGTTTCCTATGCGCGCTTCGAAGCC
droEug1	scf1800000403672:786174-786326 -		GTGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAATGTAGTTGCATTCCGTCTACGCCTCGCTTAGCTCCTCCTTAGTGT-T---A-------------C---CA---------CCT----AATCTCCTTCAATCCCCATTCCATTGGCAATTTCCTATGTGCGCTTCGCAAGCA
dm3	chr2R:11879503-11879655 -		GTGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAAATGTAGTTGCATTCCTGACGCAGTGCAC-GCAG-T---T-------------T---CA---------CCT----AATCCTGCATTCCCCATTCCATTGGATGTTTCCTATGTGCGCTTCGAAGCCC
droSim2	2r:12545287-12545439 -		GTGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAATGTAGTTGCATTCCTGACGCCGCAGCGCAGCG-T---A-------------T---CA---------CCT----AATCCGCATTCCCCATTCCATTGGATGTTTCCTATGCGCGCTTCGAAGCC
droSec2	scaffold_13537836-9378588 -		GTGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAATGTAGTTGCATTCCTGACGCAGCGCAGCG-T---A-------------T---CA---------CCT----AATCCGCATTCCCCATTCCATTGGATGTTTCCTATGCGCGCTTCGAAGCC
droYak3	2R:17103234-17103389 +		GTGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAAATGTAGTTGCATTCCTGACGCAGTCGCAGCGCTT-AAGAGCGCTT-A-A-------------C---CT---------ACT----AATCCCCATTCCATTCCCCATTGGATGTTTCCTATAAGCGCTTCGAAGCC
droEre2	scaffold_4845:1391371-1392937 +		GTGTGGACAATTTTAAGACATCGAGTATATCTTGAGCACATTCCGAAAATGTAAGTTGCATTCCTGACGCAGTCGCAGCGCTT-AAGAGCGCTT-A-A-------------C---CA---------CCT----AATCCCAATTCCATTCCCCATTGGATGTTTCCTATGCGCGCTTCGAAGCC

Generated:09/08/2015 at 07:34 PM

	PASS/FAIL
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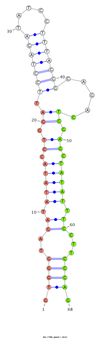
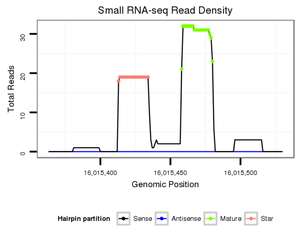
crit.loop	0
crit.mor	0
crit.stem	1
crit.total	1
crit.pairing	1
crit.top3	1
crit.tgtop3	1
crit.loop3	1
crit.back	1
rescue.total	0
rescue.pairing	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

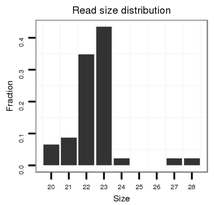
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_7206	**scaffold_12875:16015413-16015480 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

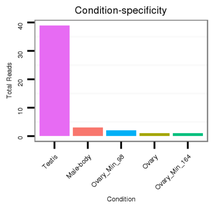
Legend: mature star mismatch in alignment mismatch in read

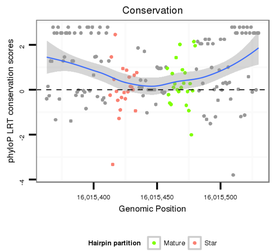
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [DviriGI221198-in]; CDS [DviriGI221198-cds]; CDS [DviriGI221198-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GTGCCACGCTCGGCACCACGGGCAGCTGCAGCTTTGACAATCTGGATGAGGTGGGTAGATATATACCTGGATCCCTAGATATCCTTTAGGGCAGACTCGAGCTATATTTCCTCCCAGATTGGCATCGTGTGCGCGAGTACAACCTGTGGCTGCATGTGGATGCGGC					SRR060679	SRR060681	SRR060683	V116	SRR060678	SRR060680	SRR060689	SRR060655	SRR2096056	SRR2096059	SRR2096081 embryo_0-2h from 15to16 day old	SRR060676	SRR2096055	M027	SRR060670	SRR2096013	SRR2096058	SRR2096060	SRR060657	SRR060659	SRR060671	SRR060677	SRR060685	SRR060686	SRR2096080 embryo_0-2h from 15to16 day old	V053	SRR060662
**********	Read size	# Mismatch	Hit Count	Total Norm	140x9_testes_total	Argx9_testes_total	160_testes_total	male body	9x140_testes_total	9x Arg_testes_total	160x9_testes_total	9x160_testes_total	Ovary_Min_46	Ovary_Min_164	nondyegenic mothers	9xArg_ovaries_total	Ovary_Min_43	male 9_testes_total	Ovary_Strain_9_oxidized	Ovary_Min_98	Ovary_Min_193	140_testes_total	Argentina_testes_total	9x160_males_carcasses_total	Argx9_ovaries_total	9xArg_0-2h_embryos_total	2h_embryos_total	nondyegenic mothers	head	2h_embryos_total
.....CTCGAGCTATATTTCCTTCCCAGATTGGCATCGTGTGCGCGAGTACAACCTGTGGCTGCATGTGGATGCGGC	23	1	1	36.00	16	12	0	12	1	2	0	1	0	0	1	0	0	1	0	0	0	1	0	0	0	0	0	1	0	0	0
.....CTCGAGCTATATTTCCTTCCCAG.....	23	0	1	12.00	12	3	0	2	1	0	0	2	1	0	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0
.....CTCGAGCTATATTTCCTTCCCAGA.....	24	1	1	12.00	12	1	0	2	1	0	0	0	4	0	1	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0
.....GTGGGTAGATATATACCTGGAT.....	22	0	1	9.00	9	5	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
.....GTGGGTAGATATATACCTGGATT.....	23	0	1	7.00	7	1	0	3	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
.....TCGAGCTATATTTCCTTCCCAG.....	22	0	1	5.00	5	3	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
.....CTCGAGCTATATTTCCTTCCCAGA.....	24	0	1	4.00	4	0	0	0	0	0	0	0	0	3	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCGAGCTATATTTCCTTCCCA.....	21	0	1	4.00	4	0	2	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CGAGCTATATTTCCTTCCCAGT.....	22	1	1	3.00	3	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
.....CGCGATACAACCTGTGGCT.....	20	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	0	0	0	0	0	0
.....CTCGAGCTATATTTCCTTCCCAGTA.....	25	2	1	2.00	2	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CTCGAGCTATATTTCCTTCCCA.....	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	0	0	0	0	0
.....TCGAGCTATATTTCCTTCCCAGA.....	23	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
.....GTGGGTAGATATATACCTGGATTCA.....	26	2	1	2.00	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
.....TCGAGCTATATTTCCTTCCCAGTA.....	24	2	1	2.00	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
.....TCGAGCTATATTTCCTTCCC.....	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
.....TGGGTAGATATATACCTGGATTC.....	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
.....TCGAGCTATATTTCCTTCCCAGTAAA.....	25	3	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
.....GATATCCTTTAGGGCAGACTCGAGCTA.....	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	0	0	0	0	0
.....TCGAGCTATATTTCCTTCCCAGT.....	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	0	0
.....AGATATCCTTTAGGGCAGAC.....	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	0	0	0	0	0
.....CGGGCACCTCGACTTTCA.....	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
.....GTGGGTAGATATATACCTGGATTCCTAG.....	28	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
.....GTGGGTAGATATATACCTGGATTC.....	24	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
.....TCGAGCTATATTTCCTTCCCAGAAAA.....	26	3	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
.....TCGAGCTATATTTCCTTCCCAGAAA.....	26	2	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
.....CTCGAGCTATATTTCCTTCC.....	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

Anti-sense strand reads

CACGGTGCGAGCCGTGGTGCCCGTCGACGTCGAAACTGTTAGACCTACTCCACCCATCTATATATGGACCTAAGGATCTATAGGAAATCCCGTCTGAGCTCGATATAAAGGAAGGGTCTAACCGTAGCACACAGCGCTCATGTTGGACACCGACGTACACCTACGCCG					SRR060667
**********	Read size	# Mismatch	Hit Count	Total Norm	160_females_carcasses_total
.....CTCGAGCTATATTTCCTTCCCAGTCTGGACTCGAGCTATATTTCCTCCCAGATTGGCATCGTGTGCGCGAGTACAACCTGTGGCTGCATGTGGATGCGGC					
.....CTCGAGCTATATTTCCTTCCCAG.....	23	1	1	36.00	16
.....CTCGAGCTATATTTCCTTCCCAGA.....	24	1	1	12.00	12
.....GTGGGTAGATATATACCTGGAT.....	22	0	1	9.00	9
.....GTGGGTAGATATATACCTGGATT.....	23	0	1	7.00	7
.....TCGAGCTATATTTCCTTCCCAG.....	22	0	1	5.00	5
.....TCGAGCTATATTTCCTTCCCAGA.....	24	0	1	4.00	4
.....TCGAGCTATATTTCCTTCCCA.....	21	0	1	4.00	4
.....CGAGCTATATTTCCTTCCCAGT.....	22	1	1	3.00	3
.....CGCGATACAACCTGTGGCT.....	20	0	1	3.00	3
.....CTCGAGCTATATTTCCTTCCCAGTA.....	25	2	1	2.00	2
.....CTCGAGCTATATTTCCTTCCCA.....	22	0	1	2.00	2
.....TCGAGCTATATTTCCTTCCCAGA.....	23	0	1	2.00	2
.....GTGGGTAGATATATACCTGGATTCA.....	26	2	1	2.00	2
.....TCGAGCTATATTTCCTTCCCAGTA.....	24	2	1	2.00	2
.....TCGAGCTATATTTCCTTCCC.....	20	0	1	1.00	1
.....TGGGTAGATATATACCTGGATTC.....	23	0	1	1.00	1
.....TCGAGCTATATTTCCTTCCCAGTAAA.....	25	3	1	1.00	1
.....GATATCCTTTAGGGCAGACTCGAGCTA.....	27	0	1	1.00	1
.....TCGAGCTATATTTCCTTCCCAGT.....	23	1	1	1.00	1
.....AGATATCCTTTAGGGCAGAC.....	20	0	1	1.00	1
.....CGGGCACCTCGACTTTCA.....	19	0	1	1.00	1
.....GTGGGTAGATATATACCTGGATTCCTAG.....	28	0	1	1.00	1
.....GTGGGTAGATATATACCTGGATTC.....	24	0	1	1.00	1
.....TCGAGCTATATTTCCTTCCCAGAAAA.....	26	3	1	1.00	1
.....TCGAGCTATATTTCCTTCCCAGAAA.....	26	2	1	1.00	1
.....CTCGAGCTATATTTCCTTCC.....	20	0	1	1.00	1

Show Alignment With Reads

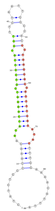
Re-alignment of all predicted orthologs

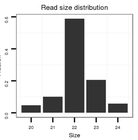
Species	Coordinate	ID	Alignment
dvi-r3	scaffold_12875:16015363-16015530 +	dvi_7206	GTGCCACGCTCGGCACCACGGGCAGCTGCAGCTTTGACAATCTGGATGAGGTGGGTAGA-----T----------A---GC---------TA------T-----------------------------AT-----------TTCCTTCCCAGATTGGCATCGTGTGTGCGCGAGTACAACCTGTGGCTGCATGTGGATGCGGC
droMo33	scaffold_6496:7765103-7765263 -		GTGCCACGCTCGGCACCACGGGCAGCTGCAGCTTTGACAATCTGGATGAGGTATATAGGGGA----A----------AC-C---TGTCCACAAATAGCTTGATC---GC---------T-------G-----------------------------AT---TTAATTTGTGCATATTCATCATTAGCTTGTGGCTGCATGTGGATGCGGC
droGri2	scaffold_15245:12821897-12822055 +		GTGCCACGCTCGGCACCACGGGCAGCTGCAGCTTTGACAATCTGGATGAGGTAGATGCGGGGT-T--AGTCAACAAT---TTAAGCTTCAA-T-----------G-----------------------------AT-----------TTACATAATGTGCATCGTGGCTGCATGTGGATGCGGC
droWil2	scaff_1100000008822269060 4:2690802 -	Dwi_2133	GTGCCACGCTCGGCACCACGGGCAGCTGCAGCTTTGACAATCTGATGAGGTGGGTGCGGGGGT-T--GGGGGGTTGCTTGAC---TCAGCCAAATCGCTGGTCCCCAAAGTGTGTGGGTCAATTCCT---GC---------T-------T-----------------------------ATCACTTTTTGTGTGTGCATGTTGATGTGGATGCGGC
dp5	11:6965898-6966072 +		GTGCCACGCTCGGCACCACGGGCAGCTGCAGCTTTGACAATCTGGATGAGGTGGGTGCTCCTGT-C--TCTGCGGACCACTAATCTGTTTCCACC-----TGAG---AACATCCACTT-CCCAG-----------------TCTTT---GC---------T-------T-----------------------------A-----------TTCAGCATAATGCGCACACCTGTGGCTGCATGTGGATGCGGC
droPer2	scaffold_27367956-7168128		GTGCCACGCTCGGCACCACGGGCAGCTGCAGCTTTGACAATCTGGATGAGGTGGGTGCTCCTGT-C--TCTGCGGACCAATAATCTGTTTCCACC-----TGAG---AAATTCCACTT-CCCAG-----------------TCCTT---GC---------T-------T-----------------------------A-----------TTCAGCATAATGCGCACACCTGTGGCTGCATGTGGATGCGGC
droAna3	Scaffold_13246:18434680-18434782 +		GCCACCACGCTCGGCACCACGGGCAGCTGCAGCTTTGACAATCTGCCGAGATGGGTAGG-----C--AGCGAGGCGTCCCGG-SG---GC---------T-------T-----------------------------A-----------GTGGGCATGTGGATGCGGC
droBip1	scf718000039575514601698-4601927 +		GTGCCACGCTCGGCACCACGGGCAGCTGCAGCTTTGACAATCTGGATGAGGTGTGCTTTGT-C--TTTGTGGCTTTTTTTTCTAGAAATTATTGGG---AGGGAGTTAAA---AAAAATACCTAATAATTGTAAAGATATTCAAGG-TGTTCTATAAAAGGCTTA---TAAATG-T-------TA-------T-----------------------------AT-----------TTCATCCAGATGCAGCGTCGTCGCTGAGTACCACCTGTGGCTGCATGTGGATGCGGC
droKik1	scf718000030281746450 8-4647485 +		GTGCCACGCTCGGCACCACGGGCAGCTGCAGCTTTGACAATCTGGATGAGGTGGGTGCTGCGGT-C--TGGGCATTTCCCAATAAGCTAGCTGCTTGAACAGCAACT-----CCCTT---TCCCTTAATGACCGTGGAAATTATACTAATTATTCGCTTGGAAAAACTTT---TATATTTTAAATTTAAA-T-------T-----------------------------AT-----------TTACGCCGATGCAGCGTCGTCGCTGCATGTGGATGCGGC
droFic1	scf718000045395527371 6-5527418 +		GCCACCACGCTCGGCACCACGGGCAGCTGCAGCTTTGACAATCTGCCGAGATGGGTAGG-----C--AGCGAGGCGTCCCGG-SA---GC---------T-------T-----------------------------A-----------GTGGGCATGTGGATGCGGC
droEle1	scf718000049127144024 2-4405444 -		GCCACCACGCTCGGCACCACGGGCAGCTGCAGCTTTGACAATCTGCCGAGATGGGTAGG-----C--AGCGAGGCGTCCCGG-SC---GC---------T-------T-----------------------------A-----------GTGGGCATGTGGATGCGGC
droRho1	scf718000076640946213 6-6622138 -		GCCACCACGCTCGGCACCACGGGCAGCTGCAGCTTTGACAATCTGCCGAGATGGGTAGG-----C--AGCGAGGCGTCCCGG-S--GC---------T-------T-----------------------------A-----------GTGGGCATGTGGATGCGGC
droBia1	scf718000030242245255297-4525395 +		GCCACCACGCTCGGCACCACAAATCTGCCGATTTGACAATCTGCCGAGATGAGTG-------T--AGCGAGGCGTCCCGG-SC---GC---------T-------T-----------------------------A-----------GTGGGCATGTGGATGCGGC
droTak1	scf718000041398728301-28403 +		GCCACCACGCTCGGCACCACGGGCAGCTGCAGCTTTGACAATCTGCCGAGATGGGTAGG-----C--AGCGAGGCGTCCCGG-SC---GC---------T-------T-----------------------------A-----------GTGGGCATGTGGATGCGGC
droEug1	scf718000040929349303-49539 -		GTGCCACGCTCGGCACCACGGGCAGCTGCAGCTTTGACAATCTGGATGAGGTGCTTGGG-TGGGAATAATTATGAAGAAAAATAGGGGG

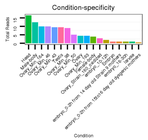
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_100	**scaffold_10322:288263-288322 -**	**confident**	**Canonical miRNA**	**intergenic**	View on UCSC Genome Browser (Cornell Mirror)

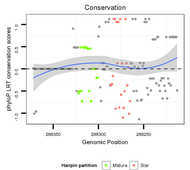
Legend: **Seed** **3p** **mismatch to pre-miRNA** **mismatch to loop**

Predicted structure









Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

name	strand
1. dvi_100 scaffold_10322:288263-288322 -	
2. dvi_2426 scaffold_12042:66422-66543 +	

Sense Strand Reads

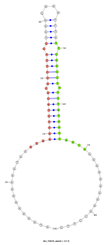
hide 3p reads show mid mismatch reads

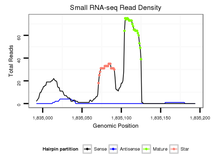
| UCUGCAUUUUAAAAACACGUUUUUAGUAAGCACUACUACUCCCCAAAAACATCAAAAATCCUCCTTATGGCTTCTAATTGUCCACCTAAAGAGCATTTTGATATCTTTGAAAACATTTACTCTTTCTCTGCCAACTTAGAATACGCAUTAAAAAU | | |

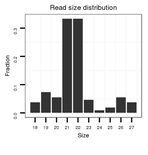
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_24634	**scaffold_13047:1835042-1835144 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

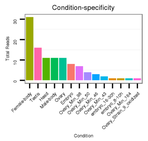
Legend: Sense 5p Artificiallyin silly mutant mismatch in bias

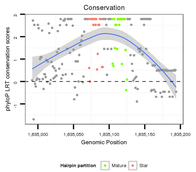
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
A-rich/low_complexity	Low_complexity	-	

