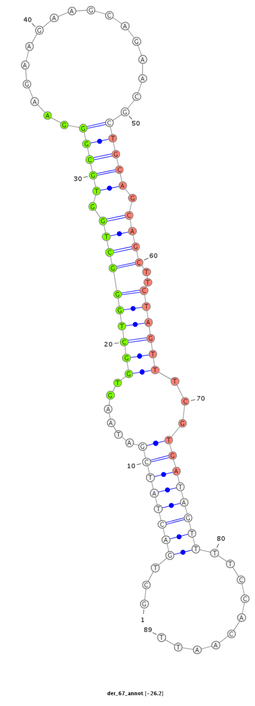
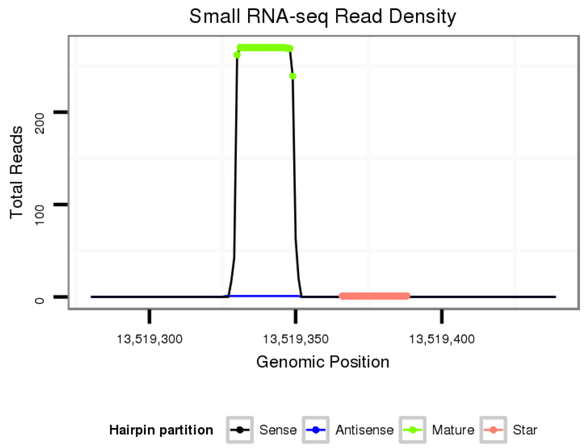
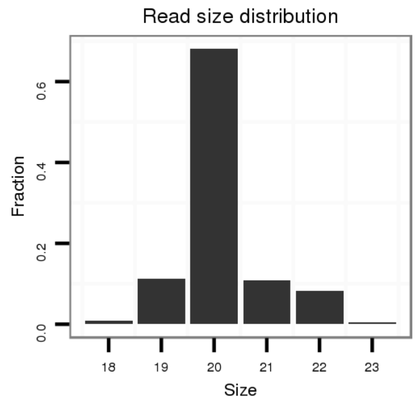
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_67	**scaffold_4784:13519330-13519389 +**	**candidate**	**Canonical miRNA**	**5pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

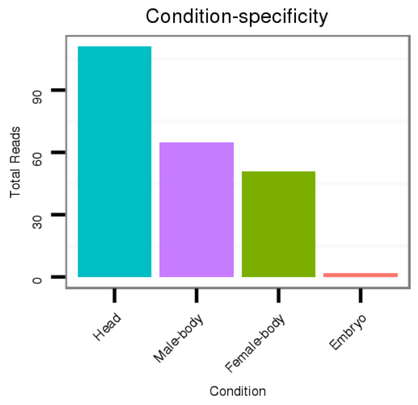
Legend: mature star mismatch in alignment mismatch in read

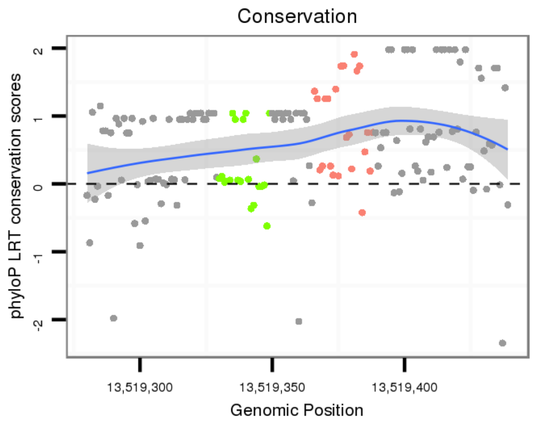
Predicted structure











Show Alternate Folds

Flybase annnotation

utr5 [utr5_plus_7949]; Antisense to utr5 [utr5_minus_6595]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AACAATCGGCCTGTTGCACACACAATCGGACGGTTGCTGACTATCGATAAGTGGCTGGGCTGGTGCGGGAAGAAGAAGCAGAACGCTGCAGCAGCTTCTAGTTTCGTGATAGTTTTCCACAATTAGTGCTGAAATTAATAACCACAAATGCCATTTTTCC	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V107 male body	M055 female body	V060 head	M057 embryo	V040 embryo
***********...(((((((((.....((((((((((.(((((.................))))).))))..)))))))...)))))))..........**********											
....................GTGGCTGGGCTGGTGCGGGA....	20	0	1	155.00	155	75	46	30	3	0	1
....................GTGGCTGGGCTGGTGCGGGAA...	21	0	1	24.00	24	11	7	5	0	1	0
....................GTGGCTGGGCTGGTGCGGG.....	19	0	1	22.00	22	9	10	3	0	0	0
....................GTGGCTGGGCTGGTGCGGGAAG...	22	0	1	19.00	19	10	2	6	1	0	0
....................AGTGGCTGGGCTGGTGCGGGA....	21	0	1	13.00	13	6	3	4	0	0	0
....................AAGTGGCTGGGCTGGTGCGGGAA...	23	0	1	10.00	10	6	2	1	1	0	0
....................AGTGGCTGGGCTGGTGCGGGAA...	22	0	1	8.00	8	5	0	3	0	0	0
....................AAGTGGCTGGGCTGGTGCGGGA....	22	0	1	4.00	4	2	0	1	1	0	0
....................TGGCTGGGCTGGTGCGGGA.....	19	0	1	4.00	4	1	0	3	0	0	0
....................AAGTGGCTGGGCTGGTGCGGG.....	21	0	1	3.00	3	1	2	0	0	0	0
....................AGTGGCTGGGCTGGTGCGGG.....	20	0	1	3.00	3	1	1	1	0	0	0
....................TGGCTGGGCTGGTGCGGG.....	18	0	1	2.00	2	0	0	2	0	0	0
....TGCAGCAGCTTCTAGTTTCGTGA....	23	0	1	1.00	1	1	0	0	0	0	0
....................GTGGCTGGGCTGGTGCGGGT.....	20	1	1	1.00	1	1	0	0	0	0	0
....................AGTGGCTGGGCTGGTGCGGGG.....	21	1	1	1.00	1	0	0	0	1	0	0
....................GTGGCTGGGCTGGTGCGGGAT.....	21	1	1	1.00	1	0	1	0	0	0	0
....................TGGCTGGGCTGGTGCGGGAAG.....	21	0	1	1.00	1	0	0	1	0	0	0
....................TGGCTGGGCTGGTGCGGGAA.....	20	0	1	1.00	1	0	0	1	0	0	0
....................GTGGCTGGGCTGGTGCGGGG.....	20	1	1	1.00	1	0	0	1	0	0	0
....................GTGGCTGGGCTGGTGCGGAG.....	21	1	1	1.00	1	1	0	0	0	0	0
....................AGTGGCTGGGCTGGTGCG.....	18	0	1	1.00	1	0	1	0	0	0	0
....................GTGGCTGGGCTGGTGCGGGAAGAAA...	25	1	1	1.00	1	1	0	0	0	0	0
....................GTGGCTGGGCTGGTGCGGA.....	19	1	2	1.00	2	2	0	0	0	0	0

Anti-sense strand reads

TTGTTAGCCGGACAACGTGTGTGTTAGCCTGCCAACGACTGATAGCTATTCACCGACCCGACCACGCCCTTCTTCTTCGTCTTGCGACGTCGTCGAAGATCAAAGCACTATCAAAAGGTGTTAATCACGACTTTAATTATTGGTGTTTACGGTAAAAAGG	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	V040 embryo
***********...(((((((((.....((((((((((.(((((.................))))).))))..)))))))...)))))))..........**********							
....................TATTCACCGACCCGACCACGCCCTTC....	26	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4784:13519280-13519439 +	der_67	AACAATCGGCCTGTTGC----ACACACAATCGGACGGTTGCTGACTATCGATAAGTGGCTGGG-CTGGT--GCG---GGAAGAAGAAGCAGAACGCTGCAGCAGC--TTCTAGTTTCGTGATA-----GTT-TTCCACAATTAGTGCTGAAATTAA-----TAACCACAA-ATGCCATTTTTC-C
droYak3	3L:13609564-13609723 +	dya_1783	AACTATCGGCCTGTTGCTCCTA----CAATCGAACGGTCGCTGACTATCGATAAGTGGCTGGG-CTGGT--GCG---GGAAGAAGAAGCAGAACGCTGCAGCAGC--TTCTATTTCGTGATA-----GTT-TTCCGCAATTAGTGCTGAAATTAA-----TAACCATAA-ATGCCATTTTACC-C
droSec2	scaffold_0:5681840-5682004 +		AACTATCGGCGTGTTGCTCCTACACACAATTGTGCGTTCGCTGACTATCGATAAGTGGCTGGG-CTGTT-TGCG---AGAAGAAGAAGCAAAACGGTGCAGCAGC--TTCTATTTCGTGATA-----GTT-TTCCGCAATTAGTGCTGAAATTAA-----TAACCATAA-ATGCCATTTTGCC-C
droSim2	3l:13210143-13210307 +		AACTATCGGCATGTTGCTCCTACACACAATTGTGCGTTTGCTGACTATCGATAAGTGGCTGGG-CTGGT-TGCG---AGAAGAAGAAGCAGAACGGTGCAGCAGC--TTCTATTTCGTGATA-----GTT-TTCCGCAATTAGTGCTGAAATTAA-----TAACCATAA-ATGCCATTTTGCC-C
dm3	chr3L:13506408-13506572 +		AACTATCGG-ATGTTGCTCCTACACACAATTCTGCGTTCGCTGACTATCGATAAGTGGCTGGG-CTGGTGTGCG---AGAAGAAGAAGCAGAACGGTGCAGCAGC--TTCTATTTCGTGATA-----GTT-TTCCGCAATTAGTGCTGAAATTAA-----TAACCATAA-ATGCCATTTTGCC-C
droEug1	scf7180000409121:52054-52216 +		ATCTATCGCCTTGCT----AAAGGAATATCGTGCGGGCGCGACTATCGATATACCTCTGGG-CTGGTA-TAGAT-AAAGAAGAAGCAAAACGGTGCAGCAGCACTTCTATTTTCGTGATA-----GTT-TTCCGCAATTAGTGCTAAAATTTA-----TAACCATAA-ATGCTATTTTGCC-G
droBia1	scf7180000302428:6397253-6397314 -		--CTATTTTCGTGATA-----TT-TTCCGCAACTAGCCCTAAAATTAA-----TAACCATAG-ATGCCATTTGTCC-C
droTak1	scf7180000415429:216431-216489 +		--CTATTTTAGTGATA-----GTTATTTTCCGCAATTAGT-----AATTAA-----TAACCATAA-ATGCCGTTTTGCC-A
droEle1	scf7180000491255:1960976-1961135 +		C----------TGTTGCTGCAATGAACTATCGTGTGGCGCGCGACTATCGATATATCGCTCTCCCTGGTG-TAGATGCAAGAAGAAGCATAACGGTGCAGCAGCAGCTCTATTTCGTGATA-----GTT-TTTCCTTAATTAGTGCTAAAATTAA-----TAACCATAG-ATGCCATTTTTC-C
droRho1	scf7180000779509:106322-106462 +		AT----------------------OGTGTGGCGCGCGACTATCGATATATCGATGGG-CTAAAG-TAGATGCAAGAAGAAGCACAACGGTGCAGCAGCTCTTCTATTTCGTGATA-----GTT-TTTCCGCAATTAGTGCTAAAATTAA-----TAACCATAG-ATGCCATTTTGCC-C
droFic1	scf7180000454048:191674-191841 -		AACTTTCGGCCTGTTGCTGCAATGGAATTTCGTGTGGCGCGCGACTATCGATATATCGCTGGG-CTGTA----GATGGAAGAAGAAGAAGAAACGGTGCAGCAGCTCTTCTATTTCGTGATA-----GTT-TTTCCGCAATTAGTGCTAAAATTAA-----TATCCATAATATGCCATTTTGCCGC
droKik1	scf7180000302808:501838-501910 -		--C--TTCTATTTTGTGATAGTGTTTTT-TTCCGCAATTTGTGCTAAAATTAATATAATAAGTAATGA-ATGCAATTT---C
droAna3	scaffold_13337:21927630-21927683 -		AACCTTT--TTGTTTCG-----GA-TTTAACAATTATTTTCGGAATTAATTTTA-AAAGAACGA-G-----------
droBip1	scf7180000396730:397255-397308 -		GT--TTCGGATTTAACAATT-----TTT-TTTCCGGAATTAATTTTAATTTTA-----AAAGAACGA-G-----------
dp5	XR_group8:6926289-6926365 -		AC--ACTGACGCCCC--ATCTATTT----TGATAG--TTTTT-TTTCCGCAATTTGTGCTAAAATTAA-----TAAGTATAG-ATGTAAATTGTC-T
droPer2	scaffold_36:381494-381570 +		AC--ACTGACGCCCC--ATCTATTT----TGATAG--TTTTT-TTTCCGCAATTTGTGCTAAAATTAA-----TAAGTATAG-ATGTAAATTGTC-T
droVir3	scaffold_13049:17621496-17621497 +		CC---

Generated: 09/08/2015 at 07:42 PM

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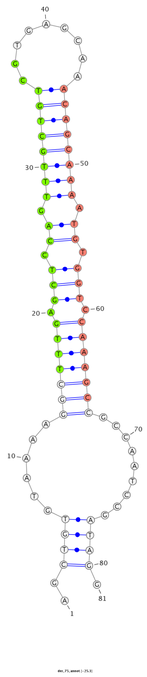
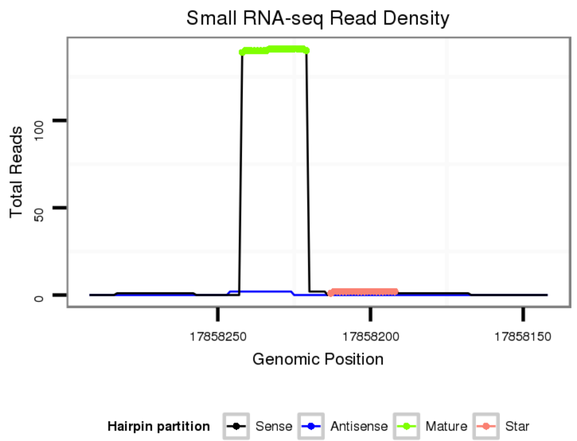
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

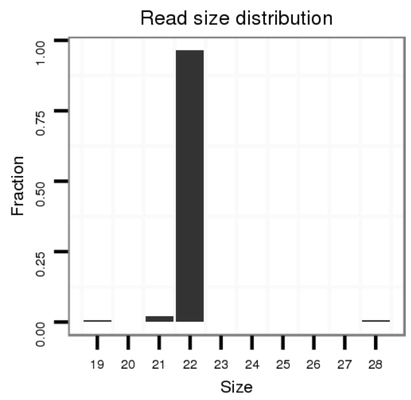
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_75	**scaffold_4929:17858192-17858242 -**	**candidate**	**Canonical miRNA**	**3pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

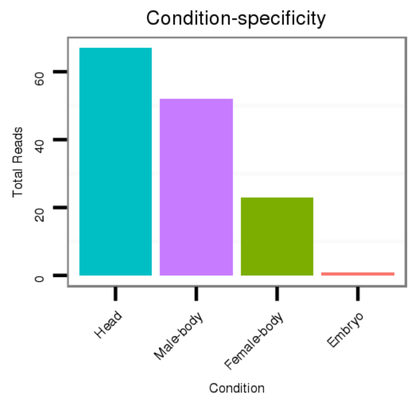
Legend: mature star mismatch in alignment mismatch in read

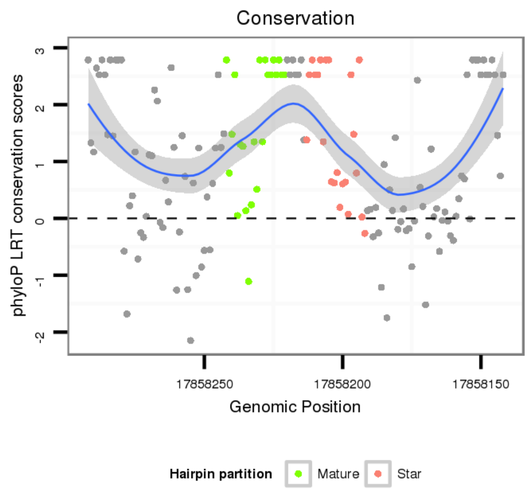
Predicted structure











Show Alternate Folds

Flybase annnotation

utr3 [utr3_plus_1952]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATCACACATTTTTGCAGAGGGCATTTTCTTTTGGAAGCTGTGTAAAAGGCTTTGAGCTCCAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGTCCAAAGCCGCCAATCCGATAGGTGCTTTGGGGGCCCCAATAATCGAAACTGCAGTCG	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V107 male body	M055 female body	V060 head	V040 embryo
**********..((((.....(((((((.(((.((.(((((((((.........)))))))).)).))).)))))))).....))))..**********										
.....TTTGAGCTCCAGTTTGCTGTCG.....	22	0	1	137.00	137	57	51	21	8	0
.....TTTGAGCTCCAGTTTGCTGTCGTGAGCA.....	28	0	1	1.00	1	0	1	0	0	0
.....TTTTGCAGAGGGCATTTTCTTTTGGA.....	26	0	1	1.00	1	0	0	1	0	0
.....CAGTTTGCTGTCGTGAGCA.....	19	0	1	1.00	1	0	0	0	0	1
.....ACAGCAAAATGTGGTCCAAAGC.....	22	0	1	1.00	1	0	0	1	0	0
.....CAGCAAAATGTGGTCCAAAGC.....	21	0	1	1.00	1	1	0	0	0	0
.....TTGAGCTCCAGTTTGCTGTCG.....	21	0	1	1.00	1	1	0	0	0	0
.....TTTGAGCTCCAGTTTGCTGTC.....	21	0	1	1.00	1	0	0	1	0	0
.....TTTGAGCTCCAGTTTGCTGTCT.....	22	1	1	1.00	1	0	1	0	0	0
.....CGCCAATCCGATAGGTGCTTTGGG.....	24	0	1	1.00	1	0	0	0	0	1

Anti-sense strand reads

TAGTGTGTAAAAACGTCTCCCGTAAAAGAAAACCTTCGACACATTTTCCGAAACTCGAGGTCAAACGACAGCACTCGTTTGTCGTTTTACACCAGGTTTCGGCGGTTAGGCTATCCACGAAACCCCCGGGGTTATTAGCTTTGACGTCAGC	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head
**********..((((.....(((((((.(((.((.(((((((((.........)))))))).)).))).)))))))).....))))..**********						
.....TCCGAAACTCGAGGTCAAACG.....	21	0	1	2.00	2	2

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4929:17858142-17858292 -	der_75	ATCACACATTTTTGC--A------GAGGGCAT--TTT----CTT---------TT--G----------GAAGCTGTGTAAAAGGCTTTGAGCTCCAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGTCCAAAGCCGCCAA----------TCC-GAT-------A------GGTGC----------TTTGGGG------GCC-CCA----------ATAATCGAAACTGCAGT-CG
droYak3	2L:17449468-17449618 +	dya_1784	ATCACACATTTTTGC--A------GAGGACAT--TTT----GCT---------TT--G----------GAACTTTGTAAAAGGTTTTGAGCTCCAGTTTGCTGTCGTGAGCAAACAGCAAAATGTAGTCCAAAGCCGACAA----------TTC-GAC-------A------GGTGT----------TTTGGGG------GCC-CCA----------CTTATCGAAACTGCAGT-CG
droSec2	scaffold_1:2429415-2429574 +	dse_1835	ATCACACGTTTTTGC--A------GACGGCAT--TTT----CTA---------TTCG--G----------AAACTGTGTAAAAGGTTTGAGCTCCAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGTCCAAAGCCGCCAT----------TGC-GAA-------A------GGCTT----------TCATGGGAGCCGCC-CCA----------TCAATCGAAACTGCAGT-CG
droSim2	2r:5600469-5600628 +	dsi_32438	ATCACACGTTTTTGC--A------GACGGCAT--TTT----CTA---------TTCG--G----------AAACTGTGTATAAAAGGTTTGAGCTCCAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGTCCAAAGCCGCCAT----------TGC-GAA-------A------GGCTT----------TCTTGGGAGCCGCC-CCA----------TCAATCGAAACTGCAGT-CG
dm3	chr2R:4791632-4791788 +	dme_379	ATCACACGTTTTTGC--A------GACGGCAT--TTT----CTA---------TTCG--G----------AAACTGTATAAAAGGTTTGAGCTCCAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGTCCAAAGCCGCCAA----------TGC-GAA-------A------GGCTT----------TCATGGGAGCC---GCC-CTA----------TCAATCGAAACTGCAGT-CG
droEug1	scf1800004091833:445694-445849 +		ATCACACATTTTTGA--A------GAGATCAT--TTTT---CTA---------TTCT-C----------AAACTTGTTATACAAGGTTTGAGCTTCAGTTTGCTGTCGTGAGCAAACAGCAAAATGCGGTCCAAAATCGCCTC----------TCC-GAA-------A------GGTGT----------TTTTGGGGG----TCA-CCA----------TAAATGTAAACTGCAGT-TG
droBia1	scf1800000302291:2735861-2736008 +		ATCACACATTTTTGC--A------GA--GCAT--TTT----CTA---------TTC--C----------AAACATGTTTACAAGGTTTCGACTACAGTTTGCTGTCGTGAGCAAACAGCAAAACGTTTTCCGAAGTCGCC------------TTC-GAA-------A------GTTAC----------TTTAAGG------GCA-CCA----------CAAATCGAAACTGCAGT-TG
droTak1	scf1800000415386:451368-451521 -		ATCACACATTTTTGC--A------GAGAGCAT--TTT----CTT---------TTT--A----------GAACATGTTTACAAGGTTTTGAACCACAGTTTGCTGTCGTGAGCAAACAGCAAAATGTTTTCCAAAATCGCCAA----------TTC-GAA-------A------GTTAT----------TTTGAGG----GCGCA-CCA----------CAAATGTAAACTGCAGT-TG
droEle1	scf1800000490483:67750-67902 -		ATCACACATTTTTGC--A------GAGG-TTATATTTT----CTT---------TTT--C----------GAATATGTTTACAAGGTTTTGAACTACAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGCCCAAAACTGAAAA----------TTC-AAA-------A------GGTTT----------TATTGGG------GCA-CCA----------CAAATCGAAACTGCAGT-TG
droRho1	scf1800000780108:150200-150349 +		ATTACACATTTTT-C-A------GAGATTAT--TTATT---CTT---------TTT--C----------AAAAATGTAGACAAGGTTCTGAACTATAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGCCCAGAATCGAAAT----------TTT-GAA-------A------GTTAT----------TTTTGGG------TCA-AAA----------CAAATCGAAACTGCAGT-TG
droFic1	scf1800000453851:1506170-1506323 -		ATCACACATTTTTGC--A------GGAGCAT--TTTT---CTT---------TTTT-A----------AAACGTGTAGAAAAGGTTTTGAACTTCAGTTTGCTGTCGTGAGCAAACAGCAAAATCGGCCCAAAACCGCAAA----------TTC-AAA-------C------AGAAT----------TTTTGGG------GCA-CTA----------CAAACCGAAACTGCAGT-TG
droKik1	scf1800000302682:1354903-1355059 +		ATCACACATTTTTAGACA------GAAGGTAT--TTC----CTT---------TTT--C----------GAACTGTTACACAAGGTTCTGGACTCCAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGCTCAGAGCCGACTT----------TCC-GAA-------AAC--G--TATTT----------TTTTGGG------GGA-CTA----------CAAATCGAAACTGCAGT-TG
droAna3	scaffold_13266:1225293-1225463 -	dan_4056	ATCACACATTTTTGC-GAAAAAAAAGAGCAT--TTTTTTTCTTC-TTTCGATTTTCCG-A----------AAAGTTGTGAAAATGGTTTTGAACTTCAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGCCCAAAGCCGCCA----T----------TCCGCC-----GAAAC--G---GGTTT----------------------AA-TTA----------CAAATCAAAACTGCAGA-TG
droBip1	scf1800000396730:2224851-2225036 -		ATCACACATTTTTTGACAAA----AAAAACAT--TTTTATGTTCGATTCGAAATTCCG-A--------AAAA----------AAAGGTTCATACAAGGTTTGAACTCCAATTGCTGTCGTGAGCAAACAGCAAAATGTGGCCCAAAGCCGCCAT----------TCC-GCC-----GAAA------GGTTG-------ACATTTTGGGT----GG-GTATTTC----------CAAGTGAAAACTGCAGAACG
dp5	3:13606084-13606243 -	dps_3844	ATCACACATTTTTGA--A------GATG-CGT--T-T----GTT---------TT--A----------AGAACTTTGTCTGAGATTTTGAACCACAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGCAAAAATGAACAT----------TCCGAT-------C------GACTT----TAAGAATTTGAG--TTAGGGCC-CTT----------CAGATCAAAACTGCAGT-TG
droPer2	scaffold_2:8013588-8013747 +		ATCACACATTTTTGA--A------GATG-CGT--T-T----GTT---------TT--A----------AGAACTTTGTCTGAGATTTTGAACCACAGTTTGCTGTCGTGAGCAAACAGCAAAATGTGGCACAAAATGAACAT----------TCCGAT-------C------GACTT----TAAGAATTTGAG--TTAGGGCC-CTT----------CAGATCAAAACTGCAGT-TG
droWil2	scf2_1100000004510:2696669-2696853 -	dwi_5429	AACACACATTTTTTT--G------------A---TTT---------TTCAGAAAATTCTCATAAAAATTGTTCTCTTTGTCAAATGTG-------GATTTTGTATCAAATTTGCTGTCGTGAGCAAACAGCAAAAATTGACACAAACACCTCGA----------ATGACCCGATCT--T---CACATAATTCCATGAATTTTCCGG------GCTTTG----------GATAGTCAAAACTGCAGT-TG
droVir3	scaffold_12875:1774794-1774970 +	dvi_24661	ATCACACATATTTACG-T------GAAAGCAT--TTG----TTT---------TCC--------AACACATTCAGATAGATTTTGAACTCTGTTCTGCTGTCGTGAGCATTCAGCAGAAAATTGTTCAAAATTGAAAA----TTT-CCTA--CGT-TAA------GAGTA---GACTC----------TTCTGGTCGCTTCCA--A-AAAAAAACAAAACAAACGAAAACTGCAGT-TG
droMoj3	scaffold_6496:13717208-13717375 -	dmo_3156	A---CACATTTTTCA--A-AAGGAAAGAGAAA--TT----CAT---------TCT--C----------GATCGCTTCAAATAGATTTTGAACTCTGTTCTGCTGTCGTGAGCATTCAGCAGAAAATTGTTCAAAATTGAATTTAAATTC-CCCA--CTC-GAA-------GAGCGGAAGGTTT----------TTCCAA------ACT-TTT----------AATACGAAACTGCAGT-TG
droGri2	scaffold_15112:3869031-3869170 +		ATCACACATTTTTTATTC------------------------G----------AACGCAATA---TAGATTTTGGACCTGTTCTGCTGTCGTGAGCATTCAGCAGAAATTGTTCAAAATTAAAA----TTCATCTACTTTC-GAA-------A------GTTA----------TTC-GGG-TCAAAATA-TTC----------CAACGTAAACTGCAGT-TG

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PASS/FAIL	
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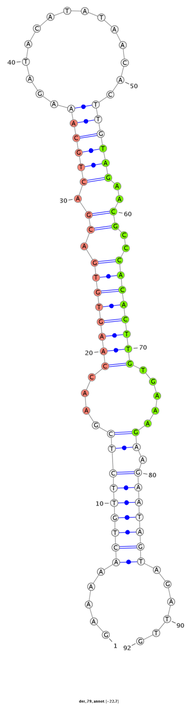
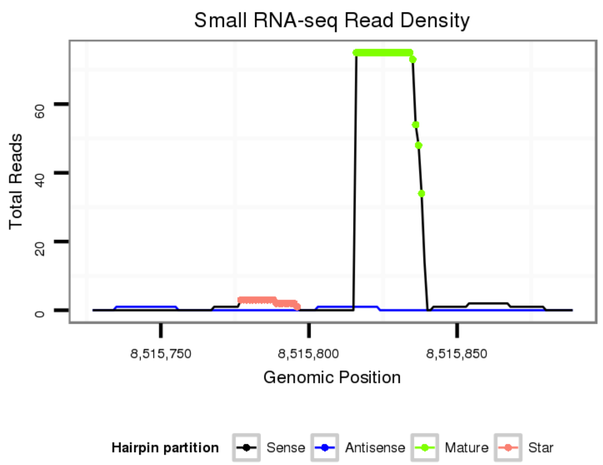
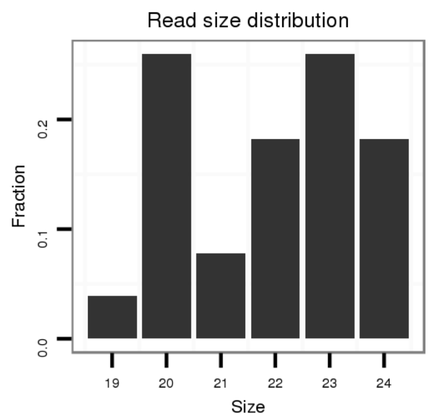
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_79	**scaffold_4929:8515777-8515839 +**	**candidate**	**Canonical miRNA**	**5pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

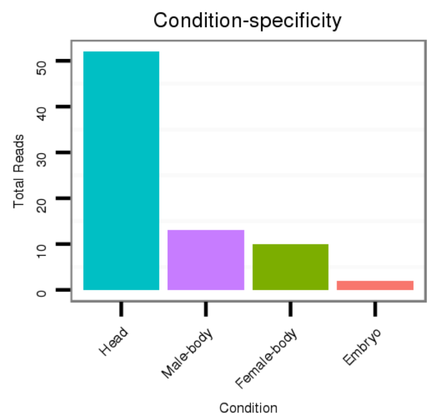
Legend: mature star **mismatch in alignment** mismatch in read

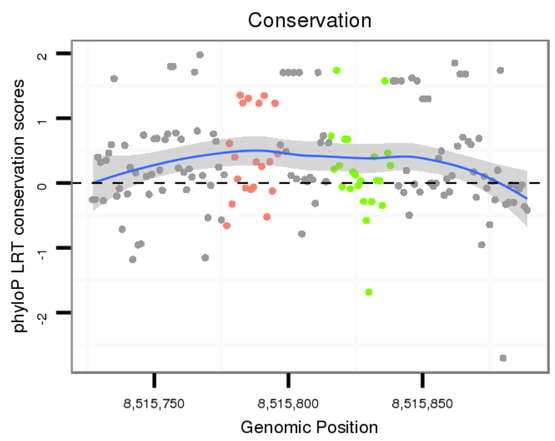
Predicted structure











Show Alternate Folds

Flybase annnotation

utr5 [utr5_minus_3088]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAAGACCTCGTCGCTTCACAAACGCCGCAGCATCCGAAAAACTGTTCTCGAACCAAGTGTGACGACTGCAAAGATACATATAACACTTGTAGAACGCCCACACTTGTGAAAGAAGAATAGTAGATTGCAGCGAAGACGTGTCTTTTAGATAAGAGTTAAGACG **********.....(((((((((....(((((((((.((.((((((..............)))))))..))..)))))))))).....)).)))))))......**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V107 male body	M055 female body	V060 head	V040 embryo	M057 embryo
.....TAGAACGCCCACACTTGTGAAAG.....	23	0	1	20.00	20	14	4	0	1	1	0
.....TAGAACGCCCACACTTGTGA.....	20	0	1	19.00	19	14	0	4	1	0	0
.....TAGAACGCCCACACTTGTGAAA.....	22	0	1	14.00	14	8	4	2	0	0	0
.....TAGAACGCCCACACTTGTGAAAGA.....	24	0	1	14.00	14	8	3	2	1	0	0
.....TAGAACGCCCACACTTGTGAA.....	21	0	1	6.00	6	2	2	2	0	0	0
.....TAGAACGCCCACACTTGTG.....	19	0	1	2.00	2	2	0	0	0	0	0
.....AACCAAGTGTGACGACTGCA.....	20	0	1	1.00	1	0	0	0	0	1	0
.....AACCAAGTGTGACGACTGC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....CAGCGAAGACGTGTCTTTTAGATAAG.....	26	0	1	1.00	1	0	1	0	0	0	0
.....TAGAACGCCCACACTTGTGAAAA.....	23	1	1	1.00	1	1	0	0	0	0	0
.....CTGTTCTCGAACCAAGTGTGA.....	21	0	1	1.00	1	0	0	0	1	0	0
.....TAGAACGCCCACACTTGTGAAAGG.....	24	1	1	1.00	1	0	0	1	0	0	0
.....AATAGTAGATTGCAGCGAAGACGTGT.....	26	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