Sense Strand Reads

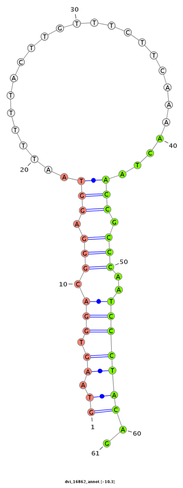
hide 3p reads show mid mismatch reads

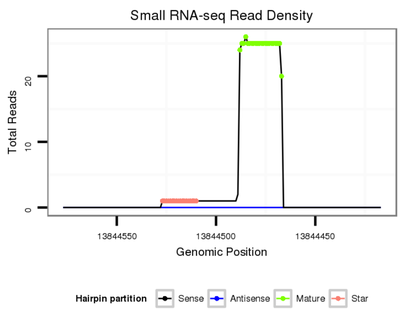
| Read # | size | M.mismatch | Count | 5 | 3 | Total | Norm | Total | MI47 female body | MI41 embryo | Y053 head | SRR040665 5 | SRR040664 females | SRR040664 males | SRR040664 carcasses | SRR040664 total | SRR296058 embryo_90 | SRR296055 Ovary_Mix_90 | SRR296056 Ovary_Mix_43 | SRR296054 Ovary_Mix_46 | SRR040678 5d145_testes_total | SRR040667 145_females | SRR040667 145_males | SRR040667 carcasses | SRR040667 total | MI28 head | SRR040672 5d145_females | SRR040672 145_males | SRR040672 carcasses | SRR040672 total | Y114 male body | SRR040674 5d145_ovaries_total | SRR040674 145_testes_total | SRR040679 | SRR296057 Ovary_Mix_50 | SRR040681 Arps9_testes_total | SRR040681 145w5_ovaries_total | SRR040681 Arps9_ovaries_total | SRR040668 145w5_males | SRR040668 carcasses | SRR040668 total | SRR040677 5d145_ovaries_total | SRR040680 Rabg_testes_total | SRR040683 145_testes_total | SRR296059 Ovary_Mix_164 | SRR040654 145w5_ovaries_total | SRR040666 145_males | SRR040666 carcasses | SRR040666 total | SRR040671 5d145_testes_total | SRR040671 145w5_females | SRR040671 carcasses | SRR040671 total | SRR040689 Arps9_0-2h_embryos_total | SRR040689 145_testes_total | SRR296013 Ovary_Strain_9_oxidized | SRR040655 5d145_testes_total | SRR040669 145w5_females | SRR040669 carcasses | SRR040669 total | V047 | SRR040658 145_ovaries_total | SRR040670 5_testes_total | SRR040676 Rabg_ovaries_total | SRR040688 145_ovaries_total | SRR1104720 embryo_8-12h | SRR1104722 embryo_10-12h | SRR1104730 embryo_14-20h | SRR296060 from 15x1L4 MI27 female nondiapausal mutant mothers | SRR040682 5d145_0-2h_embryos_total |
|---|---|---|---|---|---

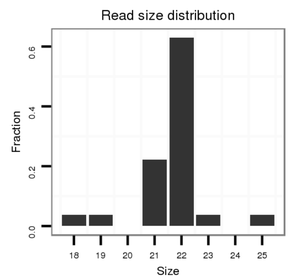
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_16862	**scaffold_13047:13844467-13844527 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

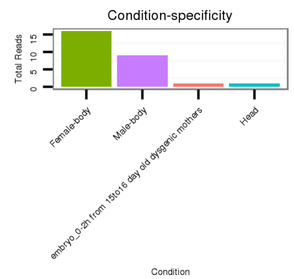
Legend: mature star mismatch in alignment mismatch in read

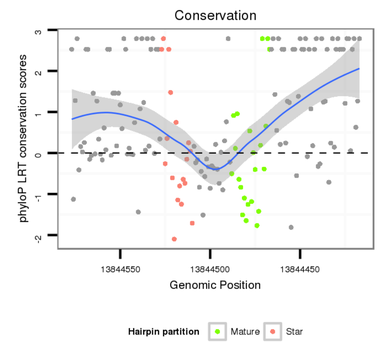
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dvir\GJ22846-in]; CDS [Dvir\GJ22846-cds]; CDS [Dvir\GJ22846-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GACTTAGTCCAAATGAGTCCCGCTTTACATCCACTTTCATGATGCAGCCGGTAAGTGGACGGGAGGTAATTTTTACTTGTTTCTTCAAAACTAACCGCCCAATCCCTACAGCAACTGGGCGTGCCCTTGCATGTTCACATGCGTCTACAGGCCAACCAAGT						SRR060672	M047	SRR060664	SRR060671	SRR060665	SRR060668	SRR060669	SRR060667		SRR060666	SRR2096072	GSM1528803	SRR060683
**********	Read size	# Mismatch	Hit Count	Total Norm	Total	9x160_females_carcasses_total	female body	9_males_carcasses_total	9x160_males_carcasses_total	9_females_carcasses_total	160x9_males_carcasses_total	160x9_females_carcasses_total	160_females_carcasses_total	head	160_males_carcasses_total	embryo_0-2h from 15to16 day old dysgenic mothers	follicle cells	160_testes_total
.....ACTAACCGCCCAATCCCTACAG.....	22	0	1	17.00	17	2	5	4	2	3	0	0	0	0	0	1	0	0
.....ACTAACCGCCCAATCCCTACAG.....	23	1	1	15.00	15	2	0	2	1	1	3	3	2	1	0	0	0	0
.....ACTAACCGCCCAATCCCTACA.....	21	0	1	5.00	5	1	1	0	0	0	0	0	1	1	1	0	0	0
.....ATTTTTACTTGTTTCTTCAAAACTA.....	25	0	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0
.....GTAAGTGGACGGGAGGTA.....	18	0	1	1.00	1	0	0	0	0	0	0	0	0	0	1	0	0	0
.....ACTAACCGCCCAATCCCTACAGC.....	24	2	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0
.....AACCGCCCAATCCCTACAG.....	19	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0
.....ACTAACCGCCCAATCCCTACAG.....	23	1	1	1.00	1	1	0	0	0	0	0	0	0	0	0	0	0	0
.....AACTAACCGCCCAATCCCTACAG.....	23	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0
.....CTAACCGCCCAATCCCTACAG.....	21	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

CTGAATCAGGTTTACTCAGGGCGAAATGTAGGTGAAAGTACTACGTCGGCCATTCACCTGCCCTCCATTAAAAATGAACAAAGAAGTTTTGATTGGCGGGTTAGGGATGTCGTTGACCCGCACGGGAACGTACAAGTGTACGCAGATGTCCGGTTGGTTCA						SRR060681	SRR060683	M047	V053	SRR2096081	SRR060666	SRR060657	SRR1106727	V116	SRR060655	SRR060672	SRR1106728	SRR1106729
**********	Read size	# Mismatch	Hit Count	Total Norm	Total	Argx9_testes_total	160_testes_total	female body	head	embryo_0-2h from 15to16 day old nondysgenic mothers	160_males_carcasses_total	140_testes_total	larvae	male body	9x160_testes_total	9x160_females_carcasses_total	larvae	mixed whole adult body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_13047:13844417-13844577 -	dvi_16862	GACTTAGTCCAAATGAGTCCCGCTTTACATCCACTTTCATGATGCAGCCGGTAAGTG-GACGGG-AGGT------A--ATTTTTAC-----TTGTT---------TCTTCAAAAC-TAACC----------GCCCAATCCCTACAGCAACTGGGCGTGCCCTTGCATG---TTCACATGCGTCTACAGGCCAACCAAGT
droMoj3	scaffold_6540:26245689-26245850 +		GCTGATTCCAAGGAGTCCCGCTTTACATCCACTGTCATGTGCAGCCGGTAAGTG-CAGAGGATCC-----G--GT-----TTCTTT--GCTT-------TCTATGAAGGTCCTT----------AGCCAATCCTACAGCAACTGGGCGTACCCTTGCAG---TCATGTGCGTCTCAGGCCAACCAGGT
droGri2	scaffold_14830:6111335-6111498 +		GCTTAAGTCCAAGTATAGAAGCAGAAGCATCAAATTTGTGTGGATACCCGTGAGTG-CTATCAT---ATA--G--AA-----TATCTC--TCTTCTTTGAAAGTAACC--T----C-----AGC-----ACGT-AAGATTTACAGCAACTGGGCGTGCCTTGCATG---CTCATATGCGTCTACAGGCCAACCAGGT
droWil2	scaf2_1100000004921:4599201-4599369 +		GCTGATCCAATGATCCAGCTTGACGTCCTCGTTGTGATCGAGCCGGTAAGTTTTAAA--AGTTCCATCCGCATTGGAGGTAGCTC--TG---------ATTCTAATC--T--A-----AT-----TCTTGTTTTGCAGCAATTGCACTCCAATGCAGAACTCATTTGCGTCTACAGGCAATCAATT
dp5	2:5315129-5315301 +		GCTCCAACCGCAGGAGTCCCGCTTGAGCTCTGTGTTCGTGTGGAACCGTAAGTG-TCATAGAGAC-----C--T------ ------ ---CTTTCTGCGCAGTCTGCC--- ----TGCAACAATTTTCCCTTCTTCCCTGCAGCAACTGGGACCCCATGCAGCGCACATCTGCGATTCCAGGCCAATCAGGT
droPer2	scaffold_19:1026876-1027048 +		GCTCCAACCGCAGGAGTCCCGCTTGAGCTCTGTGTTCGTGTGGAACCGTAAGTG-TCATAGAGAC-----C--T------ ------ ---CTTTCTGCGCCGTCTGCC--- ----TGCAACCATTTTCCCTTCTTCCATCGCAGCAACTGGGACCCCATGCAGCGCACATCTGCGATTCCAGGCCAATCAGGT
droAna3	scaffold_13340:7464525-7464695 +		GCTTAATCCGCAGGAGTCCCGATTGACGTCTTAGTTCGTGTGCAGCCGGTAAGTCGAGCACTT---CACAC--C------ ----T--TATCG-TTTTTAAACTAACC--C----TAAATAAATTATAA--ATGATTTCTTTAGCACTTGCACCCCATGCAGCGCACCGCACTGCGATTACAGGCCAATCAGGT
droBip1	scf7180000396708:1385632-1385798 -		GCTGATCCGCAGGAGTCCCGATTGACGTCCTAGTTGTGTGCAGCCGGTAAGTCGAGCTCTC---TAGGC--T-------TT--AATCTCTCCTCAGCGAACCCTAGGCC-----TC-----TTAT-TATCGCTTTAGCAACTGGCGGCGCGATGCAGCGCACCGCATGCGTTACAGGCCAATCAGGT
droKik1	scf7180000302475:126326-126493 +		GCTGATCTCCGAATTCGAGGCCGCTTGACGTCCTCGTTTTGTGTGCAGCCCGGTAAGTTCTTGTAATTGTTACTTTGATATCG----- ------TGCG---------AGGATAATC--T----GACA-----A-----ATTTTTGTTTTTAGCAACTGGCACCCCATGCAGCGCACATCTTCGTTCCAGGCCAACCAGGT
droFic1	scf7180000453796:162607-162769 +		GCTTGCAGCCGGATGATGCCGCTTGACGTCCACCTTTTGTGTGGAACCGTGGCTTCAAACACCTA-T---AACC--ATAATATGT-----A-CCG---------TTTATAATC--T----A-----CT-----CCTTTTTGTATTGCAGCAACTGGGACCCCATGCAGCGCACCGCATCTGCGTTCCAGGCCAACCAGGT
droEle1	scf7180000490967:697753-697915 -		GCTCCAGCCGAAGGAGTCCCGCTTGACGTCCACCTTCGTGTCGAACCGTAGCCCAATGTCAAGGCCGCCCCCCAA---AGCCAAGT-----CTACT---------TATACTAACC--T----T-----AT-----ACTTGTGTGTTCAGCAACTGGCACCCCATGCAGCGCACCGCATTTGCATTGCAGGCCAACCAGGT
droRho1	scf7180000778336:18053-18214 +		GCTCCAACCGCAAGGAGTCCCGCTTGACGTCCACCTTTGTGTGCAACCCGGTGAGTTGCACTTGAGAGCCCCCCCA--AAGCCAATT-----CCGCT---------TACTTAACC--T----A-----AT-----GCTTTTTGGGTTCCAGCAACTGGCATCTCCGATGCAGCGCACCGCACTGCGGTTCCAGGCCAACCAGGT
droBia1	scf7180000299102:359165-359326 -		GCTTCCCGCCGATGAGAGCCGCTTGACATCACGTTCCTCGTGCAACCCGGTAAGTTCGAATAATAGT------A--AATCAAAT-----TGCGC---------AATCTAATC--T----G-----AT-----ACGCTTTCATTCCAGCAACTGGCACCCCATGCAGCGCACCGCACTGCGGTTCCAGGCCAACCAGGT
droTak1	scf7180000415580:251650-251813 +		GCTCCAGCCGAATGAGACCGCTTGACGTCCACCTTTGTGTGGAACCGGTGAGTCCGAATCCAAGTTG-----A--ATGGGGGT-----AGCCG---------AATCTAATC--T----A-----GC-----ATTTCTAAATTCCAGCAACTGGCACCCCATGCAGCGCACCGCACTGCGGTTCCAGGCCAATCAGGT
droEug1	scf7180000409557:110665-110826 +		GCTCGAGCCGAATGAGACGCGCTTTACGTCCACCGTGGTGTGCAGCCGGTGAGTTGAATCAAAGT-----A--ACCCATAT-----TGCGC---------AATTTAATC--T----A-----AT-----ATACTTGGGGTTCAGCAACTGGCACCCCATGCAGCGCACCGCATCTGCGGTTCCAGGCCAACCAGGT
dm3	chr3R:12423425-12423586 -		GACTGCAGCCGAATGATCCGCGTTGACGTCCACCTTTGTGTGGAACCCGGTGAGTTGAATCAAAGT------A--GTCCCAGT-----TTGTGC---------AATCTAATC--T----A-----AT-----ACTTTTGGGTTCAGCAACTGGCACCCCATGCAGCGCACCGCATCTGCAGGCCAACCAGGT
droSim2	3r:8826667-8826828 +		GACTGCAGCCGAATGAGTCCGCGTTGACGTCCACCTTTGTGTGTACCCGGTAAGTTGAATCAAAGT------C--GTCCCAGT-----TGTGC---------AATCTAATC--T----A-----AT-----ACTTTTGGGATTCAGCAACTGGCACCCCATGCAGCGCACCGCATCTGCGATTCCAGGCCAACCAGGT
droSec2	scaffold_12:1724840-1725001 +		GACTGCAGCCGAATGAGTCCGCGTTGACGTCCACCTTTGTGTGGAACCCGGTAAGTTGAATCAAAGT------C--GTCCCAGT-----TGTGC---------AATCTAATC--T----A-----AT-----ACTTTTGGGTTCAGCAACTGGCACCCCATGCAGCGCACCGCATCTGCGATTCCAGGCCAACCAGGT
droYak3	3R:11969268-11969429 +		GCTCGAGCCGAATGAGTCCGCGTTGACGTCCACCTTCGTGTGGAACCCGGTCAGTTGAAGCGAAGT------A--GTCCAGGT-----TGTGC---------AATCGAATC--T----A-----AT-----ACTTTGGGGTTGAGCAAGTGGGCACCCCATGCAGCGCACCGCATCTGCGTTCCAGGCCAACCAGGT
droEre2	scaffold_4770:9213906-9214067 +		GCTCGAGCCGAATGAGTCCGCGTTGACGTCCACCTTCGTGTGGAACCCGGTCAGTG-GAATCCAAGT------A--GTCCAGGC-----TGTGC---------AATCGAATC--T----A-----AT-----ACTGTTGGGGTTGAGCAAGTGGGCACCCCATGCAGCGCACCGCATCTGCGTTCCAGGCCAACCAGGT

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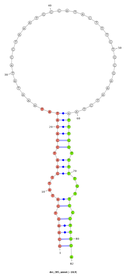
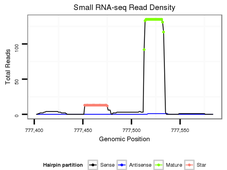
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	1
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

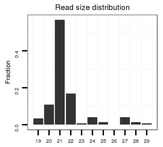
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_285	**scaffold_13047:777452-777534 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Comf2.Mmu1)]

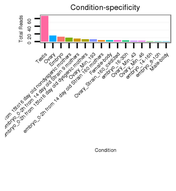
Legend: sense, star, mismatch in alignment, mismatch in star

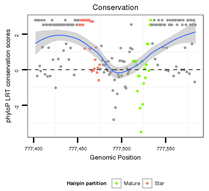
Predicted structure











Show Alternate Folds

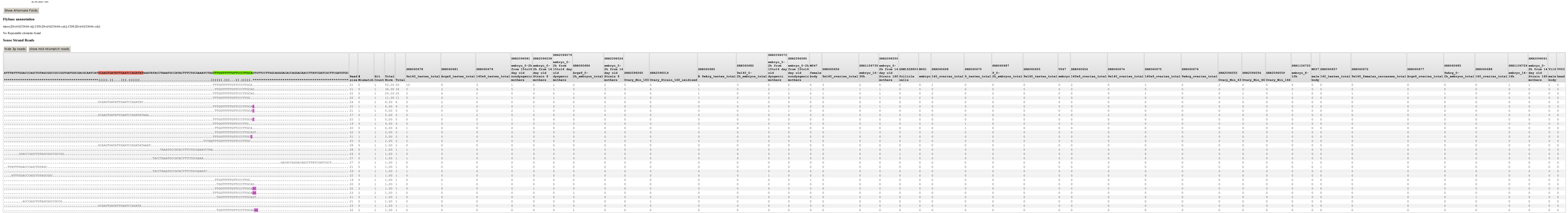
Flybase annotation

intron [DroGI23646-u], CDS [DroGI23646-cds], CDS [DroGI23646-cds]

No Repeatmir elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

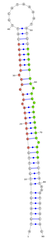
Re-alignment of all predicted orthologs

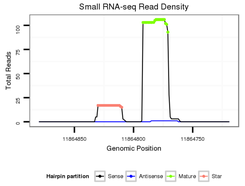
Generated 09/08/2015 at 07:07 PM

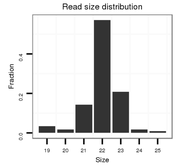
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_290	**scaffold_12875:11864769-11864830 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (Comel3.Minor)]

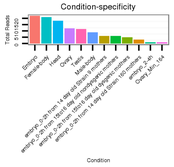
Legend: **mature** **star** **hairpin arm** **mismatch in alignment** **mismatch in seqs**

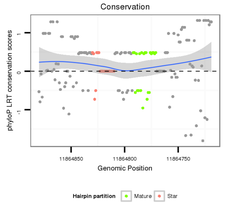
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show red mismatch reads

TGCTATAAAATACACATACAAATACACAGTTACGTATGTATGTAGTTGTGTTTATATCAGGCTCTGTGTCATTGCATGATAAAATATGGTATGGGCATGCTATAAACTACAACTATAAATATACAGTTACGCATGTATGTATGGATGGTTGTTTTATATGTA	Read #	Hit	Total	M047 female body	M024 Argw9_0-head 2h_embryos_total	ERR060486 Argw9_testes_total	ERR060681 head 2h_embryos_total	V053 9_0-head 2h_embryos_total	ERR060687 Strain 9 mothers	ERR2096026 embryo_0-2h from 14 day old male	V116 male	ERR060677 Argw9_ovaries_total	ERR060678 9x160_testes_total	ERR2096079 embryo_0-2h from 15to16 day old dyegenic mothers	ERR060676 9xArg_ovaries_total	ERR2096080 embryo_0-2h from 15to16 day old nondyegenic mothers	ERR2096081 embryo_0-2h from 15to16 day old nondyegenic mothers	Argentina_testes_total	ERR060659 9_ovaries_total	ERR060682 2h_embryos_total	M027 male	ERR060671 9x160_males_carcasses_total	ERR060673 140x9_0-9_ovaries_total	ERR060684 2h_embryos_total	ERR2096038 embryo_0-2h from 14 day old Strain 9 mothers	ERR2096050 embryo_0-2h from 14 day old Strain 160 mothers	ERR060654 160x9_ovaries_total	ERR060664 9_males_carcasses_total	ERR060668 160x9_males_carcasses_total	ERR060670 9_testes_total	ERR060672 9x160_females_carcasses_total	ERR060674 9x160_ovaries_total	ERR060675 140x9_ovaries_total	ERR060679 140x9_testes_total	ERR060685 9xArg_0-2h_embryos_total	ERR060689 160x9_testes_total	ERR1106714 embryo_2-4h	ERR2096059 Strain_160_Ovary_Min_164	ERR2096061 embryo_0-2h from 15to16 day old dyegenic mothers	ERR2096072 embryo_0-2h from 14 day old Strain_160 dyegenic mothers	V047 embryo	ERR060655 9x160_testes_total
********************************.((((((((((((((((((((.(.(.(.((((((((((.....))))))))))).)).))))))).)))))))).))))))))).********************************alignment		Mismatch	Count	Norm	Total																																				
.....	22	0	1	65.00	65	12	8	3	4	3	3	2	4	3	2	0	2	2	0	2	2	0	1	2	0	0	1	1	0	0	0	0	0	0	1	1	0	0	0	0	0
.....	23	0	1	23.00	23	1	0	8	1	0	2	2	0	0	1	2	1	0	0	1	0	2	0	0	0	1	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0
.....	21	0	1	8.00	8	3	2	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	1	0	0	0	0	0
.....	21	0	1	8.00	8	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	1	0	0	1	0	0	0
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.....	23	0	1	4.00	4	1	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
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.....	20	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	0	0
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.....	21	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
.....	25	3	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
.....	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	0	0	0	0	0	0	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	24	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	0	0	0	0
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.....	25	2	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	0	0
.....	24	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	0	0	0	0
.....	23	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	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
.....	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
.....	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	0	0	0
.....	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
.....	21	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	0	0	0	0	0	0

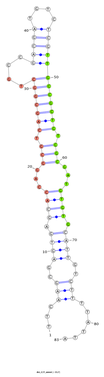
Anti-sense strand reads

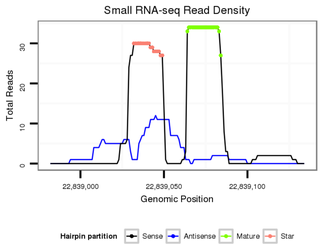
ACGATATTTTATGTGATGTTTATGTGTCAATGCATACATACATACCACACACATAATACGTATTTTATACCATACCCGTACGATATTTGATGTGTTGATATTTATATGTCAATGCGTACATACATACCTACCACACAAATATACAT																																									
********************************.((((((((((((((((((((.(.(.(.((((((((((.....))))))))))).)).))))))).)))))))).))))))))...))))))).********************************alignment	Read #	Hit	Total																																						
	Mismatch	Count	Norm	Total																																					
.....	0	1	1.00	1

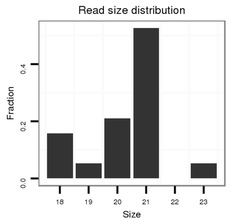
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_127	**scaffold_13049:22839032-22839084 +**	**confident**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

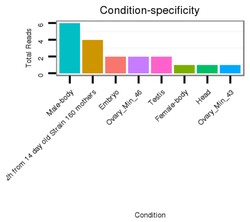
Legend: mature star **mismatch in alignment** mismatch in read

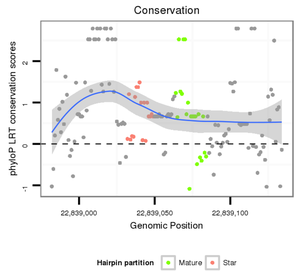
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dvir/GJ13997-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TTTCGGCAGAATATGAATACCAAACCGTGGTCAGGTTCAAGCGAGTGAGACCAGGCGTCAGCGGCTGCCGACGATGTCTCGTTGCCGCTGTCGCGATGTGTGCATTGTCTTTTATTATTGTTTTTCATTTGGTTTTGTTGTGACCAATTGAAT	Read size	# Mismatch	Hit Count	Total Norm	V116 male body Total	SRR2096056 Ovary_Min_46	SRR2096060 Ovary_Min_193	M047 female body	SRR2096055 Ovary_Min_43	SRR2096057 Ovary_Min_50	SRR2096050 embryo_0-2h from 14 day old Strain 160 mothers	SRR2096059 Ovary_Min_164	SRR060663 160_0-2h_embryos_total	M028 head	SRR060688 160_ovaries_total	V053 head	M027 male body	SRR2096058 Ovary_Min_98	SRR060656 9x160_ovaries_total	SRR060686 Argx9_0-2h_embryos_total	SRR060681 Argx9_testes_total	SRR060655 9x160_testes_total	SRR060660 Argentina_ovaries_total	SRR060675 140x9_ovaries_total	SRR060682 9x140_0-2h_embryos_total	SRR060683 140_testes_total	SRR060687 9_0-2h_embryos_total	SRR060689 140x9_testes_total	SRR2096080 embryo_0-2h from 15to16 day old nondysgenic mothers	SRR2096081 embryo_0-2h from 15to16 day old nondysgenic mothers	V047 embryo	SRR060672 9x160_females_carcasses_total
********************************...((((.(((((.((((.((.(((((((.....((((((....))))))))))))).))))..)))).))))..)))).)))).....********************************																																
.....AGCACCAGGCGTCAGCGGCTGC.....	22	0	1	11.00	11	0	2	1	0	1	1	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTGCCGCTGTCGCGATGTGTG.....	21	0	1	9.00	9	2	0	0	1	0	0	4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
.....TTGCCGCTGTCGCGATGTGTGC.....	22	0	1	9.00	9	1	0	0	2	0	0	0	0	1	2	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AGCACCAGGCGTCAGCGGCTG.....	21	0	1	7.00	7	0	1	1	1	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TTGCCGCTGTCGCGATGTGT.....	20	0	1	4.00	4	3	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
.....TTGCCGCTGTCGCGATGTGTGCA.....	23	0	1	4.00	4	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
.....GAGTGAGCACCAGGCGTCAGCGGCTG.....	26	0	1	3.00	3	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ACCAGGCGTCAGCGGCTG.....	18	0	1	3.00	3	0	2	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
.....TTGCCGCTGTCGCGATGTGTGCATT.....	25	0	1	3.00	3	0	1	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
.....TTGCCGCTGTCGCGATGTGTGT.....	22	1	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
.....TTGCCGCTGTCGCGATGTGTGCATT.....	25	2	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
.....GCACCAGGCGTCAGCGGCTGC.....	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
.....TTGCCGCTGTCGCGATGTGTG.....	22	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	0	0	0	0	0	0	0
.....TTTTCATTTGGTTTTGTTGTGACCAAT.....	27	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
.....TTGCCGCTGTCGCGATGTGT.....	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
.....GTTGCCGCTGTCGCGATGTGTGCA.....	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	0	0	0	0	0	0	0
.....CCAGGCGTCAGCGGCTGC.....	18	1	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
.....TTGCCGCTGTCGCGATGTGTGC.....	23	1	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
.....TCATTTGGTTTTGTTGTGACC.....	19	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....TTGCCGCTGTCGCGATGTG.....	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	0	0	0	0	0	0	0
.....GAGTGAGCACCAGGCGTCAG.....	20	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
.....GCACCAGGCGTCAGCGGCTG.....	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	0	0	0	0	0	0
.....CGAGTGAGCACCAGGCGTC.....	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
.....TCGTTGCCGCTGTCGCGATGTGT.....	23	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
.....TTGCCGCTGTCGCGATGTGCATG.....	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
.....GCACCAGGCGTCAGCGGCTGCC.....	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	0	0	0	0	0	0
.....GAGCACCAGGCGTCAGCGGCTGC.....	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	0	0	0

Anti-sense strand reads

AAAGCCGTCTTATACTTATGGTTTGGCACCAGTCCAAGTTCGCTCACTCGGGTCCGCAGTCGCCGAGGGCTGCTACAGAGCAACGGCGACAGCGCTACACAGTAACAGAAAATAATAACAAAAGTAAACCAAAACAACACTGGTTAACTTA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR2096056 Ovary_Min_46	SRR2096060 Ovary_Min_193	M047 female body	SRR2096055 Ovary_Min_43	SRR2096058 Ovary_Min_98	SRR2096059 Ovary_Min_164	V053 head	V047 embryo	SRR060662 9x160_0-2h_embryos_total	SRR060687 9_0-2h_embryos_total	SRR2096038 embryo_0-2h from 14 day old Strain 9 mothers	V116 male body	GSM1528803 follicle cells	M028 head	SRR060676 9xArg_ovaries_total	SRR1106728 larvae	SRR1106729 mixed whole adult body
********************************...((((.(((((.((((.((.(((((((.....((((((....))))))))))))).))))..)))).))))..)))).)))).....********************************																						
.....CACCAGTCCAAGTTCGCTCACT.....	22	0	1	3.00	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TCCGCAGTCGCCGACGGCT.....	19	0	1	3.00	3	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0
.....A CCGACGGCTGCTACAGAGCA.....	21	1	1	2.00	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CAGTCGCCGACGGCTGCTACA.....	21	0	1	2.00	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
.....TCGCCGACGGCTGCTACAGAG.....	21	0	1	2.00	2	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
.....CCGACGGCTGCTACAGAGCAA.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....CACTCGTGGTCCGCAGTCGC.....	20	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....ACACACGTAACGAAAAATAAT.....	21	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTCCAAGTTCGCTCACTC.....	18	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....CCGCAGTCGCCGACGGCT.....	18	0	1	1.00	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TACTTATGGTTTGGCACCAGT.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
.....GCGACAGCGCTACACACGTAA.....	21	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
.....TCCGCAGTCGCCGACGGCTGCTACAGAG.....	28	0	1	1.00	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AC CACTCGTGGTCCGCAG.....	19	2	1	1.00	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
.....AGTCCAAGTTCGCTCACTC.....	19	0	1	1.00	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
.....CGCAGTCGCCGACGGCTGCTAC.....	22	0	1	1.00	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
.....G TATGGTTTGGCACC.....	15	1	5	0.20	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_13049:22838982-22839134 +	dvi_127	TTTC-G----------G----CA---GAATAT-GAATACCAAACCGTGGTCAGGTTCAAGCGAGTGAGCACCAGGCGTCAGCGGCTGCCGACGATGTCTCGTTGCCGCTGTCGCGATGTGTGCAT----------T---------GTCTTTTAT-----TATTGTTTTCATTTGGTTT----T-GTTGTG-ACCAATTGA----------AT
droMoj3	scaffold_6680:17455501-17455649 +		TTTC-G----------G----CA---GAAC-T-GAATACCAAACCGTGGTCA-GTTCAAGCGAG----AC AGGCGTCAGCGGCTGCCGACGCGTGTCTCGTTGCCGC----------TGCGCGCGTGCGCGCAT----------T---------G-TGCTTAT-----TATTGTTTTCATTTGCTTT-G-GGT-GA-T-CT-T-----**********----------AT
droGri2	scaffold_15110:1811881-1811983 +		TTTC-G----------G----CA---GAATAC-GAATACCAACCGTGGTCA-TATTCAAGCGAGCGAGCGCAGGCGTCAGCGGCTGCCGACGCATGTCCGTTGCCGC----------TGCGGCGTGTGCGTCG-TCG----------TGCGGAGCGAG-GCTTTTATTTTGTT-T-TA-TT-----CT-T-T-G-GGT-C-----G----------AGTCATAA----------G-TT
droWil2	scf2_1100000004511:8606465-8606617 +		CCC-GA----AAGAGAACCAAA CCA--T-A-GAA----CAACCGTGGTCA-GTTCAAGCGAG-----G----GGTGTGTG----------TA-GGCGAGTGC-CCCT-AT-------G-A--TGGCCGACGAAA----------G-TGCCGGCG-----A ATTGTTT-----TTTTT-GGT-TGG-T-T-G-GTGTCATAGCAAATA----------AG A
dp5	XR_group6:11786927-11787045 +		-T-T-TG---------TTG--T-TA---GAAT-C-TG----AACCGTGGTCA-GTTCAAGCGC-----G----------GCATGCCGGCGCAGCGTGCGTTTCA----------A-A--CACCCCC--ATG----------CC-T-TTAT----TATTGTTT-----TG-T-T-GTC-GAAAAT-CCAAT---**********----------**
droPer2	scaffold_20:1708238-1708359 +		-T-T-TG---------TTG--T-TA---GAAT-C-TG----AACCGTGGTCA-GTTCAAGCGC-----G----------GCATGCCGGCGCAGCGTGCGTTTCA----------A-A--CACCCCC--ATG----------CC-T-TTAT---TATTATTGTT-----TG-T-T-GTC-GAAAAT-CCAAT---**********----------**
droAna3	scaffold_13337:19364337-19364472 +		A TTC-G----------CTAC-CA---GAAG-CC-GAA----CAACCGTGGTCA-GTTCAAGCGAG----TCGAGAGCGT----------GCATGCCGGCGCGTGTGCTGCT----------CG-A--TGCCCCCCTCTAGA----------GCTCCCG-T-----G ATTGTTT-----AT-T-T-AT-AAA-A-T-CCAATTGCAA----------**
droBip1	scf718000039636O:559019-559155 +		A TTC-G----------CTAC-CA---GAAG-CC-GAA----CAACCGTGGTCA-GTTCAAGCGAG----GCGAGAGCGT----------GCATGCCGGCGCAGCGTGCTGCT----------G--A--TGCCCCCCTCTAGA----------CC-T-TAT----ATTGTTT-----AT-T-T-AT-AAAAAA-T-CCAATTGCAA----------**
droKik1	scf718000302391:590683-590794 +		CG TC-T----------G----G A---GAAT-CC-GAA----CAACCGTGGTCA-GTTCAAGCGC-----G----------GCATGCCGGCGCGTGTGCC-CGCC----------CC-T--T--CCCC---TTG----------CC-CGCCG-T-----CG TGTTT-----AT-T-T-CGC-GAAA-T-ACCAATTGCA----------**
droFic1	scf718000045413:2415275-2415404 +		CG TC-G----------G----T TCC-T-A-G CC----A-CCGTGGTCA-GTTCAAGCGC-----G----------AAATGCCGGCGCGTGC-TA--------C-----**********----------T---------TC-T-T-CC-----A ATTGTTT-----AT-T-TTGG-GAAGAGC-CCAATTGCGTTTGACATTGTTGTAAGGGTAA-GA
droRle1	scf718000049193:4174608-4174714 +		TT-C-A---------TCG----T TC---GG-CC-GAA----CAACCGTGGTCA-GTTCAAGCGC-----G----------AAATGCCGGCGCGTGC-T--------C-----**********----------T---------TC-T-T-CC-----A ATTGTTT-----AT-T-TTGG-T-A-TAAT-CCAATTGCCC----------**
droRho1	scf718000077342:32446-32569 +		TT-C-A---------TCG----T TC---GG-CA-GAA----CAACCGTGGTCA-GTTCAAGCGC-----G----------AATGCCGGCG--CGTGCGCTGC--------C-----**********----------T---------TC-T-T-CC-----A ATTGTTT-----AT-T-TTGG-T-A-TAAT-CCAATTGCGA-TAGTTATTATTACCCGG-----AT
droBia1	scf718000302193:5778578-5778686 +		-TTC-G----------G----A CC---CA-GAA----CAACCGTGGTCA-GTTCAAGCGC-----G----------AATGCCGGCGCAGCGTGT-TT--------C-----**********----------T---------TC-T-T-CC-----A ATTGTTT-----AT-T-TTGGC-T-A-TAAT-CCAATTGCCAA----------AT
droYak1	scf718000041525:675468-675558 +		-TTC-G----------G----T A---****-CC-****-CAACCGTGGTCA-GTTCAAGCGC-----G----------AATGCCGGCGCAGCGTGC-TA--------C-----**********----------T---------TC-T-T-CC-----A ATTGTTT-----AT-T-TTGGC-T-A-TAAT-CCAATTGCC----------**
droEug1	scf718000040946:5044792-5044914 +		-T**-A TCGGTCGGTTG--AT-GGTC--GG-CAG----CAACCGTGGTCA-GTTCAAGCGC-----G----------AATGCCGGCGCAGCGTGC-TT--**********----------T---------TC-T-T-CC-----A ATTGTTT-----AT-T-TAAG-T-A-TAATGCCCAATTGCGAATTGT----------**
droSuz1	scf718000045413:2415275-2415404 +		AC-T-G TCCCCACCGTCG--CT-GGTC--GGC-TA----CAACCGTGGTCA-GTTCAAGCGC-----G----------AATGCCGGCGCAGCGTGC-TC--------C-----**********----------T---------TC-CCC-CC-----A ATTGTTT-----AT-T-T-CGC-GAAT-C-CCAATTGCCATGTGCATGC----------CTGT
droSoc2	scf718000045413:2415275-2415404 +		AC-T-G TCCCCACCGTCG--CT-GGTC--GGC-TA----CAACCGTGGTCA-GTTCAAGCGC-----G----------AATGCCGGCGCAGCGTGC-TC--------C-----**********----------T---------TC-CCC-CC-----A ATTGTTT-----AT-T-T-CGC-GAAT-C-CCAATTGCCATGTGCATGC----------CTGT
droYak3	3L:20673979-20674111 +		A C-G TCCCACTGTCG--CT-GGTC--GGC-TA----CAACCGTGGTCA-GTTCAAGCGC-GCGCGCTGC-TG--------C-----**********----------T---------TC-CCC-CC-----A ATTGTTT-----AT-T-T-CGC-GAT-C-CCAATTGCATGTTCATTC----------TG
droEre2	scaffold_4784:19641313-19641428 -		-T**-T TCCCACCGTCG--CT-GGTC--GGC-TA----CAACCGTGGTCA-GTTCAAGCGC-----G----------AATGCCGGCGCAGCGTGC-TG--------C-----**********----------T---------TC-CCC-CC-----A ATTGTTT-----AT-T-T-CGC-GAT-C-CCAATTGC----------**

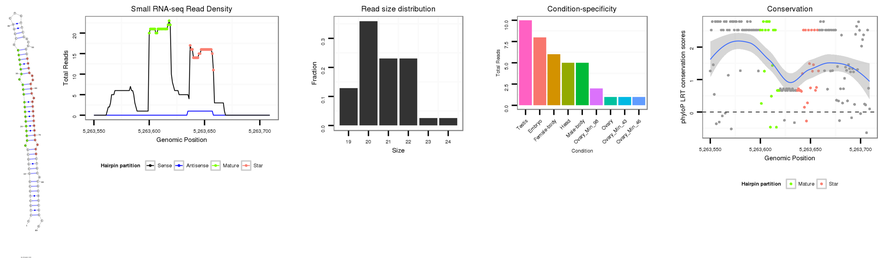
Generated: 09/08/2015 at 08:35 PM

	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.mism	0
crit.pairing	1
crit.top3	1
crit.group3	1
crit.sum	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_130	**scaffold_12928:5263600-5263659 +**	**confident**	**Canonical miRNA**	**intron**
				[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star hairpin arm mismatch in arm mismatch in star

Predicted structure



Show Alternate Folds

Fly base annotation

intron [Dvir(GI16956-aj); CDS [Dvir(GI16956-cds]