TTTCTGGAGCAGCGAAGTGTTTGCGGCGTCGTAGGCTTTTTGACAAGAGCTTGGTTCACACTGCTGACGTTCTATGTATATTGTGAACATCTTGCGGGTGTGAACACTTTCTTCTTATCATCTAACGTCGCTTCTGCACAGAAAATCTATTCTCAATTCTGC **********.....(((((((((....(((((((((.((.((((((..............)))))))..))..)))))))))).....)).)))))))......**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	V108 head	M055 female body
.....GCAGCGAAGTGTTTGCGGCGT.....	21	0	1	1.00	1	1	0	0
.....GTATATTGTGAACATCTTGCG.....	21	0	1	1.00	1	0	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4929:8515727-8515889 +	der_79	AA---------AGACCTCG-TCGCTTCACAAA----CGCCGCAGCATCCGAA-----------AAACTGTTCTCGA-A-CCAAGTGTGACGACTGCAAA-GATACATATA----------ACACTTGTAGAACGCCCACA-CT------TG-TGAAAGAAGAA-------TAGTAGATTGCAGCGAAGACGTGTCTTTTAGATAAGAG---TTAAG----------ACG
droYak3	2L:18479617-18479782 -		AG---------AGTCCTCG-TTGCTTCACAAA----CGTGGCAGCATCCGAA-----------AAACTGTTCTCGG-A-CCAAGTGGGACGACTGCAAA-GATACAGATT---TAC----------ACACTTGTAGAACGCCCACA-CT------TG-TGAAAGAAGAA-------TCGTAGATTGGAGCGAAGACGTGTCTCTAAGATAAGGG---TTAGG----------ACG
droSec2	scaffold_1:3462052-3462215 -		AA---------AGTCCTCG-TCGCTTTACAAA----CGCCGCAGCATCCTCA-----------AGACAGTTCTCGG-G-CCAAGTGGCCCTACTGCAAA-GATACACATA----------ACACTTGTGAACGCCCACA-CT------TGCCGAAAGAAGAA-------TCGTAATTGCAGCGAAGACGTGTCTCTAAGATAAGCG---TTAGG----------ACG
droSim2	2r:6628766-6628929 -		AA---------AGTCCTCG-TCGCTTTACAAA----CGCCGCAGCATCCTCA-----------AGACAGTTCTCGG-G-CCAAGTGGCCCTACTGCAAA-GATACACATA----------ACACTTGTGAACGCCCACA-CT------TGCCGAAAGAAGAA-------TCGTAATTGCAGCGAAGACGTGTCTCTAAGATAAGCG---TTAGG----------ACG
dm3	chr2R:5852244-5852407 -	dme_380	AA---------AGTCCTCG-CCGCTTTACAAA----CGCCGCAGCATCCTCA-----------AGACAGTTCTTGG-A-CCAAGTGGAACGAATCCAAA-GATACACATA----------ACACTTGTGAACGCCCACA-CT------TGTCGAAAGAAGAA-------TTGTAGATTGCAGCGAAGACGTGTATCTAAGATAAGTG---TTAGG----------ACG
droEug1	scf7180000409209:323018-323148 +		TA---------AGTCCTCG-CCGTCGCTTTAAA----CGCTACAGCATCCAAA-----------AAATAGTTCTCGA-A-CGAAGGCGAACGAATGCGAA-GATATACATA----------ACACTTAGTAGTACGCCCACG-TC------T---TAGTA---TTAGCAAGAGGTTT--AAAAAACT
droBia1	scf7180000301506:849654-849804 +		AA---------AGTCCTCG-TCGCTTCCCAAC----CACCGCAGCATCCGA-----------AACCATTCTCTGG-A-CCAAGTG----------AA-GATACACCTA----------ATACTTGTAGAACGCCCTTG-CG------GCGTTAAAGAAGAG-------TTGCAGATTGCAGCGAAGACGTGTCACTACGAAAAGAG---TTCAG----------CTG
droTak1	scf7180000415870:410200-410376 +		AA---------AGTCCTCAATCACTCCTTAAC----CGCCGCAGCATCCGAA-----------AAACAAATCTCGA-A-CCA---GGAACGAGTGCGAA-GATACACATA----------ACACTTGTAGAACGCCCAGG-CG------GAGTAGAAGAAGAG-------TCGCAGATTTCCGCCAAGACGTGTCACTAGCAAAAGAA---TTGAGCAGGGGTACGAGAATTACG
droEle1	scf7180000491107:1237594-1237757 +		AA---------AGTGCCCG-TTGCTCGCCAAA----CGCCGCAGCATCCGAA-----------AAACAATTCTCGA-A-CCAAGTGGAACGAATCGAA-GATACACACA----------ACACTTGTAGAACGCCCACA-CT------TGCTACAAGAATAG-------TCGCAATTGCAGCGAAGACGTGTCACTGGCGAAAGAG---CTAAC----------GAA
droRho1	scf7180000777200:38712-38874 -		AA---------AGTCCCG-TTGCTCGCCAAA----CGCTGCAGCATCCGAA-----------AAACCATTCTCGA-A-ACAAGTGGAACGAATGCGGA-GAAACACACA----------ACACTTGTAGACCGTCCACA-CA------TGCTAAAGAAGAG-------CCGCAGATTGCAGCGAAGACGTGTCACTACGGAAAGAG---TTAAC----------GAA
droFic1	scf7180000453858:891725-891894 +		TA---------AGCCCTCA-CAGCTCGCCAAA---CCGCCGCAGCATCCGAA-----------AAACGAATCTCGA-A-TCAAGTGGAACGAATGCGAA-GACACATATACCATAT---A---------CCACTTGTAGATCGAACACA-AA------GCGAAATCGAAGAG-------TCGCAGATTACATGTGTGAAGCGTCACTCGGGAAAGAGGCGTTA------------------A
droKik1	scf7180000302476:2829919-2830087 -		GC---------------------TTGTAACCCTTCCGCCACAGCATCCGATC----GCCGCC-AAACTAATCTCGAGA-GCCAGCGAAACGAATGCGAA-GATACACGG----------CAACTTGTAGGACGCCGGCA-GCGAGTAATGGTAAAAGAAGAT-------ACGCAGATTGAAGCGACGACGTGTCACTGAGAAACGAA---CG-AA----------ACA
droAna3	scaffold_13266:15350695-15350797 -		C---------------G-TCGTT-GCACA----AGCCGTTGCTGTTCT----------AAACAGTATTCGA-AAG----------------------------CTAACAGAACGCTCATC-CA------------------AAGAGTTG----------GGGATACGTGTCGTTGATT--TGGAG---ACTAA----------AAG
droBip1	scf7180000396547:1700856-1700953 +		C---------------CTCG-TTGCCAGCAA--------GCCTTAGCTCGTCG----------AAACATTTCAAAC-A-CCG----------------------------ACCGCTCATC-CA------------------AGGAGTT----------GGGATACGTGTCGTTGATCGGA-GG---TTGAT----------ACG
dp5	3:10917092-10917287 +		ACGTCAGCACCCGACATCT-TCGTTTCCTCTT----TGCCGCAGCATTCGATCCGCCGCCGATAAAGAATTCTGT--------------GAAGAATATACA---CACACACAAACGGTGAGATAAGTGGAATATCTTTCGACCCAGAACGATACAACAATATCCAACGATTCGAA----GCCGCAGGACGTGGAGCAATT-TAGCA---ACAAAACGAA----------ACCG
droPer2	scaffold_4:6240666-6240857 +		ACGTCAGCACCCGACATCT-TCGTTTCCTCTT----TGCCGCAGCATTCGATCCGCCGCCGATAAAGAATTCTGT--------------GAAGAATATACATA---CACACACAAACGGTGAGATAAGTGGAATATCTTTCGACCCAGAACGATACAACAATATCCAACGATTCGAA----GCCGCAGGACGTGGAGCAATT-TAGAA---ACAAA----------ACG
droMoj3	scaffold_6496:8768875-8768886 -		AG---CA---TTAGA----------ATA

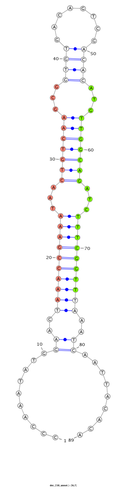
Generated: 09/08/2015 at 07:43 PM

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

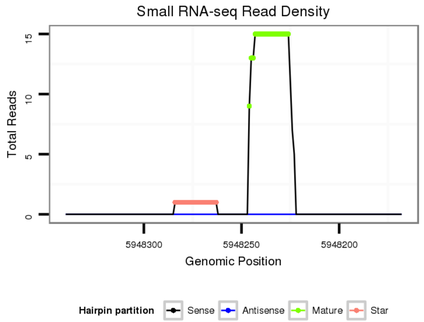
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_230	**scaffold_4770:5948218-5948290 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

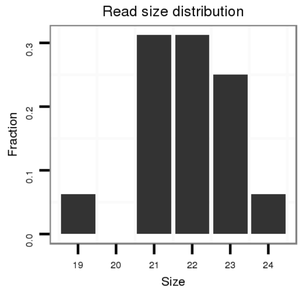
Legend: mature star mismatch in alignment mismatch in read

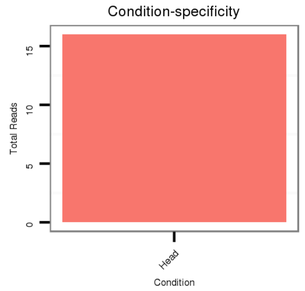
Predicted structure

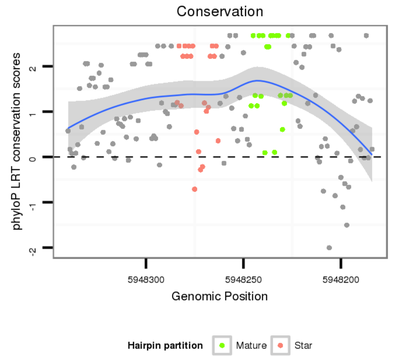


Show Alternate Folds









Flybase annotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AGGCTAATCCAAATGGCTGGGATGTCACGCTTTGTGCCCTACCCAAATATGGAACTAAACCGAAATAACTGTCAAGCGGTGTGACAGTCGACACATGTTGGCAGATCTTTCGGTTTAAATCAATTACACACCGCAAAGCAATGAAAAAAGCGTTGGTAATAAATATTCATATG	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V040 embryo
..........((..((((((((((...(((((((...((((.....))))...))))))).))))))))))..)))..........							
.....ATGTTGGCAGATCTTTCGGTTT.....	21	0	1	4.00	4	4	0
.....TGTTGGCAGATCTTTCGGTTTA.....	22	0	1	3.00	3	3	0
.....ATGTTGGCAGATCTTTCGGTTT.....	22	0	1	3.00	3	3	0
.....TTGGCAGATCTTTCGGTTTAAATT.	24	1	1	1.00	1	1	0
.....ATGTTGGCAGATCTTTCGGTTTA.....	23	0	1	1.00	1	1	0
.....TGTTGGCAGATCTTTCGGTTTA.....	22	0	1	1.00	1	1	0
.....TTGGCAGATCTTTCGGTTT.....	19	0	1	1.00	1	1	0
.....ATGTTGGCAGATCTTTCGGTTTAA.....	24	0	1	1.00	1	1	0
.....AAACCGAAATAACTGTCAAGCG.....	22	0	1	1.00	1	1	0
.....TTGGCAGATCTTTCGGTTTAA.....	21	0	1	1.00	1	1	0

Anti-sense strand reads

TCCGATTAGGTTTACCGACCCTACAGTGCGAAACACGGGATGGGTTTATACCTTGATTTGGCTTTATTGACAGTTCGGCACACTGTCAGCTGTGTACAACCGTCTAGAAAGCCAAATTTAGTTAATGTGTGGCGTTTCGTTACTTTTTCGCAACCATTATTTATAAGTATAC	Read size	# Mismatch	Hit Count	Total Norm	Total	V040 embryo	M055 female body
**********.....((..((((((((((...(((((((...((((.....))))...))))))).))))))))))..))).....**********							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4770:5948175-5948331 -	der_230	CAAATGGC----------T-GGGATGTCACGCTTTGT------GCCCTACCCAAATATGGA----------ACTAAACCGAA--------ATAACTGTCAAGC----------GGT-GTGACAGTCGACACATGT----TGGCAGATCTTTCGGTTTAAATCAATTACAC-------ACCGCAAAGCAATG----------A------AAA----AAG--------C-GTTGGTAATAA--ATAT--
droYak3	3R:4486327-4486486 +		CAAATGGC----------T-GGGATGTCACGCTTTGT------GCCCAGCCCAAAATATGGA----------ANTCAACCGAA--------ACAACTGTCAAGC----------AGT-GTGACAGTCGACACATGT----TGGCAGATCTTTCGGTTTAAATCAATTACAC-------ACCGCAAAACAATA----------A------AAACAA--AAA--------C-GTGGTAATAA--ATAT--
droSec2	scaffold_25:62639-62791 -		CAAATGGCCAAA----------T-GGGATG----------GCCCACCCAAATATGGA----------ACTAAACCGAA--------ATAACTGTCAGCT----------GGT-GTGACAGTCGACACATGT----CGGCAGATCTTTCGGTTTAAATCAATTACAC-------ACCGCAAAATAATA----------C------AAAAAA--AAA--------C-TCTGGTAATAA--ATAC--
droSim2	3r:5569642-5569793 -		CAAATGGCCAAA----------T-GGGAT----------GCCCACCCAAATATGGA----------ACTAAACCGAA--------ATAACTGTCAGCT----------GGT-GTGACAGTCGACACATGT----CGGCAGATCTTTCGGTTTAAATCAATTACAC-------ACCGCAAAATAATA----------C------AAAAAA--AAA--------C-TCTGGTAATAA--ATAC--
dm3	chr3R:15714654-15714816 +		CAAATGGCCAAA----------T-GGGATGTCACGCTTTGC------GCCCACCCAAATATGGA----------ACTAAACCGAA--------ATAACTGTCAGCT----------GGT-GTGACAGTCGACACATGT----CGGCAGATCTTTCGGTTTAAATCAATTACAC-------ACCGCAAAACAATA----------C------AAAAA---AAG--------C-GCAGGTAATAA--ATAT--
droEug1	scf7180000409804:2024025-2024192 +		CAGCTGGA----------T-GGGATGTCACGCTTTAAT------GCCCAACCCAAATATGGA----------ACTAAACCGAA--------ATAACTGTCACTT----------GAT-GTGACAGTCAACACATGTTAGGCTTGGCGATCTTTCGGTTTAAATCAATTACAC-------ACCGCAAACAATA----------A------AACAACGAAAA--------G-TCTGGTAATAA--ATAT--
droBia1	scf7180000302402:1489865-1490029 +		CAGCTGGC----------T-GGGATGTCACGCTTTAGT------GCCCGACCCAAATATGGA----------ACTAAACCGAA--------AATAACTGTCAGTC----------CCG-GTGACAGTCGACACATGTGGGGCCCGGCAGATCTTTCGGTTTAAATCAATTACAC-------ACCGCAAACAGC-A----------------------A---AAGCAAAAA---AA--------A-TATGGTAATAA--ATAT--
droTak1	scf7180000415710:93991-94175 -		CAGCC---AAA---ATCCCAGC----------T-GGGATGTCACGCTTTAAGCCTGATGCCCCAACCCAAATATGGA----------ACTAAACCGAA--------AATAACTGTCACTC----------GGT-GTGACAGTCGACACATGTTGGGTCTGGCAGATCTTTCGGTTTAAATCAATTACAC-------ACCGCAAAATAATA----------GAAAAAACAACAAA---------A-GCTGGTAATAA--ATAT--
droEle1	scf7180000491008:1192574-1192740 -		CAGATGGC----------C-GGGATGTCACGCTTAAT------GCCCAGCCCAAATATGGA----------ACTAAACCGAA--------AATAACTGTCAATC----------GGT-GTGACAGTCGACACATGTTAGGCTTGGCAGATCTTTCGGTTTAAATCAATTACAC-------ACCGCAAACAAATA----------G------AAAAACA-GAT--------A-GCTGGTAATAC--ATAT--
droRho1	scf7180000780274:115970-116137 -		CAGCTGGC----------C-GGGATGTCACGCTTTAAT------GCCCAGCCCAAATATGGA----------ACTAACCGAA--------AATAACTGTCACTC----------GGT-GTGACAGTCGACACATGTTAGGCTTGGCAGATCTTTCGGTTTAAATCAATTACAC-------ACCGCAAAACAATA----------G------AACAAATACGT--------A-GCTGGTAATAA--ATAT--
droFic1	scf7180000454126:738723-738888 +		CAGCTGGC----------T-GGGATGTCACGCTTTAAT------GCCCAGCCCAAATATGGA----------ACTAAACCGAA--------AATAACTGTCAATC----------GGT-GTGACAGTCGACACATGTTAGGCTTGGCGATCTTTCGGTTTAAATCAATTACAC-------ACCGCAAAACAC-A----------------------A---ATACAAAA---AA--------C-GTGGTAATAA--ATAT--
droKik1	scf7180000297926:102183-102349 -		CAGCTGGC----------C-GGGATGTCACGCTTTAAT------GCCCAGTCCAAATATGGA----------ACTAACCGAA--------ATAACTGTCACTT----------CAT-GTGACAGCGACACATGTTAGGCTTGGCAGATCTTTCGGTTTAAATCAATTACATATATGCCGCAAAATCAATA----------G------AAAAA---AAG--------A-GCTGGTAATAA--A----
droAna3	scaffold_13340:2295853-2296039 +		CAA---GCCAG----------GGC----------TTTCAGGGGATGTCACGCTTTAAT------GCCCAGCCCAAATATGGA----------ACTCAACCAAA--------AATAACTGTCACTT----------TGT-GTGACAGTCACACATGTTAGGCTTGGCAGATCTTTCGGTTTAAATCAATTACAC-------ACCGCAAAGCAGTGA----------------------A---ATACAAACAAA---AAATGGATATATA--TGAATAATAT--ACAT--
droBip1	scf7180000396712:2046817-2046995 -		CAACGAGC----------GGC----------TTTCAGGGGATGTCACGCTTTAAT------GCCCAGCCCAAATATGGA----------ACTAAACCAAA--------AATAACTGTCACTT----------TGT-GTGACAGTCACACATGTTAGGCTTGGCAGATCTTTCGGTTTAAATCAATTACAC-------ACCGCAAAACAAATAGA----------------------A---ATACAAAAAA---AA--------T-GCATA-TTCAA--ACAT--
dp5	2:26297029-26297310 -		TCTGT---------------------A-----------------------TTACCCTTATATGGTTTTATGGCAGCGACAACGTAAGTACAGTGAAGTCTGAAGGGATGGAGCGGACGAGCTCTTGATCGA-GAGATTACAAAATGTTGTC----------CATCAATCGATACCTGTCACTGTAACTGTCATGTAATTTGTATGTGAAATTTA-TGTGACAGTCGACACATGTTAAGGTTGGCACGATCTTTCGGTTTAAGCAATTACAC--------ACCGCAAGCATCCC---AACCAGAGATAGAACTAAAAACCATA-A-------AAACGA--CAT--------CATCGTGTATAAA--ATAAAG
droPer2	scaffold_6:1626895-1627176		TCTGT---------------------A-----------------------TTACCCTTATATGGTTTTATGGCAGCGACAACGTGAGTACAGTGAAGTCTGAAGGGATGGAGCGGACGAGCTCTTGATCGA-GAGATTACGAAATGTTGTC----------CATCAATCGATACCTGTCACTGTAACTGTCATGTAATTTGTATGTGAAAATTTA-TGTGACAGTCGACACATGTTAAGGTTGGCACGATCTTTCGGTTTAAGCAATTACAC--------ACCGCAAGCATCCC---AACCAGAGATAGAACTAAAAACCATA-A-------AAACGA--CAT--------CATCGTGTATAA--ATAAAG
droWil2	scf2_1100000004921:4099158-4099232 -		TCA-----------------------A---ACACATG----TGCCATAATTTCGGGTAAAGTTTAAT----------ACCACAAAGTGTCA----------G------A-C----AAT--------C-GTCTATAAAAGGCAATC--
droMoj3	scaffold_6540:25232951-25233133 -		CAAGG---------------------TGAGCGACAGGGG----------RCAG----------GTGGCGAGTCGGGGAGGGGACGCCCTTACATGGCA--AT---GGAACG----------CGGCTAAACC-AA--------ATAGCTGTCAATT----------CAT-GAGACAATGAGCATCTCTAGAGGTTG--AGATCTCTTGGTTAAAATCAATTAC---------CGCAAAGGCAAGCGCGC----------G------AACGAA--AAA--------G--TGA-AAACAG--AAAG--
droGri2	scaffold_15074:5443114-5443327 -		CGAATA-CGGAGACGCTTCTCAGCTGGAGGGAAGCGGCGGGG----RCAG----GT------AGT-AACCCTTATATGGC----------T-AT---GGAACGTTGGCTGGTTATCTGGCACCTAAACC-AA--------ATAACTGTCAATT----------TAT-GAGACAATCGACATGTCCAAAGGT--GAGATCTTTCGGTTCAAATCAATTAT---------CCGCAAAACAGCA----ACA----------G------AAATAG--AAA--------CAGATAATACAAACG--AAT--

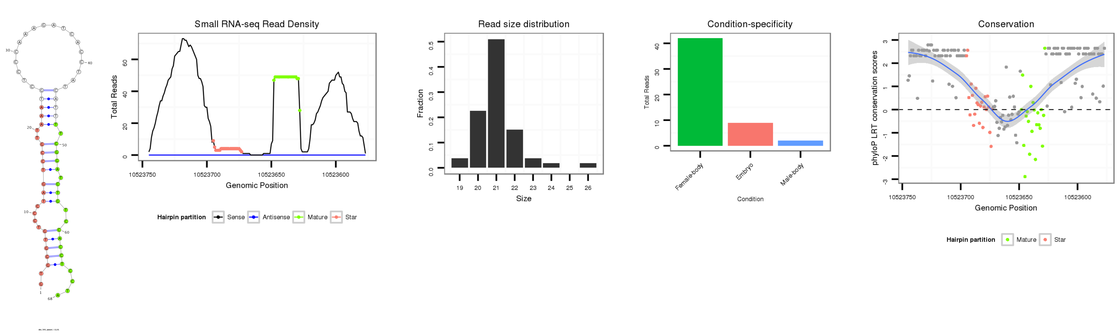
Generated: 09/08/2015 at 07:43 PM

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

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_593	scaffold_4770:10523627-10523695 -	candidate	Mirtron	intron	[View on UCSC Genome Browser (Cornell Mirror)]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annotation

intron [Dere/GG20880-in]; CDS [Dere/GG20880-cds]; CDS [Dere/GG20880-cds]; utr3 [utr3_minus_7751]; utr3 [utr3_minus_7750]; utr5 [utr5_minus_9055]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

	Read #	Mismatch	Hit Count	Total Norm	Total	W055 female body	Y107 male body	V108 head	M057 embryo	V040 embryo	V060 head
GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCTGTCCACCTCCTAGGGTACCCATCTCGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA										
********************************..((((((....((((((((..((((((.....................)))))).)))))))...))))))..********************************											
.....TTCGGATCTGTCCACCTCCTA.....	21	0	1	25.00	25	20	1	0	4	0	0
.....TTCGGATCTGTCCACCTCCT.....	20	0	1	12.00	12	12	0	0	0	0	0
.....TTCGGATCTGTCCACCTCC.....	23	0	1	5.00	5	4	1	0	0	0	0
.....TTTTCGGATCTGTCCACCTCCT.....	22	0	1	5.00	5	4	0	0	0	1	0
.....GCGATGTCCTCACTTGAAGGACA.....	24	0	1	4.00	4	4	0	0	0	0	0
.....GCTATGGTCTCTACTTGAAGGACA.....	24	0	1	3.00	3	3	0	0	0	0	0
.....TCTGCTATGGTCTCTACTTGAAG.....	24	0	1	3.00	3	3	0	0	0	0	0
..GAAGGCATGGAATGATCA.....	18	0	1	3.00	3	3	0	0	0	0	0
.....TGCAGGAGATCGAGCGCAGGTACG.....	24	3	1	3.00	3	2	0	0	0	0	1
.....TCTGCTATGGTCTCTACTTGAAGGACA.....	28	0	1	3.00	3	3	0	0	0	0	0
.....ACCCATCGCAGGAATCG.....	18	0	1	3.00	3	1	2	0	0	0	0
.....ATGCAGGAGATCGAGCGCAGGTACG.....	25	3	1	3.00	3	1	2	0	0	0	0
.....TGCAGGAGATCGAGCGCA.....	18	0	1	3.00	3	2	0	0	0	0	0
.....CTACTTGAAGGACAAGCCACTCA.....	23	0	1	2.00	2	0	1	0	1	0	0
.....ATCTGAAGCCATGCAGGA.....	19	0	1	2.00	2	0	0	2	0	0	0
.AGAAGGCATGGAATGATCATCT.....	22	0	1	2.00	2	0	0	2	0	0	0
..GCATGGAATGATCATCTGAAGCGCA.....	25	0	1	2.00	2	2	0	0	0	0	0
.....GCGCATGCAGGAGATCGAGCGCA.....	23	0	1	2.00	2	2	0	0	0	0	0
.....AGCGCATGCAGGAGATCGAGC.....	21	0	1	2.00	2	2	0	0	0	0	0
.....TACTTGAAGGACAAGCCACTCAC.....	23	0	1	2.00	2	1	0	0	1	0	0
.....GCTATGGTCTCTACTTGAAGGACA.....	23	0	1	2.00	2	1	0	0	0	1	0
.....TCGGATCTGTCCACCTCCT.....	19	0	1	2.00	2	2	0	0	0	0	0
.....ATGATCACTGAAGCGCATGCAGGA.....	25	0	1	2.00	2	1	0	0	1	0	0
.....ATCTGAAGCCATGCAGGAG.....	20	0	1	2.00	2	1	0	0	0	1	0
.....TGGTCTCTACTTGAAGGACA.....	20	0	1	2.00	2	0	0	0	0	1	1
.....ATGGAATGATCATCTGAAGCGC.....	22	0	1	2.00	2	0	0	2	0	0	0
.....GATCATCTGAAGCGCATGCAGG.....	22	0	1	2.00	2	2	0	0	0	0	0
.....AGCGCATGCAGGAGATCGAGC.....	21	0	1	2.00	2	2	0	0	0	0	0
..AAGGCATGGAATGATCATCTG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TTTCGGATCTGTCCACCTCCTA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....GCACGATGCAGGAGATCGAGCGCAG.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TGGTCTCTACTTGAAGGACAAGCC.....	24	0	1	1.00	1	1	0	0	0	0	0
.....ATCATCTGAAGCGCATGCAGGAGATC.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GGACAAGCCACTCACGCCCA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....CTACTTGAAGGACAAGCCACTCACGCC.....	27	0	1	1.00	1	1	0	0	0	0	0
.....GGTACCCATCTCGCTATGGTCTC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TATGGTCTCTACTTGAAGG.....	19	0	1	1.00	1	1	0	0	0	0	0
.....GGTACCCATCTCGCTATGGTCT.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TGATCATCTGAAGCGCATG.....	19	0	1	1.00	1	1	0	0	0	0	0
.....GATCATCTGAAGCGCATGC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....CATGGAATGATCATCTGA.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TGGAATGATCATCTGAAGCGCATGCAG.....	27	0	1	1.00	1	1	0	0	0	0	0
.....ATCTCGCTATGGTCTCTACTTGAAGGA.....	27	0	1	1.00	1	1	0	0	0	0	0
.....TGAAGGACAAGCCACTCACGC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....AAGCGCATGCAGGAGATCGAGCGC.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TGAAGCGCATGCAGGAGATC.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TCTCGCTATGGTCTCTACTTGA.....	22	0	1	1.00	1	1	0	0	0	0	0
GAGAAGGCATGGAATGATCATCT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....CTGAAGCGCATGCAGGAG.....	18	0	1	1.00	1	1	0	0	0	0	0
.....CATCTCGCTATGGTCTCTACTTGA.....	24	0	1	1.00	1	1	0	0	0	0	0
.....ACTTGAAGGACAAGCCACTCACGCCC.....	26	0	1	1.00	1	1	0	0	0	0	0
.....GTGGGTGTCCCTAGTCCGTTAAA.....	23	0	1	1.00	1	1	0	0	0	0	0
....AGGCATGGAATGATCATCTG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GAAGCGCATGCAGGAATCG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....GTCTCTACTTGAAGGACAAGCC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....ATGCAGGAGATCGAGCGCAGG.....	21	0	1	1.00	1	1	0	0	0	1	0
.....GGACAAGCCACTCACGCC.....	18	0	1	1.00	1	1	0	0	0	0	0
.....AAGCGCATGCAGGAGATCG.....	25	0	1	1.00	1	1	0	0	0	0	0
.....AATGATCATCTGAAGCGCATGC.....	22	0	1	1.00	1	1	0	0	0	0	0
.....GAATGATCATCTGAAGCGCATGCAG.....	25	0	1	1.00	1	1	0	0	0	0	0
.....TGAAGCGCATGCAGGAGATCG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CATGGAATGATCATCTGAAGC.....	21	0	1	1.00	1	0	1	0	0	0	0
.....GAAGCGCATGCAGGAGATC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....TTCGGATCTGTCCACCTCCTA.....	22	1	1	1.00	1	1	0	0	0	0	0
.....TCTCTACTTGAAGGACAAGCCACTCA.....	26	0	1	1.00	1	1	0	0	0	0	0
.....GGTACCCATCTCGCTATGGTCTC.....	23	0	1	1.00	1	1	0	0	0	0	0
.....GGTCTCTACTTGAAGGACA.....	19	0	1	1.00	1	1	0	0	0	0	0
.....ATCTCGCTATGGTCTCTACTTGAA.....	24	0	1	1.00	1	1	0	0	0	0	0
.....GCGCATGCAGGAGATCGAGCGCAGGTACG.....	29	3	1	1.00	1	0	0	0	1	0	0
.....CGCTATGGTCTCTACTTGAAG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CATCTCGCTATGGTCTCTACTTG.....	23	0	1	1.00	1	1	0	0	0	0	0
...AGGCATGGAATGATCATCTGAAGCGCA.....	27	0	1	1.00	1	1	0	0	0	0	0
.....CTCTACTTGAAGGACAAGC.....	19	0	1	1.00	1	0	1	0	0	0	0
.....AGGAGATCGAGCGCAGGT.....	18	0	1	1.00	1	1	0	0	0	0	0
.....CATCTGAAGCGCATGCAGGAGAT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....TCTGCTATGGTCTCTACTTGAAGGA.....	26	0	1	1.00	1	1	0	0	0	0	0
.....CTACTTGAAGGACAAGCCACTCACGC.....	26	0	1	1.00	1	1	0	0	0	0	0
.....TCTGAAGCGCATGCAGGAGATCG.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TCTGCTATGGTCTCTACTT.....	20	0	1	1.00	1	1	0	0	0	0	0
.....TTTTCGGATCTGTCCACCTCCTAG.....	24	0	1	1.00	1	1	0	0	0	0	0
.....CTACTTGAAGGACAAGCCACTCACGCC.....	28	0	1	1.00	1	1	0	0	0	0	0
.....TGGAATGATCATCTGAAGCGCA.....	22	0	1	1.00	1	1	0	0	0	0	0
..AAGGCATGGAATGATCATCTGAAGC.....	25	0	1	1.00	1	1	0	0	0	0	0
.....GAAGCGCATGCAGGAGATC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....GAAGCGCATGCAGGAGAT.....	18	0	1	1.00	1	1	0	0	0	0	0
..AAGGCATGGAATGATCATC.....	19	0	1	1.00	1	1	0	0	0	0	0
.....ACCCATCGCAGGAATCGAGCGCAG.....	24	0	1	1.00	1	1	0	0	0	0	0
.....GAAGCGCATGCAGGAGATCGAGCGC.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TTTCGGATCTGTCCACCTCCTAT.....	21	0	1	1.00	1	1	0	0	0	0	0
.....CGCTATGGTCTCTACTTGAA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....ACCCATCGCAGGAATCGAGCGCAGG.....	25	0	1	1.00	1	1	0	0	0	0	0
.....GTGGGTGTCCCTAGTCCGTTAA.....	22	0	1	1.00	1	1	0	0	0	0	0
.....TCTACTTGAAGGACAAGCCACTC.....	23	0	1	1.00	1	0	1	0	0	0	0
.....CGCAGGAGATCGAGCGCAGGTACG.....	24	3	1	1.00	1	0	0	0	1	0	0
.....AGGAGATCGAGCGCAGGTACG.....	21	3	1	1.00	1	0	0	0	1	0	0
.....GAGATCGAGCGCAGGTACG.....	19	3	12	0.17	2	1	1	0	0	0	0