No Repeatmk element found

Sense Strand Reads

hide 3p reads show mrd mismatch reads

CGATTTGTATTCTGTGACGGAATTGTAAGGAGTGCGCCTGCTGCGGCGGCCGCTTGATTGTGCGCTTGCACGACCGTCACAGACTGTTCGACGGCACGCAGCGCGACGCCTCTGCCAGCACACAGACACAAACTCAG						SRR060681 Arg9_testes_total	M047 female body	SRR060678 9w160_testes_total	V114 male body	M028 9_males_carcasses_total	SRR060664	SRR060669 160w9_females_carcasses_total	SRR060679 140w9_testes_total	SRR060680 A Pabrg_testes_total	SRR2096058 Ovary_Mix_88	V047 embryo	SRR060667 160_females_carcasses_total	SRR060671 9w160_males_carcasses_total	SRR060672 9w160_females_carcasses_total	V053 head	SRR060662 9w160_0-2h_embryos_total	SRR060668 160w9_males_carcasses_total	SRR060676 9Abrg_ovaries_total	SRR060683 160_testes_total	SRR060686 Arg9_0-2h_embryos_total	SRR060687 9_0-2h_embryos_total	SRR2096059 Ovary_Mix_164	SRR060684 140w9_0-2h_embryos_total	SRR110670 embryo_16-20h	SRR060655 9w160_testes_total	SRR060658 140_ovaries_total	SRR060681 140w9_0-2h_embryos_total	SRR060663 160_0-2h_embryos_total	SRR060665 9_females_carcasses_total	SRR060666 160_males_carcasses_total	SRR060674 9w160_ovaries_total	SRR060682 9w160_0-2h_embryos_total	SRR060685 9Abrg_0-2h_embryos_total	SRR2096026 embryo_0-2h from 14 day old females 8 mothers	SRR2096055 Ovary_Mix_43	SRR2096056 Ovary_Mix_46	SRR060677 Arg9_ovaries_total
**********	((((((((((.((((((((((.((((((.((((.....)))).)))) ...)))).))))))))))).))))))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total																																				
.....	..GCGTTGATGTGCGCGTGCC.....	20	0	1	20.00	20	1		1	4	1	2	0	3	0		1	0	0	0	1		1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	.....CACGAGCCCAACATCAACGGCG.....	23	0	1	12.00	12	3		2	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
.....	.....CACGAGCCCAACATCAACGGCG.....	21	0	1	4.00	4	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	1
.....	.....CACGAGCCCAACATCAACGGCG.....	19	0	1	3.00	3	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
.....	..GCGTTGATGTGCGCGTGCC.....	19	0	1	3.00	3	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
.....	..ACGGAATTGTAAGGAGTGCGCC.....	21	0	1	2.00	2	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	0	0
.....	..GCGTTGATGTGCGCGTGCCCA.....	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
.....	..GCGTTGATGTGCGCGTGCCGCA.....	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
.....	.....CCACGAACTGTTCGACGGCACG.....	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
.....	..GCGTTGATGTGCGCGTGCCGCA.....	21	0	1	2.00	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	0	0	0	0	0	0	0	0
.....	..GCGTTGATGTGCGCGTGCCGCA.....	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	0
.....	.....CACGAGCCCAACATCAACGGCG.....	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	0
.....	..GAATTGTAAGGAGTGCGCCTG.....	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
.....	.....ACACCAAGGGGCTCACGCA.....	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
.....	.....CACGAGCCCAACATCAACGGCG.....	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
.....	.....GCCACGAACTGTTCGACGGC.....	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
.....	.....CCACGAACTGTTCGACGGC.....	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	1	0	0	0
.....	..GCGTTGATGTGCGCGTGCC.....	19	1	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
.....	.....CACGAGCCCAACATCAACGGG.....	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
.....	.....GAACTCACGGCGCTGCACGCA.....	24	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	0
.....	.....ATGCGCGTGCCCACGAACT.....	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
.....	..GCGTTGATGTGCGCGTGCCACGC.....	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	0	0	0	0	0	0	0	0	0
.....	.....GAACACCAAGGGGCTCACGCA.....	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
.....	.....AACACCAAGGGGCTCACGCA.....	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	0	0	0	0	0	0	0	0	0
.....	.....CCCTCCTGCGGCGGCGCCTTG.....	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
.....	.TGTGACGGAATTGTAAGGAGTGCGCCT.....	24	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
.....	.....CGTTGATGTGCGCGTGCCACC.....	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
.....	.....CACGAGCCCAACATCAACGGCGCCA.....	25	3	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
.....	.....GCGTTGATGTGCGCGTGCCAC.....	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	0	0	0	0	0	0	0	0	0
.....	..CACGAGCCCAACATCAACGGCG.....	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	0	0	0
.....	.....ACACCAAGGGGCTCACGCA.....	24	2	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
.....	..GTCACGAATTGTAAGGAGTGCC.....	20	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	1	0	0	0	0	0	0	0	0	0
.....	..GCGTTGATGTGCGCGTGCCGCA.....	23	3	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
.....	.....GCCACGAACTGTTCGACGGCACG.....	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
.....	..GCGTTGATGTGCGCGTGCCGCA.....	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
.....	..GCGTTGATGTGCGCGTGCC.....	19	2	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	0	0	0	0	0	0	0	0	0	0
.....	.....GCACGCGCGGCGCCACC.....	17	0	20	0.05	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

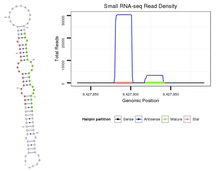
Anti-sense strand reads

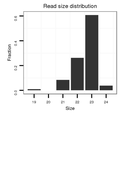
GCTAAACATAAGACACTGCCTTAACATCCTCACGCGGACGACGCCGCGCCGCAACTCACACGCCCACGCCTGCCACGACTGCCCGTGCTCGCGGTCGTTTACTTCCCGCGACGTCGGTCGTGTCTCTGTTTTGAGTC						SRR060681 Arg9_testes_total	SRR060659 Argentina_testes_total	M047 female head body	
**********	((((((((((

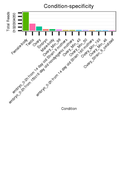
ID	Coordinate	Confidence	Class	Genome Locus
dvi_393	**scaffold_12970:9427883-9427942 +**	**confident**	**Testes-restricted**	**intron**

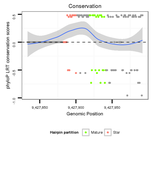
Legend: Mature Star Hairpin arm Alternative

Predicted structure









Show Alternate Forms

FlyBase annotation

intron:FBgn0259649:intron

No Repeatmasker elements found

Sense Strand Reads

Hide 2p reads show mid-mismatch reads

	Read #	Mis	Total	MEF2 Female Body	dmel0678	dmel0680	dmel0681	dmel0677	dmel0679	dmel0672	dmel0669	dmel0675	dmel0666	dmel0668	dmel0659	VCG MEF2 dmel0674	dmel0676	dmel0665	dmel0667	dmel0655	dmel0657	dmel0658	dmel0654	dmel0656	dmel0664	dmel0662	dmel0663	dmel0671	dmel0673	dmel0660	dmel0661	dmel0670	dmel0652	dmel0653	dmel0668	dmel0659	dmel0672
	size	Mismatch	Count	Norm	Total	2p2q2 testes_total	2p3q1 testes_total	2p4q0 testes_total	2p2q2 ovarian_total	2f1q2 testes_total	2f1q3 testes_total	2f2q1 testes_total	2f2q2 ovarian_total	2f2q3 testes_total	2f2q4 ovarian_total	2f3q1 male carcasses_total	2f3q2 male carcasses_total	2f3q3 male carcasses_total	2f3q4 male carcasses_total	2f4q0 ovarian_total	2f4q1 testes_total	2f4q2 ovarian_total	2f4q3 testes_total	2f4q4 ovarian_total	2f5q0 testes_total	2f5q1 ovarian_total	2f5q2 testes_total	2f5q3 ovarian_total	2f5q4 testes_total	2f5q5 ovarian_total	2f6q0 testes_total	2f6q1 ovarian_total	2f6q2 testes_total	2f6q3 ovarian_total	2f6q4 male carcasses_total	2f6q5 male carcasses_total
**********	24	0	1	16.00	16	1																															
.....	23	0	1	15.00	15	1																															
.....	22	0	1	16.00	16	1																															
.....	24	0	1	4.00	4	1																															
.....	24	0	1	4.00	4	1																															
.....	22	0	1	4.00	4	1																															
.....	23	0	1	2.00	2	1																															
.....	22	0	1	1.00	1	1																															
.....	24	0	1	1.00	1	1																															
.....	23	0	1	1.00	1	1																															
.....	18	0	1	1.00	1	1																															
.....	19	0	1	1.00	1	1																															
.....	23	0	1	1.00	1	1																															
.....	21	0	1	1.00	1	1																															
.....	21	0	1	1.00	1	1																															
.....	19	0	1	1.00	1	1																															
.....	22	0	1	1.00	1	1																															
.....	19	0	1	1.00	1	1																															
.....	22	0	1	1.00	1	1																															

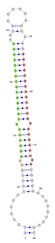
Anti-sense strand reads

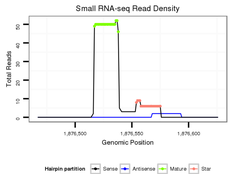
	Read #	Mis	Total	MEF2 Female Body	dmel0678	dmel0679	dmel0680	dmel0669	dmel0675	dmel0683	dmel0655	dmel0659	dmel0657	dmel0676	VCG MEF2 dmel0677	dmel0659	dmel0654	dmel0660	dmel0657	dmel0658	dmel0675	dmel0666	dmel0674	dmel0663	dmel0664	dmel0662	dmel0661	dmel0665	dmel0667	dmel0671	dmel0673	dmel0682	Y147	dmel0654	dmel0644	dmel0645	dmel1167	dmel1170	dmel0644	dmel0647	dmel0652	dmel0653	dmel0665	dmel0669	dmel0672	dmel0673	dmel0687	VCG
	size	Mismatch	Count	Norm	Total	2p2q2 testes_total	2p3q1 testes_total	2f1q2 testes_total	2f1q3 testes_total	2f2q1 testes_total	2f2q2 testes_total	2f2q3 testes_total	2f2q4 testes_total	2f3q1 testes_total	2f3q2 testes_total	2f3q3 testes_total	2f3q4 testes_total	2f4q0 ovarian_total	2f4q1 testes_total	2f4q2 ovarian_total	2f4q3 testes_total	2f4q4 ovarian_total	2f5q0 testes_total	2f5q1 ovarian_total	2f5q2 testes_total	2f5q3 ovarian_total	2f5q4 testes_total	2f5q5 ovarian_total	2f6q0 testes_total	2f6q1 ovarian_total	2f6q2 testes_total	2f6q3 ovarian_total	2f6q4 male carcasses_total	2f6q5 male carcasses_total	2f7q0 testes_total	2f7q1 male carcasses_total	2f7q2 male carcasses_total	2f7q3 testes_total	2f7q4 male carcasses_total	2f7q5 male carcasses_total	2f7q6 male carcasses_total	2f7q7 male carcasses_total	2f7q8 male carcasses_total	2f7q9 male carcasses_total	2f7q10 male carcasses_total	2f7q11 male carcasses_total	2f7q12 male carcasses_total	2f7q13 male carcasses_total

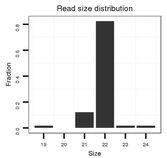
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_406	**scaffold_13050:1876517-1876576 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (Gonell Mirror)]

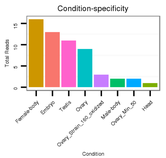
Legend: **mature** **star** **sub-mature in stly-loop** **mismatch in star**

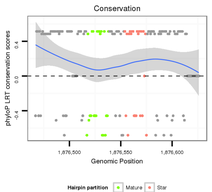
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

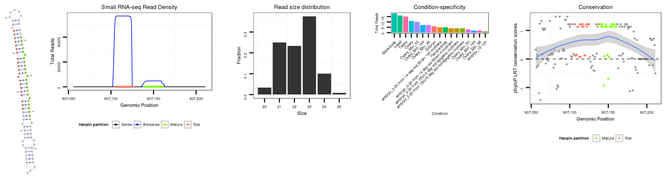
hide 3p reads show mid mismatch reads

| | | |

ID	Coordinate	Confidence	Class	Genomic Locale	
dvi_115	**scaffold_13042:907106-907161 +**	**confident**	**Testes-restricted**	**intron**	Chr6:44153C Genome Browser (Cactus3/Mmus1)

Layer: DNA RNA-seq Small RNA-seq Homologs

Predicted structure



Show Alternate Folds

Flybase annotation

intron(Dvir\GI39574-na)

No Repeatmk elements found

Sense Strand Reads

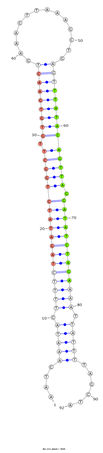
hide 5p reads show red mismatch reads

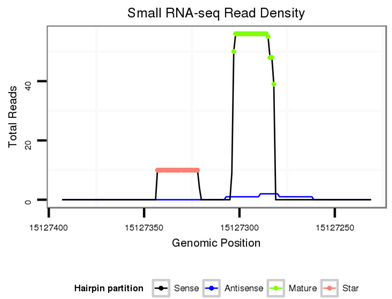
| | | |

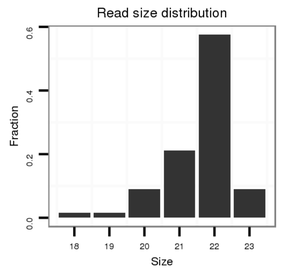
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_113	**scaffold_12875:15127281-15127343 -**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

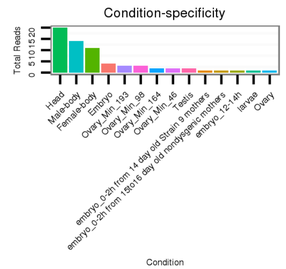
Legend: mature star mismatch in alignment mismatch in read

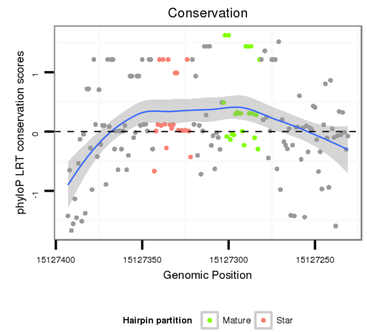
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

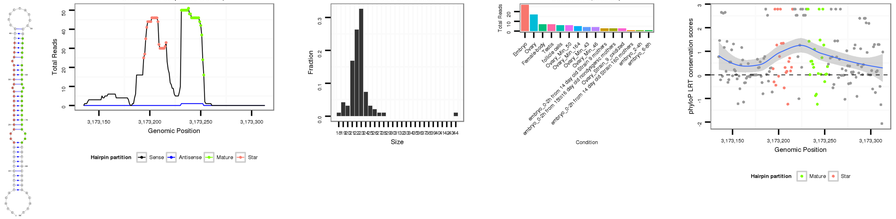
hide 3p reads show mid mismatch reads

| | | |

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_23447	**scaffold_13047:3173185-3173263 +**	**Candidate**	**Unknown**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: **mature** star **sub-match in an alignment** **mismatch in total**

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatile elements found

Sense Strand Reads

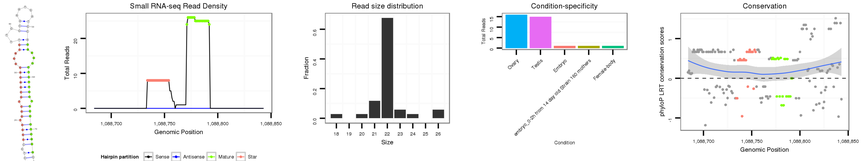
hide 3p reads show mid mismatch reads

Read Alignment	Read #	Mismatch	Hit Count	Total Norm	Total	SRR060684 140w9_0-2h_embryos_total	SRR2096055 Ovary_Min_43	SGM1528032 follicle cells	M047 female body	M041 embryo	SRR060676 9wkrg_ovaries_total	SRR060681 4rg9_testes_total	SRR2094057 Ovary_Min_50	SRR2096013 Ovary_Strain_9_unidissed	SRR060674 9w140_ovaries_total	SRR2096059 4rg9_0-2h_embryos_total	SRR060686 V047	SRR060675 140w9_ovaries_total	SRR060680 9wkrg_testes_total	SRR2096056 Ovary_Min_46	SRR060458 140_ovaries_total	SRR060673 9_ovaries_total	SRR060679 140w9_testes_total	SRR060685 9wkrg_0-2h_embryos_total	SRR2094038 embryo_0-2h from 14 day old Strain 9 mothers	SRR060454 140w9_ovaries_total	SRR060682 9w140_0-2h_embryos_total	SRR060688 140_ovaries_total	SRR1106729 mixed whole adult body	SRR2096080 embryo_0-2h from 15to16 day old nondygenic mothers	SRR2096081 embryo_0-2h from 15to16 day old nondygenic mothers	SRR060666 140_males_carcasses_total	SRR060670 9_testes_total	SRR060677 4rg9_ovaries_total	SRR060678 9w140_testes_total	SRR060687 9_0-2h_embryos_total	SRR060689 140w9_testes_total	SRR1106714 embryo_6-8h	SRR1106717 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096024 embryo_0-2h from 14 day old Strain 140 mothers	SRR2096041 embryo_0-2h from 15to16 day old Dygenic mothers	SRR2096072 embryo_0-2h from 15to16 day old Strain 140 mothers	SRR2096014 Ovary_Strain_140_unidissed	V053 head
**********	1	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
....TTCTTTGTGATTCCCCTACTCTATCCTATCGCTTTCTATTGTGAAAGTACATTTTGTTATATCTCTGAATTTTGACCAATTTGTTTGCTCGCTATCCCAAAAGCATTGGCCAAAATTCGTAATATACAAAAACATTTTTTTTGTATTTTCCAAATATTTTTCCTAGCATTTTTCCAA	22	0	1	8.00	8	0	0	0	0	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	0	0	0	0	0	0	0	0	0	0
....AAAGCATTGGCCAAAATTCGTTA	23	0	1	14.00	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....AAAGCATTGGCCAAAATTCGTTATCGCTTTCTATTGTGAAAGTACATTTTGTTATATCTCTGAATTTTGACCAATTTGTTTGCTCGCTATCCCAAAAGCATTGGCCAAAATTCGTAATATACAAAAACATTTTTTTTGTATTTTCCTAGCATTTTTCCAA	23	0	1	15.00	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....AAAGCATTGGCCAAAATTCGTTA	23	0	1	14.00	14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....AAAGCATTGGCCAAAATTCGTTA	23	0	1	15.00	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
....AAAGCATTGGCCAAAATTCGTTA	23	0	1	14.00	14

ID:	Coordinate:	Confidence:	Class:	Genomic Locdi:	
dvi_291	**scaffold_12928:1088734-1088793 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: **Sense** **Antisense** **Mature 3p alignment** **Mature 5p alignment**

Predicted structure



Show Alternate Folds

Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CAACACTGGCTGAATGCAAGCTGCCACCTGAGCGCGCAGGCATCTGGCTG	TGGCTGGCTGCGACAGGGATT	TTTTGGCAAATGATGCA	AGAGCTGTTGCTGCCGTCAGA	GCCTGTTGGCCAATCAGCGACCGTTGCGTTCAGTGTGCGAGCGAGCTGGC
**********	((((.(((((.((((.((((((.(((.(((.(((.))))))).)))))))).))))).))))).)))....	**********		

Read #	Hit	Total	V116 male body	MD47 female body	SRR6040682 2h_embryos_total	SRR6040686 Arge4_0-2h_embryos_total	SRR6040679 140w9_males_total	SRR6040684 140w9_0-2h_embryos_total	SRR6040674 Pahrg_ovaries_total	SRR6040662 9w160_0-2h_embryos_total	V053 head	SRR6040681 Arge9_testes_total	SRR6040687 3_0-2h_embryos_total	SRR2296081 embryo_0-2h from 15to16 day old mothers	SRR2296080 embryo_0-2h from 15to16 day old mothers	MD41 embryo	SRR6040658 140_ovaries_total	SRR6040675 140w9_ovaries_total	SRR6040685 2h_embryos_total	SRR6040677 Arge9_ovaries_total	SRR2296072 embryo_0-2h from 15to16 day old mothers	SRR6040663 140_0-2h_embryos_total	SRR2296050 embryo_0-2h from 14 day old mothers	SRR6040661 140w9_0-2h_embryos_total	V047 embryo	SRR6040657 140_testes_total	SRR6040660 Argentina_ovaries_total	SRR6040673 9_ovaries_total	SRR2296057 Ovary_Mix_50	SRR6040659 Argentina_testes_total	SRR2296079 embryo_0-2h from 15to16 day old mothers	SRR6040665 9_females_carcasses_total	SRR6040683 140_testes_total	SRR2296014 Ovary_Strain_160_ovidised	M27 male follicle cells	GSM1528803 9w160_males_carcasses_total	SRR6040671 140_ovaries_total	SRR1106727 mixed whole adult body	SRR1106729 160_males_carcasses_total	SRR6040666 140w9_males_carcasses_total	SRR6040668 9w140_testes_total	SRR6040678 Pahrg_testes_total	SRR6040680 Strain 9 mothers	SRR2296026 embryo_0-2h from 14 day old mothers	SRR6040674 9w140_ovaries_total
22	0	1	23.00 22	0	1	0	0	9	0	4	0	0	3	0	0	0	0	3	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
21	0	1	3.00 3	0	0	0	0	0	0	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
23	0	1	2.00 2	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	0	0
26	0	1	2.00 2	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	0	0	0	0
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	0	0
18	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
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
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
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
25	2	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	1	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

GTTGTGACCGACTTACGTTCCGACGGTGGACTCGCGTCCGTAGACCGACG	ACCGACCGACGCTCTCCCTA	AAACCTTTTACTA	TTCCGACAACGACGCATCTCGACCAGCCCAAGTCACACGCTCGCTCGACCG	
**********	((((.(((((.((((.((((((.(((.(((.(((.))))))).)))))))).))))).))))).)))....	**********		

Read #	Hit	Total	MD47 female body	M027 male follicle cells	SRR6040689 140w9_testes_total	MD41 embryo	SRR6040687 3_0-2h_embryos_total	SRR2296014 Ovary_Strain_160_ovidised	V053 head	SRR6040685 embryo	Pahrg_0-2h_embryos_total	SRR6040681 Arge9_testes_total	V116 male body

Show Alignment With Reads:

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dvi-291		dvi_291	CAACACTGGCTGAATGCAAGCTG--GCCACCTGAGCGCAGG------CATGTGGC----TGGTGGCTGCGACAGGGATTTTTGGCAAATGATGCACAGAGCTGTTGCTGCCGTCAGAGCCTGTTGGCCAATCAGCGACCGTTGCGTTCAGTGTGCGAGCGAGCTGGC----------
drosRU3	chrX:8[illegible]:2[illegible]:-		[illegible]
drosRU3	chrX:8[illegible]:2[illegible]:-		CAACACTGGCTGAATG[illegible]GCT--G[illegible]ACCTGA[illegible]G[illegible]GCAGCAGG[illegible]CATGTGGC[illegible]TGGTGGCTGCGACAGGGA[illegible]TTTTGGCAAATGATGCA[illegible]AGAGCTGTTGCTGCCGTCAGAGCCTGTTGGCCAATCAGCGACCGTTGCGTTCAGTGTGCGAGCGAGCTGGC----------
drosFR3	Scaffold_14853:1617530-1661528:+		CAACACTGGCTGAATG[illegible]G[illegible]ACCTGA[illegible]G[illegible]GCAGCAGG[illegible]CATGTGGC[illegible]TGGTGGCTGCGACAGGGA[illegible]TTTTGGCAAATGATGCA[illegible]AGAGCTGTTGCTGCCGTCAGAGCCTGTTGGCCAATCAGCGACCGTTGCGTTCAGTGTGCGAGCGAGCTGGC----------
dp5	AL_group14:3289265-3289426:-		GG[illegible]CCAATCAGCGACCGTTGCGTTCAGTGTGCATGCGAT
drsEle1	chr[illegible]:4[illegible]:-		[illegible]
drsEle1	chr[illegible]:4[illegible]:-		CUTT[illegible]CCAATCAGCGACCGTTGCGTTCAGTGTGCGAGCGAGCTGGC----------
drsEle1	chr[illegible]:4[illegible]:-		[illegible]CCAATCAGCGACCGTTGCGTTCAGTGTGCGAGCGAGCTGGC----------

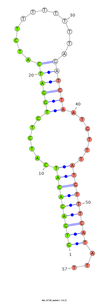
Generated on 2025-07-28 09:13 PM

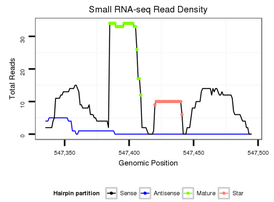
version	1.0
species	dvi
chrom	scaffold_12928
strand	+
chr_start	1088734
chr_end	1088793
genomic_locdi	intergenic
mature_strand	both
mature_alignment	
mature_coordinates	

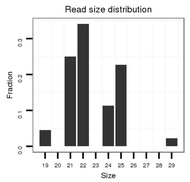
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_4736	**scaffold_12875:547385-547445 +**	**confident**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

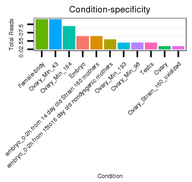
Legend: mature star mismatch in alignment mismatch in read

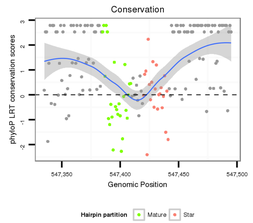
Predicted structure











Show Alternate Folds

Flybase annotation

intron [DviGG21226-in]; CDS [DviGG21226-cds]; CDS [DviGG21226-cds]

No Repeatible elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GGCGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGG	Read # size	Mismatch	Hit Count	Total Norm	Total	M047 female body	SRR2096055 Ovary_Min_43	SRR2096059 Ovary_Min_164	SRR2096014 Ovary_Strain_160_oxidised	SRR2096060 Ovary_Min_193	SRR2096057 Ovary_Min_50	M061 embryo Strain 160 mothers	SRR2096050 embryo_0-2h from 14 day old 160_0-2h_embryos_total	SRR060663 160a9_0-2h_embryos_total	SRR060684 160a9_0-2h_embryos_total	SRR060688 160_ovaries_total	SRR2096058 Ovary_Min_98	SRR060667 160_females_carcasses_total	SRR060669 160a9_females_carcasses_total	SRR060677 Arga9_ovaries_total	SRR060689 160a9_testes_total	SRR2096013 Ovary_Strain_9_oxidised	SRR2096081 embryo_0-2h from 15to16 day old nondyspenic mothers	SRR060687 9_0-2h_embryos_total	V053	M028	SRR2096079 embryo_0-2h from 15to16 day old dyspenic mothers	SRR060686 Arga9_0-2h_embryos_total	SRR060656 9x160_ovaries_total	SRR060668 160a9_males_carcasses_total	SRR060678 9x140_testes_total	SRR060680 Â 9xArg_testes_total	SRR060681 Arga9_testes_total	SRR060685 9xArg_0-2h_embryos_total	SRR1106724 embryo_12-14h	SRR2096072 embryo_0-2h from 15to16 day old dyspenic mothers	SRR2096080 embryo_0-2h from 15to16 day old nondyspenic mothers	SRR1106729 V116 mixed male whole adult body	
((((((((((.....(((((((.....))))))).....))))))))))	25	0	1	10.00	10	0	0	0	1	0	0	0	3	0	0	1	0	0	0	0	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
GTGAGACATCATCTCTGGATCATCT	22	0	1	9.00	9	0	3	2	0	0	0	1	1	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
GTGAGACATCATCTCTGGATC	21	0	1	7.00	7	0	0	5	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
GTGAGACATCATCTCTGGATCATCT	22	0	1	5.00	5	3	0	0	0	0	0	0	0	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
GTGAGACATCATCTCTGGATCATC	24	0	1	5.00	5	0	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ACGCCTCCAGCTCTTCTG	19	0	1	4.00	4	0	0	0	0	0	0	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
TCTAATGTTTATGTTTCATATT	21	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	0	0	0	0	0	0	0	0	0	0	0
GGCATGCTTTGTCGCTGGTTC	19	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTTTGTCGCTGGTTCAAATATT	22	1	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
TCGCTGGTTCAAATATCTTTACGAT	25	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
TGCTACACGAGAATTTCCCAAGGCGA	28	2	1	2.00	2	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
ATGCTTTGTCGCTGGTTC	18	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
CAAATATCTTTACGATT	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	0	0	0	0	0	0	0	0	0	0	0
TGCTACACGAGAATTTCCCAAG	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	0	0
GTGAGACATCATCTCTGGA	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AATATCTTTACGATTCCGAGATCA	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
TTTGTCGCTGGTTCAAATATCTTTACGA	28	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	0	0
CTAATGTTTATGTTTCATATT	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TCGCTGGTTCAAATATCTTTACGAT	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
CTACGCCCTGCAGCTCTTCTGCTACAACGAGAATTTCCCCAAGG	44	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	1	0	0	0	0	0
ACGCCTCCAGCTCTTCTGCTACAACG	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
GGCGCTCTACGCCCTGCAGCTCTCTGCT	29	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	0	0	0
ACGCCTCCAGCTCTTCT	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	1	0	0	0	0	0	0	0	0	0	0	0	0	0
TCTTTACGATTCCGAGATCA	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	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CGCTGGTTCAAATATCTTTACGAT	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	1	0	0	0	0	0	0	0	0	0	0	0	0	0
CCTGCAGCTCTTCTGCTACAACGAGAAT	28	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	0	0
TCTCTTCTGCTACAACGAG	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ACAGAGAATTTCCCAAGGCG	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
TCGCTGGTTCAAATATCTTTACGATT	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	1	0	0	0	0	0	0	0	0	0	0	0	0	0
GGCGCTCTACGCCCTGCAGCTCTTC	25	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	0	0
GTGAGACATCATCTCTGGATCATCTTTTT	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
ATGCTTTGTCGCTGGTTCAAAT	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	1	0	0	0	0	0	0	0	0	0	0	0	0	0
TACGCCCTGCAGCTCTTC	18	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	0	0	0	0	0	0	0	0	0	0	0
CTTTACGATTCCGAGATCATT	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	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
AATATCTTTACGATTCCGAGATCATT	26	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	0	0
TGCTTTGTCGCTGGTTCAAATATC	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CTACGCCCTGCAGCTCTTCTGCTACAACG	29	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	0	0	0
CTCTTCTGCTACAACGAG	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	0	0	0	0	0	0	0	0	0	0	0
ACAACGAGAATTTCCCAAGGCG	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	1	0	0	0	0	0
CTACAACGAGAATTTCCCAAGGCG	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	0	0
TCTTTGTCGCTGGTTCAAA	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	1	0	0	0
CAAATATCTTTACGATTCCGAGA	23	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

Anti-sense strand reads

CCGCGAGATGCGGGACGTCGAGAAGACGATGTTGCTCTTAAAGGGTTCC	Read # size	Mismatch	Hit Count	Total Norm	Total	SRR2096057 Ovary_Min_50	SRR2096058 Ovary_Min_98	V116 mixed male body	SRR060645 9_females_carcasses_total	SRR2096014 Ovary_Strain_160_oxidised	SRR2096060 Ovary_Min_193	SRR060663 160_0-2h_embryos_total	SRR060666 160_males_carcasses_total	V053 head	SRR2096056 head Ovary_Min_46	M061 embryo	SRR060684 140a9_0-2h_embryos_total	SRR060687 9_0-2h_embryos_total
((((((((((.....(((((((.....))))))).....))))))))))	21	0	1	3.00	3	1	1	0	0	0	1	0	0	0	0	0	0	0
CCGCGAGATGCGGGACGTCGA	20	0	1	1.00	1	0	0	0	0	1	0	0	0	0	0	0	0	0
CGATGTGCTCTTAAAGGGTTCCCACT	28	0	1	1.00	1	0	0	0	0	0	0	0	0	0	0	0	0	0
CCGCGAGATGCGGGACGT	18	0	1	1.00	1	0	1	0	0	0	0	0	0	0	0	0	0	0
CGAGATGCGGGACGTCGAGAA	21	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_12875:547335-547435 +	dvi_4736	GGCGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------CA--------CT--CTGGATC----A---TCTTTT--------TG----------TAG--AGGAATGTTTATGTTTCCCAAGGCATATTCAGGCGATGCTTTGTCGCTGGTTCAAATATCTTTACGATTCCGAGATCATTGAG
droMoj3	scaffold_6496:3546324-3546490 +		GGCGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--TATAAT--------A---------T--TGCTTTGTCGCTGGTTCAATATCTCACGATTCCGAGATCATTGAG
droGri2	scaffold_10245:10417232-10417390 +		GGCGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGTAGC---AGTC-A--------AATTTCAA--TC--A-C---ACCCATAT-------TTATC----------A--T----------A-T---TTATTATTTCTTATAGGCATGCTCTGCGCTGGTTCAAATATCTTACGATTCCGAGATCAT-GAG
droWil2	Super_11000000245101:1088375-1088515 +		GACGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--CCAGCGTAATGAATTCAA-CC--A-C---------TCCC--ACCAATTCTTATCTACC--------A---------T--A-C--A-C---TTTTTATCATCTTAGGCATGCTCTGCGCTGGTTCAAATATCTCATATTCGATTCCGAG
dp5	Super_15:1435638-1435878 +		GACGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--TATGCGAATGTCCCCCTAAC--------A---------T--A-C--C-A-TTTTTATCATCTTAGGCATGCTCCGCGCTGGTTCAAATATCTCACGATTCCGAGATCAT-GAG
droPer2	Scaffold_4:4382037-382237 +		GACGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--TATGCGATGAAGAATGTCCCCCTAAC--------A---------T--A-C--C-A-TTTTTATCATCTTAGGCATGCTCCGCGCTGGTTCAAATATCTCACGATTCCGAGATCAT-GAG
droAna3	Scaffold_13:3266:8235116:8238167 +		GACGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--CCAGCGCATGCAGCTCAA-CC--A-C---------TCCC--ACCAATTCTTATCTACC--------A---------T--A-C--A-C---TTTTTATCATCTTAGGCATGCTCCGCGCTGGTTCAAATATCTCATCGATTCCGAG
droRip1	Scf718500095839:435526-435687 +		GACGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--CCAT-CCC-T--A-C---------TCCC--T-------------------A-AAA-CAAAAATCAATTTTTTTCCCCTAAC--A---------T--TTTT--A-C---TTTTTATCATCTTAGGCATGCTCTGCGCTGGTTCAAATATCTTTACGATTCCGAGATCATTGAG
droKik1	Scf718500002670:237212-237392 +		GACGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--TGATGC--TGAGTCC-T--A-C---------TCCC--T-------------------A-AGCCA-TAAACCCCTGCCCCCTAAC--A---------T--TTTT--A-C---TTTTTATCATCTTAGGCATGCTCTGCGCTGGTTCAAATATCTCATCGATTCCGAGATCAT-GAG
droFic1	Scf718000045406146890-446424 +		GGCGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--CTTC-TC--C-A-C---------TCCC--T-------------------A-CCGTA-CAGTTTTTTTCCCCTAAC--A---------T--TTTT--A-C---TTTTTATCATCTTAGGCATGCTCTGCGCTGGTTCAAATATCTTTACGATTCCGAGATCAT-GAG
droEle1	Scf718000049215:234341-234513 +		GGCGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--ACC-A-C---------TCCC--T-------------------A-CCGTA-CAGTTTTTTTCCCCTAAC--A---------T--TTTT--A-C---TTTTTATCATCTTAGGCATGCTCTGCGCTGGTTCAAATATCTTTACGATTCCGAGATCAT-GAG
droRho1	Scf718000079957:87201-87368 +		GGCGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--GCA---------A---------T--TCCC-TAATT--------ATTT----------TCCCATTCCC-TTTATCATCTTAGGCATGCTCTGCGCTGGTTCAAATATCTTTACGATTCCGAGATCAT-GAG
droBia1	Scf718000002292:1855365-1855508 +		GGCGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--GCA---------A---------T--TCCC-TTTCC--T-A-C---------TCCC--T-------------------A-CCGTA-CAGTTTTTTTCCCCTAAC--A---------T--TTTT--A-C---TTTTTATCATCTTAGGCATGCTCTGCGCTGGTTCAAATATCTTTACGATTCCGAGATCAT-GAG
droTak1	Scf718000015782:325346-325531 +		GGCGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--GCA---------A---------T--TTTCCC-TTTCC--T-A-C---------TCCC--T-------------------A-CCGTA-CAGTTTTTTTCCCCTAAC--A---------T--TTTT--A-C---TTTTTATCATCTTAGGCATGCTCTGCGCTGGTTCAAATATCTTTACGATTCCGAGATCAT-GAG
droEug1	Scf718000040472:1823301-1823461 +		GGCGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--GCA---------A---------T--GTTT-TTT--T-A-C---------TCCCAAACA-CAGTTTTTTTCCCCTAAC--A---------T--TTTT--A-C---TTTTTATCATCTTAGGCATGCTCTGCGCTGGTTCAAATATCTTTACGATTCCGAGATCAT-GAG
dmJ	GRZ28:8815266-8816433 +		GGCGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--ATTT-TAA--C---A---------A--A-C-T---------TTATC----------A--T--A-CCGTA-CAGTTTTTTTCCCCTAAC--A---------T--TTTT--A-C---TTTTTATCATCTTAGGCATGCTCTGCGCTGGTTCAAATATCTTTACGATTCCGAGATCAT-GAG
droCan2	Scf718000014182555:824061 +		GGCGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--GTGC---------A---------T--ATT-TAA--C---A---------A--A-C---------TTATC----------A--T--A-CCGTA-CAGTTTTTTTCCCCTAAC--A---------T--TTTT--A-C---TTTTTATCATCTTAGGCATGCTCTGCGCTGGTTCAAATATCTTTACGATTCCGAGATCAT-GAG
droTak3	GR:3139236:3139320 +		GGCGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--GCA---------A---------T--TTTT-TTT--T-A-C---------TCCC--T-------------------A-CCGTA-CAGTTTTTTTCCCCTAAC--A---------T--TTTT--A-C---TTTTTATCATCTTAGGCATGCTCTGCGCTGGTTCAAATATCTTTACGATTCCGAGATCAT-GAG
droEre2	Scaffold_4845:1701382-1701368 -		GGCGCTCTACGCCCTGCAGCTCTCTGCTACAACGAGAATTTCCCCAAGGTGAGACAT--------A---------T--GCA---------CA---------T--ATT-TAA--C---A---------A--A-C---------TTATC----------A--T--A-CCGTA-CAGTTTTTTTCCCCTAAC--A---------T--TTTT--A-C---TTTTTATCATCTTAGGCATGCTCTGCGCTGGTTCAAATATCTTTACGATTCCGAGATCAT-GAG