Anti-sense strand reads

	Read #	Mismatch	Hit Count	Total Norm	Total	W055 female body	Y107 male body
CTCTTCCGTACCTTACTAGTAGACTCGCGTACGTCCTCTAGCTCGCGTCCACCCACAGGGATCAGGCATTTACGAGGGTTTCTAGTGGATAGTAAAGGCCTAGACAGGTGGAGGATCCATGGGTAGAGCGATACCAGAGATGAACTTCCTGTTCGGTGAGTGCGGGT							
********************************..((((((....((((((((..((((((.....................)))))).)))))))...))))))..********************************							
.....TTCGGATCTGTCCACCTCCTAG.....	24	0	1	1.00	1	1	0
.....TCGCTATGGTCTCTACTTGA.....	20	0	1	1.00	1	1	0
.....TTCGGATCTGTCCACCTCCTAT.....	23	1	1	1.00	1	1	0
.....GGCATGGAATGATCATCTGAAGCGC.....	25	0	1	1.00	1	1	0
.....GGCATGGAATGATCATCTGA.....	20	0	1	1.00	1	1	0
.....TCTGAAGCGCATGCAGGAGATC.....	22	0	1	1.00	1	1	0
.....TGATCATCTGAAGCGCATGCAGGAG.....	25	0	1	1.00	1	1	0
.....TCTGCTATGGTCTCTACTT.....	20	0	1	1.00	1	1	0
.....GCTATGGTCTCTACTTGAAGGACA.....	24	0	1	1.00	1	1	0
.....TCTGCTATGGTCTCTACTTGAAG.....	24	0	1	1.00	1	1	0
.....TCTCTACTTGAAGGACAAGCCACTCACGC.....	29	0	1	1.00	1	1	0
.....GCTATGGTCTCTACTTGAAGGACA.....	28	0	1	1.00	1	1	0
.....TCTGCTATGGTCTCTACTT.....	20	0	1	1.00	1	1	0
.....TCTGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA.....	31	0	1	1.00	1	1	0
.....TCTCTACTTGAAGGACAAGCCACTCACGCCCA.....	32	0	1	1.00	1	1	0
.....TCTCTACTTGAAGGACAAGCCACTCACGCC.....	30	0	1	1.00	1	1	0
.....TCTCTACTTGAAGGACAAGCCACTCACGCCC.....	31	0	1	1.00	1	1	0
.....TCTCTACTTGAAGGACAAGCCACTCACGCCCA.....	32	0	1	1.00	1	1	0

Show Alignment With Reads

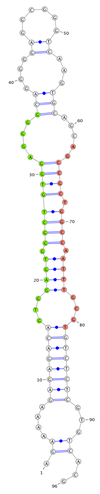
Re-alignment of all predicted orthologs

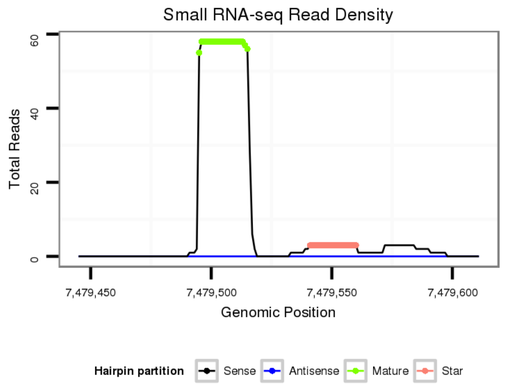
Species	Coordinate	ID	Alignment
droEre	scaffold_4770:10523627-10523745 -	der_593	GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCTGTCCACCTCCTAGGGTACCCATCTCGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA
droYak	UR:1:8323722-15432895: +		GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCTGTCCACCTCCTAGGGTACCCATCTCGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA
droSec	scaffold_2:12943765-12943833: +		GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCTGTCCACCTCCTAGGGTACCCATCTCGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA
droSim	UR:1:10224868:10227065: +	dsi_21519	GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCTGTCCACCTCCTAGGGTACCCATCTCGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA
dmj	ch:3R:11201954:11002115: -		GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCTGTCCACCTCCTAGGGTACCCATCTCGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA
droKyp	scaffold_8000004091000:67182: -		GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCATGATCATCTAAGTTT
droBia	scaffold_3:1378523: -		GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCTGTCCACCTCCTAGGGTACCCATCTCGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA
droTak	scaffold_3:1378523: -		GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCTGTCCACCTCCTAGGGTACCCATCTCGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA
droEle	scaffold_3:1378523: -		GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCTGTCCACCTCCTAGGGTACCCATCTCGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA
droRho	scaffold_3:1378523: -		GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCTGTCCACCTCCTAGGGTACCCATCTCGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA
droFic	scaffold_3:1378523: -		GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCTGTCCACCTCCTAGGGTACCCATCTCGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA
droKik	scaffold_3:1378523: -		GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCTGTCCACCTCCTAGGGTACCCATCTCGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA
droAna	scaffold_13340:6085732: -		GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCTGTCCACCTCCTAGGGTACCCATCTCGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA
droBip	scaffold_3:1378523: -		GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCTGTCCACCTCCTAGGGTACCCATCTCGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA
dpo	scaffold_3:1378523: -		GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCTGTCCACCTCCTAGGGTACCCATCTCGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA
droPer	scaffold_3:1378523: -		GAGAAGGCATGGAATGATCATCTGAAGCGCATGCAGGAGATCGAGCGCAGGTGGGTGTCCCTAGTCCGTTAAAGGCTCCACCATGTCATTTCGGATCTGTCCACCTCCTAGGGTACCCATCTCGCTATGGTCTCTACTTGAAGGACAAGCCACTCACGCCCA
droWil	scf_1150000004343:7243042: -		AT----------TCATC----------T----------T----------T

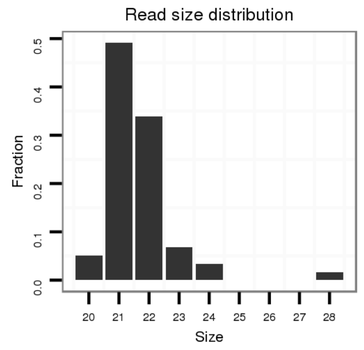
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_80	**scaffold_4845:7479495-7479561 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

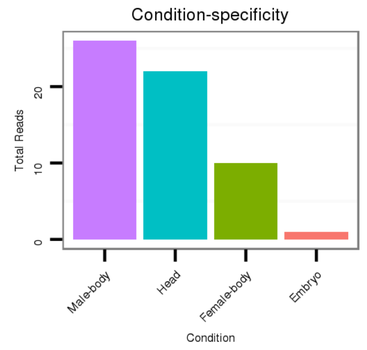
Legend: mature star mismatch in alignment mismatch in read

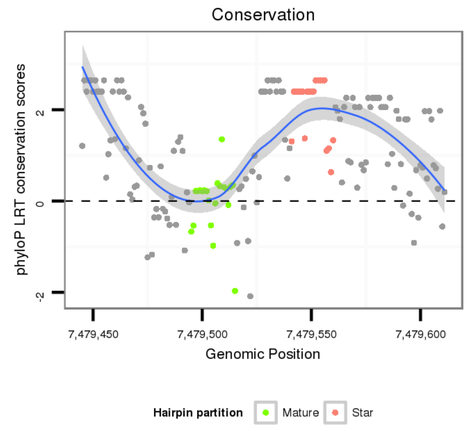
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG21784-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTGATGAGGCAGCTCAAGTGGCAGAGGGGCACAAGAGAAAAAGAGAGACAGTGGAGTGGGCTGTGGAGGGGCAGGGGGAGGCGGGTCAAGTGCAGCAGCCGCTGGCCAATTTGCGTGTCTCTCGTGTCACGACAAAAGGCCAATTCAAGCAGTGAAATTTGAATAAA

Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	V108 head	M055 female body	V060 head	M057 embryo	V040 embryo	GSM1528801 follicle cells
21	0	1	27.00	27	19	5	3	0	0	0	0
22	0	1	19.00	19	3	10	3	2	0	1	0
23	0	1	4.00	4	1	1	2	0	0	0	0
22	1	1	3.00	3	3	0	0	0	0	0	0
24	0	1	2.00	2	2	0	0	0	0	0	0
21	0	1	2.00	2	0	2	0	0	0	0	0
20	0	1	1.00	1	0	1	0	0	0	0	0
26	0	1	1.00	1	0	1	0	0	0	0	0
23	0	1	1.00	1	0	0	0	0	1	0	0
20	0	1	1.00	1	1	0	0	0	0	0	0
28	0	1	1.00	1	0	0	1	0	0	0	0
22	0	1	1.00	1	0	1	0	0	0	0	0
19	0	1	1.00	1	1	0	0	0	0	0	0
22	1	1	1.00	1	1	0	0	0	0	0	0
23	0	1	1.00	1	0	0	0	0	1	0	0
20	0	1	1.00	1	0	0	1	0	0	0	0
21	1	1	1.00	1	0	0	1	0	0	0	0
24	0	1	1.00	1	0	0	1	0	0	0	0
26	3	1	1.00	1	1	0	0	0	0	0	0
20	1	2	0.50	1	0	1	0	0	0	0	0

Anti-sense strand reads

AACTACTCCGTCGAGTTCACCGTCTCCCCGTGTTCTCTTTTTCTCTCTGTCACCTCACCCGACACCTCCCCGTCCCCCTCCGCCCAGTTCACGTCGTCGGGCGACCGGTTAAACGCACAGAGAGCACAGTGCTGTTTCCGGTTAAGTTCGTCACTTTAAACTTATTT

Read size	# Mismatch	Hit Count	Total Norm	Total

No data available in table

Show Alignment With Reads

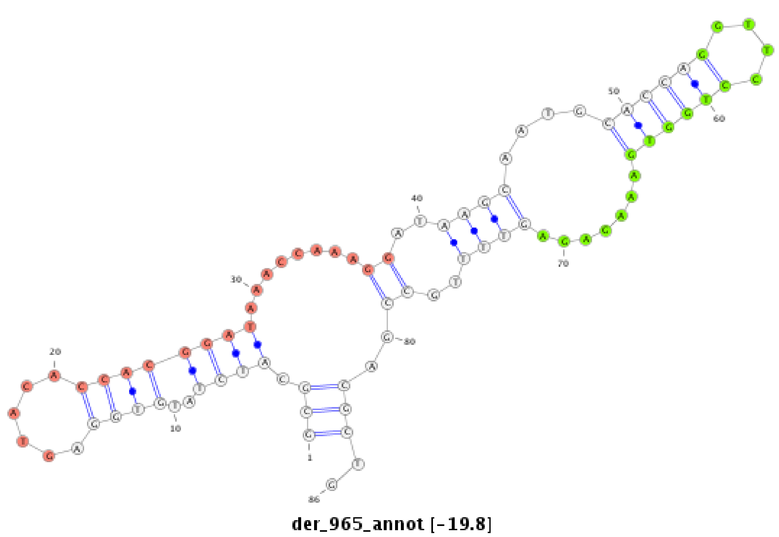
Re-alignment of all predicted orthologs

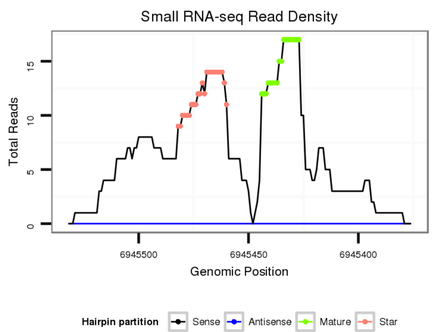
Species	Coordinate	ID	Alignment
droEre2	scaffold_4845:7479445-7479611 +	der_80	TTGATGAGGC--AGCTCAAGTGGCAGA--G-GG----------GCACAAGAGA-AAAAGA-GAGACA----------GTGGAGTG----------GGCTGTGGAGGGGCA----------GGGGGAGGCGGGTCAAGTGCAGC---AG---------CCGCTGGCCAATTTGCGTGTCTC----CTCGTGTCACGAC--AAAAGGCCAATTCAA----GCAGTGAA-ATTTG-AATAAA
droYak3	2R:15939115-15939312 -		TTGATGAGGC--AGCTCAAGTGGCAGA--G-GG----------GGGC-----------AGAGAGGCGCTGGAGTGGAATGCTGGAGGGGATGGGGATGGGGAAGGGCGAGGGTAAGGGTAAGGAGTAGGCG---GG----------AGAGGGGTCAAGTGCAGC---AG---------CCGCTGGCCAATTTGCGTGTCTC----CTCGTGTCACGAC--AAAAGGCCAACTCAA----GCAGTGGA-ATTTG-AATAAA
droSec2	scaffold_9:1774118-1774278 -		TTGATGAGGC--AGCTCAAGTGGCAGA--G-GG----------GAGC--------GTCGGAGAGCAGAGGAAGCAGAGAGGCGCA------AGA----------GGGGTAGGCGGGTCAAGTGCAGC---AG---------CCGCAGGCCAATTTGCGTGTCTC----CTCGTGTCACGAC--AAAAGGCCAATTCAA----GCGTGTGAA-ATTTG-AATAAA
droSim2	2r:19001682-19001842 -		TTGATGAGGC--AGCTCAAGTGGCAGA--G-GG----------GCGG--------GTCGGAGAGCAGAAGAAGCAGAGAGGCGCA------AGA----------GGGGTAGGCGGGTCAAGTGCAGC---AG---------CCGCTGGCCAATTTGCGTGTCTC----CTCGTGTCACGAC--AAAAGGCCAATTCAA----GCGTGTGAA-ATTTG-AATAAA
dm3	chr2R:18475460-18475620 -		TTGATGAGGC--AGCTCAAGTGGCAGA--G-GG----------CCGG--------GTCGGAGAGCATAAGAAGCAGAGCGGCGCA------AGA----------TGAGGGGCAGGCGGGTCAAGTGCAGC---AG---------CCGCTGGCCAATTTGCGTGTCTC----CTCGTGTCACGAC--AAAAGGCCAATTCAA----GCGTGTGAA-ATTTG-AATAAA
droEug1	scf7180000409672:6400675-6400798 -		TTGATGAGGC--AGCTCAAGTGGCAGA--G-GG----------GG--------------------------------------GTTGC----------AGGCGGGTCAAGTGCAGC---AG---------CCGCTGGCCAATTTGCGTGTCTC----CTCGTGTCACGAC--AAAAGGCCAATTCAA----GCGTGTGAA-ATTTG-AATAAA
droBia1	scf7180000302143:2192740-2192863 +		TTGATGAGGC--AGCTCAAGTGGCGGA--G-GG----------GG--------------------------------------GATGC----------AGGCGGGTCAAGTGCGGC---AG---------CCGCTGGCCAATTTGCGTGTCTC----CTCGTGTCACGAC--AAAAGGCCAATTCAG----GCGTGTGAA-ATTTG-AATAAA
droTak1	scf7180000415739:368329-368454 -		TTGATGAGGC--AGCTCAAGTGGCAGAGA-G-GG----------GG--------------------------------------GATGC----------AGGCGGGTCAAGTGCAGC---AG---------CCGCTGGCCAATTTGCGTGTCTC----CTCGTGTCACGAC--AAAAGGCCAATTCAA----GCGTGGCGA-ATTTG-AATAGA
droEle1	scf7180000491022:52596-52719 -		TTGATGAGGC--AGCTCAAGTGGCAGA--G-GG----------GG--------------------------------------CATGC----------AGGCGGGTCAAGTGCAGC---AG---------CCGCTGGCCAATTTGCGTGTCTC----CTCGTGTCACGAC--AAAAGGCCAATTCAA----GCGTGTGAA-ATTTG-AAGAGA
droRho1	scf7180000780232:6070-6193 -		TTGATGAGGC--AGCTCAAGTGGCAGA--G-GG----------GG--------------------------------------GATGA----------AGGCGGGTCAAGTGCAGC---AG---------CCGCTGGCCAATTTGCGTGTCTC----CTCGTGTCACGAC--AAAAGGCCAATTCAA----GCGTGTGAA-ATTTG-AATAGA
droFic1	scf7180000454066:2414984-2415109 -		TTGATGAGGC--AGCTCAAGTGGCAAA-G-GG----------GG--------------------------------------GTTGC----------AGGCGGGTCAAGTGCAC---AG---------CCGCTGGCCAATTTGCGTGTCTC----CTCGTGACACGAC--AAAAGGCCAGGTGGA----GGTCAAGATATTTG-AATAAA
droKik1	scf7180000302476:1550070-1550211 +		TTGATGAGGC--AGCTCAAGTGGCAGG--G-AGGCTGGA----------C-----------------------------------ACGACAA-GACCACGGA---------------CGAGGGGTCAAGTGCAGC---AG---------CCGCTGGCCAATTTGCGTGTCTC---CGTCGTGTGCGAC--AAAAGGCCAATTCAG----GCGTGAGAA-ATTTG-AATAGC
droAna3	scaffold_13266:7282376-7282511 +		TTGATGAGGC--AGCTCAAGTGGCAAC-A-AAGGCCAGA----------C-----GA---CA--GCGGGTGGCAGGAGGGTCAAGTGCAGC---AG---------CCGCTGGCCAATTTGCGTGTCTC----CTCGTGTCACGAC--AAAAGGCCAATTCAG----GCGGCGTA-ATGTG-AATAGC
droBip1	scf7180000396384:98201-98385 +		TTGATGAGGC--AGCTCAAGTGGCAAG--A-AAGCTAGAGAAGGGGGGG--------C---GATGTGTGCAGATAGCAGAACAAGGGGGTACTGGATGGGGACAGTAGGTGCCAGGAGGGTCAAGTGCAGC---AG---------CCGCTGGCCAATTTGCGTGTCTC----CTCGTGTCAGTAC--AAAAGGCCAATTCAA----GCGCGTA-ATGTG-AATAGC
dp5	3:7084077-7084241 -		TTGATGAGGC--AGCTCAAGTGGCAGCT-G-CAG----------C-C-----C---CGA-GAGCAG--GCGGCGGCGGTGGCGGCAGG----------GGGAGGGGTGGGTCAAGTGCAGC---AG---------CCGCTGGCCAATTTGCGTGTCATTGCCTCATGCCATGAC--AAAAGGCCAATTCAACAGAGGTCCGAG-CGCTGGGGGAGA
droPer2	scaffold_2:7283629-7283773 -		TTGATGAGGC--AGCTCAAGTGGCAGCT-G-CAG----------C-C-----C---CGA-GAGCAG--GCGGCGGCGGTGGCGGCAGG----------GGGAGGGGTGGGTCAAGTGCAGC---AG---------CCGCTGGCCAATTTGCGTGTCATTGCCTCATGCCATGAC--AAAAGGCCAATTCA----------------AGAGA
droWil2	scf2_1100000004558:355501-355643 -		TTGATGAGGCCTAAGACAAGTGACGAC--A-AGGC----------GC---ACAGGTTGTCGC-GAGCGC--GTGGGAGGGTGGCAAAAAG----------GT--AGACAAAGGGGTCAAGTGCAGT--CAG---------CCGCTGGCCAATTTTTTA---G----CTTGTGC--GACCAAAAAGGCAAA---

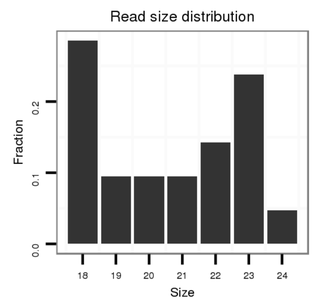
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_965	**scaffold_4820:6945426-6945482 -**	**candidate**	**Canonical miRNA**	**3pUTR**	[View on UCSC Genome Browser [Cornell Mirror]]

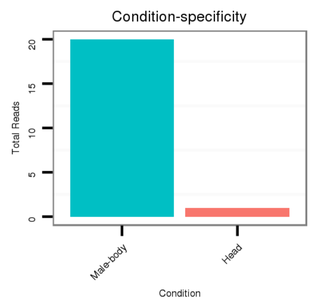
Legend: mature star mismatch in alignment mismatch in read

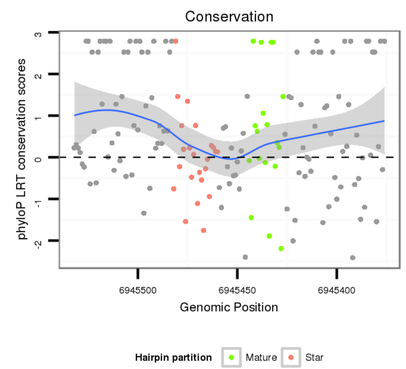
Predicted structure











Show Alternate Folds

Flybase annotation

utr3 [utr3_plus_6792]; intron [Dere\GG11389-in]; CDS [Dere\GG11389-cds]; CDS [Dere\GG11389-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTCGGCAATGCGGAGAACTACTCCAGCGTGATCACGCGCATCTATGTGGAGTACACCACGGATAAACCAAAGGATAAGCAATGCACCAGGTTCCTGGTGAAAGAGATTTTGCCGACGCTGGTCCGGCGGCGCAGGTTCTCCTGAGTTACGGAGTGT	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	M055 female body	V108 head	GSM1528801 follicle cells
**********(((.(((((..((((.....)))))))).....((..((((....((((((....))))))....))))..))))..)))..**********									
.....GGTTCCTGGTGAAAGAGA.....	18	0	1	6.00	6	5	0	1	0
.....GTACACCACGGATAAACCAAAGG.....	23	0	1	4.00	4	4	0	0	0
.....GGTTCCTGGTGAAAGAGAGT.....	20	0	1	2.00	2	2	0	0	0
.....GTACACCACGGATAAACCAAAG.....	22	0	1	2.00	2	2	0	0	0
.....CCAGCGTGATCACGCGCATCTATGTGGA.....	28	0	1	2.00	2	0	2	0	0
...GGCAATGCGGAGAACTACTCCAGCGT.....	26	0	1	1.00	1	1	0	0	0
.....GTACACCACGGATAAACCAAA.....	21	0	1	1.00	1	1	0	0	0
.....GAAAGAGAGTTTTGCCGAC.....	19	0	1	1.00	1	1	0	0	0
.....GAACTACTCCAGCGTGATCACGCGCATCT.....	29	0	1	1.00	1	0	1	0	0
.....GATAAACCAAAGGATAAGCAATGC.....	24	0	1	1.00	1	1	0	0	0
.....GTTCTCCTGAGTTACGGA.....	18	0	1	1.00	1	0	0	1	0
.....GACGCTGGTCCGGCGGCGCAGGTT.....	24	0	1	1.00	1	0	1	0	0
.....ATCTATGTGGAGTACACCACGGA.....	23	0	1	1.00	1	1	0	0	0
.....CACGCGCATCTATGTGGAGTACACCACG.....	28	0	1	1.00	1	1	0	0	0
.....CCAGGTTCCTGGTGAAAGAGAGT.....	23	0	1	1.00	1	1	0	0	0
.....TCCTGGTGAAAGAGAGTTTT.....	20	0	1	1.00	1	0	0	1	0
.....GACGCTGGTCCGGCGGCGCAGGTTCT.....	26	0	1	1.00	1	0	1	0	0
.....GTGAAAGAGAGTTTTGCCGAC.....	21	0	1	1.00	1	1	0	0	0
.....ATAAACCAAAGGATAAGCAATG.....	22	0	1	1.00	1	1	0	0	0
.....GGATAAACCAAAGGATAAGC.....	20	0	1	1.00	1	1	0	0	0
.....AGGTTCCTGGTGAAAGAGAGT.....	21	0	1	1.00	1	1	0	0	0
.....ACTACTCCAGCGTGATCACGCGC.....	23	0	1	1.00	1	0	0	1	0
.....ATCACGCGCATCTATGTGGA.....	20	0	1	1.00	1	1	0	0	0
.....CAGGTTCCTGGTGAAAGAGAGT.....	22	0	1	1.00	1	1	0	0	0
.....CACGGATAAACCAAAGGATAAGC.....	23	0	1	1.00	1	1	0	0	0
.....AGGTTCCTGGTGAAAGAGA.....	19	0	1	1.00	1	1	0	0	0
.....AAACCAAAGGATAAGCAAT.....	19	0	1	1.00	1	1	0	0	0
.....GAACTACTCCAGCGTGATCACGCGC.....	25	0	1	1.00	1	1	0	0	0
.....ACACCACGGATAAACCAAAGG.....	21	0	1	1.00	1	1	0	0	0
.....GTGATCACGCGCATCTATGTGGA.....	23	0	1	1.00	1	0	0	1	0
.....GAAAGAGAGTTTTGCCGACGCT.....	22	0	1	1.00	1	1	0	0	0
.....GTGAAAGAGAGTTTTGCCGACGCT.....	24	0	1	1.00	1	1	0	0	0
.....CGACGCTGGTCCGGCGGCGCAGGTT.....	25	0	1	1.00	1	0	1	0	0
.....GGATAAACCAAAGGATAAGC.....	20	0	1	1.00	1	1	0	0	0
.....AGGTTCCTGGTGAAAGAGAGT.....	21	0	1	1.00	1	1	0	0	0
.....ACTACTCCAGCGTGATCACGCGC.....	23	0	1	1.00	1	0	0	1	0
.....ATCACGCGCATCTATGTGGA.....	20	0	1	1.00	1	1	0	0	0
.....CAGGTTCCTGGTGAAAGAGAGT.....	22	0	1	1.00	1	1	0	0	0
.....CACGGATAAACCAAAGGATAAGC.....	23	0	1	1.00	1	1	0	0	0
.....AGGTTCCTGGTGAAAGAGA.....	19	0	1	1.00	1	1	0	0	0
.....AAACCAAAGGATAAGCAAT.....	19	0	1	1.00	1	1	0	0	0
.....GAACTACTCCAGCGTGATCACGCGC.....	25	0	1	1.00	1	1	0	0	0
.....ACACCACGGATAAACCAAAGG.....	21	0	1	1.00	1	1	0	0	0
.....GTGATCACGCGCATCTATGTGGA.....	23	0	1	1.00	1	0	0	1	0
.....GAAAGAGAGTTTTGCCGACGCT.....	22	0	1	1.00	1	1	0	0	0
.....GTGAAAGAGAGTTTTGCCGACGCT.....	24	0	1	1.00	1	1	0	0	0
.....CGACGCTGGTCCGGCGGCGCAGGTT.....	25	0	1	1.00	1	0	1	0	0
.....ATCTATGTGGAGTACACCACGGA.....	23	0	1	1.00	1	1	0	0	0
.....CACGCGCATCTATGTGGAGTACACCACG.....	28	0	1	1.00	1	1	0	0	0
.....CCAGGTTCCTGGTGAAAGAGAGT.....	23	0	1	1.00	1	1	0	0	0
.....TCCTGGTGAAAGAGAGTTTT.....	20	0	1	1.00	1	0	0	1	0
.....GACGCTGGTCCGGCGGCGCAGGTTCT.....	26	0	1	1.00	1	0	1	0	0
.....GTGAAAGAGAGTTTTGCCGAC.....	21	0	1	1.00	1	1	0	0	0
.....ATAAACCAAAGGATAAGCAATG.....	22	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

GAGCCGTTACGCCTCTTGATGAGGTCGCACTAGTGCGCGTAGATACACCTCATGTGGTGCCTATTTGGTTTCCTATTCGTTACGTGGTCCAAGGACCACTTTCTCTCAAAACGGCTGCGACCAGGCCGCCGCGTCCAAGAGGACTCAATGCCTCACA	Read size	# Mismatch	Hit Count	Total Norm	Total	V040 embryo	M057 embryo
**********(((.(((((..((((.....)))))))).....((..((((....((((((....))))))....))))..))))..)))..**********							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4820:6945376-6945532 -	der_965	CTCGGCAATGCGGAGAACTACTCCAGCGTGATCACGCGCATCTATGTGGAGTACACCACGGATAAA--CCAAAGGATA-----AG---CAATGCACCAGGTTCCTGGTGAAAGAGAGTTTTGCCGACGCTGGTCCGGCGGCGCAGGTTCTCCTGAGTTACGGAGTGT
droYak3	3R:25390915-25391071 -		CTCGGCAACGCGGAGAACTACTCCAGCGTGATCACGCGCATCSATGTGGAGTACACCACGGATAAA--TCAAAGGASA-----AG---CAATGCACCAGATTCCTGGTGAACGAGAGTTTGCCGACGCTGGTCCGGCGGCGCAGGTTCTCCTGAGTTACGGCGTGT
droSec2	scaffold_33:359033-359189 +		CTCGGCAACGCGGAGAACTACTCCAGCGTGATCACGCGCATCTATGTGGAATATACCACGATAAC--TCAAAGGATA-----AA---CAATGCACCAGATTCCTGGTGAAAGAGAGTTTGCCGACGCTGGTCCGGCGGCGCAGGTTCTCCTGAGTTACGGAGTGT
droSim2	3r:20607771-20607927 +		CTCGGCAACGCGGAGAACTACTCCAGCGTGATCACGCGCATCTATTGGAATATACCACGGATAAC--TCAAAGGATA-----AG---CAATGCACCAGATTCCTGGTGAAAGAGAGTTTGCCGACGCTGGTCCGGCGGCGCAGGTTCTCCTGAGTTACGGAGTGT
dm3	chr3R:21097728-21097876 +		CTCGGCAACGCGGAGAACTACTCAAGCGTGATCACGCGCATCTATGTGGAGTATACCACGGATAAA--TCAAAGGATA-----AA---CAATGCACCAGATTCC--------ACCAGATTTGCCGACGCTGGTCCGGCGGCGCAGGTTCTCCTGAGTTACGGAGTGT
droEug1	scf7180000409692:287562-287718 -		CTCGGCAATGCGGAGAACTACTCCAGCGTGATCACGCGCATCTATGTGGATACAGTACGAGAACAC--TCAAGCAGAA-----AG---CAATGCACCAGATTCTTGGTTAAGACACGTTCGCCGACGATCCGGCGGCGCAGGTCCTATGAGTTATGGAGGAGTGT
droBia1	scf7180000302136:1912714-1912870 +		CTCGGCAACGCGGAGAACTACTCCAGCGTGATCACGCGCATCTATGTGGATACACGAGAGATGGCAAGC-TGCCAGGAAA-----AG---CAATGCACCAGATTCCTGGTAAGACCCGTTCCCGACGATCCCGGCGGCGCAGGTCCTATGAGTTATGGCGTGT
droTak1	scf7180000413457:134565-134721 -		CTCGGCAATGCGGAGAACTTGGCCAGCGTGATCACGCGCATCTATGTGGAATACACCACGAAGATAC--TGCAAGGATA-----AG---CAATGCACTCGATTCCTGGCTATGACACAGTTTTGCCGACGATCCCGGCGGCGCAGGTCCTAATGCGTTATGGCGTGT
droEle1	scf7180000491212:452317-452467 +		CTCGGCAACGCGGAGAACTTATGCCAGCGTGATCACGCGCATCTATGTGGAATATAGTACGAAAGCC-ATA-------------AG---GCAATGCCAGATTCTTGGCCATGACGCAGTTTTGCCGACGATCCCGGCGGCGCAGGTCCTAATGCGTTATGGAGTGT
droRho1	scf7180000779365:155752-155908 -		ACAGCCAATGCGAGGAACTACTCCAGCGTGATCACGCGCATCTATGTGGAGTACACCACGAAGGATC-AAAAAGGATA-----AG---CAGGACGCCACGTTCCTGCTGAAAACACACGTTCGCCGAGAAGATCCCGCGGCGCAGATCCTATGCGCGACTAGGGAGTGT
droFic1	scf7180000454055:1008252-1008408 +		CTCGGCAATGCGGAGAACTACTCCAGCGTGATCACGCGCATCTAAAGTGGAATATAGTACGAATAGCC-TGCAAAACCCA-----AG---CAATCCACAAGGTTCCTGGTAAAACACACGTTTCCGAGAAGGATCCCGCTGCGAGCAGATCCTATGCGCGACTAGGGAGTGT
droKik1	scf7180000302307:737872-738031 +		ATGGCCAACGGAGAGAACTACTCAAGCGTGATCACGCGCATCACGTGGAGTACACCACCAGGGC-TGCAAGGCTA-----AGAGAGGATCCACGAAGTCCGGCTTTTGCCGAGAAGATCCCGGCTGCCAGTCCTATCTATCACGGGAGTGT
droAna3	scaffold_13340:1289262-1289418 +		ATCCCCAATGGTGAGAACTACCCAGCAGTGATCACGCGATCTATGTGGAGTACACCACAAAGGGT-TGCAAGGCCA-----AG---CTTTCCACCAACTTCCTCTTGAACACTACGTTCGCCGAAGGATCCCAGCGCCACGTTCTGGTTCACTAAGGCAATGT
droBip1	scf7180000396712:537802-537958 -		ATCCCAATGGTGAGAACTACCCAGCGTGATCACGCAGTCTATGTGGAGTACACCACAAAGGGT-TGCAAGGACA-----AG---CTTGCCACGAACTTCCTCTTGAACACTACTTTTGCTGAAAGGATCCCAGCGCCACGTCTGGTTCACTAAGGCAATGT
dp5	2:20570184-20570340 -		ATGGCGAATGGCGAGAACTTTGCAAGTGTGATCACGCGATCTATTTGGAATATAGTACGAAACCC-TGCAAGGCCA-----AA---CAGACCACTACGTTTTTGGTGAAGACTACTTTTACGAGCAAGGATCCCGGCTGCTGATGTCCTCTCCCCTTAAGGCGTTT
droPer2	scaffold_3:3321476-3321632 -		ATTGCGAATGGCGAGAACTTTGCAAGTGTGATCACGCGATCTATTTGGAATATAGTACGAAACCC-TGCAAGGCCA-----AA---CAGACCACTACGTTTTTGGTGAAGACTACTTTTACGAGCAAGGATCCCGGCTGCTGATGTCCTCTCCCCTTAAGGCGTTT
droWil2	scf2_1100000004943:13534349-13534507 -		GATCCCAATGGTGAGAACTTTGCCAGCGTGATTACGCGATAATATGTGGACTACTTACGGATATTT-GTAAAAATATG-----AACCACAACATGCCACATTTCTGGTCAACGCCATCGCGTGAGAATGCATCCCGCTTCTGATTTCCTTAAAAGAATTAGGGTATGT
droVir3	scaffold_13047:7285894-7286047 -		ACGACGCAATGCGGAGAACTATGCCAGCGTGATCACGCGCATCTATGTGGAGTTTTTGGACAAGGATT--GTATTTTAAGTAGCACGAG---------GATTCCCATTTAAGTAAACACGCCTTTGTCGCATGCATCCAGCGGCTGATTTCCTGGAACAATAAGGCGTCT
droMoj3	scaffold_6540:3207271-3207424 -		ACGCCCAATGCGGAGAACTATGCCAGCGTCATCACGACGATCATCGTTAGATCACGGACAAGGATT---TTTATTGTCC-----AGAGCCATACAGACACACTTATAGTTATGACCCGCGTCCGCGAGAAGCATCCGGCTTTTCACTTCCTGGAACAATAAGGCGTAT
droGri2	scaffold_14624:2873639-2873798 -		ACGCCAAAGCGTGAGAATTATAGTGGCTGTTCTCACCGCATTCCAGTGGAGTTCGAGGAAACAGGCAGTCGTCCTGCA-----GTTCGCTCACGCCACCGTAATCTCCTGAACGAAGCTGTTCCGAGCGAAGCAGTTCCGCCACGGGAAGCGTCTTGCCGAGTACGGTGTGCT