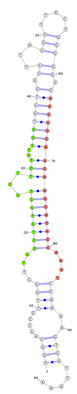
Generated: 09/08/2015 at 07:30 PM

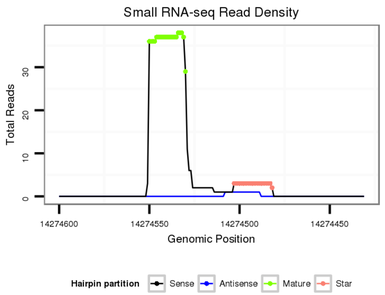
PASSFAIL	
crit.star	1
crit.loop	0
crit.stem	0
crit.half	0
crit.total	1
crit.bulge	0
crit.bp3	1
crit.bpsp3	1
crit.bp5	1
crit.back	1
rescue.total	0
rescue.mature	0
rescue.known	0
rescue.confident	0
rescue.candidate	0

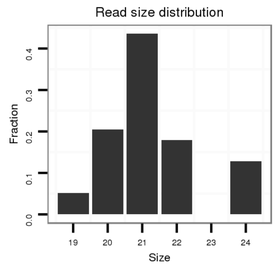
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_178	**scaffold_12875:14274481-14274550 -**	**confident-exception**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser [Cornell Mirror]]

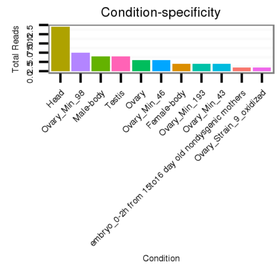
Legend: mature star mismatch in alignment mismatch in read

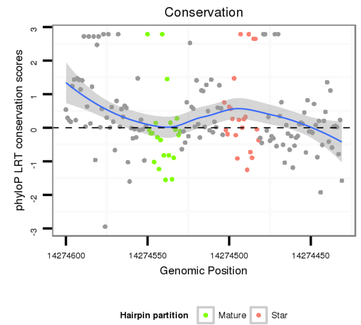
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [DvirGJ20282-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

GTATCAGTTCTATCTGCTGGATGTAATTAGCTTTGTGGCAGCCGTTGGCTTGGCTGTGCTCCTTCTGCTGCTGCTGGCCTTACGCTTGCTGCGGGGCAGCGGCAAGAAGCATAGCAAATCCAAAAGTCATTAAATCATCAACTATTTAATCTAGCTGCAATTATTGCCGT						M028	SRR2096058	M027	SRR2096056	SRR2096060	SRR2096055	M047	SRR060655	SRR060657	SRR060665	SRR060673	SRR060676	SRR060677	SRR060679	SRR060681	SRR2096013	SRR2096080			SRR1106720
**********	Read # size	Mismatch	Hit Count	Total Norm	Total	head	Ovary_Min_98	male body	Ovary_Min_46	Ovary_Min_193	Ovary_Min_43	female body	9x160_testes_total	140_testes_total	9_females_carcasses_total	9_ovaries_total	9xArg_ovaries_total	Argx9_ovaries_total	140x9_testes_total	Argx9_testes_total	Ovary_Strain_9_oxidized	embryo_0-2h from 15to16 day old nondysgenic mothers	V053 head	M061 embryo	embryo_8-10h
**********	21	0	1	16.00	16	5	4	3	2	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
**********	20	0	1	7.00	7	2	0	0	0	0	0	0	0	1	0	0	1	0	0	1	0	1	1	0	0
**********	22	0	1	5.00	5	2	0	1	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0
**********	24	0	1	4.00	4	1	1	0	0	1	1	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
**********	22	0	1	2.00	2	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0
**********	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
**********	22	2	1	1.00	1	0	0	0	0	1	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
**********	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
**********	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
**********	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	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

Anti-sense strand reads

CATAGTCAAGATAGACGACCTACATTAATCGAAACACCGTCGGCAACCGAACCGACGAGGAAGACGACGACGACCGGAATGCGAACGACGCCCCGGTCGCCGTTCTTCGTATCGTTTAGGTTTTCAGTAATTTAGTAGTTGATAAATTAGATCGACGTTAATAACGGCA						GSM1528803	SRR1106722	V047
**********	Read # size	Mismatch	Hit Count	Total Norm	Total	follicle cells	embryo_10-12h	embryo
**********	20	0	1	1.00	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12875:14274431-14274600 -	dvi_178	GTATCAGTTCTATCTGCTGGATGTAATTAGCTTTG---TGGCAGCCGTTGGCTTGG---CTGTGCTCC-TTCT----------GCTGCTGCTGGCCTTACGCTTGCTGCGGGG----------CAGCGGCAAGAAGCATAGCAAATCCAAAAGTCATTAAATCATC--AACTATTTAATCTAG----------CTGCAATTATTGC--CG--T
droMoj3	scaffold_6496:9721249-9721424 -		GTATCAGTTCTATTTGCTGGATGTGATTGCATTGCCTTTG---TGACAGTGATTGCACTGG---CCCCCTGTTGTCT----------GCTCTGCTGGCCATACGCTGCTGCAGGG----------CAGCGGCGAAGCAGCAAAGTGAAAACACATTAACTCAATT--------GATCGTATAAATTCTAGTTTCAATTACTGGCTTGC--A
droGri2	scaffold_2262:1553-1730 +		GTATCAGTTCTATCTGCTGATGTGATTGCTTTTG---TGACAGTGATTGCCTTGG---CTGTGTGTCT----------CCCGGTGCTGGCCATCGCTGTGCAGGAA----------CAGCGCAGAACAGCATATGCAAAATGAAAGCAAATTAAATGTACT--------GAATTAGTAATTAATATTGTATTTAACAAATCAAATG
droWil2	scaf2_11000000004514:111631-116475 +		GGTCAGTTCTATCTGCTGATGTGATTGCCTTTG---TGGCTCAGCATGTTTTGG---TCTCTTCTGCTTGG----------GCTCTGCTGGCCATCGCCATTTAAGG----------TGCTTACAAAAAGCAATATAGCTTAAAAAGCAATCTGTTTATATCA-ATTTCGTGCAC----------AATAT--------T---T
dp5	3:3573039-3573172 -		GTTCCAGTTCTATCTGCTGGATGTGATTGCCTTTG---TGGCTGCCATTGCCTTGG---CCCCTCTGTTGT-TGGC----------CGCCTGTTGCCATCGCCTGCTGATGGG----------CAGCGCAAACAGCACAGAAATCCAAGCAGCAGTGAA-----T----------T----------T--T-T
droPerZ	scaffold_23761681-3761814 -		GTTCCAGTTCTATCTGCTGGATGTGATTGCCTTTG---TGGCTGCCATTGCCTTGG---CCCCTCTGTTGT-TGGC----------CGCCTGTTGCCATCGCCTGCTGATGGG----------CAGCGCAAACAGCACAGAAATCCAAGCAGCAGTGAA-----T----------T----------T--T-T
droAna3	scaffold_13266:4882184-4882337 -		GTATCAGTTCTATCTGCTGGATGTGATGCGCATGG---TTTGCGCCATATTTTCCCTTCCCATTG-CTGTATA-------CTTCTATTTTTGG--AAAAGTCTCAAATAAGATGGTCAAGAAGATTAGCCTTTT-------TGCAAT------T--T
droBip1	scf7180000396566:525316-525458 +		CATCTTCTG----------ATAAATAGCATTG---TATCCTGTTATCCTCTGCTGCGATTCGTGTGG-AAATTTGTTTGG--AAGAAGCTAGA------AGCAAGCGAA---AAGGTCTTCCAAAAGTCCCAAAAACAAAAGAAGAATTAGTT----T-------TAATT--T----------T----------A--T
droKik1	scf7180000302471:308064-308241 +		GTTCCAAGTGCCTTTTTATCCTCTTTGTGTTCTATGGGCAGTTCTACGCCCTTGTGTGTTGTGGG-AGTCCTGGCTTG--TGCGCGCCCTA------TGTTGCAGAAAAA---CTAGAATGCCAAGTTCTCC-----AAATGTAAATTTAGTTTCC--ATGTGCGGAATATAA----------TGCAATCATGC--AG--T
droFic1	scf7180000453811:176880-177012 +		CATTCAGTTCTATCTGCTGGATGTGATAGCTTTG---TCTGCTGTTATCTTCGAGTTTGCAATTGGAAATG-GAG----------CTTCGCTTGGCCATTCGCTGCTGATGGG----------CAGTAACAGCAAGCAAGCAAGCTGAAAAACAATTAA-----T----------T----------T----------T--T-T
droEle1	scf7180000491232:282879-283011 +		GTTCCAGTTCTATCTGCTGATGTAGATGCATTTG---TGGCCTTCATTGGCTTGA--CCTGCATCC-TGGC----------CTTCTATTTGCCATTCATTGCTGATGGG----------CAGTAACAAAAAGCAGCAGCAAGCTTAAGCAAAAATAA-----T----------T----------T----------T--T-T
droRho1	scf7180000780219:71830-71962 -		GTTCCAGTTCTATCTGCTGCAGCTGATGCAGCTTTG---TGGCCCTTCATTCTTTGA--CTTGAATCC-TGCC----------CTTTGCATTGCCATTCATTGCTGATGGG----------CAGTAACAAAAAGCAGCAGCAAGCTAAGCAAGAATTAA-----T----------T----------T----------T--T-T
droBia1	scf7180000302143:1316499-1316632 +		GTTCCAATTTCTATTTGCTGAAGTGCCGCCTTTG---TGGCTGCCTTCCTTTGG---CAGAATCC-TGTC----------CTTCTATTGGGCTATTCATTTGCTAATGGG----------CAGTAACAAAAAGCACAGCAAGCCCAAGCAAAATTAGA-----T----------T----------T----------T--T-T
droTak1	scf7180000410787:39215-39370 +		GTTCCAATTCTATTTGCTGGATGTGCGTGGCTTTG---TGGCGCATTATTGCTTTGA--GTGCAATTC-TGGC----------CTTCTGTTGGGCTATTCATTTGCTAATGGG---TTAGCAA---CAGCAACAAAAAGTGAGCAAGGCTAAGCAAAAATAAAATCC-T--------ATTAA----------GATTT--------T--T-A
droEug1	scf7180000409474:843257-843389 +		GTTCCAATTCTATTTGCTGGATGTGATAGCATTTG---TGGCCTTCATTCTTTGA--CTTGAATCT-TGC----------CTTCTATTGGGCCATTCATTGCTGATGGG----------CAGTAACAAAGCAAAGCAAAGTAAGCAAAGCAAATAA-----T----------T----------T----------T--T-T
dm3	chr2R:17103019-17103156 -		GTTCCAATTTCTATTTGCTGGATGTGATAGCATTTG---TGGCTATCATTTCTTTGG---CTTGCGCTCA-TGGC----------TTCTCATTGGGCCATTCCTTTATGAATGGG----------CAGTAACAAGAAACACAGCAAGCTAAGCAAAATTAAAGTATT-T----------T----------T----------T--T-T
droSim2	scaffold_9142923:6-17658139 +		GTTCCAATTTCTATTTGCTGGATGTGATAGCATTTG---TGGCTATCATTTCTTTGG---CTTGCGCTCA-TGGC----------TTCTCATTGGGCCATTCCTTTATGAATGGG----------CAGTAACAAGAAACACAGCAAGCTAAGCAAAATTAAAGTATT-T----------T----------T----------T--T-T
droYak3	2R:12086802-12086963 +		GTTCCAATTTCTATTTGCTGGATGTGATAGCATTTG---TGGCTATCATTTCTTTGG---CTTGCGCTCA-TGGC----------TTCTCATTGGGCCATTCCTTTATGAATGGG----------CAGTAACAAGAAGACACAGCAAGCTAAGCAAAATTTGAATCATTTTACGGGGTTTAATTAAA----------GTAAA------T--T-T
droEre2	scaffold_4845:11246360-11246521 -		GTTCCAATTTCTATTTGCTGGATGTGATAGCATTTG---TGGCTATCATTTCTTTGG---CTTGCGCTCA-TGGC----------TTCTCATTGGGCCATTCCTTTATGAATGGG----------CAGTAACAAGAAGACACAGCAAGCTAAGCAAAATTTAAAATATTGTTCAAGGGTTTAATTAAA----------ATGCAA------T--T-T

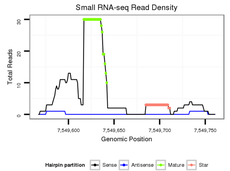
Generated: 09/08/2015 at 08:37 PM

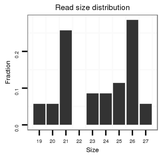
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	1
crit.total	1
crit.pairing	1
crit.top3	1
crit.stem	0
crit.back	1
rescue.total	0
rescue.dominant	0
rescue.known	0
rescue.confident	1
rescue.candidate	0

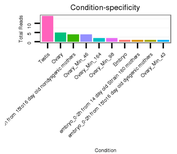
ID:	Coordinate:	Confidence:	Class:	Genome Locale:	
dvi_9288	**scaffold_12928:7549617-7549711 +**	**confident**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

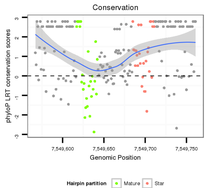
Legend: seed; nt; nt mismatch in alignment; mismatch in seed

Predicted structure









Show Alternate Folds

Flybase annotation

intron [Dvir(GI17971-ia), CDS [Dvir(GI17971-cds), CDS [Dvir(GI17971-cds]

No Repeatmir elements found

Sense Strand Reads

hide 5p reads show mid mismatch reads

Read #	Hit Count	Total Nucs	Total Total	GEM528803 Argentina_testes_total	GEM528803 Argentina_total	SRR2096056 follicle cells	SRR2096056 Ovary_Min_46	SRR2096056 140_testes_total	SRR2096056 body	W047 female 140_ovaries_total	SRR2096058 9_testes_total	SRR2096058 Argo9_testes_total	SRR2096058 embryo	SRR2096058 160a9_testes_total	M041	SRR2096089	SRR2096059 Ovary_Min_144	SRR2096059 9a140_testes_total	SRR2096059 2h_embryos_total	SRR2096082 9a149_0-2h_embryos_total	SRR2096055 Ovary_Min_43	SRR2096058 Ovary_Min_98	SRR2096060 Ovary_Min_193	SRR2096080 embryo_0-2h from 15to16 day old nondypenic mothers	SRR2096081 embryo_0-2h from 15to16 day old nondypenic mothers	SRR2096057 male body	W029 male head	W028 body	SRR2096055 9a160_testes_total	SRR2096060 Argentina_ovaries_total	SRR2096068 160a9_males_carcasses_total	SRR2096073 9_ovaries_total	SRR2096075 140a9_ovaries_total	SRR2096076 9a4rg_ovaries_total	SRR2096079 140a9_testes_total	SRR2096080 A 9a4rg_testes_total	SRR2096086 Argo9_0-2h_embryos_total	SRR2096088 160_ovaries_total	SRR1106715 embryo_4-6h	SRR1106723 embryo_14-16h	SRR2096041 embryo_0-2h from 14 day old Strain 160 mothers	SRR2096072 embryo_0-2h from 15to16 day old dypenic mothers	V053 head	SRR2096071 9a160_males_carcasses_total	SRR2096069 160a9_females_carcasses_total	SRR2096074 9a140_ovaries_total
size	Mismatch	Count	Nucs	Total																																												
26	0	1	10.00 10	0			0	1	0	0	0	0	0	0	0	0	0	0	1	1	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
21	0	1	7.00 7	0			0	1	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	0	0	0	0	0	0	0
23	0	1	3.00 3	0			0	0	0	0	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	0	0	0	0
24	0	1	3.00 3	0			0	0	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	0	0
25	0	1	3.00 3	0			0	0	0	0	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	0	0	0	0	0	0	0	0	0	0	0	0	0
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17	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	0
20	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	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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	0	0	0	0	0	0
21	0	1	2.00 2	0			0	0	0	0	0	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	0	0	0	0	0
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	0
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	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	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
20	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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	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	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	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	0	0	0	0	0	0
19	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	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	0	0	0	0	0	0	0
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	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	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	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	0
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	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	0	0	0	0	0	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	0	0	0	0	0	0	0	0	0	0	0	0	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	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	0	0	0	0	0	0
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	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

Read #	Hit Count	Total Nucs	Total Total	GEM528803 follicle cells	GEM528803 160_ovaries_total	SRR2096089 male body	W027 Ovary_Strain_8_ovidized	SRR2096013 embryo_0-2h	SRR2096055 Ovary_Min_43	V047 embryo	W041 embryo
size	Mismatch	Count	Nucs	Total							
21	0	1	1.00 1	0	1	0	0	0	0	0	0
20	0	1	1.00 1	0	1	0	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
dsrv(+)	scaffold_12928:7549617- 7549711:+	dvi_9288	CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsim(3)	scaffold_6473:2683773- 2683838:-		CCTCGATTGGTTCGCAGGGCACTGCGGGTCTGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsrv(2)	scaffold_14853:9023236- 9023261:-	dsr_L16	CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsim(12)	scaffold_13000000043591:4727566- 4727681:+		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
5p5	ss_group1:6:7337:4:7133:1		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsrv(+)	scaffold_6:15136934:15137126:+		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsim(2)	scaffold_14930:2111138- 2111208:-		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsim(2)	scaffold_6500001962782:3914747- 3914818:-		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsim(2)	scaffold_6500001924966:1317026- 1317097:-		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsrv(2)	scaffold_6500001840721:1118204- 1118276:-		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsim(4)	scaffold_6500001491411:1006140- 1006213:-		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsim(6)	scaffold_6500001772886:760283- 760388:-		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsim(8)	scaffold_6500001501761:1314828- 1314898:-		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsrv(5)	scaffold_6500001415381:1137331- 1137404:-		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsim(9)	scaffold_6500001402631:935097- 935169:-		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsh3	chr3:6243676-6243745:+		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsrv(4)	scaffold_6500001[illegible]:1848194:+		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsrv(2)	scaffold_6500001[illegible]:5068548:-		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsrv(3)	scaffold_6500001[illegible]:2253119:-		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA
dsrv(6)	scaffold_6500001[illegible]:4609112:2657547- 2657619:-		CCTCGATTGGTTCGCAGGGCACCGTTGGCGGTCTCGTTGTTGCCGCATTGTAAATATTGGTTGTCTGCTGCCGTCTATTATACCGGCTGCCTGACAGGTGCTATTATATCGCTATGTTCCCCCTGATTATCGCCGGCTGCCGTTCTTGTTGGCATTGGTGCCCTCTA

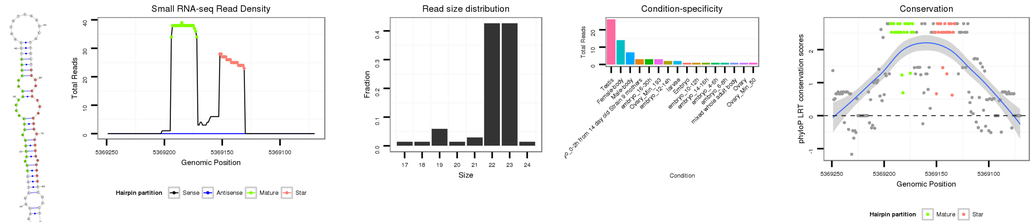
Generated: 09/05/2015 at 07:10 PM

```
      PASSPAL
    ------------
    crb.star    |
    crb.star    |
    crb.star    |
```

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_24642	**scaffold_12970:5369120-5369199 -**	**confident**	**Canonical miRNA**	**intron**
				[View on UCSC Genome Browser [CorcoLB Mirror]]