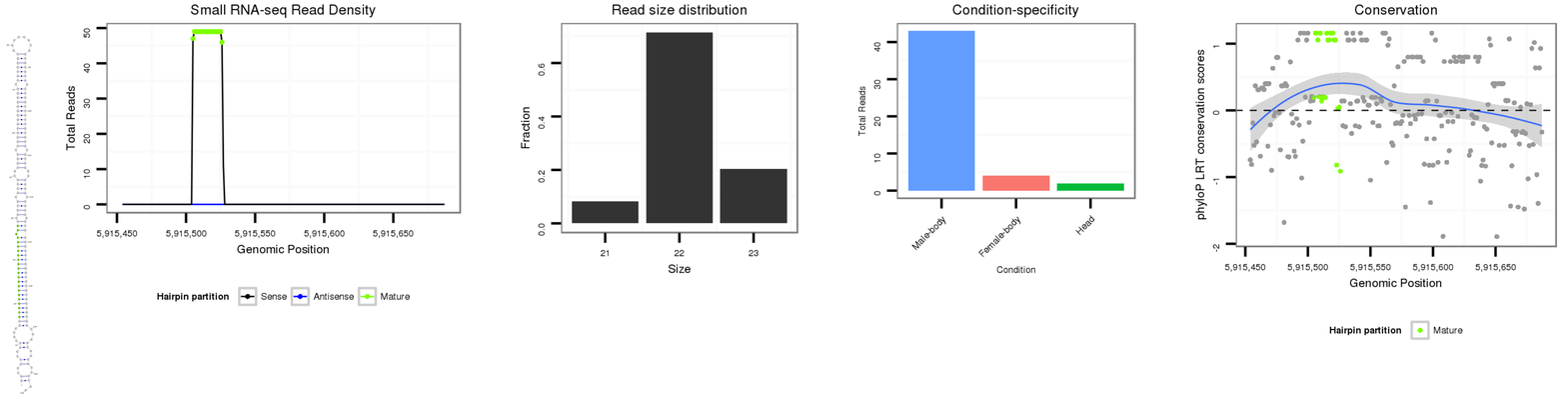
Generated: 09/08/2015 at 07:43 PM

	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	0
crit.tploop3	0
crit.uri	1
crit.back	0
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1455	**scaffold_4770:5915504-5915637 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

Legend: mature star mismatch in alignment mismatch in read

Predicted structure



Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TCATCACGGAACATTTGGTGAAATGGCCAGGGCATAGTCCTCGATCACCTCATTGTACAAATCGTTTCCTAGGCGGGTGCCTTCCACGACTCCCACAAGAACGGATTATGCACAGCCCATGGTGTATACTTTGTTTTTGTGGGTGTCGGAGAAGTCACCAGTCAGGGAACGATTTGTACAATGACAAGTAAAGTTCTAAAATAGTTTTTGATGGGTATAAACGGCTTTGCACC

**********	((..((..((....(((((((((((((((((((.(((..((((.((((..((((.(((((((((((((((.(((((((.........))))))).)))))))))))))))).)))).)))))).)))))))))))))))))))...))..)).)).)..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	M055 female body	V108 head	V040 embryo
.....	ATTGTACAAATCGTTTCCTAGG	22	0	1	34.00	34	31	3	0	0
.....	ATTGTACAAATCGTTTCCTAGGC	23	0	1	10.00	10	9	0	1	0
.....	ATTGTACAAATCGTTTCCTAG	21	0	1	3.00	3	2	0	1	0
.....	ATTGTACAAATCGTTTCCTAGGT	23	1	1	2.00	2	2	0	0	0
.....	TTGTACAAATCGTTTCCTAGGC	22	0	1	1.00	1	1	0	0	0
.....	TTGTACAAATCGTTTCCTAGG	21	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

AGTAGTGCCTTGTAAACCACTTTACCGGTCCCGTATCAGGAGCTAGTGGAGTAACATGTTTAGCAAAGGATCCGCCCACGGAAGGTGCTGAGGGTGTTCTTGCCTAATACGTGTCGGGTACCACATATGAAACAAAAACACCCACAGCCTCTTCAGTGGTCAGTCCCTTGCTAAACATGTTACTGTTCATTTCAAGATTTTATCAAAAAACTACCCATATTTGCCGAAACGTGG

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

No data available in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4770:5915454-5915687 +	der_1455	TCATCACGGAACATTTGGTGAAATGG----------CCAGGGCATAGTCCTCGATCACCTCATTGTA-CAAATCGTTTCCTAGGCGGGTGCCTTCCACGACTCCCACAAGAACGGATTATGCACAGCCCATG--GTGTATACTTTGTTTTTGTGGGTGTCGGAGAAGTCACCAGTCAGG-GAACGATTTGTACAATGAC----------AAGTA-AAGTTCTAAAATAGTTTTTG----------ATG--------GGTATAAACGGCTT-------TGCACC
droYak3	3R:4520190-4520495 -		TCATCACGAACATTTGGTGAAATGGCAGCCCTTAAGGTGGCGGCT---TGTTGAATGGTCAAAC-AGTTGGTGGATAAG-----CGATGGATGCAAATTAAAGCCGCATTA-GAGGCATATGTTATACGATCTCATTGTA-CAATCGTTTCCTAGGCGGTGCCTTCCAGCAACTCCCACAAGAACGGATTATGCACAGCCCATG--GTGTATACTTTGTTTTTGTGGGTGTCGGAGAAGCATTTCAGCAGG-GAACGATTTGTACAATGA----------AG-GTAAGTTCTGATAGTTTTGCC----------ATG--------GGTCAGCACGGCTT-------TGCACC
droSec2	scaffold_25:31118-31423 +	dse_1816	TCATCACGGAACATTTGGTGAAATGGCCTTTCTTAA------GCA---TGCTGAGTGACCAAAGAAGTTTATTGCTGTTGCTTGCGATGGCGGAAAAATAAAACCCATTA-GAGGCATATGTTATACCGATCTCATTGTA-CAATCGTTTCCTAGGCGGTGCCTTCCAGCAACTCCCACAAGAACGGATTATGCACAGCCCATG--GTGTATACTTTGTTTTTGTGGGTGTCGGAGAAGCGATTTCAGCAGG-GAACGATTTGTACAATGA----------AG-GTAAGTTCTAAAATAGTTTTTGC----------AGT--------GGG--GGGGCTT-------TGACC
droSim2	3r:5537921-5538235 +	dsi_32097	TCATCACGAACATTTGGTGAAATGGCAGCCA---TGCTGACTGACCAAAGAAGTTCATTGCTAAG-----CAATGGCGAGAAAATAAAACCCATTA-GAGGCATATGTTATACCGATCTCATTGTA-CAATCGTTTCCTAGGCGGTGCCTTCCAGCAACTCCCACAAGAACGGATTATGCACAGCCCATG--GTGTATACTTTGTTTTTGTGGGTGTCGGAGAAGCGATTTCACAATGA----------AG-GTAAGTTCTGAAATAGTTTTTAC----------AGT--------TTGTAGCGGGCTT-------TGACC
dm3	chr3R:15746389-15746704 -		TCATCACGGAACATTTGGTGAAATGGATTCCCTTAAGGTGGCGGTATGCTGCTGAGTGACCAAAGAAGTTCATTGCTAAG-----CAATGGCGAGAAACTTGACCCCATTA-GAGGCATATGTTATACCGATCTCATTGTA-CAATCGTTTCCTAGGCGGTGCCTTCCAGCAACTCCCACAAGAACGGATTATGCACAGCCCATG--GTGTATACTTTGTTTTTGTGGGTGTCGGAGAAGCGACCAGTCAGG-GAACGATTTGTACAATGA----------AG-GGGAAGTACTGAAATAGTTGACC----------GCT--------CTTAGCGTGGCTT-------TGCACC
droEug1	scf7180000409804:2056287-2056492 -		GT----------GAAAT----------GGCATTG-TTGATCATCATTGTA-CAAATCGTTTCCT-CTAATGCGTTGCCATACTTCGCAAGAAGCGATATGCAA---TATA--TGCATATGTTTATTTTTGCGGCATTAGCTAACGCAATGCGTAAGAAACGATTTGTAC-GATGACGACAT----------ATCAGTA-GAC----------TTTTATGTTCGCCGAGTGAGACGTAGATACC----------GC----------CTTAGCGTGGCTT-------TGCACC
droBia1	scf7180000302402:1524831-1525025 -		----------CCTTGATCATCCATTGTA-CAAATCGTTTCCTCTA-GTGGCGCTGCCGACTCCCGTAAGAGCACCTATC----------AAAGATCCTTCGTTTTTGCAGCATCGCCGGCGCACTTGTTAGGCGAACGATTTGCATAAGAC----------AGCC----------GTCCAAGGAAT----GTATCGGTCTTTGC-ACA--------G-CGGGGATAGCTCTAGTCATTCACG
droTak1	scf7180000415212:143585-143805 -		TG----------AGTGAAAT----------AAACCACCCTCGATCATCATTGTA-CAAATCGTTTCCTCAGGGTGCGCTGCCGACTCCCGCAAAACGGATTATCAGC-------T----G----------TGACCGTTAC----------CACGTTGTTAATCAGCTCCATGATCAGCA-CAG----------TTTTACCCACGCCGGCACCGCCAAACAGGCCAATTTTAC-CTCCTTGGCAAGGGAGCCAGAAGATCCACGAACGTTGATT----CC
droEle1	scf7180000491238:86250-86451 +		----------CCTCATCATCCATTGTA-CAACTCGTTTCCTCCGGGTGCGCTGCCGACTCCCGTAAGAACGATTATCAGC-------T----G----------TGACCGTTAC----------CACGTTATTAATCAGCTCCATAATCAGCA-CAG----------TTTTGCCGACGCCGGCACCGCGAACAAGCCAATTTTAC-CACCCTTGGCAAGGGAGCCAGAGGTCCACGACGTTGATT----CC
droFic1	scf7180000454040:625704-625905		----------CCTCATCATCCATTGTA-CAAATCGTTTCCTCCGGGTGCGCTGCCGACTCCCGTAAGAACGGATTATCAGC-------T----G----------TGACCGTTAC----------CACGTTGTTAATCAGCTCCATAATCAGCA-CAG----------TTTTGCCGACGCCAGCTCCGCCAAACAGACCGATTTTAC-CGCCTTTGGCAAGGAGCCAAGATCAACACATTGATT----CC

PASS/FAIL

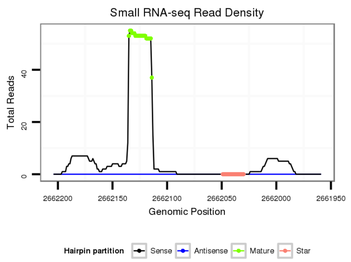
crit.star	0
crit.long	0
crit.short	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

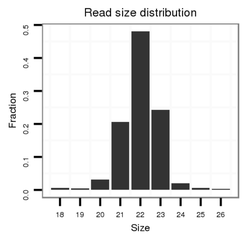
Generated: Oct 30 2015 at 07:44 PM

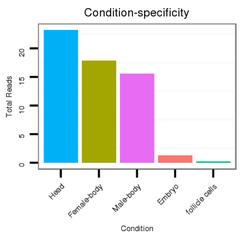
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1439	scaffold_4690:2662009-2662154 -	candidate	Canonical miRNA	intergenic	[View on UCSC Genome Browser [Cornell Mirror]]

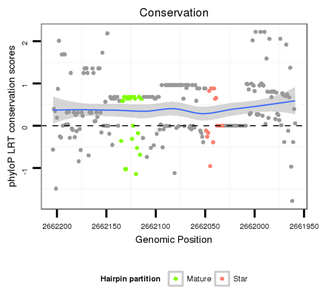
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
	1. der_1439 scaffold_4690:2662030-2662049 - 2. scaffold_4690:3509500-3509519 - 3. scaffold_4690:3510416-3510435 + 4. scaffold_4784:22922366-22922385 + 5. scaffold_4784:23481146-23481165 - 6. scaffold_4929:20298952-20298971 +

Sense Strand Reads

hide 3p reads | show mid mismatch reads

							M055	V108	V107	V040	M057	V060	GSM1528801
AAAGAAACCATTTAAATGCAGACAGAGTAACGTTACAAATTCTAATTAACTATACACTTGTCAGAAAAAATATGCGTACACCACCCAATGCATAACTTTGATGGCAAAAAAGTATATTTATATAAAATGATATCGACTTCATTTCTTTTTCAGTTATGCATTGAGTGTGTACGCATACTTTTTCTGGCAAGTATATATGCGTGTGTGCCATTGTTAGTCAACAAACAAACATAACAAACAAAACAA	Read size	# Mismatch	Hit Count	Total Norm	Total	female body	head	male body	embryo	embryo	head	follicle cells
..........ATATGCGTACACCACCCAATGC..	22	0	1	20.00	20	5	8	6	0	0	1	0
..........ATATGCGTACACCACCCAATGCA..	23	0	1	13.00	13	5	4	4	0	0	0	0
..........ATATGCGTACACCACCCAATG..	21	0	1	8.00	8	2	5	1	0	0	0	0
..........AATATGCGTACACCACCCAATG..	22	0	1	6.00	6	2	3	1	0	0	0	0
..........TGCAGACAGAGTAACGTTACAAATTC..	26	0	1	1.00	1	1	0	0	0	0	0	0
..........TATGCGTACACCACCCAATGC..	21	0	1	1.00	1	0	0	1	0	0	0	0
..........TTTCTGGCAAGTATATATGCGTGTGT..	26	0	1	1.00	1	1	0	0	0	0	0	0
..........ATGCGTGTGTGCCATTGTTA..	20	0	1	1.00	1	0	0	0	1	0	0	0
..........ATATGCGTGTGTGCCATTGTTAGTCAAC..	28	0	1	1.00	1	0	0	1	0	0	0	0
..........TATGCGTACACCACCCAATG..	20	0	1	1.00	1	1	0	0	0	0	0	0
..........ATATGCGTACACCACCCAATGC.	23	1	1	1.00	1	0	1	0	0	0	0	0
..........TAAATGCAGACAGAGTAACGTTACAAAT..	28	0	1	1.00	1	1	0	0	0	0	0	0
..........ATATATGCGTGTGTGCCATTGTTAGT..	26	0	1	1.00	1	0	0	0	0	1	0	0
..........AATATGCGTACACCACCCAATGC.	23	1	1	1.00	1	0	1	0	0	0	0	0
..........GAAAAAATATGCGTACACCAC..	22	0	1	1.00	1	0	0	1	0	0	0	0
..........AAATTCTAATTAACTATACACTTG..	24	0	1	1.00	1	1	0	0	0	0	0	0
..........AAATATGCGTACACCACCCAATGC..	24	0	1	1.00	1	0	0	1	0	0	0	0
..........CTATACACTTGTCAGAAAAAATATGCG..	27	0	1	1.00	1	1	0	0	0	0	0	0
..........TACACCACCCAATGCATAACT..	21	0	1	1.00	1	1	0	0	0	0	0	0
..........ATAACTTTGATGGCAAAAAGT..	22	0	1	1.00	1	0	0	0	0	1	0	0
..........TATATAATGCGTGTGTGCCATTGTTAGTC..	28	0	1	1.00	1	1	0	0	0	0	0	0
..........TTAACTATACACTTGTCAGAAAAAATA..	27	0	1	1.00	1	1	0	0	0	0	0	0
..........CACTTGTCAGAAAAAATATGC..	21	0	1	1.00	1	1	0	0	0	0	0	0
..........AATATGCGTACACCACCCAATGC..	23	0	1	1.00	1	0	1	0	0	0	0	0
..........ATATGCGTACACCACCCAATGC.	23	1	1	1.00	1	0	1	0	0	0	0	0
..........AATGCAGACAGAGTAACGTTACA..	20	0	1	1.00	1	1	0	0	0	0	0	0
..........GCAGACAGAGTAACGTTACAA..	21	0	1	1.00	1	0	0	0	0	1	0	0
..........ATATGCGTACACCACCCAATGCA.	24	1	1	1.00	1	1	0	0	0	0	0	0
..........TGCAGACAGAGTAACGTTACAAAT..	24	0	1	1.00	1	0	0	0	1	0	0	0
.....CATTTAAATGCAGACAGAGTAACGT..	25	0	1	1.00	1	1	0	0	0	0	0	0
..........ATGCATTGAGTGTGTACGCA..	20	0	6	0.50	3	0	3	0	0	0	0	0
..........CATTGAGTGTGTACGCATACT..	21	0	6	0.33	2	1	1	0	0	0	0	0
..........CATACTTTTTCTGGCAAGT..	19	0	8	0.25	2	0	0	0	0	0	0	2
..........CATAACTTTGATGGCAAA..	18	0	5	0.20	1	1	0	0	0	0	0	0
..........CAATGCATAACTTTGATGGCA..	21	0	5	0.20	1	0	1	0	0	0	0	0
..........TGCATTGAGTGTGTACGCATACTTTT..	26	0	6	0.17	1	0	0	0	1	0	0	0
..........TATGCATTGAGTGTGTACGCATACT..	25	0	6	0.17	1	1	0	0	0	0	0	0
..........TATATAAATGATATCGACTTCATT..	24	0	6	0.17	1	1	0	0	0	0	0	0
..........TGCATTGAGTGTGTACGCATA..	21	0	6	0.17	1	1	0	0	0	0	0	0
..........TATGCATTGAGTGTGTACGCA..	21	0	6	0.17	1	0	0	1	0	0	0	0
..........CATTGAGTGTGTACGCATAC..	20	0	6	0.17	1	0	0	1	0	0	0	0
..........TGCATTGAGTGTGTACGCATACT..	23	0	6	0.17	1	0	1	0	0	0	0	0
..........TGCATTGAGTGTGTACGCATACTTT..	25	0	6	0.17	1	1	0	0	0	0	0	0
..........GTTATGCATTGAGTGTGTACG..	21	0	7	0.14	1	0	0	1	0	0	0	0
..........ATTGAGTGTGTACGCATA..	18	0	7	0.14	1	0	0	0	1	0	0	0
..........TTATGCATTGAGTGTGTACG..	20	0	7	0.14	1	0	0	1	0	0	0	0

Anti-sense strand reads

						V108	M055	V107	V040
TTTCTTTGGTAAATTTACGTCTGTCTCATTGCAATGTTTAAGATTAATTGATATGTGAACAGTCTTTTTATACGCATGTGGTGGGTTACGTATTGAAACTACCGTTTTTCATATAAATATATTTACTATAGCTGAAGTAAAGAAAAAGTCAAFACGTAACTCACACATGCGTATGAAAAAGACCGTTCATATATACGCACACACGGTAACAATCAGTTGTTTGTTTGTATTGTTTGTTTTGTT	Read size	# Mismatch	Hit Count	Total Norm	Total	head	female body	male body	embryo
..........GTATTGAAACTACCGTTTTTT..	21	0	5	0.40	2	1	1	0	0
..........ACGTAACTCACACATGCGTAT..	21	0	6	0.33	2	0	2	0	0
..........CGTAACTCACACATGCGTAT..	20	0	7	0.29	2	1	1	0	0
..........ACGTATTGAAACTACCGTTTT..	21	0	5	0.20	1	1	0	0	0
..........ACGTATTGAAACTACCGTTT..	20	0	5	0.20	1	0	1	0	0
..........GTAACTCACACATGCGTATGA..	21	0	6	0.17	1	1	0	0	0
..........ACGTAACTCACACATGCGTA..	20	0	6	0.17	1	0	0	1	0
..........CACACATGCGTATGAAAAAGA..	21	0	6	0.17	1	0	1	0	0
..........CATGCGTATGAAAAAGACCGT..	21	0	7	0.14	1	1	0	0	0
..........ATTTACTATAGCTGAAGTAAA..	21	0	7	0.14	1	1	0	0	0
..........ATGCGTATGAAAAAGACCGTTC..	22	0	7	0.14	1	0	0	1	0
..........CATGCGTATGAAAAAGACCGTT..	22	0	7	0.14	1	1	0	0	0
..........GTAACTCACACATGCGTA..	18	0	7	0.14	1	0	0	0	1
..........CGTAACTCACACATGCGTA..	19	0	7	0.14	1	1	0	0	0

Show Alignment With Reads

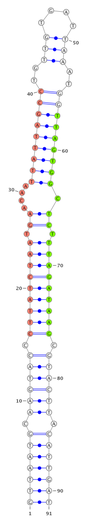
Re-alignment of all predicted orthologs

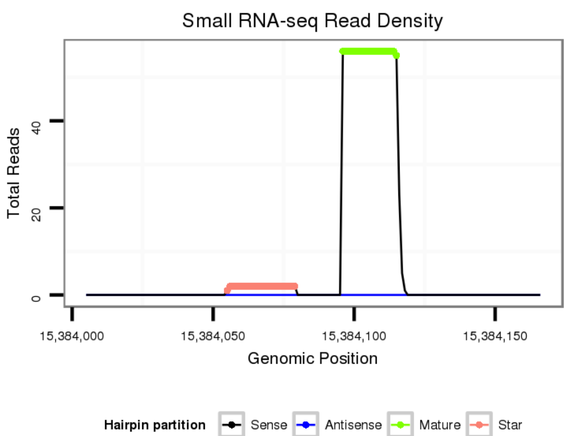
Species	Coordinate	ID	Alignment
droEre2	scaffold_4690:2661959-2662204 +	der_1439	AAAGAAA--------CCATTTAAA--------TGCAGA--C--AGAGTAACGTTA-CAAATTCTAATTAACTATACACTTGTCAGAAAAATATGCGTACACCACCCAATGCATAACTTTGATGGCAAA-AAGTATATTTATATAAATGATATCGACTTCATTTCTTTTT---TC-----AGTTATGCATTGAGTGTGTACGCATACTTTTTCTGGCAAGTATATATGCGTGTGTGCCATTGTTAGTCAACAAA--CAAACATAACAAACA--A----------AACAA
droYak3	scaffold_4929:3161675-3161887 +		AAAAAAAA--------CCATTTAAA--------AGCGA--C--AGAGTACGTTA-CAAATTCTAATTAACT--TATACACTTGTCAGAAAAATATGCGTACACCACCCAATGCATAACTTTGATGGCAAA-AAGTATATTTATATAAATGATATCGACTTCATTTCTTTTT---TC-----AGTTATGCATTGAGTGTGTACGCATACTTTTTCTGGCAAGTATATATGCGTGTGTGCCATTGTTAGTCAACAAA--CAAACATAACAAACA--AGAAATGGATACTTTTC---CCCCA----------AACCCATTGTAAATAAATCCATTTTGGACAGACAAA----------GGAA
droSec2	scaffold_28:140531-140629 +		TAAAAAA--------CCATTTAAA--------AGCGA--C--AGAGTACGTTA-CAAATTCTAATTAACT--TATACACTTGTCAGAAAAATATGCGTACACCACCCAATGCATAACTTTGATGGCAAAAAGTATATTTATATAAATGATATCGACTTCATTTCTTTTT---TC-----AGTTATGCATTGAGTGTGTACGCATACTTTTTCTGGCAAGTATATATGCGTGTGTGCCATTGTTAGTCAACAAA--CAAACATAACAAACA--A----------TT-----AAAA
droSim2	gi|14714531|14714620 -		TAAAAAA--------CCATTTAAA--------AGCGA--C--AGAGTACGTTA-CAAATTCTAATTAACT--TATACACTTGTCAGAAAAATATGCGTACACCACCCAATGCATAACTTTGATGGCAAAAAGTATATTTATATAAATGATATCGACTTCATTTCTTTTT---TC-----AGTTATGCATTGAGTGTGTACGCATACTTTTTCTGGCAAGTATATATGCGTGTGTGCCATTGTTAGTCAACAAA--CAAACATAACAAACA--A----------TT-----AAAA
dm3	chrX:5307937-5307999 -		AAAGAAA--------CCATTTAAA--------AGCAGATAA--AGAGTACGTTA-CAATTCTAATTAACT--TATACACTTGTCAGAAAAATATGCGTACACCACCCAATGCATAACTTTGATGGCAAA-AAGTATATTTATATAAATGATATCGACTTCATTTCTTTTT---TC-----AGTTATGCATTGAGTGTGTACGCATACTTTTTCTGGCAAGTATATATGCGTGTGTGCCATTGTTAGTCAACAAA--CAAACATAACAAACA--A----------TT-----AAAA
droEug1	scaffold_4780000040904:154669-154901 +		AAGAGAAAACAAAAAAACCATTTAAATGAAAAACAAAAGCAGA--C--AGAGTAACGTTA-CAATTCTAATTAACTATACACTTGTCAGAAAAATATGCGTACACCACCCAATGCATAACTTTGATGGCAAA-AAGTATATTTATATAAATGATATCGACTTCATTTCTTTTT---TC-----AGTTATGCATTGAGTGTGTACGCATACTTTTTCTGGCAAGTATATATGCGTGTGTGCCATTGTTAGTCAACAAA--CAAACATAACAAACA--AC-A-----TAC-----A-------AGAGAAAGAAAAAACCAGAA-AAACCTATAAAGCTAAA----------ACAAATGGATACTACTTCTTCCCAAA-A----------AAAAAACCCATTGTAAATAAATCCATTTTGGCAGACAAAGAAA----------GGAA
droBia1	scaffold_4780000031345:184050-184107 +		------------------

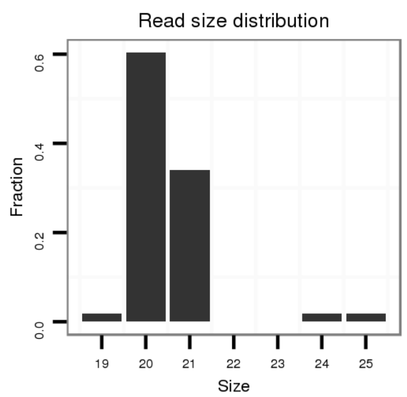
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_228	**scaffold_4929:15384055-15384116 +**	**candidate**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

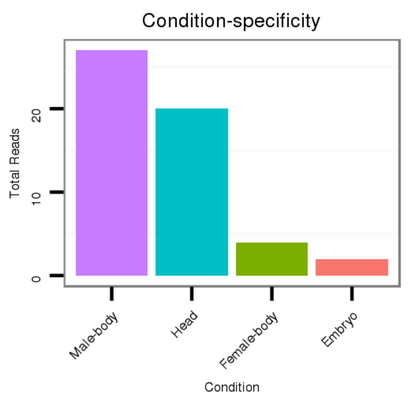
Legend: mature star **mismatch in alignment** mismatch in read

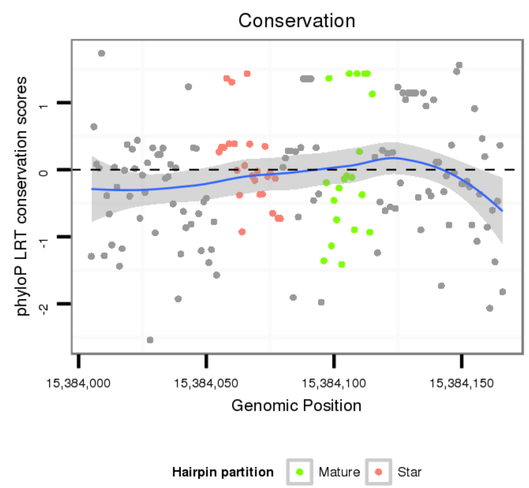
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dere\GG23619-in]; utr5 [utr5_plus_933]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CATAATGTATACATAATAACAAACTAATTATTCAAGTTAATGCAAGTACCCTTATCTAATGAACAATTATTAGCCTGTTGTGATTAAATGGTTAGTGGCTCTTTAGATAAGCGTACTTACATTGATATCAAGACAATCAAGTTAAACCCCAAAATACGACTA	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	V108 head	M055 female body	V040 embryo	V060 head	M057 embryo
**********(((((((.((((((.((((((((((.((....((((((((((..(((....)))..)))))))))).)).)))))))))).)))))))**********											
..........TAGTGGCTCTTTAGATAAG..........	20	0	1	32.00	32	22	9	0	1	0	0
..........TAGTGGCTCTTTAGATAAGC..........	21	0	1	18.00	18	4	11	3	0	0	0
..........TAGTGGCTCTTTAGATAAGCG..........	22	0	1	4.00	4	4	0	0	0	0	0
..........TAGTGGCTCTTTAGATAAGCGT..........	23	0	1	1.00	1	0	1	0	0	0	0
..........TAGTGGCTCTTTAGATAA..........	19	0	1	1.00	1	1	0	0	0	0	0
..........TAGTGGCTCTTTAGATAAGG..........	21	1	1	1.00	1	0	1	0	0	0	0
..........TAGTGGCTCTTTAGATAAGCA..........	22	1	1	1.00	1	0	1	0	0	0	0
..........CTTATCTAATGAACAATTATTAGCC..........	25	0	1	1.00	1	0	0	1	0	0	0
..........TTATCTAATGAACAATTATTAGCC..........	24	0	1	1.00	1	0	0	0	0	0	1

Anti-sense strand reads

GTATTACATATGTATTATTGTTTGATTAATAAGTTCAATTACGTTCATGGGAATAGATTACTTGTTAATAATCGGACAACACTAATTTACCAATCACCGAGAAATCTATTCGCATGAATGTAACTATAGTTCTGTTAGTTCAATTTGGGGTTTTATGCTGAT	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	V040 embryo
**********(((((((.((((((.((((((((((.((....((((((((((..(((....)))..)))))))))).)).)))))))))).)))))))**********							

Show Alignment With Reads

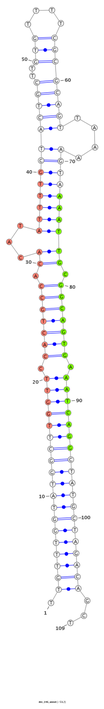
Re-alignment of all predicted orthologs

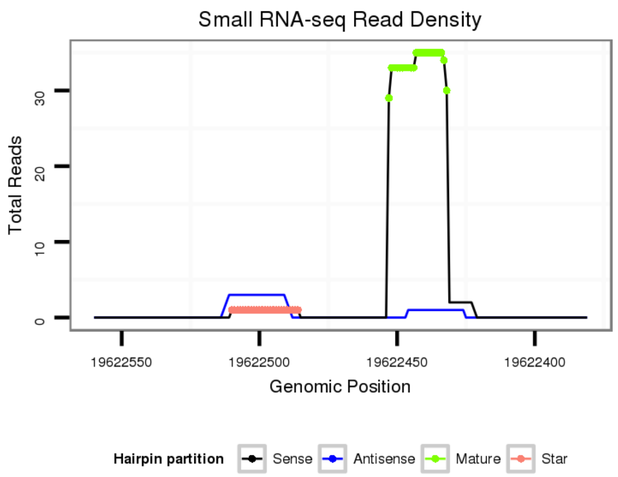
Species	Coordinate	ID	Alignment
droEre2	scaffold_4929:15384005-15384166 +	der_228	CATA--ATGT-AT-ACATAATAACAAACTAATT----------ATTCAAGTTAATGCA--AG----------TACCCTTATCTAATGAACAATTATTAGCCTGTT------GTGATTAAATGGTTAGTG-G----------CTCTTTAGATA----AGCGTACTTACATTGATATCAAGACAATCAAGTTAAACCCC-AAAATACGACTA
droYak3	2L:6441504-6441665 -		CATA--ATGT-AT-TAATAATACCAGAATAATT----------ATTCATGTTAATGCT--AG----------TACTCTTATCTAATGAACAATAATTAGCCTGTT------CTGATTAAATGGTTAGTG-C----------CTCTTTAGATA----AGCGTACTGGATTGATATCAAGACAATTAAGTTAAGTCCCC-AAAATACGACTA
droSec2	scaffold_5:4524512-4524664 +		CACACCATGT-AA-ACATAATAAC--ATTAATT----------ATTCAGCTAATGCA--AG----------TACTCTTATCTAATGAGCAATTATTAGCCTGTT------GTGATTAAATGTTTAGCG-G----------CTCTTTAGATA----AGCGTACTTAATTGATATCGAGACAATCCAGTTAAAC--T-------GATA
droSim2	2L:6250168-6250317 +		CACACCATGT-AA-ACATAATAACATTATAATT----------ATTCAGCTAATGCA--AG----------TACTCTTATCTAATGAGCAATTATTAGCCTGTT------GTGATTAAATGTTTAGCG-G----------CTCTTTAGATA----AGCGTACTGAATTGATATCGAGACAATCCAGTTAA-----T---------CTG
dm3	chr2L:6475292-6475430 +		CACA--ATGT-AA-ACATTA--------TAATT----------ATTTAAGCTAATGCA--AA----------AACTCTTATCTAATGAGCAATTATTAGCCTGTT------GTGATTAAATGTTAGTG-G----------CTCTTTAGATA----AGCGTACTTAATTGATATCGAGACAATCCAGTTAAAC----T----------
droEug1	scf7180000409463:1899855-1900010 +		AATA--AGAA-GT-TCGTAAAAAGCAACT---T----------ATTCGATC-AGTAAT--TG----------AGAGCTTATCTAAAGAACAATTATTAGCTGTT------ATGATTAATTGCGAAATT-G----------TTCTTAAGATA----AGCATACTTAATTGATATCAAGAAAGATTT-ACAAATCCA--TGAATATACTG
droBia1	scf7180000302422:3000939-3001041 -		CAGT--ATGT---T-------------------------------------GGGGCGCAATAGTTTGG----------CCTGCCTATCTAAAGAACCAATAATTAGGTGTA------ATCATTAAATAGGTAATGAG----------GTCTTTAGATA----GGCATAGTTAGA----------ACTG
droTak1	scf7180000415858:230073-230178 -		AC---T----T--T----------ACAATCATT----------ACCCAACACAATTAAA--A----------TTGCTTATCTAGAGAACAACAAAC-------------AATT-G----------GTCTTAAGATA----AGCGCACTTAAATTGATATGTA----------AATCT--A-GAAAAAGTGCTG
droEle1	scf7180000490970:493542-493705 -		CATTAA-GAT-GT-TGTCAGACACTAATTCACT----------GTTCACCAC-AGTAAT--TG----------CGCATTATCTAGAGAATACAATTTCAATTGCT------GTGATTAAACAAC-----A----------ATT-TAAAAATCCTCTAGCTA----AGCAC--CCAATAATGATATCGAGCAATCAACTCAAATCAGTAAGGAGCTGATA
droRho1	scf7180000779524:171746-171921 +		CATT--AAAATT-TGCT---G-TTAATCTATTTTAGATACCCGTGTAAG--GCCATTGAAGCATTTT--------------TT-TTAAGT----ACAG-CCCCTTTTGAAAGTCAAAATAATTAAAAATAAAACTACTATT-AAAAAAGCTTGAAGTTACTTAG--TTAATTAATTGATATCGAGACAATTAGTTCAACT---T-------CTCT
droFic1	scf7180000453973:75230-75415 -		GATA--AAAATTAATATT---AAT-AATTAATCATTAATAATTTATAAAGCCCAAAATCATTGTT--------TACC--AA----------TATTCTTATCTTATAAACAATTAGTTAGTCGTT------ATGATTAAATAATTATTT--------------------------------------CTTTAAACACCCTTAAGTTA----G--GCACTTAAACGTGATATGGAGGTAATTAAGTCAAATCCG-GAAAATTGCTG
droKik1	scf7180000302590:39853-40004 +		AATA--ATTA-AT-TAAAATAAAAAAATTATTT----------AATAAATT-AAAAAT--AATAAACTCCATCAAAGAATACTTTCATCTGACAAAA-GTTATAATACCTTTCCAAATTATTATTAGTACAGAA-G----------GAATCTATATA----TGTATCT----------TC--AAAACGGTTCT
droMoj3	scaffold_6500:7576364-7576403 -		TATA--AAAT-AT-ACATAGAAATAAT------AGAAGCG------T--T----------TACTTTT

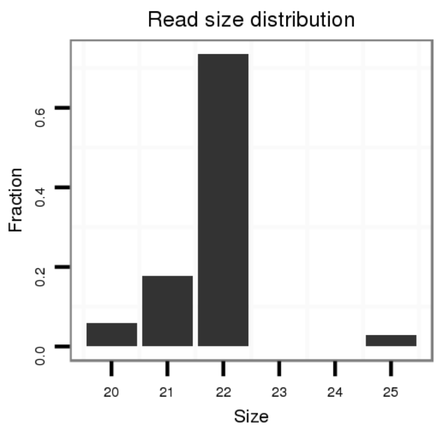
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_146	**scaffold_4929:19622431-19622510 -**	**candidate**	**Canonical miRNA**	**antisense_to_3pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

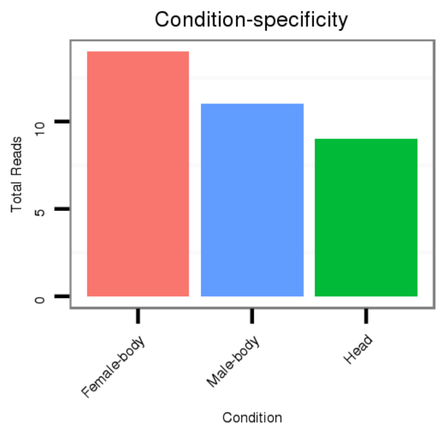
Legend: mature star mismatch in alignment mismatch in read

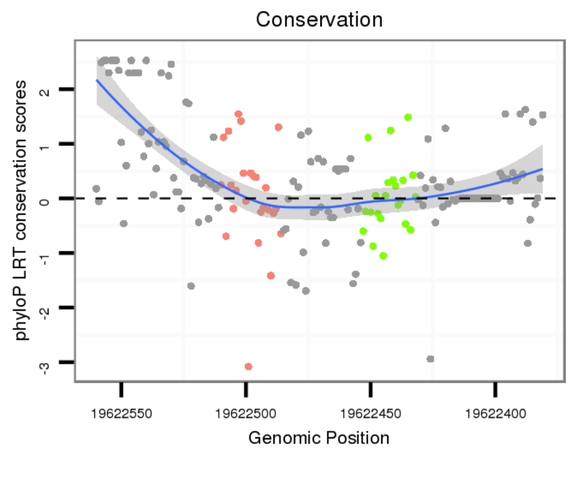
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to utr3 [utr3_minus_2290]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAAAACAATTCATGTGGGTCTGTATCGGTGTACGATTGTTTGGTATGGCTTGGTTCCACTGCCACACATATTTTGCTACTGCTTGTGTTTTCGCGCAGTTAAAAGTAAAATTGCGGCAGTGAAATCAGGCTATGCTAGACAGCTGGACAGCAGGTCTGCGGGTCTGCCGGTTTCTGAAGT	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	V107 male body	V108 head
**********.((((((((((((((((((.(((((((.((...((((((((((((..(((....))))))))).....))))))))))).)))))))..))))))))))))))...**********								
.....AAATTGCGGCAGTGAAATCAGG.....	22	0	1	25.00	25	8	9	8
.....AAATTGCGGCAGTGAAATCAGGT.....	23	1	1	7.00	7	3	4	0
.....AAATTGCGGCAGTGAAATCAGT.....	22	1	1	4.00	4	1	2	1
.....AAATTGCGGCAGTGAAATCAG.....	21	0	1	3.00	3	3	0	0
.....AATTGCGGCAGTGAAATCAGG.....	21	0	1	3.00	3	0	2	1
.....AATTGCGGCAGTGAAATCAG.....	20	0	1	1.00	1	1	0	0
.....AAATTGCGGCAGTGAAATCAGGA.....	23	1	1	1.00	1	0	0	1
.....TGCGGCAGTGAAATCAGGT.....	19	1	1	1.00	1	1	0	0
.....TGGTTCCACTGCCACACATATTTTG.....	25	0	1	1.00	1	1	0	0
.....AGTGAAATCAGGCTATGCTAG.....	21	0	1	1.00	1	0	1	0
.....AAATTGCGGCAGTGAAATCA.....	20	0	1	1.00	1	1	0	0
.....AGTGAAATCAGGCTATGCTAGA.....	22	0	1	1.00	1	1	0	0

Anti-sense strand reads

TTTTTGTTAAGTACACCCAGACATAGCCACATGCTAACAAACCATACCGAACCAAGGTGACGGTGTGTATAAAACGATGACGAACACAAAAGCGCGTCAATTTTCATTTTAACGCCGTCACTTTAGTCCGATACGATCTGTCGACCTGTCGTCCAGACGCCCAGACGGCCAAAGACTTCA	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V107 male body	M055 female body	V040 embryo
**********.((((((((((((((((((.(((((((.((...((((((((((((..(((....))))))))).....))))))))))).)))))))..))))))))))))))...**********									
.....CCGTCACTTTAGTCCGATACG.....	21	0	1	1.00	1	0	0	1	0
.....GAACCAAGGTGACGGTGTGTAT.....	22	0	1	1.00	1	1	0	0	0
.....AACCAAGGTGACGGTGTGTATAA.....	23	0	1	1.00	1	0	1	0	0
.....CGAACCAAGGTGACGGTGTGTATA.....	24	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

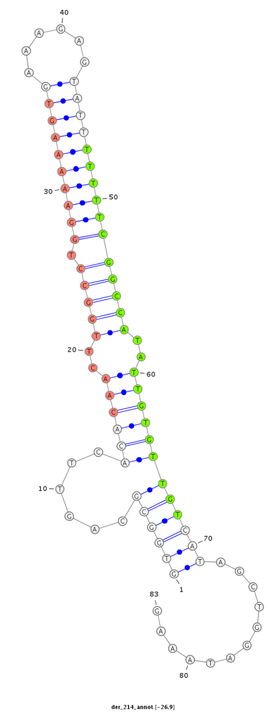
Re-alignment of all predicted orthologs

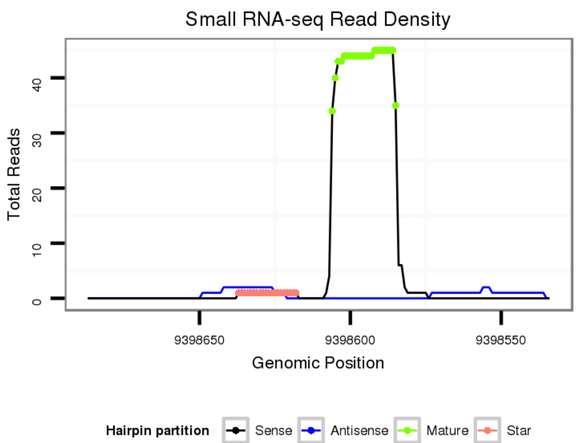
Species	Coordinate	ID	Alignment
droEre2	scaffold_4929:19622381-19622560 -	der_146	AAAAACAATTCATGTGGGTCTGTATCGGTGTACGATTGT-TTGGTATGGCTTGGTTCCACTGCCACACATATT-TTGCTAC--------TGCTTGTGTTTTCGCGCAGTTAAAAGTAA----------AATTGCGGCAGTGAAATCAGGCTATGCTAGACAGCTGGACAGCAGGTCTGCGGGTCTGCCGGTTTCTGAAGT
droYak3	2L:15658606-15658737 +		AA-AACAATTCATGTGGGTCTGTATCGGTGTACGATTGT-TTGGAAAAGCCTGATTCCACTGGCACACATACTTTTGCTAG--------TGCTCAT----------GTGAAACCAGGCTATGCTAGACAGGAGG----------TCTGCAGGTGTCTGAAGT
droSec2	scaffold_1:613241-613384 +		AAAAACAATTCATGTGGGTCTGTATCGGTGTACGTTGT-TTGGTAAAGCCTGGTTTCACTGCCACGCATATT-TTGCTGC--------TACTCAT----------TA----------AATTGGCACAGTGAAATCAGGCTATGGTAGACAGCAGG----------ACTGCAGGTGTCCGAAGT
droSim2	2r:3795017-3795160 +		AAAAACAATTCATGTGGGTCTGTATCGGTGTACGATTGT-TTGGTAAAGCCTGGTTTCACTGCCACGCATATT-TTGCTGC--------TGCTCAT----------TA----------AATTGGCACAGTGAAATCAGGCTATGATAGACAGCAGG----------ACTGCAGGTGTCTGAAGT
dm3	chr2R:2945349-2945512 +		AAAAACAATTCAGTGGGTCTGTATCGGTGTACGATTGT-TTGGTAAAGACTGGTTCCACTGTCACACATATG-TTGCTGC--------TGCTCATGTTTACGCGCAGTTAAAATATTA----------AATTGCCACAGTGAAATCAGGCTTGTTAGACAACAGG----------ACTGCAGGTGTCTGAAGT
droEug1	scf7180000409672:4962466-4962634 +		AAAAACAATTCTTGTGGGTCTGTATCGGTGTACGGTTGC-TTAGTGAAGCCTGGTTCCACTGCAGTTATTCT--TCCAA-----TATTAC----------ATAAATTTCGATCTTTTCATT------GAGAGAATTGAGAAGTGTCAGTGGAATCGCACT--GCTGAACAGCTAG----------TCTGTAGGTGTATGCGT
droBia1	scf7180000302292:3197844-3197984 -		AAAAACAATTCATGTGGGTCTGTATCGGTGTA---TTGT-TTGCTGAAGCTTGGTTGCACTGCACATACACC-GTTATAT--------CCCTTTTGGATTCATATAGTTAGAGTAGG----------AACGTATCAGTCGAACCGTGCTAT--TA----------GTTGGGT
droTak1	scf7180000415382:173185-173316 +		AAAAACAATTCATGTGGGTCTGTATCGGTGTACGTTGCAGTGGTGCAGCCGATTCCACTGGCACATC----------GT----------TACGTTTGGGTAA----------CGAATGG-AAAAGTGTCCGAGGAATCGGG----------AA----------TCTGCAGGTGTCTGGT
droEle1	scf7180000491265:50570-50649 +		GAAAACAATTCTTGTGGGTCTGTATCGGTGTTGGTTGA-TTGGTGAAGCCTGCTCTCACTGGCACATATTCT--TCTAC--------TGC----------
droRho1	scf7180000780072:211579-211753 -		AAAAACAATTCTTGTGGGTCTGCATCGGTGTTCAGTTGT-TTTGTGAAGCCTGGTTCCACTGTCACTAATTTT-TT-GCACCACTACTTTA----------GATAATTTTTGATCATTTGATTATTGCTGCTCTAATGGAGAATGTGACAGTGGTATCGGGCTTT--TGGATAGCTAG----------TTTGCAGGTGTT------
droFic1	scf7180000453955:320676-320833 -		AAAAACAATTCATGTGGGTCTGTATCGGTGTTCGGTTGA-TGGGTGAAGCCTGGTTCCACTGCCACATCTTCT--ATCA--------CTTTTTGGATTCTT-------GATATTT----------TATT------GCGGG-----AATTCTCAGAGTGGAACCAGGCT--GTTAGACAGCTAG----------TCTGCAGGTGTTTGTGT
droKik1	scf7180000302640:41556-41648 +		ACAAACAATTCTTGTGGGTCTGTTTCGGTGTTAGT-GTTAGTGT----------TCGGT---GT-TT-----------------------------AGTGTTGTCAGGTCAG-------GCTAG----------TCTAGAGGTGTCTGGT
droAna3	scaffold_13266:3182387-3182424 +		AAAAACAATTGTTGTGGGTCTGTTCCGG-GTTCGTTTGG-----------------------------

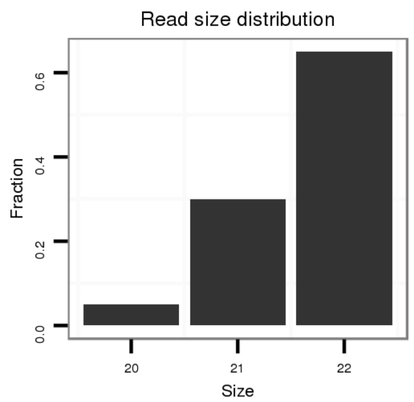
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_214	**scaffold_4770:9398584-9398637 -**	**candidate**	**Canonical miRNA**	**5pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

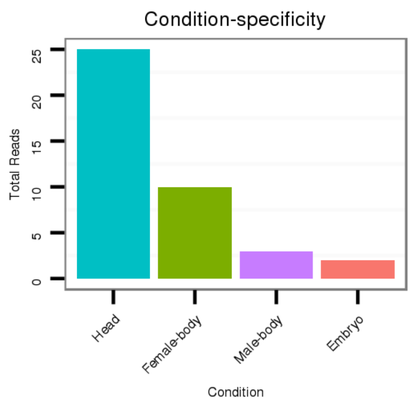
Legend: mature star mismatch in alignment mismatch in read

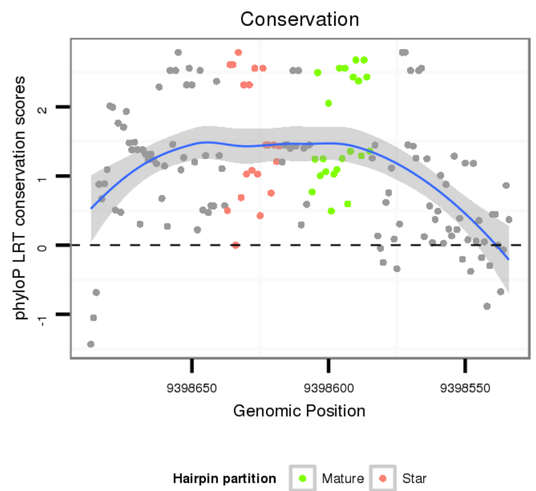
Predicted structure











Show Alternate Folds

Flybase annnotation

utr5 [utr5_minus_8921]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CCCGTGTGTGTGTGTGTGTGTGTGCGCGCGTGTGTGTGGCGCAGTTCACACAACTTGGCCTGGAAAAAGTGAAAGAGTATTTTTTTCGGCCATATTGTGTTGTCATAGCTGGATAAAGTGCATTTCCGGCCATATGGAGTTTCTGATCATATGC											
***********************************(((((((.....(((((((..(((((.((((((((((.....)))))))))))))))..)))))))))))).....***********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	M055 female body	V107 male body	M057 embryo	V040 embryo	V060 head
.....TTTTTCGGCCATATTGTGTTGT.....	22	0	1	23.00	23	14	4	3	1	0	1
.....TTTTTCGGCCATATTGTGTTG.....	21	0	1	7.00	7	6	0	0	0	1	0
.....TTTTCGGCCATATTGTGTTGT.....	21	0	1	5.00	5	2	3	0	0	0	0
.....TTTTTTCGGCCATATTGTGTTG.....	22	0	1	3.00	3	2	1	0	0	0	0
.....TTTTCGGCCATATTGTGTTGTCT.....	23	1	1	2.00	2	0	2	0	0	0	0
.....TTTTCGGCCATATTGTGTTGTT.....	22	1	1	2.00	2	2	0	0	0	0	0
.....TTTCGGCCATATTGTGTTGTCA.....	22	0	1	2.00	2	0	1	1	0	0	0
.....TTTCGGCCATATTGTGTTGT.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TCGGCCATATTGTGTTGTCAT.....	21	0	1	1.00	1	0	1	0	0	0	0
.....TTTTTTTCGGCCATATTGTGTTGTCA.....	26	0	1	1.00	1	0	0	1	0	0	0
.....CAACTTGGCCTGGAAAAAGT.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TGTGTTGTCATAGCTGGA.....	18	0	1	1.00	1	1	0	0	0	0	0
.....TTTTCGGCCATATTGTGTTGTCA.....	23	0	1	1.00	1	0	0	1	0	0	0
.....TGTGTGTGCGCGCGTGTGT.....	19	0	15	0.07	1	0	1	0	0	0	0
CCCGTGTGTGTGTGTGTGTGTG.....	22	0	17	0.06	1	0	1	0	0	0	0
....TGTGTGTGTGTGTGTGTG.....	20	0	20	0.05	1	1	0	0	0	0	0

Anti-sense strand reads

GGGCACACACACACACACACACGCGCGCACACACACCGCGTCAAGTGTGTTGAACCGGACCTTTTTCACTTTCTCATAAAAAAGCCGGTATAACACAACAGTATCGACCTATTTCACGTAAAGGCCGGTATACCTCAAAGACTAGTATACG						V107 male body	V108 head	V040 embryo
***********************************(((((((.....(((((((..(((((.((((((((((.....)))))))))))))))..)))))))))))).....***********************************	Read size	# Mismatch	Hit Count	Total Norm	Total			
.....CGCGTCAAGTGTGTTGAACCGGAC.....	24	0	1	1.00	1	0	1	0
.....TTTCACGTAAAGGCCGGTAT.....	20	0	1	1.00	1	1	0	0
.....AGTGTGTTGAACCGGACCTTT.....	21	0	1	1.00	1	0	1	0
.....TATACCTCAAAGACTAGTATA..	21	0	1	1.00	1	1	0	0

Show Alignment With Reads

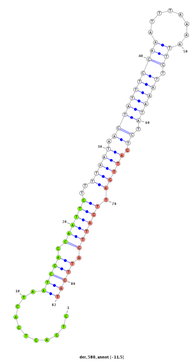
Re-alignment of all predicted orthologs

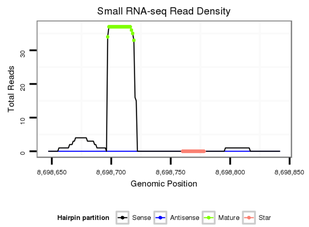
Species	Coordinate	ID	Alignment
droEre2	scaffold_4770:9398534-9398687 -	der_214	CCCGTGT--------GTGTGTG-TGTGTGTGTG------------CG---CGCGTGTGTGTGGCGCAGTTCACACAACTTGGCCTGGAA-AAAGTGAAAGA---------GTATTTTTTCGGCCATATT----------------GTGTTGTCATAGCT--GGATAAAGTGCATTTC-CGGCCATATGGAGTTTCTGATCATATGC
droYak3	3R:16575809-16575953 +		CCCGTGT--------GT-----------------------GTGTGTG---AGCGTGTGTGTGGCGCAGTTCACACAACTTGGCCTGGAA-AAAGTGAAAGA---------GTATTTTTTCGGCCATATT----------------GTGTTGTCATAGCT--GGAAAAAGTGCATTTTCCGGCCATATGGAGATTGTGTTCATATGC
droSec2	scaffold_0:12157454-12157599 +		CCCGTGA--------GT-----GT----------------GTGTGTG---AGCGTGTGTGTGGCGCAGTTCACACAACTTGGCCTGGAA-AAAGTGAAAGA---------GTATTT-TTTCGACCATATT----------------GTGTTGTCATAGCT--GGAAAAAGTGCATTTCCGGCCATATGGAGATTCAGATCATAGGC
droSim2	3r:11327517-11327664 +		CCCGTGA--------GTGT---GT----------------GTGTGTG---AGCGTGTGTGTGGCGCAGTTCACACAACTTGGCCTGGAA-AAAGTGAAAGA---------GTATTT-TTTCGGCCATATT----------------GTGTTGTCATAGCT--GGAAAAAGTGCATTTCCGGCCGTATGGAGATTCAGATCATATGC
dm3	chr3R:9857401-9857546 -		CTCGTGT--------GT-----GT----------------GTGTAT---AGCGTGTGTGTGGCGCAGTTCACACAACTTGGCCTGGAA-AAAGTGAAAGA---------GTATTT-TTTCGGCCATATT----------------GTGTTGTCATAGCT--GGAAAAAGTGCATTTCCGGCCATATGGAGATTCAGATCATATGC
droEug1	scf7180000409802:89352-89492 +		G---TGT--------------GC----------------TTGTGTG---AGCGTGTGTGTGGCGCAGTTCACACAACTTGGCCTGGAA-AAAGTGAAAGA---------GTATTT-TTTCGGCCATATT----------------GTGTTGTCATAGCT--GGAAAAAGTGCATTTCCGGCCATATGGAGATTCTGGCCATCTGC
droBia1	scf7180000302402:2639899-2640022 -		G---T--------------GT----------------GTATGTG---AGCGTGTGTGTGGCGCAGTTCACACAACTTGGCCTGGAA-AAAGTGAAAGA---------GTATTTTTTCGGCCATATT----------------GTGTTGTCAGAGCT--GGAAAAAGTGCATTTCCGGCCACTCG----------------GC
droTak1	scf7180000415380:743006-743136 -		G---T--------------GT----------------GTATGTG---AGCGTGTGTGTGGCGCAGTTCACACAACTTGGCCTGGAA-AAAGTGAAAGA---------GTATTTTTTCGGCCATATT----------------GTGTTGTCATAGCT--GAAAAAAGTGCATTTCCGGCCATATGGAGATTCTG---------
droEle1	scf7180000491047:1306593-1306722 +		AGT----------------------------------GTGTGTGTGTGGCGCAGTTCACACAACTTGGCCTGGAA-AAAGTGAAAGA---------GTATTT-TTTCGGCCATATT----------------GTGTTGTCATAGCT--GGAAAAAGTGCATTTCCGGTCATATGGAGATTCTGGCACTTGC
droRho1	scf7180000779165:39265-39395 -		GG-----------------------------------AGTGTGTGTGGCGCAGTTCACACAACTTGGCCTGGAA-AAAGTGAAAGA---------GTATTT-TTTCGGCCATATT----------------GTGTTGTCATAGCT--GGAAAAAGTGCATTTCCGGGTCATATGGAGATTCTGGCACCTGC
droFic1	scf7180000453912:363371-363510 -		CGTGT--------------------------------TTGGTGTGTGTGGCGCAGTTCACACAACTTGGCCTGGAA-AAAGTGAAAGA---------GTATTT-TTTCGGCCATATT----------------GTGTTGTCATAGCT--GGAAAAAGTGCATTTCCGGCCGTATGCATATTCTAGGCATCTGC
droKik1	scf7180000302475:1286833-1286958 +		CGGCGAGT--------G-------------------------TGTGTGTGTGGCGCAGTTCACACAACTTGGCCTGGAA-AAAGTGAAAGA---------GTATTT-TTTCGGCCATATT----------------GTGTTGTCATAGCT-GGGGAAAAGTGCATTTCGCGCCATATGGAGTTAG---------C
droAna3	scaffold_13340:20616985-20617140 +		CCTCTCT--------GTGTGTGA----------GTGTGT---TGTGTGTGAGTGGCGCAGTTCACACAACTTGGCCTGGAA-AAAGTGAAAGAAGCAAATAGGGTATTT-TTTCGGCCATACT----------------GTGT-TTGTCATTATT-GGCAAAAAGTGCACTTATCAGCCATATGGAGATTCA------ATGC
droBip1	scf7180000396413:1785935-1786074 -		CGCGTGT--------G-------------------------TGTGTGTGAGTGGCGCAGTTCACACAACTTGGCCTGGAA-AAAGTGAAAGAAGCAA-TAAGGTATTTTTTCGGCCATACT----------------GTGTTGTCATAGCT--GGGAAAAGTGCACTTAGCAGCCATATGGAGATTCT------ATGC
dp5	2:13539578-13539748 +		TCTGTGT--------GTTCTG-TGTGCGTGTGCGTGCGTG-TGTGTGTTGTGTGTGTGTGGTG----------TTTGGCCTGGAA-AAAGTGAAAGAAGCAA-TAAGGTATTTTTTCGGCCATATT----------------GTGTGTTGTCATTGCTCGGGGAAAAGTGCATTTCGAATGCACATGCAACTGCCACACAACGGA
droPer2	scaffold_0:6910015-6910179 -		CT-GTGTGTTTCTGTGTGTGTGC-GTGCG----------TG-CGTGTG---AGTGTGTGTGTGGTG----------TTTGGCCTGGAA-AAAGTGAAAGAAGCAA-TAAGGTATTTTTTCGGCCATATT----------------GTGTGTTGTCATTGCTCGGGGAAAAGTGCATTTCGAATGCACATGCAACTGCCACACAACGGA
droWil2	scf2_1100000004837:1141310-1141422 +		TGTGTGT--------GTGTGTG-TGTGTGTGTG------------TG---TGTGTGT-----GTGTAAGGCGTCTAATTG--------A-ATATTTGAACGA---------GGCTTT-T----------AGTGTTTGACTTTATTAGCGTGTTGCCA-CGTT-GCCCAAAGTGC-----------------------------------

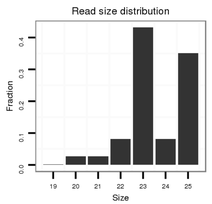
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_580	**scaffold_4770:8698697-8698792 +**	**candidate**	**3p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

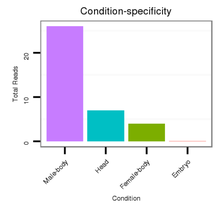
Legend: mature star mismatch in alignment mismatch in read

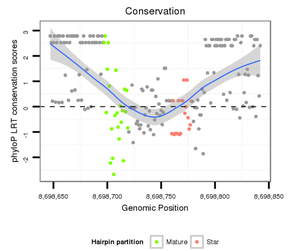
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dere/GG16792-inI]; CDS [Dere/GG16792-cdsJ]; CDS [Dere/GG16792-cdsJ]

Repeatable elements

Name	Class	Family	Strand
(ATTGTn	Simple_repeat	Simple_repeat	+

mature **star**

1. scaffold_4644:1901756-1901774 +
2. scaffold_4690:13182936-13182954 +
3. scaffold_4690:13391007-13391025 +
4. scaffold_4690:14432476-14432494 -
5. scaffold_4770:6259706-6259724 -
6. der_580 scaffold_4770:8698760-8698778 +
7. scaffold_4770:10736609-10736627 -
8. scaffold_4770:16674064-16674082 +
9. scaffold_4784:6628675-6628693 -
10. scaffold_4784:7036990-7036008 +
11. scaffold_4784:8607519-8607537 +
12. scaffold_4784:16239630-16239648 +
13. scaffold_4845:1156978-1154936 +
14. scaffold_4929:12890233-12890251 +

Sense Strand Reads

hide 3p reads | show mid mismatch reads

							V107	GSM1528801	V108	M055	V040	M057
										female		
	Read size	# Mismatch	Hit Count	Total Norm	Total		male body	follicle cells	head	body	embryo	embryo
TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG												
..........GTGAGTGACTAATCGAGCAATTG..	23	0	1	16.00	16		10	0	4	2	0	0
..........GTGAGTGACTAATCGAGCAATTGTT..	25	0	1	13.00	13		10	0	3	0	0	0
..........TGAGTGACTAATCGAGCAATTGTT..	24	0	1	2.00	2		1	0	0	1	0	0
..........GTGAGTGACTAATCGAGCAATT..	22	0	1	2.00	2		2	0	0	0	0	0
..........ATTTGTGATGACCGTTTTCCC..	21	0	1	1.00	1		0	0	0	1	0	0
..........GTTCTCAGAGGTTGAAGTGCCATGCA..	26	0	1	1.00	1		1	0	0	0	0	0
........ACCTGCCAGGTGAAGTTCTCAGAG..	24	0	1	1.00	1		0	0	1	0	0	0
..........GTGAGTGACTAATCGAGCAAT..	21	0	1	1.00	1		1	0	0	0	0	0
..........TGAGTGACTAATCGAGCAATTG..	22	0	1	1.00	1		0	0	0	1	0	0
..........GTGAGTGACTAATCGAGCAA..	20	0	1	1.00	1		1	0	0	0	0	0
..........GTGAGTGACTAATCGAGCAATTGT..	24	0	1	1.00	1		1	0	0	0	0	0
..........AGTTCTCAGAGGTTGAA..	18	0	1	1.00	1		0	0	0	1	0	0
..........GTGAGTTCTCAGAGGTTGAAGT..	23	0	1	1.00	1		0	0	0	1	0	0
..........GATTGATTGATTGATTGAT..	19	0	20	0.05	1		0	0	0	1	0	0

Anti-sense strand reads

						V040	V107
	Read size	# Mismatch	Hit Count	Total Norm	Total	embryo	male body
AGGCACGAGTGGACGGTCCACTTCAAGAGTCTCCAACTTCACGGTACGTCCACTCACTGATTAGCTCGTTAACAAAATTATTCATAAACGTTTAAATTTTAACAATTTATAGACTAACTAACTAACTAACTAAACAAGGGGAGTCAGGTAAACACTACTGGCAAAAGGGGTTAGTCTTGGGTGGTTCCATTTCC							
..........((((((.(((((((..((((((.(((((((((((.........)))).)))))).)).)))))).))))))))))))..							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4770:8698647-8698842_+	der_580	TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTG----------CAA----------ATT---TAAAATTG----------TAAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droYak3	scaffold_14642:11452476_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droSec1	scaffold_12112:6928-7025_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droSim2	tr|B3P676:8329676_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
dm3	chr3R:12930582-12930780_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droEug1	scf1800004939804:37440E-374600_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droBia1	scf1800003920754:4126321-4126530_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droTak1	scf1800004145613:39276-39558_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droEle1	scf1800004491080:1369439-1369798_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droRho1	scf1800000795721:28046-28397_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droFic1	scf1800000453912:2559664-2559872_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droKik1	scf1800003027061:2267443-2267532_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droAna3	scaffold_13340:6550503-6550693_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droBip1	scf1800003967082:2293319-2293476_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
dp5	s:4957368-4957530_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droPer2	scaffold_19:655397-655559_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droWil2	scf_3100000004902:1130293-1130481_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droVir3	scaffold_12855:2605184-2605343_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droMoj3	scaffold_6546:11808107-11808265_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG
droGri2	scaffold_14624:2339477-2339646_+		TCCGTGCTCACCTGCCAGGTGAAGTTCTCAGAGGTTGAAGTGCCATGCAGGTGAGTGACTAATCGAGCAATTGTTTAATAATAGTATTTGCAAATTTAAAATTGTTAAATATCTGATTGATTGATTGATTGTTGTTCCCCTCAGTCCATTTGTGATGACCGTTTTCCCCAAATCAGAACCCACCAAGGTAAAGG