Legend: mature star mismatch in alignment mismatch to seed

Predicted structure



Show Alternate Folds

Flybase annnotation

intron [DviGI18884-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mrd mismatch reads

TCAGCTGCACAATTTTGGTTCCATATGGGTATACAAAGGGTTCTTTAAGAGGTTACTGATGGGACTCCACCTAGAACGATGTGGATATTAAGCATTGCTGCACTTCAGAGCCTCAGCATTACGCCTAGAGAAATATCAACTACGTTTACCTAAGATCCTAGAATAAAGGTGGCGGTGCAGG	Read #	Hit Mismatch	Total Count	Total Norm	Total	M047 female body	SRR060678 9x140_testes_total	SRR060681 Argx9_testes_total	SRR060679 140x9_testes_total	SRR060671 9x160_males_carcasses_total	SRR060665 9_females_carcasses_total	SRR060672 9x160_females_carcasses_total	SRR1106730 embryo_16-30h	SRR2096038 embryo_0-2h from 14-day old Strain 9 mothers	SRR2096060 Ovary_Min_193	M027 body	SRR060657 140_testes_total	SRR060683 160_testes_total	SRR1106728 larvae	V116 male body	W061 embryo	SRR060660 Argentina_ovaries_total	SRR060664 9_males_carcasses_total	SRR060666 160_males_carcasses_total	SRR060676 9xArg_ovaries_total	SRR060680 9xArg_testes_total	SRR1106716 embryo_4-6h	SRR1106717 embryo_6-8h	SRR1106722 embryo_10-12h	SRR1106723 embryo_12-14h	SRR1106724 embryo_14-16h	SRR1106725 mixed whole adult body	SRR1106729 embryo_0-2h from 14-day old Strain 9 mothers	SRR2096026 SRR2096057 Ovary_Min_50	V047 embryo	V053 head	SRR2096014 Ovary_Strain_160_oxidised	SRR2096072 embryo_2-2h from 15to16 day old dyegenic mothers
********** ((((((.(..((((((.(((((.(((((.(((((((.....))))))).)).)))).)))))).))))))).))))).....	size	Mismatch	Count	Norm	Total																																		
.....TGATGGGACTCACCTAGAACGAG.....	23	0	1	29.00	29	5	1	2	1	2	2	0	2	3	0	0	2	2	0	0	0	0	0	1	1	1	0	1	0	1	1	1	0	0	0	0	0	0	0
.....CGCACTTCAGAGCCTCAGCATT.....	22	0	1	23.00	23	0	6	1	2	1	0	0	1	0	3	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
.....GATGGGACTCACCTAGAACGAG.....	22	0	1	4.00	4	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0
.....TGATGGGACTCACCTAGAACGAG.....	24	1	1	2.00	2	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
.....TGGAGTATTAAGCATTGCT.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGATGGGACTCACCTAGAACGA.....	22	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGATGGGACTCACCTAGAACG.....	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
.....TCACCTAGAACGAGTGGA.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AGAGGTAGTGATGGGACT.....	19	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
.....GAATATTAAGCATTGCTCG.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GCATTGCTGCACTTCAGAGCTC.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0
.....TGATGGGACTCACCTAGAAC.....	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
.....TAAGCATTGCTCGCACT.....	17	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	0
.....CGCACTTCAGAGCCTCAGCAT.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....AGCATTGCTGCACTTCAG.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0

Anti-sense strand reads

AGTCGACGTGTTAAAACCAAGGTATACCCATATGTTCCGCAAGAATTCTCCATC ACTACCCTGAGTGGATCTTGCTC ACCTTATAATTCGTAACGA GCGTGAAGTCTCGGAGTCGTAA TGCCGATCTCTTTATAGTTGATGCAAATGGATTCTAGGATCTTATTTCACCGCCACGTCC	Read #	Hit Mismatch	Total Count	Total Norm	Total	V053 head	SRR060670 9_testes_total	SRR060672 9x160_females_carcasses_total
********** ((((((.(..((((((.(((((.(((((.(((((((.....))))))).)).)))).)))))).))))))).))))).....	size	Mismatch	Count	Norm	Total			

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
DroYak1	scaffold_12970:13639200-13639279:-	dvi_24642	TCAGCTGCACAATTTTGGTTCCATATGGGTATACAA----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------GGTGGCGGTGCAGG
DroMoj3	scaffold_6731:4951681-4951837:-:-	dmo_3154	ACTGCACAATTTTGGTTCCATATGGGTATACAAAGAACTGTGTTGCTTTT---TAAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATT---TGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACTGT-------------GTGTAGATACATTTTTTTTAGTATTATTTTTCTATAATACCACTGGTTGGTGGCGGTGCAGG
DroGri3	scaffold_15203:9467725-9467788:-	dgr_467	TCAGCTGCACATTTTGGTTCCATATGGGTATACAA--------AAGCTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA-AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACTGT-GTACAAAAGAAAATGTGTGTATACATTTTTTTTAGTGGCGGTGCAGG
DroWil2	scaffold_11000000004909:115061939-115062011:-		----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCCTGGGTTTCGAAGGAATGCGAATTATTTAAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------
Dp5	Dp_group3b:100283-100362:+	Dpg_160	----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------
DroPer2	scaffold_9511858:8128187:+	Dpe_137	----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------
DroAna2	scaffold_2338:42135:42282:-	Dan_8033	----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------
DroBip1	scf7180000396431:1081273:1081358:-		----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------
DroWil4	scf7180003026391:307851:307934:-		----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------
DroFic1	scf7180003545073:1443039:1443145:-		----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------
DroEle1	scf7180003491041:215117:215215:+		----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------
DroRho1	scf7180000779310:38440:38523:-		----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------
DroSim1	scf7180000302041:163722:163815:+		----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------
DroYak1	scf7180002414391:30873:30961:+		----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------
DroSuz1	scf7180002408358:35982-36065:-		----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------
Dm3	chrX:13533607-13533691:+		----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------
DroSim2	scf2830226:12830603:+		----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------
DroSec1	scf7180000_96:193548:193631:+		----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------
DroYak3	scf7180431:733534:3:+		----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------
DroRer2	scaffold_4690:13329705-13329788:+		----------AGCGTTCTTT---AAGAGGTAGTGATGGGACTCC---ACCTAGAACGATGTGGATATTA---AAGCATTGCTGCACTTCAG-AGCCTCAGCATTACGCCT-AGAGAAATATCAACT-AC---------GTTTACCTAAGATCCTAGAATA-AA----------

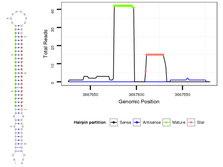
Generated 09/08/2015 at 09:14 PM

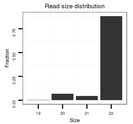
	PASS/FAIL
crit.star	1
crit.loop	0
crit.miss	0
crit.half	0
crit.total	1
crit.score	0
crit.bp3	1
crit.gc	0
crit.un	0
rescue.loop	0
rescue.miss	0
rescue.dominant	0
rescue.half	0
rescue.confident	0
rescue.candidate	0

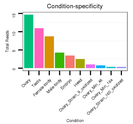
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_390	**scaffold_13049:36675570-36676624 -**	**confident**	**Canonical miRNA**	**intron**
				[View on UCSC Genome Browser (Crated Mince)]

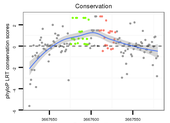
Legend: Loop 5p 3prime's 5b 3b 3prime's 3b 3b mismatch 5b mismatch

Predicted structure









Show Alternate Folds

Flybase annotation

mmu:Zfp423[ENSG]

Repeatable elements

Name	Class	Family	Divergence
MuSmel_Zfpm2	DNA	Zfp	0.0
ACATATAA	Simple_repeat	Simple_repeat	0.0

mature

```
1. scaffold_2267:64343-64424(+)
2. scaffold_3282:87438-87520(+)
3. scaffold_2961:98456-98537(+)
4. dvi_390 scaffold_13049:36675570-36676624 -
```

star

```
1. scaffold_4314:68-427 -
2. scaffold_2372:34-535(+)
3. scaffold_2372:70842-71040(+)
4. scaffold_2929:35843-35970(+)
5. scaffold_2929:35843-35970(+)
6. scaffold_2929:65115-65271 -
7. scaffold_2961:67866-67986(+)
8. scaffold_2961:67866-67986(+)
9. scaffold_2961:127578-127788(+)
10. dvi_2969 scaffold_2969:127788(1.127788)(+)
11. scaffold_3047:37-187(+)
12. scaffold_3047:37-187(+)
13. scaffold_3047:38477-38677(+)
14. scaffold_3047:38477-38677(+)
15. scaffold_3047:38477-38677(+)
16. scaffold_3282:98456-98656(+)
17. dvi_390 scaffold_13049:36675570-36676788 -
18. scaffold_3282:87438-87520(+)
19. scaffold_3282:87438-87520(+)
20. dvi_2969 scaffold_2969:2674424-2674524(+)
21. dvi_2969 scaffold_2969:2674424-2674524(+)
22. scaffold_2961:67866-67986(+)
23. scaffold_3282:87438-87520(+)
24. scaffold_2961:67866-67986(+)
25. scaffold_2962:6736-6919(+)
26. scaffold_2962:6736-6919(+)
27. scaffold_2962:6736-6919(+)
28. scaffold_3282:87438-87520(+)
29. scaffold_3282:87438-87520(+)
30. scaffold_3282:87438-87520(+)
31. scaffold_3282:51125-51244(+)
```

Sense Strand Reads

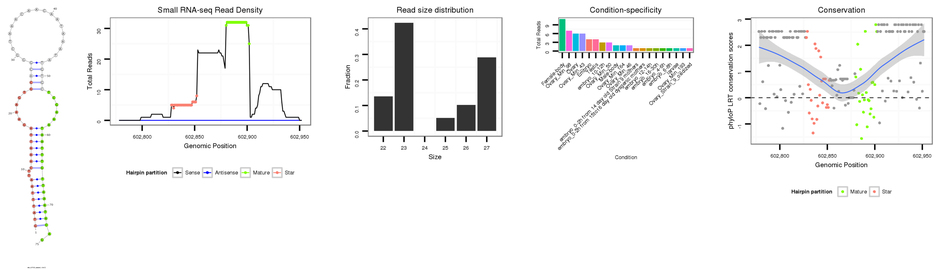
Hide 3p reads | show red mismatch reads

```
TTGTGATCGACGAAAATTGACGACAAATTTGAGTATATCCATTAACTAAAATGTATCGTTTTTTGATGCCAATTCACAAATCCCGCTACTCCTCCGCAACGCATCA
                                                
```

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dvi_17715	**scaffold_13049:602828-602902 +**	**confident-exception**	**Mirtron**	**intron**
				[View on UCSC Genome Browser (Cornell Mirror)]

Legend: **mature** **star** **mismatch in sfg seq** **mismatch in read**

Predicted structure



Show Alternate Folds

Flybase annotation

intron [DroVirGI12734-in], CDS [DroVirGI12734-cds], CDS [DroVirGI12734-cds]

No Repeatmiler elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

Read #	size	MismatchCount	Hit Num	Total Total	W047 female body	SRR2096055 Ovary_Min_43	SRR2096058 Ovary_Min_98	SRR2096056 Ovary_Min_46	SRR2096060 Ovary_Min_193	SRR060677 Arge9_ovaries_total	SRR060679 140x9_testes_total	SRR2096057 Ovary_Min_50	SRR060669 160x9_females_carcasses_total	SRR060676 9Akrg_ovaries_total	M028 male	M041 embryo	SRR060681 Arge9_testes_total	SRR1106722 embryo_10-12h	SRR2096059 Ovary_Min_144	SRR060665 9_females_carcasses_total	SRR060664 9_males_carcasses_total	SRR060671 9x160_males_carcasses_total	SRR060672 9x160_females_carcasses_total	SRR060674 9x140_ovaries_total	SRR060675 140x9_ovaries_total	SRR060678 9x140_testes_total	SRR060683 160_testes_total	SRR060684 140x9_0-2h_embryos_total	SRR060685 9Akrg_0-2h_embryos_total	SRR060686 Arge9_0-2h_embryos_total	SRR060687 9_0-2h_embryos_total	SRR1106715 embryo_4-8h	SRR1106718 embryo_6-12h	SRR1106721 embryo_10-14h	SRR1106724 embryo_12-larvae	SRR1106728 embryo_16-30h	SRR2096013 Ovary_Strain_9_ovidissed	SRR2096014 Ovary_Strain_160_ovidissed	SRR2096039 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096072 embryo_0-2h from 15to16 day old dygenic mothers	Y114 male body
CACAACAACCATGGTACGAAATTTGCCCGCAGTCGCCATGGATTATAAGGTATTTAATTCAAATTAGAAAGTGCACGGCTAAACAACAATAAATATGTG-TCGAAATAATTTGTTAAATACAGGTACACATAGATGCCGGCAAGGAGGACTGCTATCATCAGTATGTGCAGGC																																								
**********	Read # size	MismatchCount	Hit Num	Total Total	body	Ovary_Min_43	Ovary_Min_98	Ovary_Min_46	Ovary_Min_193	Arge9_ovaries_total	140x9_testes_total	Ovary_Min_50	160x9_females_carcasses_total	9Akrg_ovaries_total	head	embryo	Arge9_testes_total	12h	Ovary_Min_144								160_testes_total	2h_embryos_total	2h_embryos_total	2h_embryos_total	4h	8h	12h	14h	larvae	30h	Ovary_Strain_9_ovidissed	Ovary_Strain_160_ovidissed	mothers	mothers	body
.....	23	0	1	24.00	24	4	2	1	2	0	1	1	1	2		0	1	2	0	2	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	27	0	1	16.00	16	0	3	4	0	0	1	1	0	0		0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	22	0	1	6.00	6	2	0	0	0	0	0	0	0	0		0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
.....	23	1	1	4.00	4	0	0	1	0	0	0	0	0	0		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
.....	25	0	1	3.00	3	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	1	0	0	0	0
.....	26	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
.....	26	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	0
.....	26	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	0	0	0	0	0	0	0
.....	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	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	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	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	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	0	0	0
.....	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0
.....	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	0	0	0	0	0	0	0	0	0	0
.....	22	0	1	1.00	1	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
.....	18	0	1	1.00	0	0	0	0	0	0	0	0	0	0		0	0	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	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
.....	22	0	1	1.00	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
.....	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	1	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	0	0	1	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	0	0	0
.....	26	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
.....	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	0	0	0	0	0	0	0	0	0
.....	18	0	2	0.50	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	0
.....	18	0	2	0.50	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

Anti-sense strand reads

GTGTTGTTGGTACCATGCTTTTAAACGGGCGTCAGCGGTACCTAATATTCCAATAAATTAAGTTTAATCTTTCACGTGCCCGATTTGTTGTTATTTATACAC-AGCTTTATTAACCATTTATGTCCATGTGTATCTACGCCGTTCCTCTGACGATAGTAGTCATACACGTCCG

Read #	size	MismatchCount	Hit Num	Total Total	V053 head	SRR1106728 larvae
**********						

Show Alignment With Reads

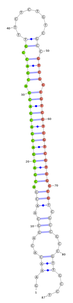
Re-alignment of all predicted orthologs

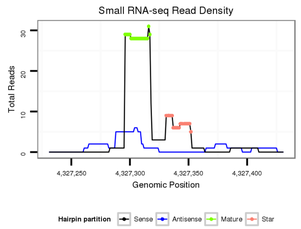
Species	Coordinate	ID	Alignment
			CACAACAACCATGGTACGAAATTTGCCCGCAGTCGCCATGGATTATAAGGTATTTAATTCAAATTAGAAAGTGCACGGCTAAACAACAATAAATATGTG-TCGAAATAATTTGTTAAATACAGGTACACATAGATGCCGGCAAGGAGGACTGCTATCATCAGTATGTGCAGGC
drosvir1	scaffold_13049:602778-602842, +	dvi_17715	CACAACCATGGTACGAAATTTGCCCGCAGTCGCCATGGATTATAAGGTATTTAATTCAAATTAGAAAGTGCACGGCTAAACAACAATAAATATGTG-CGTGGAGAAAGCCAATTTTT

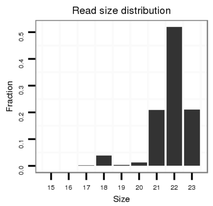
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_24645	**scaffold_13042:4327281-4327381 +**	**confident**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

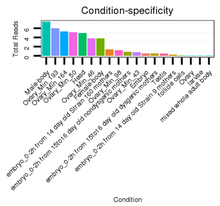
Legend: mature star sub-match in alignment mismatch in read

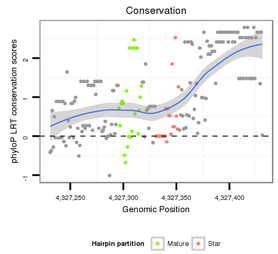
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
(CGA)n	Simple_repeat	Simple_repeat	+
(TCG)n	Simple_repeat	Simple_repeat	+

mature	star
1. scaffold_12970:11790250-11790271 + 2. dvi_24645 scaffold_13042:4327296-4327317 +	1. scaffold_10324:263128-263149 + 2. dvi_24645 scaffold_13042:4327331-4327352 +

Sense Strand Reads

hide 3p reads show mid mismatch reads

CAGAAAAATAAATACATTTTCGTTGTTTTTGCTGCTGCGTCAATTGAACGAAACACAGGCAACGACGACGACGACGACGACGACGACGTTTCTCTGTCGCCTTCGCCGTCGTCGTCGTCGCCGTCGCCGCCGTTGCCTCTATCCGCACAACACAAAAACAGTCAGTTTTCATTCTCATTTGACATCATCAACATTGAAAATT	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR2096060 Ovary_Min_193	SRR2096059 Ovary_Min_164	SRR2096057 Ovary_Min_50	M028 head	M027 male body	SRR2096056 Ovary_Min_46	V116 male body	M047 female body	SRR2096058 Ovary_Min_98	SRR2096061 embryo_0-2h from 14 day old Strain 160 mothers	SRR060672 9x160_females_carcasses_total	SRR060684 140x9_0-2h_embryos_total	SRR2096055 Ovary_Min_43	SRR2096081 embryo_0-2h from 15to16 day old nondypgenic mothers	M061 embryo	SRR060681 Argx9_testes_total	SRR2096072 embryo_0-2h from 15to16 day old dypgenic mothers	SRR2096014 Ovary_Strain_160_oxidized	GSM1528803 follicle cells	SRR060667 160_females_carcasses_total	SRR2096026 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096050 embryo_0-2h from 14 day old Strain 160 mothers	SRR2096079 embryo_0-2h from 15to16 day old dypgenic mothers	SRR2096080 embryo_0-2h from 15to16 day old nondypgenic mothers	SRR060666 160_males_carcasses_total	SRR060677 Argx9_ovaries_total	SRR060686 Argx9_0-2h_embryos_total	SRR1106728 larvae	SRR1106729 mixed whole adult body
ACGACGACGACGACGACGCG	22	0	2	17.50	35	5	0	6	4	3	0	3	5	0	2	2	0	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ACGACGACGACGACGACGTC	23	0	1	9.00	9	1	3	0	1	3	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
GTCGCCGTCGTCGTCGTCGCCG	22	0	2	4.00	8	1	3	3	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
CGTTTCTCTGTGCCGTGCCC	21	0	1	3.00	3	0	0	0	0	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
ACGACGACGACGACGACGAC	21	0	8	2.75	22	4	6	1	0	1	0	0	1	0	0	1	0	2	2	0	0	0	0	0	0	2	0	0	1	0	0	0	0	0	0
GTCGCCGTCGTCGTCGTCGCC	21	0	4	2.00	8	5	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
AACACAGGCAACGACGAC	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
GTCGTCGCCGTCGTCGCCGTT	21	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
AACAGTCAGTTTTCATTCTCATTT	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
GCCGTCGTCGTCGTCGCCGTCG	22	0	2	0.50	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
GTCGCCGTCGTCGTCGTCGCC	20	0	3	0.25	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
TCGCCGTCGTCGTCGTCGCC	20	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	1	0	0	0	0	0	0	0
GTCGCCGTCGTCGTCGTCGC	20	0	6	0.17	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
GACGACGACGACGACGAC	18	0	20	0.15	3	0	0	0	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
TCGTCGTCGTCGCCGTGCCG	21	0	7	0.14	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
CGCCGTCGCCGTCGTCGTC	19	0	20	0.10	2	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
GTCGCCGTCGCCGTCGTC	18	0	20	0.10	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
TCGCCGTCGCCGTCGTC	17	0	20	0.10	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0
GCCGTCGCCGTCGTCGTCG	22	0	17	0.06	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
CGTCGCCGTCGCCGTCGCC	19	0	19	0.05	1	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
AACGACGACGACGACGACGA	20	0	20	0.05	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
GTCGTCGTCGCCGTCGCC	18	0	20	0.05	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
GTCGCCGTCGCCGTCGCC	15	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	0	1
CGACGACGACGACGACGAC	22	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	0	0
AACGACGACGACGACGACG	22	0	20	0.05	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
GACGACGACGACGACGAC	16	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
TCGCCGTCGTCGTCGTCGC	18	0	20	0.05	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
CGACGACGACGACGACGACG	20	0	20	0.05	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
CAACGACGACGACGACGAC	22	0	20	0.05	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
CGTCGCCGTCGTCGTCGTCG	22	1	20	0.05	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
CGTCGCCGTCGTCGTCGTCG	20	0	20	0.05	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
GTCGCCGTCGCCGTCGTCGTC	21	0	20	0.05	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