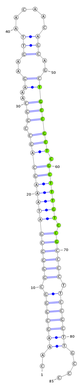
Generated: 09/08/2015 at 10:33 PM

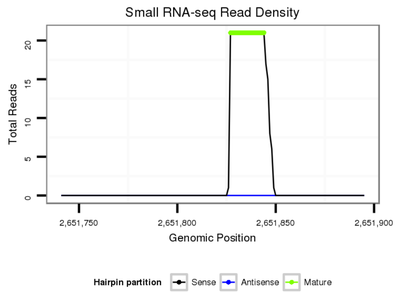
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.loop5	1
crit.loop3	1
crit.3ploy3	1
crit.back	1
rescue.total	1
rescue.confident	0
rescue.known	0
rescue.confident	0
rescue.candidate	1

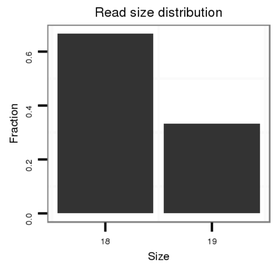
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_144	**scaffold_4784:2651791-2651845 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

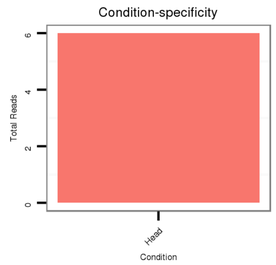
Legend: mature star mismatch in alignment mismatch in read

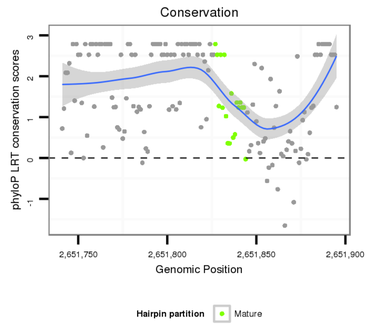
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere/GG14877-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TCGGCAAAGCAGAGCATGTGATGAAAATCGTTGGCAAAGCGGGCGGGGCGATAAAGCAGCCGGCAAAGAAGTTAACAACAGCAGCTGCCGCTCGCTTTGTCCGCCCCTTCCGCTTGCCCCCCTCCGCCCCCTTGGAAGAGCGCAGAAAATCGGG	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	M055 female body	V040 embryo	GSM1528801 follicle cells
**********..(((((((.(((((((((((((((((.(((..((..(((.....))).)))))))).))))))).))))))).....**********									
.....TGCCGCTCGCTTTGTCCGCCC.....	20	0	1	6.00	6	3	3	0	0
.....TGCCGCTCGCTTTGTCCGCCCC.....	22	0	1	5.00	5	2	3	0	0
.....TGCCGCTCGCTTTGTCCGCC.....	21	0	1	4.00	4	4	0	0	0
.....TGCCGCTCGCTTTGTCCGC.....	19	0	1	2.00	2	2	0	0	0
.....TGCCGCTCGCTTTGTCCGCCCG.....	22	1	1	1.00	1	0	1	0	0
.....CTGCCGCTCGCTTTGTCCGCC.....	21	0	1	1.00	1	0	1	0	0
.....TGCCGCTCGCTTTGTCCGCCCT.....	23	0	1	1.00	1	1	0	0	0
.....TGCCGCTCGCTTTGTCCGCT.....	21	1	1	1.00	1	1	0	0	0
.....TGCCGCTCGCTTTGTCCGCCG.....	22	1	1	1.00	1	1	0	0	0

Anti-sense strand reads

AGGCGGTTTCGTCTCGTACACTACTTTAGCAACCGTTTCGCCCGCCCCGCTATTTCGTCGGCCGTTTCTTCAATTGTTGTCGTCGACGGCGAGCGAAACAGGCGGGGAAGGCGAACGGGGGGAGGCGGGGGAACCTTCTCGCGTCTTTTAGCCC	Read size	# Mismatch	Hit Count	Total Norm	Total	V040 embryo	V060 head	M057 embryo	V107 male body
**********..(((((((.(((((((((((((((((.(((..((..(((.....))).)))))))).))))))).))))))).....**********									

Show Alignment With Reads

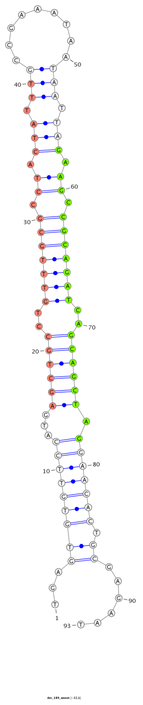
Re-alignment of all predicted orthologs

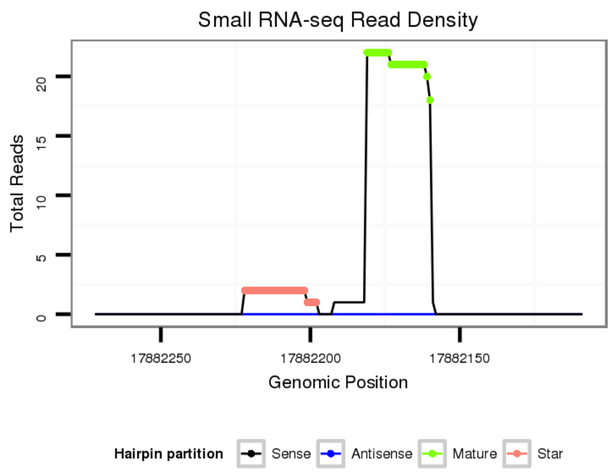
Species	Coordinate	ID	Alignment
droEre2	scaffold_4784:2651741-2651895 +	der_144	TCCGC--------CAAAG-CAGAGCATGTGATGAAAATCGTTGGCAAAGCGGGCGGGGCGATAAAGCAGCCGGC--AAAGAAGTTAACA----------ACAGCAGCTGCCG----CTCGCTTTGTCCGCC--C----C----CTTC----C--GCTTG----------CCC---------CCCT----------C----------CGC-C--CCCTTG--GAAGA---GCGCAGAAAATCGGG
droYak3	3L:9303675-9303836 -	dya_1785	TCCGC--------CAAAG-CAGAGCATGTGATGAAAATCGTTGGCAAAGCGGGCGGGGCGATAAAGCAGCCGGC--AAAGAAGTTAACA----------ACAGCAGCTGCCG----CTCGCTTTGTCCGCC--C----C----CTTC----C--GCTTG----------CCC---------CCTC--TC----CT----------CCCT--TC----------GCC-C--CCCTTG--GAAGA---GCGCAGAAAATCGGG
droSec2	scaffold_2:2656183-2656349 -		TCCGC--------CAAAG-CAGAGCATGTGATGAAAATCGTTGGCAAAGCGGGCGGGGCGATAAAGCAGCCGGC--AAAGAAGTTAACA----------ACAGCAGCTGCCG-CCCTCGCTTTGTCCGCC--T----C----CTTC----C--GCTGC----------CCC---------CCCT----------GC----------CCCT--TC----------ACC-C--CATTG--GAAGA---GCGCAGAAAATCGGG
droSim2	3L:2519985-2520151 +		TCCGC--------CAAAG-CAGAGCATGTGATGAAAATCGTTGGCAAAGCGGGCGGGGCGATAAAGCAGCCGGC--AAAGAAGTTAACA----------ACAGCAGCTGCCG-CCCTCGCTTTGTCCGCC--T----C----CTTC----C--GCTGC----------CCC---------CCCT----------GC----------CCCT--TC----------ACC-C--CATTG--GAAGA---GCGCAGAAAATCGGG
dm3	chr3L:2632658-2632824 +		TCCGC--------CAAAG-CAGAGCATGTGATGAAAATCGTTGGCAAAGCGGGCGGGGCGATAAAGCAGCCGGC--AAAGAAGTTAACA----------ACAGCAGCTGCCG-CCCTCGCTTTGTCCGCC--T----C----CTTC----C--GCTGC----------CCC---------CCCT----------GC----------CCCT--TC----------ACC-C--CATTG--GAAGA---GCGCAGAAAATCGGG
droEug1	scf7180000409466:359423-359588 +		TCCGC--------TAAAG-CAGAAGATGTGATGAAAATCGTTGGCAAAGCGGGCGGGGCGATAAAGCAGCCGGC--AAAGAAGTTAACA----------ACAGCAGCTGCCG----CTCGCTTTGTCCGCC--T----C----CTTC----C--GCTGC----------CCCA---GAGCCCT----GC----------TCCCG--TT----------CGC-C--CCTTG--GAAGA---GCGCAGAAAATCGGG
droBia1	scf7180000302428:9411124-9411297 +		TCCGC--------TAAAG-CAGAAGATGTGATGAAAATCGTGGCAAAGCGGGCGGGGCGATAAAGCAGCCGGC--AAAGAAGTTAACA----------AGCAAGCTGCCG----CTCGCTTTGTCCGCC--T----C----CTTC----C--GCTTG----------CCCG-GGC---CCGCCCCCTTCCTGCCCCCGGC----T----------HC----------CCCC--TCCTTG--GAAGA---GCGCAGAAAATCGGG
droTak1	scf7180000415857:429832-429974 +		TCCGC--------TAAAG-CAGAAGATGTGATGAAAATCGTTGGCAAAGCGGGCGGGGCGATAAAGCAGCCGGC--AAAGAAGTTAACA----------AGCAAGCTGCCG----CTCGCTTTGTCCGCC--T----C----CTTC----C--GCTGC----------CCCCCC-CCCTCCCT----GC----------TCCCT--CC----------CGC-C--C-----C-----CG-GCAGAAAATCGGG
droEle1	scf7180000491249:2747837-2748000 -		TCCGC--------TAAAG-CAGAAGATGTGATGAAAATCGTTGGCAAAGCGGGCGGGGCGATAAAGCAGCCGGC--AAAGAAGTTAACA----------ACAGCAGCTGCCG----CTCGCTTTGTCGCC--T----C----CTTC----C--GTTG----------CCCCCC---GCCT----------TCACTCCGT----------C-C--CCCTTG--GAAGA---GCGCAGAAAATCGGG
droRho1	scf7180000758401:30366-30523 -		TCCGC--------TAAAG-CAGAAGATGTGATGAAAATCGTTGGCAAAGCGGGCGGGGCGATAAAGCAGCCGGC--AAAGAAGTTAACA----------ACAGCAGCTGCCG----CTCGCTTTGTCCGCC--T----C----CTTC----C--GTTG----------CCCC---GCCT----------TCACC----------T-C--CCCTTG--GAGA---GCGCAGAAAATCGGG
droFic1	scf7180000454105:959676-959832 +		TCCGC--------TAAAG-CAGAGCATGTGATAAAATCGTTGGCAAAGCGGGCGGGGCGATAAAGCAGCCGGC--AAAGAAGTTAACA----------ACAGCAGCTGCCG----CTGCTTTGTCCGCC--T----C----CTTC----C--GCTTG----------CCCG-T----CGCT----------GC----------TC----------CCC---C--CGTTG--GAAGA---GCGCAGAAAATCGGG
droKik1	scf7180000302441:1073450-1073687 -		TCCGCTGCTCCGCAAAG-CAGAGCATGTGATGAAAATCGTTGGCAAAGCGGGCGAAGCGATAAAGCAGCCGGC--AAAGAAGTTAACA----------ACAGCAGCTGCCG-GCGCTCGCTTTGTCGCGGTCTCCCCTTCGCCGGTTTCTTCTTCTTCTTCGTCGCTTGCTTGCTCCCTGCTTC----CCGTTGCCCGCCAC----------CCC----------C----------CGCTC----------C-C--CGTTG--GAAGA---GCGCAGAAAATCGGG
droAna3	scaffold_13337:9448858-9449057 -		C--C---------CAAAG-CAGAGCATGTGATGAAAATCGTGGCAAAGCGGGCGGGGCGATAAAGCAGCCGGC--AAAGAAGTTAACA----------C---AGCTGTGG-GTGCTC----------C----------CCT----CT----C-----CTGCGTCCCCT----------CGTTCTCCCT--CAGCTCTTCGGCTTCGTCGTT-C-GTG-----CCCGCCTCCTC----------TTCCCCT--TCAGTTCGTTATATT----C----TTCTT----CT---TC--GGA---GCGCAGAAAATCGGG
droBip1	scf7180000396544:259775-259991 -		C--C---------CAAAG-CAGAGCATGTGATGAAAATCGTGGCAAAGCGGGCGATGCGATAAAGCAGCCGGC--AAAGAAGTTAACA----------C---AGCTGTGG-GTGCTC----------C----------CCT----CT----C-----TTGCGTCCCCT----------CGTTCTCCCT--CAGCTCTTCGGCTTCGTCGTT-C-GTG---CCCGCCTACTC----------TTCC--CCT--ACGGTTCGTTATATT----CTTCTTCTTCTTT---CT---TC--GGA---GCGCAGAAAATCGGG
dp5	XR_group3a:1305442-1305680 -		TCCGC--------CAAAG-CAGAGCATGTGATGAAAATCGTAGCAAAGGCGAGGCGCGATAAAGCAGCCGGC--AAAGAAGTTAACAAATAACAGCAGCTGCCTGCCG----------C----------C----TGTTCTGCTTCTGCTGCTG

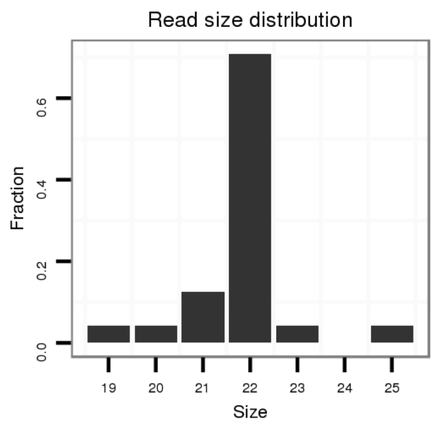
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_189	**scaffold_4784:17882159-17882222 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

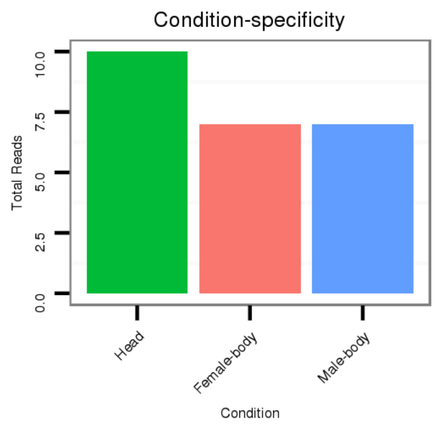
Legend: mature star mismatch in alignment mismatch in read

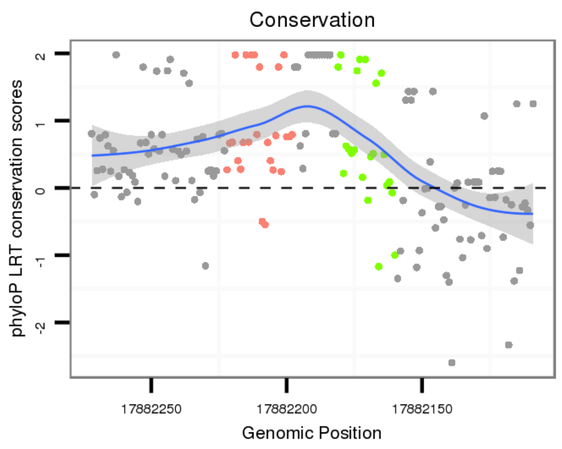
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG13532-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACATCTCACAGCTTTGCTGGCTAATAAACAATAAATGAGTGTGTTCCATGAGCTGCCTGTTTGCGCCTACTATTTGCCGAAATAATAATTAGAAGCCGCAGATCAGCAGCTAGGAACACTGCGAGAATATCGACGTGCCATTTATAGATAAAAATATACTTTAA	Read size	# Mismatch	Hit Count	Total Norm	Total		M055 female body	V108 head	V107 male	V060 head	GSM1528801 follicle cells
**********...(((((((((...(((((..(((((((.((.(((.(((.........))).))).)).)))))))..)))))).))))))).))).....**********											
.....GAAGCCGCAGATCAGCAGCTAG.....	22	0	1	17.00	17	5	4	6	2	0	
.....GAAGCCGCAGATCAGCAGCTAGT.....	23	1	1	3.00	3	2	1	0	0	0	
.....GAAGCCGCAGATCAGCAGCTAC.....	22	1	1	2.00	2	2	0	0	0	0	
.....GAAGCCGCAGATCAGCAGCTA.....	21	0	1	2.00	2	0	1	0	1	0	
.....GAAGCCGCAGATCAGCAGT.....	19	1	1	2.00	2	2	0	0	0	0	
.....AGCTGCCTGTTTGCGCCTACTATTT.....	25	0	1	1.00	1	1	0	0	0	0	
.....AATAATAATTAGAAGCCGC.....	19	0	1	1.00	1	0	1	0	0	0	
.....GAAGCCGCAGATCAGCAGCTAGG.....	23	0	1	1.00	1	0	1	0	0	0	
.....AGCTGCCTGTTTGCGCCTACT.....	21	0	1	1.00	1	1	0	0	0	0	
.....AAGCCGCAGATCAGCAGCTAC.....	21	1	1	1.00	1	1	0	0	0	0	
.....GAAGCCGCAGATCAGCAGCTAGA.....	23	1	1	1.00	1	1	0	0	0	0	
.....GAAGCCGCAGATCAGCAGCT.....	20	0	1	1.00	1	0	0	1	0	0	

Anti-sense strand reads

TGTAGAGTGTCGAAACGACCGATTATTTGTTATTTACTCACACAAGGTACTCGACGGACAAACGCGGATGATAAACGGCTTTATTATTAATCTTCGGCGTCTAGTCGTCGATCCTTGTGACGCTCTTATAGCTGCACGGTAAATATCTATTTTTATATGAAATT	Read size	# Mismatch	Hit Count	Total Norm	Total	V060 head	V040 embryo	M055 female body	GSM1528801 follicle cells
**********...(((((((((...(((((((..(((((((.((.(((.(((.........))).))).)).)))))))..)))))).))))))).))).....**********									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4784:17882109-17882272 -	der_189	ACATCTCACAGCTTT-G---CTGGCTAATAAACAATAAATGAGTGTGTTCCATGAGCTGCCTGTTTGCGCC-T-AC-TATTTGCC-GA--AATAATAATTAGAAGCCGCAGATCAGCAGCTAGGAACACTGCGAGAA----------TATCG-----A------CGTGCCATTTATAGATAAAAATATA--C----------TTT----------AA------
droYak3	3L:18172320-18172482 -		ACATTTCACAGCTCT-G---CTGGCTAATAAACAATAAATGAGTGTGTTCCATGAGCTGCCTGTTTGCGCC-T-AC-TATTTGCC-AA--AATAATAATTAGAAGCCGCAGATC-GAAGCTAAAACACTGCAAAAA----------TACCA-----A------AGCGCCATTTATAGATAAAAACATA--T----------TTT----------AA------
droSec2	scaffold_0:7736760-7736929 -		ATATTTCACAGCTTT-G---CTGGCTAATAAACAATAAATGAGTGTGTTCCATGAGCTGACTGTTTGCGCC-T-AC-TATTTGCC-AA--AATAATAATTAGAAGCCGCAGATCAGAAGCTAAAACACTGCAAAAA----------TTATCACGAAAT------CGTGTCAGTTATAGATAAAAACATA--T----------TTT----------AA------
droSim2	3L:15255536-15255705 -		AATATTTCACAGCTTT-G---CTGGCTAATAAACAATAAATGAGTGTGTTCCATGAGCTGCCTGTTTGCGCC-T-AC-TATTTGCC-AA--AATAATAATTAGAAGCCGCAGATCAGAAGCTAAAACACTGCAAAAA--A----------TTATCACGAAAA------TGTGCCATTTA-AAATAAAAACAAA--T----------TTT----------GA------
dm3	chr3L:15624115-15624303 -		ACATTTCACAGCTTT-G---CTGGCTAATAAACAATAAATGAGTGTGTTCCATGAGCTGCCTGTTTGCGCC-T-AC-TATTTGCC-AA--AATAATAATTAGAAGCCGCAGATCAGAAGCTAATAACACTGCAAAAA----------TTATCACAAAAT------CGTGCCATTTAAAATAAAAACATA--T----------TCTGATAAAATTAATACAATTTAA------
droEug1	scf7180000408844:356204-356388 -		TCATTTCACAGCTTC-G---CCGGCTAATAAACAATACATGAGTCTATTGTATGAGCTGTCTGTTTGCACCGAACCGATATTTGCC-AA--AATAATAATCAGAAGCCGCAGAACAGTAACCAAATACACTTGCGGAAA--A----------ATATTTTGAATATCAGTTAGGTTTT------AGTTAAAGAAAGA--A------AAGTAGGTTAGGCG----------GA------
droBia1	scf7180000302334:760437-760561 +		ACATTTGTCAGGCTG-G---CTGGCTAATAAACAATACATGAGTGTATTGTAACGGCGTGTCTGTTTGCGCC-A-AC-AATTTGCC-GA--AATAATAATTAGAAGCCGCAGAACAGGAGCTAG--GCACTGGGCAAA----------.....-----.-------.....-.---.....---.....--
droTak1	scf7180000415268:19552-19677 -		ACATTTCACAGCTTG-G---GTGGCTAATAAACAATACATGTGTGTACATGTATGATTTGTCTGTTTGCGCC-A-AC-AATTTGCC-AT--AATAATAATTAGAAGCCGCAGAACAGCAGATAA-ACCACTGAAAAAA----------.....-----.-------.....-.---.....---.....--
droEle1	scf7180000491000:1038733-1038923 -		ACATTGTGCAGTTCT-G---CTGGCTAATAAACAATACACGAGTGTATTGTATGAGCTGTCTGTTTGGCC-A-AC-AATTTGCC-AA--AATAATAATTGGAAGCCGCAGAACAGCAGCTGC-CACACTAAAAATAAAA----------ATATCACGAAAATTAG---GTTATGTTTG---TAAAGACCAA--ATCTTACAAATAAAATTATTTT----------AA------
droRho1	scf7180000778197:5838-6005 +		ACCTTTGCGCAGCTCT-T---CTGGCTAATAAACAATACAGCGAGTGTGTTGTATGAGCTGTCTATTTGCGCC-A-AC-AATTTGCC-AA--AATAATAATTAGAGGCCGCAAAGCAGAAGCTGA-CGCACTGAAAAAAAATAAATAACAAATA--TTATTAAGCA-A------.....----------ATTGAATCCTA--A----------TTC----------AA------
droFic1	scf7180000454065:1687308-1687499 +		ACATTTCACAGCTTT-G---CTGGCTAATAAACAAAACATGATTGTGTTCTATGAGCTGTCTGTTTGCACC-A-AC-AATTTGCC-AA--AATAATAATTAGAAGCCGCAGAACAGCAGCTTG-GCCACTCAAAAAAAATGTG---CA---ATTATC-A------.....-TGTTCTAAAATAGAAAGAAAATATTT---ACTTTTAAAATGA----------TTTAAAGGGTC
droKik1	scf7180000302686:1134818-1134974 +		ACATTTCACAGCTCT-GGCCCCGGCTAATAAACAATGCATGATGTGTATTCTATGAGCTGTCTGTTCGGTCC-G-AC-AATTTGCCCAA--AATAATAATTAGAAGCCACAGAATGCGAGTCAA-GGCACTTGAAAAA----------.....A----.-----.-----.....CATTAGAAATAACGTTCA--G----------.....ATT----------.....TA------
droAna3	scaffold_13337:11534984-11535067 +		AAATTTCACAGCTTTG-G---CCAGCCAGTCA----------GCACAATATATGAGCTATCTGTTTGTCCGA-AAAC-GACTTGCC-AA--AATAATAATTAGA----------.....-----.-------.....-.---.....---.....--
droBip1	scf7180000396589:2439139-2439231 -		AAATTTCACAACTTTG-G---CCAGCCAGTCAGCA----------CCATATATGAGCTATCTGTTTGCCGA-AAAC-GACATGCC-AA--AATAATAATTAGAGAAGACAGA----------.....-----.-------.....-.---.....---.....--
dp5	XR_group6:140525-140635 +		ATGGCCAAGAATATTCA---GGGGTCG---GCCAGCACATGTATATCTCTAGTCGGCTATTTGTTTGGCTA-A-AC-AATTCGCA-AAATAATAATAATTAGAAGCCACAAAGCAGAAGCT----------.....-----.-------.....-.---.....---.....--
droPer2	scaffold_12:825009-825119 +		ATGGCCAAGAATATTCA---GGGGTCG---GCCAGCACATGTATATCTCTAGTCGGCTATTTGTTTGGCTA-A-AC-AATTCGCA-AAATAATAATAATTAGAAGCCACAAAGCAGAAGCT----------.....-----.-------.....-.---.....---.....--

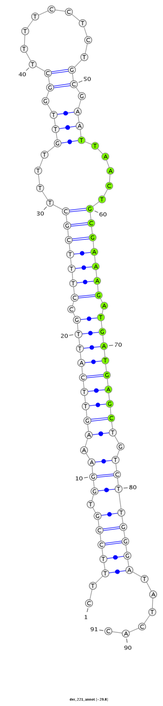
Generated: 09/08/2015 at 07:45 PM

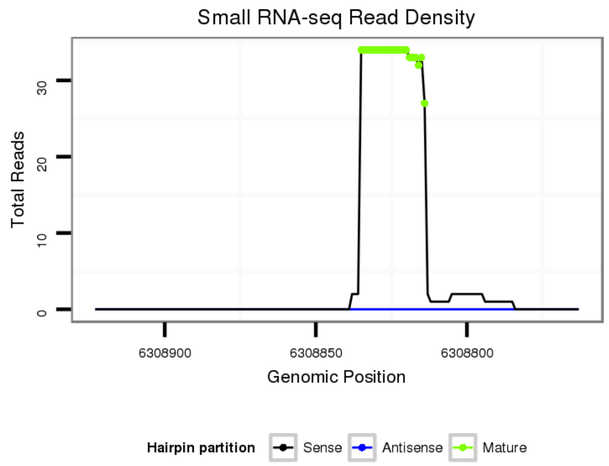
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

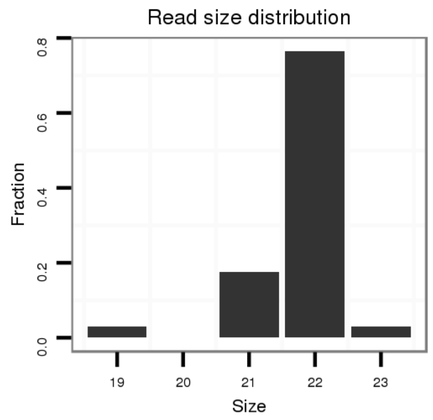
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_221	**scaffold_4770:6308813-6308873 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

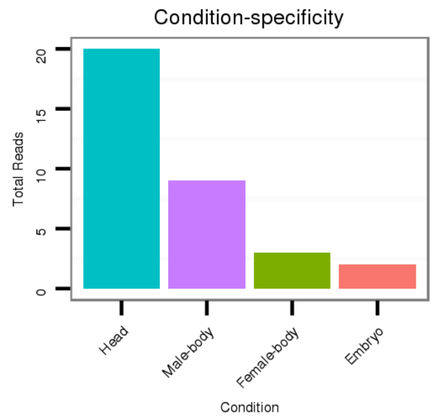
Legend: mature star mismatch in alignment mismatch in read

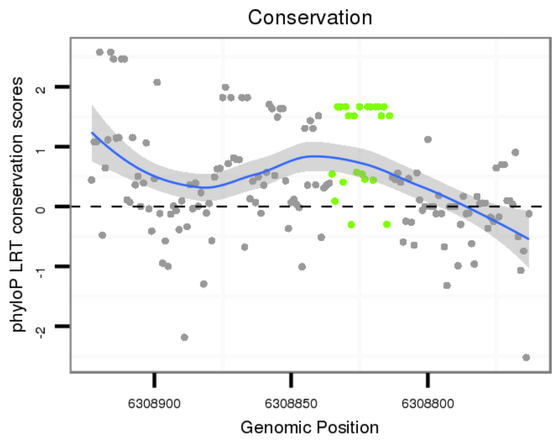
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG23350-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTGAAAGATTTATTCAGTGTATAAAGCGCAACCTCCTTTCCGTGGAAAGTTCATTGCCTTTCGCTTTTGTTGGCTTTTCCTCTGCGAATTAACTGCGAAAGATGATGAGCTGTCTTGGGATATCACTGCATCCCAGCTGAATAAAAGGCATTTTTATGTTA						V108	V107	V040	M055 female	M057	V060				
********************************..(((((.(((.(((((((((.(((((((....(((.((.........)).))).....)))))))).)))))))).)))))))).....**********************************	Read size	# Mismatch	Hit Count	Total Norm	Total	head	male body	embryo	body	embryo	head				
.....TTAACTGCGAAAGATGATGAGC.....	22	0	1	25.00	25	15	7	1	1	1	0				
.....TTAACTGCGAAAGATGATGAG.....	21	0	1	6.00	6	4	0	0	2	0	0				
.....GAATTAACTGCGAAAGATGATG.....	22	0	1	1.00	1	1	0	0	0	0	0				
.....GATATCACTGCATCCCAGCTG.....	21	0	1	1.00	1	0	0	1	0	0	0				
.....TTAACTGCGAAAGATGATGAGCT.....	23	0	1	1.00	1	0	1	0	0	0	0				
.....TTAACTGCGAAAGATGATGAGG.....	22	1	1	1.00	1	1	0	0	0	0	0				
.....GAATTAACTGCGAAAGATG.....	19	0	1	1.00	1	0	1	0	0	0	0				
.....TTAACTGCGAAAGATGATGAGT.....	22	1	1	1.00	1	0	0	0	0	0	1				
.....GCTGTCTTGGGATATCACTGC.....	21	0	1	1.00	1	0	1	0	0	0	0				

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4770:6308763-6308923 -	der_221	TTGA----AAGATTTATTCAGTGTATAAA----------GC-GCAACCTCCTTTCCGTGGAAAGTTCATTGCCTTTCGCTTTTGTTGGCTTTTCCTCTGCGAATTAACTGCGAAAGATGATGAGCTGTCTTGGGATATCACTGCATCCCAGCTGAATAA---AAGGCATT----------T-TTAT----GTTA
droYak3	3R:4072488-4072643 +		TTGA----AAGATTTATTCAGTGTATAAA----------GG-GCAATCTCCTTTCCGTGGAAAGTTCATTGCCTTTCGCTTTTGTTGGTTTTCCTCTGCGAATTAACTGCGTAAGATGATGAGCTGTCATGGGAAG-C--AGTGA---TGGGAAATAA---AG------GGAATTTCTTAT----GTGA
droSec2	scaffold_25:443215-443370 -		TTGA----AAGATTTATTTAGTGTATAAA----------GA-GCAAATCTCCTTCCGTGGAAAGTTCATTGCCTTTCGCTTTTGTTGCACTTTCCTCTGCGAATTAACTGCGAAAGATGATGAGCATGTCATGGAATG-C--AGTGA---TGCTAAGCAA---TG------GGAATTTTTTAT----ATGA
droSim2	3r:5933289-5933444 -		TTGA----AAGATTTATTTAGTGTATAAA----------GA-GCAAATCTCCTTCCTTCGTGGAAAGTTCATTGCCATTCGCTTTTGTTGACTTTTCCTCTGCGAATTAACTGCGAAAGATGATGAGCATGTCATGGGATG-C--AGTGA---TGCTAAATAA---TG------GGAATTTCTTAT----ATGA
dm3	chr3R:15332896-15333049 +		TTGA----AAGATTTATTTAGTGTATGAA----------GA-GCAAATCTCCTCTCCGTGAAAGTTCATTGCCTTTCGCTTTTGTTGACTTTCCTCTGCGAATTAACTGCGAAAGATGATGAACAGTGCGCGGGATA-C--AGTGA---TGCTAAATAA---TG------GGAATTTTTT----ACGA
droEug1	scf7180000409804:1614957-1615094 +		TTGA----CAGATTTATGCATTGTATAAA----------GA-GAATTTTCATTTCCTTGGAAAGTTCATTGCCTTTCGCTTTTGTTGGCTTACGATGGGAGAATAACTGCGAAAGATGATGAGCAGTCGGGAGTA-C--AGTGT---TCGAATT---------------T-----------TT
droBia1	scf7180000302402:1101150-1101309 +		TTGA----CAGATTTATGTAGTTTATTAA----------AG-GCGTTCGCCTTTCCACGACAAGTTCATTGCCTTTCGCTTTTGTTGGCCTACGATCTGCGAGTAAACTGCGAAAGATGATGAGCAGTCATGAAACA-C--AGTGG---GGCTATATAT---AA------GGAAGAACCCATTAAACTGA
droTak1	scf7180000415710:510287-510437 -		TTGA----CAGATTTATGTAGTTTATAAA----------GA-AGGTTCGGCTTCCCGTGGAAAGTTCATTGCCTTTCGCTTTTGTTGGCTTAAGATCTGTGAATAACTGCGAAAGATGATGAGCAGTCATGGGATA-C--AATGG---GGCTAAATAT---AAGGGCGTT----------T-----------ATAA
droEle1	scf7180000490994:1129701-1129851 +		TTGA----CAGATTTATGCAGTGTATAAA----------AAAACATTTTCTTTTTCGTGG-AAGTTCATTGACTTTCGCTT-----GTCTGACGATCTGAGAATAACTGCGAAAGATGATGACCATGTCATGGGATA-C--TGAAT---ACATATCTTTTTAAAAGCATT----------TGT-----AATA
droRho1	scf7180000779431:117842-118004 -		TTGA----CAGATTTATGCAGTGTATAGA----------AA-AAATGTTGTTTCTCATGG-AAGTTCGTTGACTTTCGCTTTTGTTGGCTGGCGATCTGAGAATAACTGCGAAAGATGATGACCATGTCATGGGATA-C--AGTCG---GGCTAA-TAT---AAGCCATTAGTGATGGGA---C-TTAC---AATAA
droFic1	scf7180000454126:321328-321450 +		GTGA----ATGA----------------------------AAATTT-GCTTTCCCGCGAAAGTTCATTGTCTATTCTTTTGTTGGGAGACGATCTGCACAATAACTGCGAAAGATTATGAACAGCCGTAAAATA-C--AGTGG---GGCTTA-T---------------------T-TTAA----GCTT
droKik1	scf7180000302803:15693-15813 +		TTGA----CAGATTTATGCAGTGTTCGTA----------TA-CTGTTT-ATTTTCTTGGAAAGTTCAACGCTTTCTCTTTTGTTGCCTGAAGATCTGCGAATAACTGAGAAAGATGATGAGCAGTCAAGAGATA---
droBip1	scf7180000395971:120235-120316 +		--GA----ATAATCTATACAGATTATAAA--TCTTCTTGTGG-A-AGTCTGCAATCT----------C----------G----CGAATGTGAATAATGATGAGCAATAATGGGAT---
dp5	2:29811237-29811321 +		TTGA----CAGATTTATGCACTGAAGGAATTTCTTATTGTGGG-GTGGCCGGCTGTCTGTGG---GTTCATTGACTCGCCGATTCGTTGTTT--
droPer2	scaffold_6:5180794-5180878 +		TTGA----CAGATTTATGCACTGAAGGAATTTCTTATTGTGGG-GTGGCCGGCTGTCTGTGG---GTTCATTGACTCGCCGATTCGTTGTTT--
droWil2	scf2_1100000004943:4145767-4145790 +		TTGA----TAGATTTATTATACTGTATAAA----------T--
droVir3	scaffold_13047:16267989-16268041 -		GTGA----AAGATTAATGGTCGCCA--AA----------GT-GC---TTCTCTTCAGTCCAAGGTGCATTGCC--
droGri2	scaffold_15116:1150297-1150319 -		TCAAGGCACAGATTTATGCACTG------------------T--

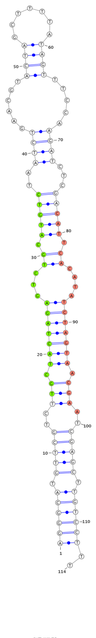
Generated: 09/08/2015 at 07:45 PM

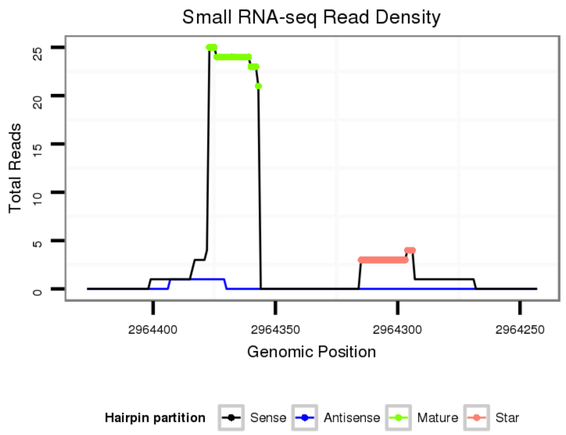
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

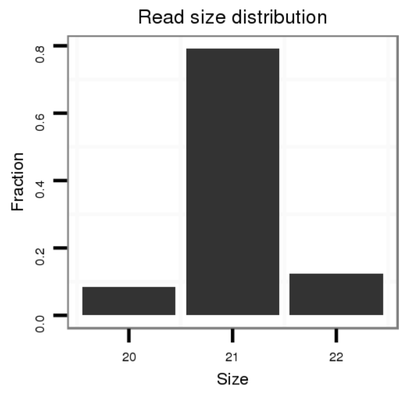
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_191	**scaffold_4845:2964293-2964377 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

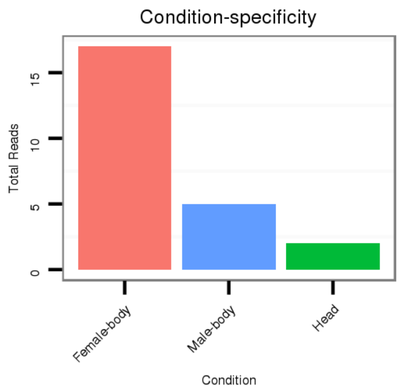
Legend: mature star mismatch in alignment mismatch in read

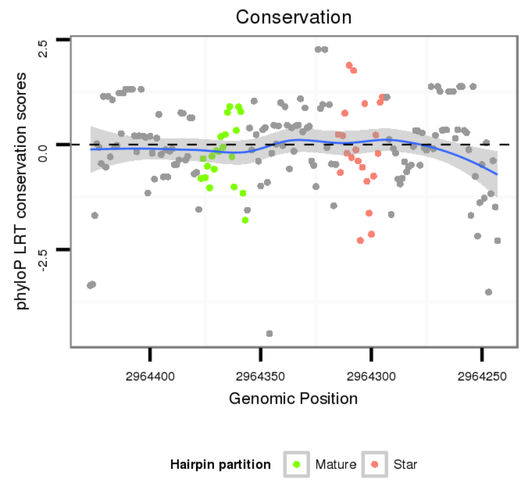
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
DNAREP1_DM	RC	Helitron	+
DNAREP1_DM	RC	Helitron	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	female body	V107 male body	V108 head	M057 embryo
ACAACGAAACTGCGACATATACATATATTCAGCAGAGGGCATGTTCGTCTTGCTACTAGAGTCTGCATGTCTAATCTGAACGTACTAGCTTTTATAGTTTCCAAGATCTCGACATTCACATATCTAGTAACGAATCGAGCTTGTCCTTTTCTCTACGAGTAACGGGTATAAAAATTATTAGTTTC									
**********(((((((.(((((..(((.(((((((...((.(((((..((((.....((((.......))))).....))))...))))))..)).....)))))))..))))).))....))))..**********(((((.(((((..(((.(((((((...((.(((((..((((.....((((.......))))).....))))...))))))..)).....)))))))..))))).))....))))..**********									
.....TGCTACTAGAGTCTGCATGTC.....	21	0	1	19.00	19	13	4	2	0
.....CATTCACATATCTAGTAACGAA.....	22	0	1	3.00	3	3	0	0	0
.....TGCTACTAGAGTCTGCATGT.....	20	0	1	2.00	2	1	1	0	0
.....ATTCAGCAGAGGGCATGTTCGTCTTGC.....	27	0	1	1.00	1	0	0	0	1
.....TTGCTACTAGAGTCTGCATGTCA.....	23	1	1	1.00	1	1	0	0	0
.....TTCGTCTTGCTACTAGAGTCTGCA.....	24	0	1	1.00	1	1	0	0	0
.....TCGTCTTGCTACTAGAGTCTGCATGTC.....	27	0	1	1.00	1	0	0	1	0
.....TTGCTACTAGAGTCTGCATGTC.....	22	0	1	1.00	1	0	0	1	0
.....GAATCGAGCTTGTCCTTTTCTCTACGAG.....	28	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M057 embryo	M055 female body	V108 head
TGTTGCTTTGACGCTGTATATGTATATAAGTCGTCTCCCGTACAAGCAGAACGATGATCTCAGACGTACAGATTAGACTTGCATGATCGAAAATATCAAAGGTTCTAGAGCTGTAAGTGTATAGATCATTGCTTAGCTCGAACAGGAAAAGAGATGCTCATTGCCCATATTTTTAATAATCAAAG								
**********(((((((.(((((..(((.(((((((...((.(((((..((((.....((((.......))))).....))))...))))))..)).....)))))))..))))).))....))))..**********(((((.(((((..(((.(((((((...((.(((((..((((.....((((.......))))).....))))...))))))..)).....)))))))..))))).))....))))..**********								
.....CTCCCGTACAAGCAGAACGATGA.....	23	0	1	1.00	1	1	0	0
TGTTGCTTTGACGCTGTATAT.....	21	0	20	0.05	1	0	0	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4845:2964243-2964427 -	der_191	ACAACGAAACT----------GCGACATATACATATATTCA----------GCAGAGGGCA----------TGTTCG-TCTTGCTACTAGAGTCTGCATGTCTAA-TCTGAACGTACTAGCTTTTATAGTTTCCAAGATCTC-----GACATTCACATATCTAG---T----------AACGAATCGAGCTTGTCCTT---TTCTCTACGAGTAACGGGTATAAAAATTA---TTA--GTTTC
droYak3	3R:358604-358724 -		CGT--------|----------|----------|----------|----------|------CTATGTCACTGGAGTCTGCATGCTGAA-TCTTAAGTATCTAGCTTTTATAGTTTTGAGATCTC-----GACGTTC----------|---|----------|--------TAGTATACCCTT--TTACTTACGAGTAACGGGAATAAAAACAT---T---AGTTT
droSec2	scaffold_1098:450-617 -		CTG--------|----------|----------|----------|----------|-----GGATATCGATAGATAGATATCAACAAACTTGT---TCTGCTCTTTAGAATCTGTATGCTTAA-TCTCAACATTTAGCTTTTATAGTACTTAAGATCTC-----CACGTTCATATGG----|---|----------|----------AATGCAGTATAACATT--TTACTCGACGAGCAACGGGTATAAATTATTA---AAAAACTTTC
droSim2	node_36324:1130-1297 +		CTG--------|----------|----------|----------|----------|-----GGATATCGATAGATAGATATCAACAAACTTGT---TCTGCTCTTTAGAATCTGTATGCTTAA-TCTCAACATTTAGCTTTTATAGTACTTAAGATCTC-----CACGTTCATATGG----|---|----------|----------AATGCAGTATAACATT--TTACTCGACGAGCAACGGGTATAAATTATTA---AAAAACTTTC
dm3	chrYHet:227838-227997 -		AGT--------|----------|----------|----------|----------|-----GGGCGTGGAT----------GC---GCTTTCTCTAGAATCTATATGCTCAG-TCTCAACATTCTAGCTTTTATAGTTTGTGAGATCTGTTCCTGACAGTTACATACTTTT---C----------AACGAATGTCGTGTACCTT--TTAGACTACGAGTGCCGGGTATAATGACGA---AAA--TTACT
droEug1	scf7180000408193:292592-292711 -		TAT--------|----------|----------|----------|----------|------|--TCATCTACAGAATCTACATGCTTAA-TCCAAGTTTGTAATCTTATTGTTCCTGAGATCTC-----AGCGTACATACGG--AC----A----------AAC------GG-GCGCACAT--TTACTCTACGAGTAACGGGTATAAAAA----|---|---|--
droBia1	scf7180000301518:13691-13816 -		CTT--------|----------|----------|----------|----------|------|--------CAATAACCTGCATGGCAAA-TCCCAAGTTTCAAGCTTTAATAGTTTCCGAGATCTA-----AACTTT-ATAC--TTTC---C----------GAAGAATACAGTACACTTT---CGGCTCTAAGAGTAACGGGTATAAACACAA---TT---|---A
droTak1	scf7180000412540:8503-8634 -		A---------|----------|----------|----------|----------|------|----------GAATATGTGTGGAAA-TCTCAACTTCTAGCTTTTGTAGTTTCCGAGATCTC-----AGCTGTTACATACTTTT---G----------CTCGAATACAAAACACCTTT--TTACTCTACGAGTAACGGGTATAAAAATATCTTAGA--TGCCC
droEle1	scf7180000487683:3390-3513 -		----------|----------|----------|----------|----------|------|---------TATAATCTGCATGCCAAA-TCCCAATTCTCTAGCTTGTATAGTTTCCGAGATCTC-----GACGTTCATACAG--ACGGAC----------AACGAATACAATATACCCTTT--TTACTCTACGAGTAACGGGTATAATAATTC---|---|----T
droRho1	scf7180000776861:9988-10108 -		CTC--------|----------|----------|----------|----------|------|--------CTAAATCTACATGCAAAA-TGCCAATCTTCTAGCTTTTATAGTTTCCGAGATCTC-----AGCGTTCATATCGG----|---|----------|----------ACAGACCCTTT--TTACTCTACGAGTAACGGGTATAATTATAA---ATCCCGTTGC
droFic1	scf7180000453879:9610-9680 +		TTT--------|----------|----------|----------|----------|------|---TATGTCTAGAATCTGCATGTCTAA-TCCCAATATTCTAGCTTATAATAGTTTTCCAGATATC-----GATATTCA---------|---|----------|----------|---|----------|---|---|-----
droKik1	scf7180000302660:227421-227446 +		ATC--------|----------|--GACATATATATATCTACA----------|----------|----------|------|----------|----------GTGGA-|----------|----------|---|----------|----------|---|----------|---|---|-----
droAna3	scaffold_13047:1059840-1060018 +		GCAACAACAATAACAACAACAACGGTCAGGACTTGACATATACATAAGT-TGCA----ATTTAAG--GAAAAA----|----------|----------|------|----------|----------|----------|----------|----------|----------|---|----------|----------TATATTT---TAATTAACAATATCTATGAATAAAGTTTGCTTCACATTCTGACATTAGTAACGCTATTCAAATTT---AAA--AATTT
droBip1	scf7180000394510:16549-16682 -		AGAACAACA-|-------ACATCGAGCATGATTTGACATATTCTTGATC-AGGATCACCTCCTGAGTTGATATGAGCA----------|----------|----------TGTCCG-TCT------GTCCGTCTGTCTGTCTTGTTCTACGGGAACTAGTCT-CTCAGTTTTAAAGCTATC-----GAC----------|---|----------|----------|---|----------|---|---|-----
droWil2	scf2_1100000004909:1116797-1116868 -		TAC--------|----------|----------|----------|----------|------|------CAGACGAGTCTGCATATCAAA-TTTGATGCTCTAGCTCTTATAGTTCCCGAGATCTC-----CGTCTTTATACA-----|---|----------|----------|---|----------|---|---|-----
droVir3	scaffold_13036:602909-602998 -		ATTCGCAGACT----------TCGCCATATATATATATA----------|----------|----------|------|---CTATTCTAGTAGCTAAATGCCAATTTCGGATTTTCTTTCTCTTATAACTTGCTAGATTT-----|----------|---|----------|----------|---|----------|---|---|-----
droMoj3	scaffold_6495:88582-88632 -		A---------|----------|----------|----------|----------|------|----------|----------A-TTGAAGTCTCTAGCTTTTATATCTTGTGAAATGGA-----CGCGTTCATACAT-----|---|----------|----------|---|----------|---|---|-----

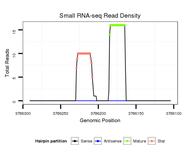
Generated: 09/08/2015 at 07:46 PM

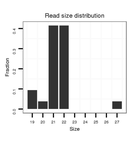
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

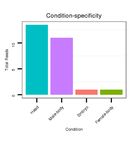
ID	Coordinate	Confidence	Class	Genomic Locale	
der_367	scaffold_4690:3786154-3786241 -	candidate	Canonical miRNA	intron	[View on UCSC Genome Browser (Cotton3.Mitos)]

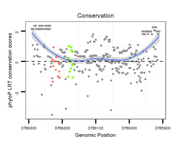
Legend: Genic Intergenic Antisense to the annotated Mismatch/Indel

Predicted structure









Show Alternate Folds

FlyBase annotation

intron:Dmoj\GG004194.sq2

No flyexpalte elements found

Sense Strand Reads

Hide 3p reads | show mid mismatch reads

	Read #	Size	Mismatch	Count	Mismatches	Total	Total	VLST V10K V04K V04C body					MOSS male head	MOSS female body
ATTACTAATTTAAATGAGAAATTTAATGTATTACACATAAACACATATGTGAAAATAAAAG-CACAGTTGTCTGTAGCCGTAA-AATTGCGCTTGGATTAAAAAAA-ATTTC-TCATTGCGACCGTTTGC														
.....	22	0	1	5.00	5	4	0	1	0					
.....	22	0	1	2.00	2	0	0	1	1					
.....	22	0	1	2.00	2	0	2	0	0					
.....	22	0	1	2.00	2	1	0	1	0					
.....	21	0	1	2.00	2	1	0	1	0					
.....	22	0	1	2.00	2	1	0	1	0					
.....	22	1	1	2.00	2	1	0	0	1					
.....	19	0	2	1.50	3	1	2	0	0					
.....	19	0	1	1.00	1	0	0	0	0					
.....	21	0	1	1.00	1	1	0	0	0					
.....	22	0	1	1.00	1	0	0	0	0					
.....	22	1	1	0.69	1	0	1	0	0					

Anti-sense strand reads

TAAGTGGTAAATTCACTCCTTAAATTACCATATGTTGTTGTTGTCATCACTTTTATTTTCCCATGTTGCACAGACTACTGCCGATT-TTACGCCCGACCTTATTTTTTAA-TAATAACGACGCCGTTGCAC | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | Read # | Size | Mismatch | Count | Mismatches | Total | Total | | |
| ********** | | | | | | | | | |

No data available in table

Show Alignment With Reads

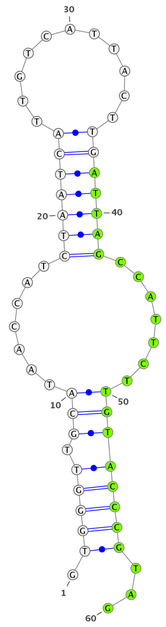
Re-alignment of all predicted orthologs

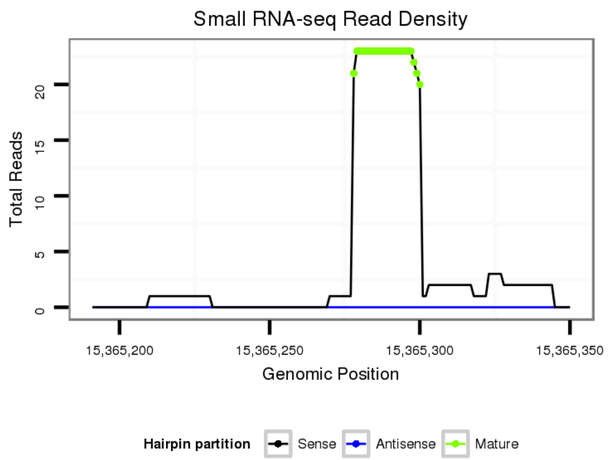
Species Coordinate	ID	Alignment
Gorai.004G194000.2	der_367	
Gorai.004G194000.1		
Gohir.D04G194000.2		
Gohir.D04G194000.1		
Gosti.D04G194000.2		
Gosti.D04G194000.1		
Gaz3		
Gaz2		
Gaz1		
Gaz4		
Gaz5		
Gaz6		
Gaz7		
Gaz8		
Gaz9		
Gaz10		
Gaz11		

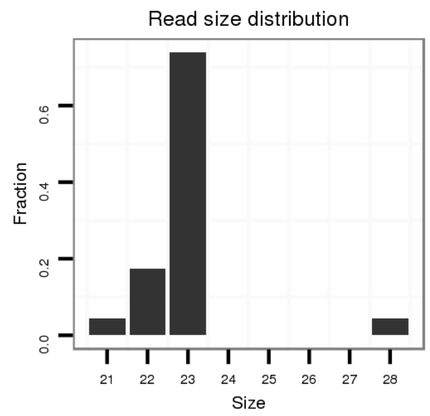
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1320	**scaffold_4929:15365241-15365300 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

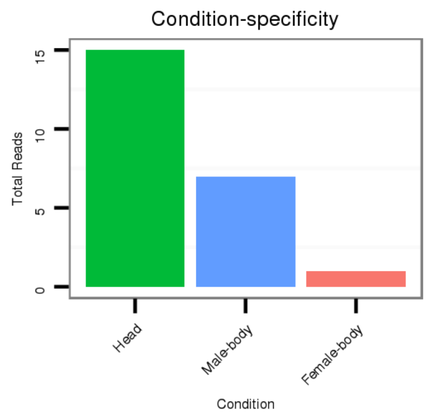
Legend: mature star mismatch in alignment mismatch in read

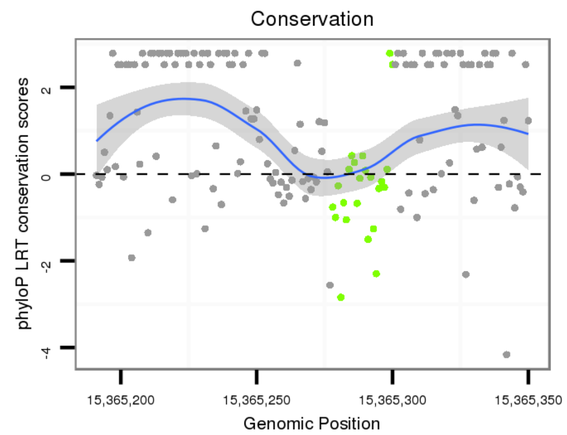
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG10412-in]; CDS [Dere\GG10412-cds]; CDS [Dere\GG10412-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAGGCATTCCCGGGCACACCAACATGATACAAATGCTACTGACACTGAAGGTGGGTTGCATAACCATCTAATCATTGTCATTACTTGATTAGCCATTCTTGTACCCGTAGGTTTCGGGTATTGCCTTCGAGAGGACGGCCGCCTGGAAGAGGCTGCTGGC **********.(((((.(((.......(((((((.....)))))))).....)))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V107 male body	M055 female body	V040 embryo
.....ATTAGCCATTCTTGTACCCGTAG.....	23	0	1	17.00	17	12	5	0	0
.....GGACGGCCGCCTGGAAGAGGCT.....	22	0	1	2.00	2	1	1	0	0
.....TTAGCCATTCTTGTACCCGTAG.....	22	0	1	2.00	2	2	0	0	0
.....ATTAGCCATTCTTGTACCCGTA.....	22	0	1	2.00	2	1	1	0	0
.....CAACATGATACAAATGCTACT.....	21	0	1	1.00	1	0	0	1	0
.....GGTTTCGGGTATTGCCTT.....	18	0	1	1.00	1	1	0	0	0
.....ATTAGCCATTCTTGTACCCGT.....	21	0	1	1.00	1	0	1	0	0
.....ATTACTTGATTAGCCATTCTTGTACCCG.....	28	0	1	1.00	1	0	0	1	0
.....ATTAGCCATTCTTGTACCCGTAA.....	23	1	1	1.00	1	1	0	0	0
.....TTCGGGTATTGCCTTCGAGAGGACG.....	25	0	1	1.00	1	0	0	1	0
.....ATTAGCCATTCTTGTACCCGTAT.....	23	1	1	1.00	1	1	0	0	0

Anti-sense strand reads

TTCCGTAAGGGCCCGTGTGGTTGTACTATGTTTACGATGACTGTGACTTCCACCCAACGTATTGGTAGATTAGTAACAGTAATGAACTTAATCGGTAAGAACATGGGCATCCAAAGCCCATAACGGAAGCTCTCCTGCCGGCGGACCTTCTCCGACGACCG **********.(((((.(((.......(((((((.....)))))))).....)))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V040 embryo	M055 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4929:15365191-15365350 +	der_1320	AAGG-------CATTCCCGGGCACACCAACATGATACAAATGCTACTGACACTGAAGGTGGG-----TTGCATAACCA---TC-TAATCATT---GTCAT-TACTTGATTAG-C----------CATTCTTGT-----------ACCC----GTAGGTTTCGGGTATTGCCTTCGAGAGGACGGCCGCCTGGAAGAGGCTGCTGGC
droYak3	2L:6460708-6460867 -		TAGG-------CATTCCCGGCCACACCAACATGATACAAATGATACTTACACTGAAGGTGGG-----TTGCATAACCA---TC-TAATCATT---GCCAT-TACTCCACTCG-C----------CATTCTTGT-----------GCCG----GCAGGTTTCGGGTATTGCCTTCGAGAAGACGGCCGCCTGGAAGCGCTGCAGGC
droSec2	scaffold_5:4506000-4506159 +		TAGG-------CATTCCCGGCCACACGAACATGATACAAATGATACTAACATGAAGGTGGG-----TTGCATAACCA---TC-TAATCATT---GCCAT-AACTTGACTCG-T----------CATCTTGC-----------CTG----GCAGGTTTCGGGCATTGCCTTCGAGAAGAGTGCCGCCTGGAAGCGGCTGCAGGC
droSim2	2L:6231261-6231420 +		TAGG-------CATTCCCGGCCACACGAACATGATACAAATGATACTAACATGAAGGTGGG-----TTGCATAACCA---TC-TAATCATT---GCCAT-AACTTGACTCG-T----------CATCTTGC-----------ATC----GCAGGTTTCGGGCATTGCCTTCGAGAAGAGTGCCGCCTGGAAGCGGCTGCAGGC
dm3	chr2L:6456815-6456970 +		TCGG-------CATTCCCGGCCACACGAACATGATACAAATGATACTAACACTAAGGTGGG-----TTGCATAACCA---T---TCATT---GGCAT-TACTTAGCTCG-T----------AATCTTGC-----------ATG----GCAGGTTTCGGGCATTGCCTTCGAGAAGACTGCCGCCTGGAAGCGACTGCAAGC
droEug1	scf7180000409463:1879084-1879242 +		TCGG-------CATTCCCGGCCACACCAACATGATACAAATGATACTGACGTTAAAGGTAAG-----TTGCATAACCA---TGATAACCAT-----CAAT-TACTTGACATT-C----------AATTCTTGC-----------ATCG----GCAGGTCTCGGGCATTGGTTTTGAAAAGAGAGGTGCCTGGAAACGGATTCAGGC
droBia1	scf7180000302422:3021953-3022111 -		TGGG-------CATTCCCGGACACACAAACATGATCCAAATGGTGCTCACCTGAAGGTAGG-----TTGCATAACCA---TC-TA-TCATT---TGAGT-AACTTTGCTGA-T----------AACCCCACC-----------ATTC----GCAGGTTTCGGGTATCGCCTTTGAGAAGAGCAGCCGCCTGGAAACGCCTGAGGC
droTak1	scf7180000415858:255296-255453 -		TGGG-------CATTCCCGGCCACACCAACATGATTCAAATGATACTCACCTGAAGGTGGG-----TTATGGCAACCA---TC-CA-TCATT---ACAAT-TACTTACGTGT-C----------AGTCC-TCC-----------AACG----ACAGGTTTCTGGTATTGCCTTCGAGAAGACCGCCGCCTGGAAGCGTCTGCAGGC
droEle1	scf7180000490970:522733-522899 -		TGGG-------CATTCCCGGCCACACCAACATGATACAAATGATACTGACCTGAAGGTGTGTTCCAGTTGCATAACCA---TC-AG-TCGTT---AGTTGTAAACTTGATTGC-T----------AATCCTTCC-----------ACAGC----GCAGGTGTCGGGCATTGCCTTCGAGAAGACAGCCGCCTGGAACGACTGCAGGC
droRho1	scf7180000779524:143833-143991 +		TGGG-------CATTCCCGGGCACACCAACATGATACAAATGATACTCACCTGAAGGTGGG-----TTGCATAACCT---GC-T-GCATT---ACAAC-TACTTGATTCC-C----------AATCCTTCC-----------AACG----TCAGGTTTCGGGTGTGGCCTTCGAGAAGACAGCCGCCTGGAAACGACTGCAGGC
droFic1	scf7180000453973:96263-96421 -		TGGG-------AATTCCGGCCACACGAACATGATCCAAATGATGCTCACCTGAAGGTGGG-----TTGCATAACCC---TC-TA-CCATT---ACAAT-TACTTTACCAC-A----------AATCATCCC-----------AATG----GCAGGTTTCGGGTATCGCCTTCGAGAAGAGTGCCGCCTGGAAACGCCTAGAGGC
droKik1	scf7180000302590:14835-14998 +		TGGG-------CATCGCTGGCCACACCAACATGATCCAAATGATTCTCACCTGAAGGTCAG-----TTGCACAACGAGCGTC-TGTCTTTTGGGGCGCGT-TACTGAATTCA-A----------AATGAATGT-----------GT------ACAGGTTTCCGGCATTGCCTTTGAGAAAACTGCGTCCTGGAAGCGGCTGCAGGC
droAna3	scaffold_12943:2736072-2736229 -		TGGG-------AATTCGTGGACACACGAACATGATACAAATGATACTCACCTGAAGGTTAG-----TTGCATAATCC---AC-TC-CACATT---GCCAG-TAATTGCTTTA-A----------AACGATTTC-----------A-TT----TCAGGTGTCTGGAATCGCATTTGAGAAACGGCAGCATGGAAGAAATAAAGGC
droBip1	scf7180000396535:2133250-2133407 -		TGGG-------AATCGCGTGGCCACACGAACATGATTCAAATGATACTCACCTGAAGGTTAG-----TTGCATAATGC---AC-TC-CAATT---GCCAG-TAATTGATTTA-A----------AACGATTC-----------TGTT----TCAGGTGTCTGGAATAGCTTTTGAGAAAACGGCAGCATGGAAACGAATAAATGC
dp5	4_group1:1507445-1507597 +		GGAG-------CATTCGTGGGCACACGAACATGATACAAATGATACTTACACTAAGGTTAG-----TTGCATAATAA---TG-AGGTGATT---G----A-TATTCACG--T----------CTTCACTTTCTGCG----CCAGGTCTCGGGTGTTGCCTTTGAAAAACAGCCGCCTGGAACGCATACGCGA
droPer2	scaffold_5:3700892-3701044 -		GGAG-------CATTCGTGGGCACACGAACATGATACAAATGATACTTACACTAAGGTTAG-----TTGCATAATAA---TG-AGGTGATT---G----A-TATTCACG--T----------CTTCACTTTCTGCG----CCAGGTCTCGGGTGTTGCCTTTGAAAAACAGCCGCCTGGAACGCATACGCGA
droWil2	scf2_1100000004884:556340-556497 +		TAAG-------CATTCCCGGGCATACGAATATGATTCAAATGTTACTTACACTAAGGTTAG-----TTGCATAACAA---AA-A-------TA-----TACACGCTATA-G----------AA--GTCTC-ATTTC---TTCTGGTTCTTAAGGTCTCTGGCATAGCCTTTGAAAAACGGCTTCTTGGAAGCGACTCATGGC
droVir3	scaffold_12963:5157189-5157347 -		GGCG-------GTGCCCGGCCATACCAACATGATACAAATGTTGCTCACACTGAAGGTTAG-----TTGCATAACTT---TA-----ATT---GGCGT-AGC-------C-CTTGACCGGCTTTTCTTAACTAT--------GCAC----TTAGGTGTCTGGCATTGCGTTTGAGAAACGCAGCCTGGAAGCGTTTAAAGGC
droMoj3	scaffold_6500:17436242-17436406 +		GGGCTGCCTACTGTGCGTGGGCCAACAAATATGATACAAATGTTGCTCACGCTCAAGGTTAG-----TTGCATAACCA---TC-A-----TT---G----A------AATAAGAAACGAACAGCT--------AATTAAACTACTATC----TTAGGTATCTGGCATTGCATTCGAGAAAACTGCAGCCTGGAAGCGCATTCGAGC
droGri2	scaffold_15252:7819654-7819812 -		CATC-------TGTTCGTGGACACACCAATATGATACAAATGCTGCTTACCTAAGGTTAGTGGTCACTGCATAATCA---AT-CATTCATC---A-----A-GCTCCCTA--T----------ATCCTAATCCTTCA----TCAGGTCTCGGGTATTGCGTTTGAGAAAACAGCTGCCTGGAAGCGAATTCGTGC

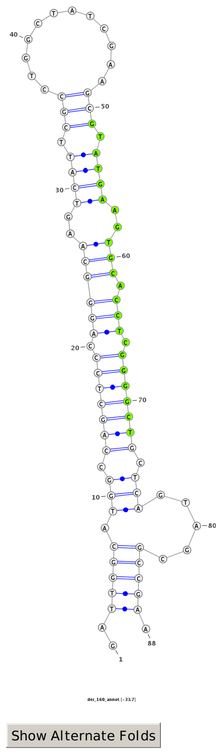
Generated: 09/08/2015 at 10:32 PM

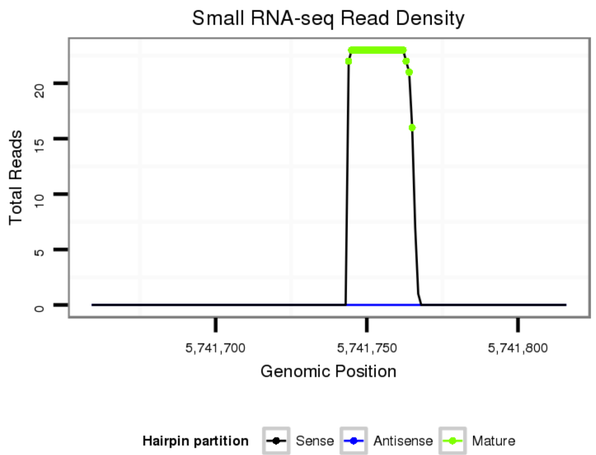
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