Anti-sense strand reads

GTCTTTTTATTTATGTAAAAGCAACAAAAACGACGACGCGAGTTAACTTGCTTTGTGTCCGTTGCTGCTGCTGCTGCTGCTGGCAAAGAGACAGCGGCAAGCGGCAGCGGCAGCGGCGGCAGCGGCGGCGGCAACGGAGATAGGCGTGTTGTGTTTTTTGTCAGTCAAAAGTAAGAGTAAACTGTAGTAGTTGTAACTTTTAA	Read size	# Mismatch	Hit Count	Total Norm	Total	SRR2096055 Ovary_Min_43	SRR060656 9x160_ovaries_total	SRR2096059 Ovary_Min_164	SRR2096060 Ovary_Min_193	SRR060655 9x160_testes_total	M027 male body	SRR060658 140_ovaries_total	SRR060664 9_males_carcasses_total	SRR060673 9_ovaries_total	SRR060670 9_testes_total	V116 male body	SRR060678 9x140_testes_total	SRR2096080 embryo_0-2h from 15to16 day old nondypgenic mothers	SRR2096057 Ovary_Min_50	M028 head	SRR2096081 embryo_0-2h from 15to16 day old nondypgenic mothers	M047 female head body	SRR060677 Argx9_ovaries_total	SRR2096038 embryo_0-2h from 14 day old Strain 9 mothers	SRR2096056 Ovary_Min_46	V047 embryo
TCCGTTGCTGCTGCTGCTG	22	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	0
TCTCCGTTGCTGCTGCTGCTG	25	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	0
TCCGTTGCTGCTGCTGCTGCT	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	0
GGAGATAGGCGTGTTGTG	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
AGTAAACTGTAGTAGTTGTAAC	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
CTGCTGCTGCTGGCAAAGAGA	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	0	0
GACGCGAGTTAACTTGCTTTG	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
TCTCCGTTGCTGCTGCTGCTG	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	0	0
GCGTGTTGTGTTTTTGTCAGTCA	23	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
CTGCTGCTGCTGGCAAA	18	1	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
CGACGACGCGAGTTAACTTGC	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
GGCAGCGGCAGCAGCAGCGCG	22	0	2	0.50	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
GCGGCAGCAGCAGCAGCGGCA	21	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
AGCGGCAGCAGCAGCGGCGCA	22	0	2	0.50	1	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0
GCAGCGGCAGCAGCAGCGCG	21	0	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
CCGTTGCTGCTGCTGCTGCTGCT	26	0	8	0.25	2	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
GCGGCAGCAGCAGCAGCG	18	0	11	0.10	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
CCGTTGCTGCTGCTGCTGCTG	24	0	10	0.10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
CCGTTGCTGCTGCTGCTGCTGC	22	0	10	0.10	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
CTGCTGCTGCTGCTGCTGCT	20	0	20	0.10	2	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
CGTTGCTGCTGCTGCTGCTGC	21	0	14	0.07	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
CTGCTGCTGCTGCTGTGG	19	0	14	0.07	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GGGCAGCGGCAGCAGCAGCAG	21	0	20	0.05	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
TTGCTGCTGCTGCTGCTG	18	0	20	0.05	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GGCAGCGGCAGCAGCAGC	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	1
GCAGCGGCAGCAGCAGCAG	19	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
CGGCAGCGGCAGCAGCAGCA	18	0	20	0.05	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0

Show Alignment With Reads

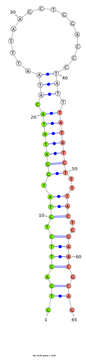
Re-alignment of all predicted orthologs

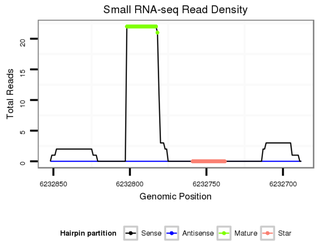
Species	Coordinate	ID	Alignment
droVir3	scaffold_13042:4327231-4327431 +	dvi_24645	CAGA-AAAATAAATACATTTTCG----------TT----------GTTTTTGCTGCTGC---G-CTCAATTGAACG-------AAACACAGGC------AACGACGACGAC---------GACGACGACGACGA----------CCGTTT--TCTCTGTCGCCGTGCGCCGTCGTCGTCGCCGTCGCCGCCGTTGCCTCTATCCGCCACACACAAAAACAGTCAGTTTTCATTCTCATTTGACATCATCAACATTGAAAATT
droMoj3	scaffold_6359:2105775-2105970 +	dmo_262	CA-A-AAAATAAATACATTTTCGTGTTTTTGCGCG----------TT-T-T-TTGCTGCTGC---G-CTCAATTGAACG-------AAACCAGGC------AACGA------------ACGAAACGACGA----------CCGTTT--TCTCG----------G-CGCGCGCGCGCGCGCG-------G-CGCGCGCGCGCG--AC--CACACAAAA--------ACAGTCAGTTTTCATTCTCATTTGACATCATCAACATTGAAAGCG
droGri2	scaffold_14853:7184289-7184509 +		CA-A----------AT-T-T----------CCGTTATTTGTTGTGTCGCGCTGCTGC-GCG-CTCAATTGAACG-------AAACAGAGGC-ACGACGCGACGTCGACGCGCGACGCGCGCGTCGCGCGCGCGCG

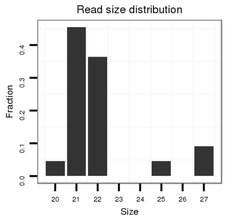
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dvi_4158	**scaffold_12855:6232738-6232802 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

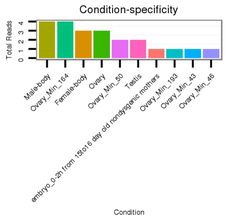
Legend: mature star mismatch in alignment mismatch in read

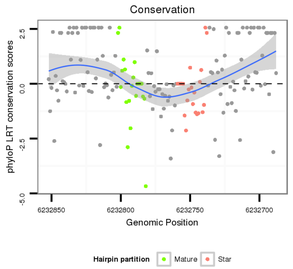
Predicted structure











Show Alternate Folds

Flybase annotation

intron [DvirGJ10234-in]; CDS [DvirGJ10234-cds]; CDS [DvirGJ10234-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

AAGTGCAAGGCAGCGAGGATTGCCTGTACCTGAATGTATATACCAGAGAGGTGAGTTCTGTATGGATATACATAATTTAAGCTGGACCCTATTTATATCTTTTACTCGAACGCAGCTGCATCCACAAAAGCCGCTGCCCGTGCTCGTTTGGATCTATGGCGGCGG						SRR2096057	SRR2096059	SRR2096056	V116	M047	SRR2096060	SRR060664	SRR060667	SRR060677	SRR060680	SRR060681	SRR060688	SRR060668	M061	SRR060672	SRR060674	SRR060675	SRR2096055	SRR2096058	SRR2096080 embryo_0-2h from 15to16 day old mothers	SRR060669		SRR060662	V053	9x160_0-2h_embryos_total
**********	Read size	# Mismatch	Hit Count	Total Norm	Total	Ovary_Min_50	Ovary_Min_164	Ovary_Min_46	male body	female body	Ovary_Min_193	9_males_carcasses_total	160_females_carcasses_total	Argx9_ovaries_total	9xArg_testes_total	Argx9_testes_total	160_ovaries_total	160x9_males_carcasses_total	embryo	9x160_females_carcasses_total	9x140_ovaries_total	140x9_ovaries_total	Ovary_Min_43	Ovary_Min_98	male mothers	160x9_females_carcasses_total	head body	0	0	0
.....TATATCTTTTACTCGAACGCAGC.	23	1	1	16.00	16	4	2	2	0	1	2	0	1	0	2	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0
.....GTGAGTTCTGTATGGATATAC.....	21	0	1	10.00	10	1	3	1	2	0	0	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
.....GTGAGTTCTGTATGGATATACA.....	22	0	1	8.00	8	1	1	1	0	0	2	1	0	0	0	0	0	0	0	1	0	1	1	0	1	0	0	0	0	0
.....TATATCTTTTACTCGAACGCAGC.	23	1	1	2.00	2	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
.....GTGCTCGTTTGGATCTATG.....	19	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
.....GTGAGTTCTGTATGGATATACATAATT.	27	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	0	0	0	0
.AGTGCAAGGCAGCGAGGATTGCCTGTA.....	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
.....GTGAGTTCTGTATGGATATA.....	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
.....GCTCGTTTGGATCTATGGCGGC..	22	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
.....GTGAGTTCTGTATGGATATACATAA.....	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	0	0	0	0	0
....GCAAGGCAGCGAGGATTGCCTGTACCT.....	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	0	0	0	0

Anti-sense strand reads

TTCACGTTCCGTCGCTCCTAACGGACATGGACTTACATATATGGTCTCTCACTCAAGACATACCTATATGTATTAAATTCGACCTGGGATAAATATAGAAAATGAGCTTGCGTCGACGTAGGTGTTTTCGGCGACGGGCACGAGCAAACCTAGATACCGCGCGC						SRR2096060	SRR2096013	V053	SRR060683	V116	SRR2096055	SRR060655	M047	V047
**********	Read size	# Mismatch	Hit Count	Total Norm	Total	Ovary_Min_193	Ovary_Strain_9_oxidized	head	160_testes_total	male body	Ovary_Min_43	9x160_testes_total	female body	embryo
.....GTGAGTTCTGTATGGATATACATAA.....	25	0	1	1.00	1	0	0	0	1	0	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droVir3	scaffold_12855:6232688-6232852 -	dvi_4158	AAGTG-CAAGGCAGCGAGGATTGCCTGTACCTGAATGTATATACCAGAGAGGTGAGTTCTGTATGGATATACA----------TAA-T--TT----------AAGCTGGA-CCC-TATTTATATCTTTT--ACTCGAACGCAG-CTGCATCCACAAAAGCCGCTGCCCGTGCTCGTTTGGATCTATGGCGGCGG
droMoj3	scaffold_6540:6572652-6572816 -		-GTG-CAGGGCAGCGAGGATGCCTGTACCTGAATGTATACCAG-GAGGTGAGTCTAA-------GA-TAGTT-----TA---C-T-AAAGGT----------AAAGCTAGATTTC--CAAAAGCCGCTGCCCGTGCTCGTTGGATCTATGGCGGCGG
droGri2	scaffold_14906:7875280-7875437 +		AA-TGACTGGCTCGAGGATTGTTGTACCTGAATGTATATGCAGAGTGAAGTAAT-------A-A-------AT-------G---T--TGAG--AGAGCTGT---A----------AT----------AT----------G---CTGA-TATGCCTTTCGAGTCGCAGCGCGATCATGTGATGGGATCTATGGCGGCGG
dp5	2:26732707-26732871 -		TCGT-T-CAAGGCAGCGAGGATTGTTGTACCTGAATGTATACACCAGAGAGGTAAGTCTA-------ATATCGAT-------AT---C-TAAACGAT----------AAAATATCAAATT--AA-T-AT-------CTTT-TTTCGTCTATCGAGTGCATCCACATAAGCCATCCCGTTGTTTGGATCTATGGCGGCGG
droPer2	scaffold_8:2050880-2050844 -		TCGT-T-CAAGGCAGCGAGGATTGTTGTACCTGAATGTATACACAGAGAGGTAGGTCTA-------ATATCGAT-------AT---C-TAAACGAT----------AAAATATCAAATT--AA-T-AT-------CTTT-TTTCGTCTATCGAGTGCATCCACATAAGCCATCCCGTTGTTTGGATCTATGGCGGCGG
droAna3	scaffold_13348:3109484-3109642 -		TCGT-T-CAGGGCAGCGAGGATGCCTGTACCTGAATGTATACACAG-GAGGTAAGTCT-------CT-------AACG---T-A-T--TT----ATTATCCTT-------A----------AA----------------G---A--TAAATATC------AGG---TTT-ACTTTTCAGCTGCATCCACATAAGCCATCCCGTTGTTTGGATCTATGGCGGCGG
droRip1	scaffk7180000396712:1241416-1241680 +		TCGT-T-CAGGGCAGCGAGGATGCCTGTACCTGAATGTATACACAG-GAGTGAGTCTG-------CT-T-----AAAG---T-A-T--TTATTAT----CCTT--------A----------AAGATCTTGGGCT----------AA---A--TAA-ATA--------AGG---CAATTTTCAGCTGCATCCACATAAGCCATCCCGTTGTTTGGATCTATGGCGGCGG
droKik1	scaffk7180000302706:81749-81911 -		CTT-T-CCAGGGCAGCGAGGATTGCCTGTACCTGAATGTATACACAG-GAGTGAGTCTAA-------GG-T------STAGTAG---C-T-AATTTC----------GAATACAGAAATT--AAAA-GAA------AAC---T-TTTCTTTTCAGCTGCATCCACATAAGCCATCCCGTTGTTTGGATCTATGGCGGCGG
droPic1	scaffk7180000454063:319443-319606 +		AAGAGCGGCGGCCAGAGGATTGCCTGTACCTGAATGTATACACAG-GAGTGAGTCTATAATT-------AGCAAA---AA-AAAAAG----------CCGCAA-CCTA-TA-TAA-TAT-T-------AC---C-TTTCTTTTCAGCTGCATCCACATAAGCCATCCCGGGCGGCGG
droEle1	scaffk7180000491104:1041479-1041637 +		AAGAGCGGCGGCCTGAAGATTGCCTGTACCTAATGTATATCTGAAGAGTGAGTCTAA-------A--CGT-------TG---T-CGTAGCAA----------CAA---ACAG----------AGCG---CTTCTCTTTTCAGCTGCATCCACATAAGCCATCCCGTTGTTTGGATCTATGGCGGCGG
droRho1	scaffk7180000277138:2064-2227 +		TCGTG-T-GGGCAGCGAGGATTGCCTATACTGAATGTATACACAG-GAGTGAACCTAAT-------C-G-------CC---TAA-T--TT----AAACATGAC-----ACTAAAAGGTC--AATTA-TAT-------TTAATACTGCATTTTAATCTGCT---TCGGCCGATCTGCCATCCACATAAGCCATCCCGTTGTTTGGATCTATGGCGGCGG
droRia1	scaffk7180000302155:1284759-1284918 +		AAGAGCGGCGGCCAGAGGATTGCCTATACCTGAATGTATACACAG-GAGTGAACCTAT-------C-A-------GAAA---T-TG-ATT-T----------TAGTTATT----------------------------G-TGTTATTATT-T-------GTCTTTTTAAGTGCCATCCACATAAGCCATCCCGTTGTTTGGATCTATGGCGGCGG
droTak1	scaffk7180000415875:482819-482973 -		CCCC-TGCGGCGCCAGAGGATGCCTGTACCTGAATGTATACGTTGAGAGTGAAGTCTA-------A----------A---T-TAA-A--T--TTGTTT--GTTG-TTTTGTGTTA-T-TAA-------CCT---TTTGGCTTTAAGTGCCATCCACATAAGCCATCCCGTTGTTTGGATCTATGGCGGCGG
droEug1	scaffk7180000409760:213109-213269 -		TCCC-TGCGGCGCCAGAGGATGCCTATACCTGAATGTATACTGAGAGTGAAGTAAGATT-------A----------AA---T-TAA-A--T--TAAG--AAGTTA--GTTAT-TAGCAGA-TA-TAA-------CCT---TTTCTATTTCCAGCTGCATCCACATAAGCCATCCCGTTGTTTGGATCTATGGCGGCGG
dm3	chr3R:3361556-3361717 +		AAGAGCGGCGGCCAGAGGATTGCTGTACCTGAATGTATACAG-GAGTGAACCTAG-------AAAG---ACT-CCGTT----------TCTTTAAT----------------------TACTGA----------AAG---AG-TGG-------GAC---TTTATTTAGAGTGCAAGTGTGAGCCATCCACATAAGCCATCCCGTTGTTTGGATCTATGGCGGCGG
droSim2	Gr:3232286-3232455 -		AAGAGCGGCGGCCAGAGGATGCCTGTACCTGAATGTATGTGTAAGTGTGAGTCTAT----------CC---G-T-----CGTATGGATCTTGTG-GAGTTTGTGTTT-T-GTA-TATTCTAT-TAT-------CCC---TTTCGCTTTCAGCTGCATCCACATAAGCCATCCCGTTGTTTGGATCTATGGCGGCGG
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droYak3	GK17023066:7023240 +		AAGAGCGGCGGCCAGAGGATGCCTGTACCTGAATGTATACGAGAGTGAAGTAGGTCGG-------A-TTC-T-----CT---T-TAACC-------TGCT----A----------TTAGTGCCTTATGGGTCTAATCC----------CCC---T--AATTGTAT-------GA---TTTCGCTTTCAGCTGCATCCACATAAGCCATCCCGTTGTTTGGATCTATGGCGGCGG
droEre2	scaffold_4770:3575460-3575621 -		CTT-T-CCCGGGCCAGAGGATGCCTGTACCTGAATGTATACGAGAGTGAAGTAGGTCGG-------A-TTC-T-----AT---G-T-AT----------CCCT----A----------CAGATCTAATCC----------CCC---AGT-TGTAT-------GA---TTTCGCTTTCAGCTGCATCCACATAAGCCATCCCGTTGTTTGGATCTATGGCGGCGG

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crit.frac	1
crit.back	1
rescue.total	0
rescue.pairing	0
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rescue.candidate	0