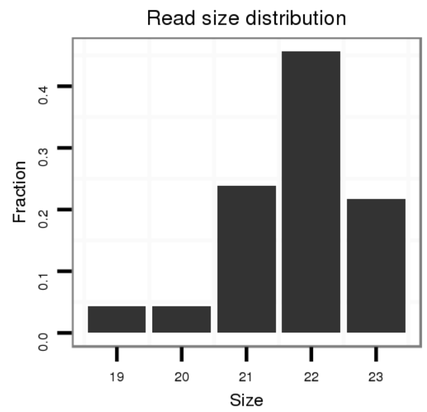
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_160	**scaffold_4784:5741709-5741766 +**	**candidate**	**Canonical miRNA**	**antisense_to_CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

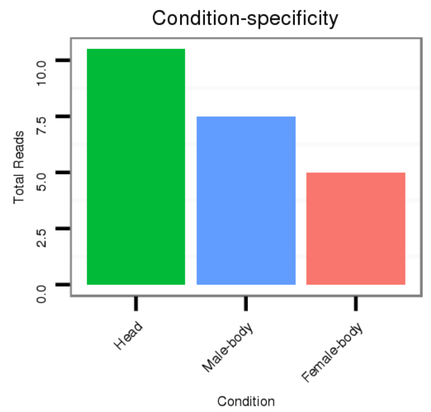
Legend: mature star mismatch in alignment mismatch in read

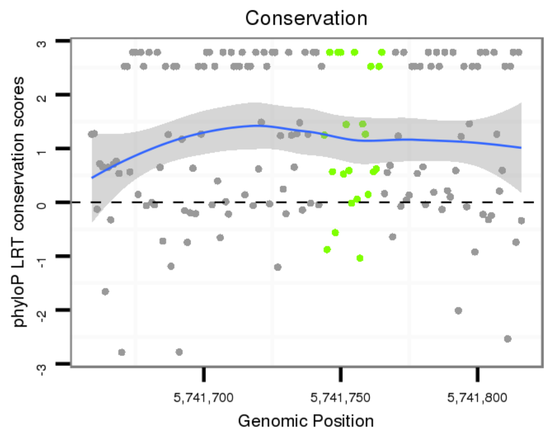
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to CDS [Dere\GG14297-cds]; Antisense to utr5 [utr5_plus_7189]

No Repeatable elements found

mature	star
1. der_166 scaffold_4784:5737030-5737051 + 2. der_160 scaffold_4784:5741744-5741765 +	

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTCTTTACCTGGGGGAAGACAATTAGAGAGGGCGTGATTGGCATGGCCAGCTCCCAGGGCAAGTCATTCGCCTGGCTATCGAAGCGTATGAAGTGCACCTCGGGGCTGCTCAGTAGCGCCGAAACCTGCAGAAATGCTTGGGATAGAACGGCGGACAG						V108	V107	M055			V060
**********..((((((.(((.(((((((.((((((..((((.(((.....)))).)))))..))))..)))).)))))))..)))).....))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	head	male body	female body	embryo	head
.....GTATGAAGTGCACCTCGGGGCT.....	22	0	2	9.50	19	10	8	1	0	0
.....GTATGAAGTGCACCTCGGGGCTG.....	23	0	2	5.00	10	3	2	5	0	0
.....GTATGAAGTGCACCTCGGGGC.....	21	0	2	5.00	10	5	3	2	0	0
.....TATGAAGTGCACCTCGGGGCTG.....	22	0	2	1.00	2	1	1	0	0	0
.....GTATGAAGTGCACCTCGGGG.....	20	0	2	1.00	2	0	0	2	0	0
.....GTATGAAGTGCACCTCGGGGCTGC.....	24	0	2	1.00	2	2	0	0	0	0
.....GTATGAAGTGCACCTCGGG.....	19	0	2	1.00	2	1	1	0	0	0
.....CTTGGGATAGAACGGCGGACA.	21	0	2	0.50	1	0	0	1	0	0
.....TATGAAGTGCACCTCGGGGCT.....	21	0	2	0.50	1	1	0	0	0	0
GTCTTTACCTGGGGGAAGACA.....	21	0	2	0.50	1	0	1	0	0	0
.....GTATGAAGTGCACCTCGGGGCTGA.....	24	1	2	0.50	1	0	0	1	0	0
.....GTATGAAGTGCACCTCGGTTT.....	20	2	2	0.50	1	0	1	0	0	0
.....GCTCAGTAGCGCCGAAACCTG.....	21	0	2	0.50	1	0	0	1	0	0

Anti-sense strand reads

CAGAAATGGACCCCCTTCTGTTAATCTCTCCCGCACTAACCGTACCGGTCGAGGGTCCCGTTCAGTAAGCGGACCGATAGCTTCGCATACTTCACGTGGAGCCCCGACGAGTCATCGCGGCTTTGGACGTCTTTACGAACCCTATCTTGCCGCCTGTC						M055	V107	V108	M057	V040
**********..((((((.(((.(((((((.((((((..((((.(((.....)))).)))))..))))..)))).)))))))..)))).....))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	female body	male body	head	embryo	embryo
.....CCGTTCAGTAAGCGGACCGATA.....	22	0	2	0.50	1	0	0	0	1	0
..GAAATGGACCCCCTTCTGTTA.....	21	0	2	0.50	1	0	1	0	0	0
.....CGTTCAGTAAGCGGACCGATA.....	21	0	2	0.50	1	1	0	0	0	0
.....GGACCGATAGCTTCGCATACT.....	21	0	2	0.50	1	1	0	0	0	0
.....GGTCGAGGGTCCCGTTCAGTA.....	21	0	2	0.50	1	0	1	0	0	0
.....CGAGTCATCGCGGCTTTGGACGTCTT.....	26	0	2	0.50	1	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4784:5741659-5741816 +	der_160	GTCTTTACCTGGGGGAAGACAATTAGAGAGGGCGTGATTGGCATGGCCAGCTCCCAGGGCAAGTCATTCGCCTGGCTATCGAAGCGTATGAAGTGCACCTCGGGGCTGCTCAGTAGCGCCGAAACCTGCAGAAATGCTTGGGATAGAACGGCGGACAG
droYak3	3L:3604368-3604525 +		GTCTTTGCCTGCGGGAAGACAATTAGAGACGGCGTAATGGCATGGCTAGCTCCCAGGGCAGATCATTCGACTGGCTATCGAAGCGTACGAAGTGCACCTCGGGGCTACTGAGTAGCGCCGAAACCTGCAGAAATGCTTGGGACAGAACGGCGGACAA
droSec2	scaffold_0:575588-575745 -		GTCTTTGCCTGGGGGAAGACAATAGAGAGGGCGTGATTGGCATAGCCAGCTCCCAGGGCAGATCATTAGCCTGGCTATCGAAGCGTACGAAGTGCACCTCGGGGCTGCGAGTAGCGCCGAAACCTGCAGAAATGCTTGGGATAGAACGGCGGACAG
droSim2	3l:8099237-8099394 -		CTCTTTGCCTGGGGGAAGACAATTAGAGACGGCGTGATTGGCATAGCCAGCTCCCAGGGCAGATCATTAGCCTGGCTATCGAAACGTACGAAGTGCACCTCGGGGCTGCGAGTAGCGCCGAAACCTGCAGAAATGCTTGGGATAGAACGGCGGACAG
dm3	chr3L:8294860-8295017 -		CTCTTTGCCTGGGGGAAGACAATTAGAGACGGCGTGGTTGGCATGGCCAACTCCCAGGGCAGATCATTAGCCTGGCTATCGAAGCGTACAAGTGCACCTCGGGGCTGCGCAGCAGCGCCGAAACCTGCAGAAATGCTTGGGATAGAACGGCTGACAG
droEug1	scf7180000409524:350464-350621 +		GGCTTTGATTGAGGGAAGACGATCAGCGATGGAGTGATCGGCATAGCCAATTCCCAGGGCAGATCATTAGCCTTGCTATCGAAGCGTACAAAGTGCACTTCAGGACTGCTTAGTAGCGCCGAAACCTGTAGCAACGCTTGCGACAAAAGTGCTGATAA
droBia1	scf7180000302428:10235653-10235810 -		GGCTTTGGCCTGGGGAAAGACGACGCAGCGAGGGCGAGATCGGCATGGCCAGTTCCCAGGGCAGATCATTAGCCTGGCCGTCGAAGCGCACAAAGTGCACCTCGGCAGCTGCTGAGCAGCGCCGAAACCTGCAGCGAACGGCTGCGACAAAACGCCTGATAA
droTak1	scf7180000415862:394638-394795 -		GGCTTTGGCCCGCGGGAAGACAATCAGCGAGGGCGACATTGGCATGGCCATTCCCAGGGCAGATCGTTCGCCTGGCTATCGAAGCGCACGAAGTGCAACTCGGCAGCTGCTGAGTAGCGCCGAAACCTGCAGCGAATGCCTGCGACAGAACGGCGGATAG
droEle1	scf7180000491268:398468-398625 +		GGCTTTGCCTGCGGGAAGACAATCAGCGACGGCGAGATCGGCATGGCCAGTTCCCAGGGCAGATCGTTGGCCTGGCTATCGAAGCTACGAAGTGCAGTTCGGCGCTGCTCAGTAGCGCCGAAACCTGCAGCGAAGCGTTGCGACAAAACGCCAGATAG
droRho1	scf7180000767967:155453-155610 -		GGCTTTGTCCTGCGGGAAGACAATCAGTGACGGCGAGATCGGCATGGCCAGTTCCCAGGGCAGATCGTTCGCTTGGCTATCGAAGCTACAAAGTGCACCTCGGGGCTGCTGAGTAGCGCCGAAACCTGCAGCGAAAGCTTGCGACAAAACGCCGGATAA
droFic1	scf7180000453833:464593-464750 -		GGCTTTGACTGAGGGAAGACAATCAACGAGGGTGTTGTCGGCATGGCCAGTTCCCAGGGCAGATCGTTCGGACTGACTGTCGAAGCGCACGAAGTGCACCTCGGGGCTGCTGAGCAGAGCCGAAACTTGCGAGCAAAGCTTGCTGACAGAACGGCAGACAA
droKik1	scf7180000302351:80721-80878 +		GGCTTTGTTTGCGGGAACACAATCAGCGAGGGCGAGATCGGCATGGCCAGTTCCCAGGGTAGATCGTTATTTTGGCTGTCAAAGCGGACAAAGTGCACCTCGGGGCTGCTGAGAAGAGCCGAAACCTGCAGCGAAGGCTGCGATAATACGGCGGATAA
droAna3	scaffold_13337:19860722-19860879 -		GGCTTGGTTCTAGGAAAGACAATCAGCGAGGGTGATATTGGCATGGCTAGTTCCCAGGGCAGATCGTTCGCTTGACTGTCGAATCCGGATGAAGTGCACTTCGGGGCTGCTGAGCAAAGCCGTAACCTGCAACAAGCGTTGCGACAGAACAGCAGATAA
droBip1	scf7180000395962:145271-145428 -		GGCTTAGTTTTAGGAAAGACTATCAGCGAGGGGCGATATTGGCATGGCTAGCTCCCAGGGCAGATCGTTCGCTTGACTATCAAATCGGATGAAGTGACACCTCGGGGCTGCTGAGCAAAGCCGTGACCTGCAAGAAGCGCTTGGGATAGCAGAGGAGACAA
dp5	XR_group3a:20674-20831 +		GGACGCGTTTCCGGAAAGACAACGCAGAGAGGGCGACGAGCGGCATGGAGAACTCCCATGGCAAGATCGTTCGCCTGGCTGTCAAAGCGTATGAAATTTAGGCTTGGACTGGTGAGCAACGCCGACACCTGCAGAAATGCTTGAGATAGTACGGCGGACAA
droPer2	scaffold_23:21401-21558 +		GGACGCGTTTCCGGAAAGACAACGCAGAGAGGGCCAGAGCGGCATGGAGAAGTCCCATGGCAAGATCGTTCGCCTGGCTGTCAAAGCGTATGAAATTTAGGCTTGGACTGGTGAGCAACGCCGACACCTGCGAGAAATGCTTGAGATAGTACGGCGGACAA
droWil2	scf2_1100000004511:2255389-2255546 -		GGATTGGATTGGGGAAAACAATGAGAGCAGGAGTTTCCGGCATAGATAGTCCCAGGGTAGATCATTCGCCTGGCTATCGAAACGTATGAATGTAGATCCGGACTCTTCAGCAATGCCGAAACTTGCGAGAAAGGCCTGCGACAGCAGTGGCTGATAA
droVir3	scaffold_13049:7404931-7405088 +		GGTCGAGATTGTGGAAACAGCAGTAGCGCTGGTGACGCCGGCATAGTCAGTTCCCAGGGCAAATCGTTTGGTTGGCTATCGAAGCGCAATAAAGCTCAGTTCGGGACTGCGTAACATAGCTGCCACTTGCATCAGCTCGTTGACATCACGGCCGAGAG
droMoj3	scaffold_6680:5659718-5659875 +		GGACGCGATTGGGGAAAGACGACGCAGCGCCGGCGTCACTGACATAGTTAGCTCCCAAGGCAAATCGTTTGCCTGGCTATTAAAGCGTATAAAATTCACATGGGACTTCGTAAGAAAGCTGCTACTTGCATCACTTCTTGGGACATAATGGCGGAGAG
droGri2	scaffold_15110:5473448-5473605 -		GGTCGAGATTGGGGAAACACAACAATGCTGGCGTCTCCGGCATGGTAAGCTCCCAGGGCAAATCATTTGGCTTGGCTATCGAACCGTATAAAATTCAGTTCGGGACTGCGCAACAGAGCTGCCACCTGCATCAGCTCCAGTGACATCACGGCAGACAA

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

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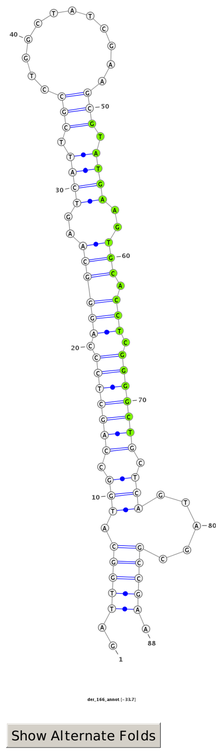
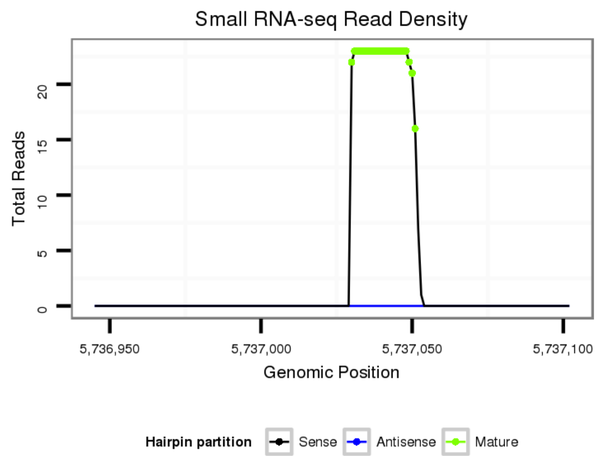
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

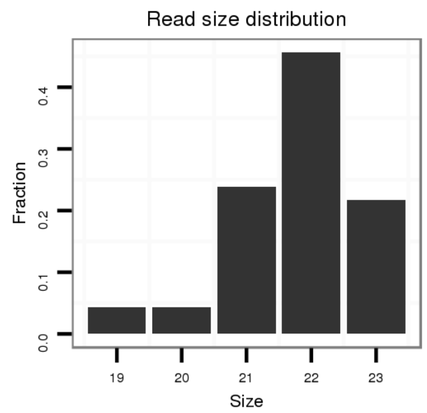
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_166	**scaffold_4784:5736995-5737052 +**	**candidate**	**Canonical miRNA**	**antisense_to_CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

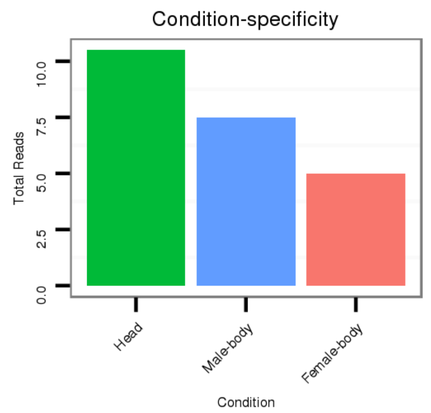
Legend: mature star mismatch in alignment mismatch in read

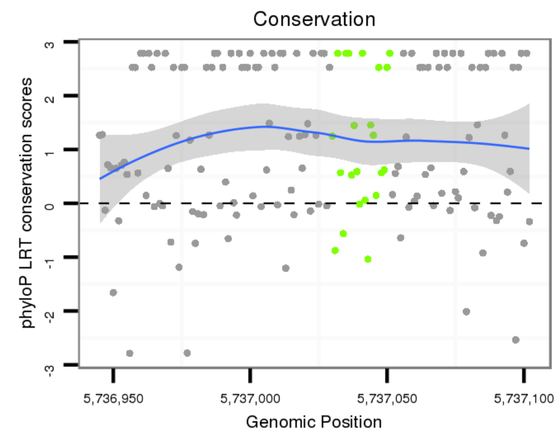
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to CDS [Dere\GG14298-cds]; Antisense to utr3 [utr3_plus_4073]

No Repeatable elements found

mature	star
1. der_166 scaffold_4784:5737030-5737051 + 2. der_160 scaffold_4784:5741744-5741765 +	

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTCTTTACCTGGGGGAAGACAATTAGAGAGGGCGTGATTGGCATGGCCAGCTCCCAGGGCAAGTCATTCGCCTGGCTATCGAAGCGTATGAAGTGCACCTCGGGGCTGCTCAGTAGCGCCGAAACCTGCAGAAATGCTTGGGATAGAACGGCGGACAG **********..((((((.(((.(((((((.((((((..((((.(((.....)))).)))))..))))..)))).)))))))..)))).....))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V107 male body	M055 female body	M057 embryo	V060 head
.....GTATGAAGTGCACCTCGGGGCT.....	22	0	2	9.50	19	10	8	1	0	0
.....GTATGAAGTGCACCTCGGGGC.....	21	0	2	5.00	10	5	3	2	0	0
.....GTATGAAGTGCACCTCGGGGCTG.....	23	0	2	5.00	10	3	2	5	0	0
.....TATGAAGTGCACCTCGGGGCTG.....	22	0	2	1.00	2	1	1	0	0	0
.....GTATGAAGTGCACCTCGGGGCTGC.....	24	0	2	1.00	2	2	0	0	0	0
.....GTATGAAGTGCACCTCGGG.....	19	0	2	1.00	2	1	1	0	0	0
.....GTATGAAGTGCACCTCGGGG.....	20	0	2	1.00	2	0	0	2	0	0
.....TATGAAGTGCACCTCGGGGCT.....	21	0	2	0.50	1	1	0	0	0	0
.....CTTGGGATAGAACGGCGGACA.	21	0	2	0.50	1	0	0	1	0	0
.....GTATGAAGTGCACCTCGGTT.....	20	2	2	0.50	1	0	1	0	0	0
.....GCTCAGTAGCGCCGAAACCTG.....	21	0	2	0.50	1	0	0	1	0	0
.....GTATGAAGTGCACCTCGGGGCTGA.....	24	1	2	0.50	1	0	0	1	0	0
GTCTTTACCTGGGGGAAGACA.....	21	0	2	0.50	1	0	1	0	0	0

Anti-sense strand reads

CAGAAATGGACCCCCTTCTGTTAATCTCTCCCGCACTAACCGTACCGGTCGAGGGTCCCGTTCAGTAAGCGGACCGATAGCTTCGCATACTTCACGTGGAGCCCCGACGAGTCATCGCGGCTTTGGACGTCTTTACGAACCCTATCTTGCCGCCTGTC **********..((((((.(((.(((((((.((((((..((((.(((.....)))).)))))..))))..)))).)))))))..)))).....))))).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	V107 male body	V108 head	M057 embryo	V040 embryo
.....CCGTTCAGTAAGCGGACCGATA.....	22	0	2	0.50	1	0	0	0	1	0
.....CGTTCAGTAAGCGGACCGATA.....	21	0	2	0.50	1	1	0	0	0	0
.....GGTCGAGGGTCCCGTTCAGTA.....	21	0	2	0.50	1	0	1	0	0	0
.....GGACCGATAGCTTCGCATACT.....	21	0	2	0.50	1	1	0	0	0	0
.....CGAGTCATCGCGGCTTTGGACGTCTT.....	26	0	2	0.50	1	1	0	0	0	0
..GAAATGGACCCCCTTCTGTTA.....	21	0	2	0.50	1	0	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4784:5736945-5737102 +	der_166	GTCTTTACCTGGGGGAAGACAATTAGAGAGGGCGTGATTGGCATGGCCAGCTCCCAGGGCAAGTCATTCGCCTGGCTATCGAAGCGTATGAAGTGCACCTCGGGGCTGCTCAGTAGCGCCGAAACCTGCAGAAATGCTTGGGATAGAACGGCGGACAG
droYak3	3L:3604368-3604525 +		GTCTTTGCCTGCGGGAAGACAATTAGAGACGGCGTAATGGCATGGCTAGCTCCCAGGGCAGATCATTCGACTGGCTATCGAAGCGTACGAAGTGCACCTCGGGGCTACTGAGTAGCGCCGAAACCTGCAGAAATGCTTGGGACAGAACGGCGGACAA
droSec2	scaffold_0:575588-575745 -		GTCTTTGCCTGGGGGAAGACAATAGAGAGGGCGTGATTGGCATAGCCAGCTCCCAGGGCAGATCATTAGCCTGGCTATCGAAGCGTACGAAGTGCACCTCGGGGCTGCGAGTAGCGCCGAAACCTGCAGAAATGCTTGGGATAGAACGGCGGACAG
droSim2	3l:8099237-8099394 -		GTCTTTGCCTGGGGGAAGACAATTAGAGACGGCGTGATTGGCATAGCCAGCTCCCAGGGCAGATCATTAGCCTGGCTATCGAAACGTACGAAGTGCACCTCGGGGCTGCGAGTAGCGCCGAAACCTGCAGAAATGCTTGGGATAGAACGGCGGACAG
dm3	chr3L:8294860-8295017 -		GTCTTTGCCTGGGGGAAGACAATTAGAGACGGCGTGGTTGGCATGGCCAACTCCCAGGGCAGATCATTAGCCTGGCTATCGAAGCGTACAAGTGCACCTCGGGGCTGCGCAGCAGCGCCGAAACCTGCAGAAATGCTTGGGATAGAACGGCGTGACAG
droEug1	scf7180000409524:350464-350621 +		GGCTTTGATTGAGGGAAGACGATCAGCGATGGAGTGATCGGCATAGCCAATTCCCAGGGCAGATCATTAGCCTTGCTATCGAAGCGTACAAAGTGCACTTCAGGACTGCTTAGTAGCGCCGAAACCTGTAGCAACGCTTGCGACAAAAGTGCTGATAA
droBia1	scf7180000302428:10235653-10235810 -		GGCTTTGGCCTGGGGAAAGACGACGCAGCGAGGGCGAGATCGGCATGGCCAGTTCCCAGGGCAGATCATTAGCCTGGCCGTCGAAGCGCACAAAGTGCACCTCGGCAGCTGCTGAGCAGCGCCGAAACCTGCAGCGAACGGCTGCGACAAAACGCCTGATAA
droTak1	scf7180000415862:394638-394795 -		GGCTTTGGCCCGCGGGAAGACAATCAGCGAGGGCGACATTGGCATGGCCATTCCCAGGGCAGATCGTTCGCCTGGCTATCGAAGCGCACGAAGTGCAACTCGGCAGCTGCTGAGTAGCGCCGAAACCTGCAGCGAATGCCTGCGACAGAACGGCGGATAG
droEle1	scf7180000491268:398468-398625 +		GGCTTTGCCTGCGGGAAGACAATCAGCGACGGCGAGATCGGCATGGCCAGTTCCCAGGGCAGATCGTTGGCCTGGCTATCGAAGCTACGAAGTGCAGTTCGGCGCTGCTCAGTAGCGCCGAAACCTGCAGCGAAGCGTTGCGACAAAACGCCAGATAG
droRho1	scf7180000767967:155453-155610 -		GGCTTTGTCCTGCGGGAAGACAATCAGTGACGGCGAGATCGGCATGGCCAGTTCCCAGGGCAGATCGTTCGCTTGGCTATCGAAGCTACAAAGTGCACCTCGGGGCTGCTGAGTAGCGCCGAAACCTGCAGCGAAAGCTTGCGACAAAACGCCGGATAA
droFic1	scf7180000453833:464593-464750 -		GGCTTTGACTGAGGGAAGACAATCAACGAGGGTGTTGTCGGCATGGCCAGTTCCCAGGGCAGATCGTTCGATGACTGACTGTCGAAGCGCACGAAGTGCACCTCGGGGCTGCTGAGCAGAGCCGAAACTTGCGAGCAAAGCTTGCTGACAGAACGGCAGACAA
droKik1	scf7180000302351:80721-80878 +		GGCTTTGTTTGCGGGAACACAATCAGCGAGGGCGAGATCGGCATGGCCAGTTCCCAGGGTAGATCGTTATTTTGGCTGTCAAAGCGGACAAAGTGCACCTCGGGGCTGCTGAGAAGAGCCGAAACCTGCAGCGAAGGCTGCGATAATACGGCGGATAA
droAna3	scaffold_13337:19860722-19860879 -		GGCTTGGTTCTAGGAAAGACAATCAGCGAGGGTGATATTGGCATGGCTAGTTCCCAGGGCAGATCGTTCGCTTGACTGTCGAATCCGGATGAAGTGCACTTCGGGGCTGCTGAGCAAAGCGGTAACCTGCAACAAGCGTTGCGACAGAACAGCAGATAA
droBip1	scf7180000395962:145271-145428 -		GGCTTAGTTTTAGGAAAGACTATCAGCGAGGGGCGATATTGGCATGGCTAGCTCCCAGGGCAGATCGTTCGCTTGACTATCAAATCGGATGAAGTGACACCTCGGGGCTGCTGAGCAAAGCGGTGACCTGCAAGAAGCGCTTGGGATAGCAGAGGAGACAA
dp5	XR_group3a:20674-20831 +		GGACGCGGTTCCGGAAAGACAACGCAGAGAGGGCGACGAGCGGCATGGAGAACTCCCATGGCAAGATCGTTCGCCTGGCTGTCAAAGCGTATGAATTTAGCGCTTGGACTGGTGAGCAACGCCGACACCTGCAGAAATGCTTGATGATAGTACGGCGGACAA
droPer2	scaffold_23:21401-21558 +		GGACGCGGTTCCGGAAAGACAACGCAGAGAGGGCGAGCGGCATGGAGAACTCCCATGGCAAGATCGTTCGCCTGGCTGTCAAAGCGTATGAATTTAGCGCTTGGACTGGTGAGCAACGCCGACACCTGCAGAAATGCTTGATGATAGTACGGCGGACAA
droWil2	scf2_1100000004511:2255389-2255546 -		GGATTTGGATTGGGGAAAACAATGAGAGCAGGAGTTTCCGGCATAGATAGTTCCCAGGGTAGATCATTCGCCTGGCTATCGAAACGTATGAATGTAGATCCGGACTCTTCAGCAATGCCGAAACTTGCGAGAAACGGCTGCGACAGCAGTGGCTGATAA
droVir3	scaffold_13049:7404931-7405088 +		GGTCGAGATTGTGGAAACAGCAGTAGCGCTGGTGACGCCGGCATAGTGAGTTCCCAGGGCAAATCGTTTGGTTGGCTATCGAAGCGAATAAAGCTGAGTTCGGGACTGCGTAACATAGCTGCCACTTGCATCAGCTGCTGTTGACATCACGGCCGAGAG
droMoj3	scaffold_6680:5659718-5659875 +		GGACGCGATTGGGGAAAGACGACGCAGCGCCGGCGTCACTGACATAGTTAGCTCCCAAGGCAAATCGTTTGCCTGGCTATTAAAGCGTATAAAATTCACATGGGACTTCGTAAGAAAGCTGCTACTTGCATCACTTCTTGGGACATAATGGCGGAGAG
droGri2	scaffold_15110:5473448-5473605 -		GGTCGAGATTGGGGAAACACAACAATGCTGGCGTCTCCGGCATGGTAAGCTCCCAGGGCAAATCATTTGGCTTGGCTATCGAACCGTATAAAATTCAGTTCGGGACTGCGCAACAGAGCTGCCACCTGCATCAGCTCCAGTGACATCACGGCAGACAA

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

	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
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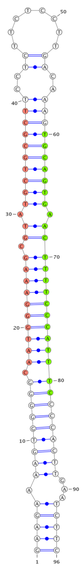
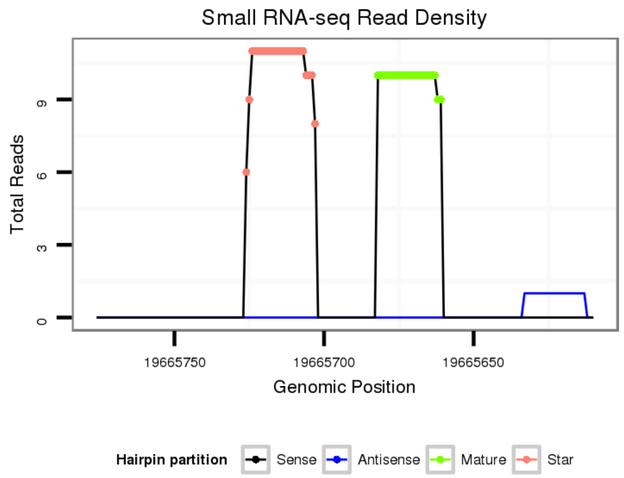
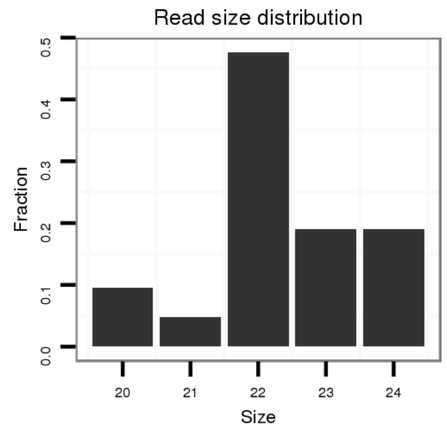
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_97	**scaffold_4929:19665660-19665726 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

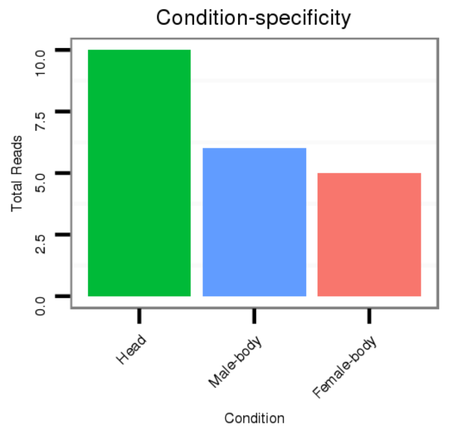
Legend: mature star mismatch in alignment mismatch in read

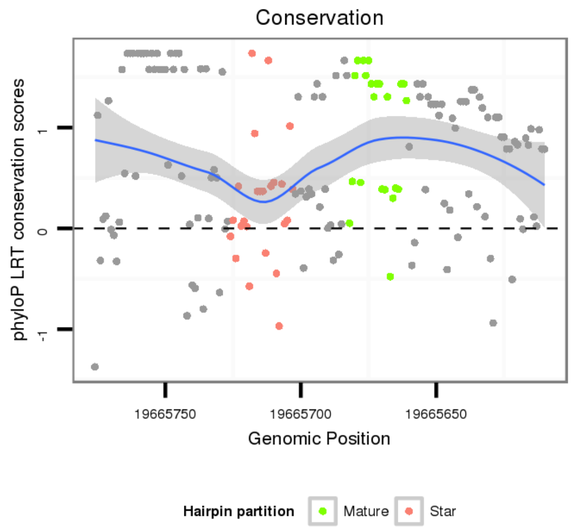
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

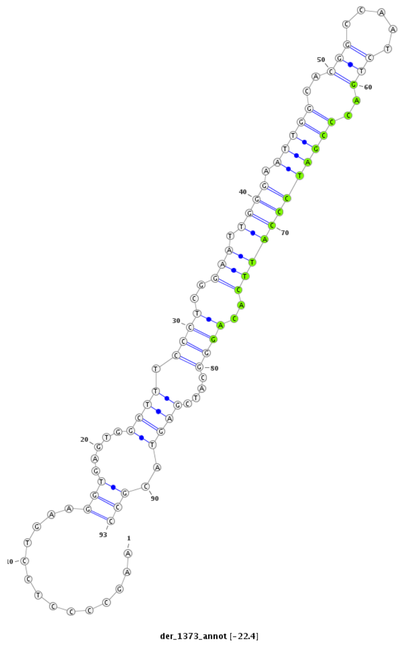
hide 3p reads | show mid mismatch reads

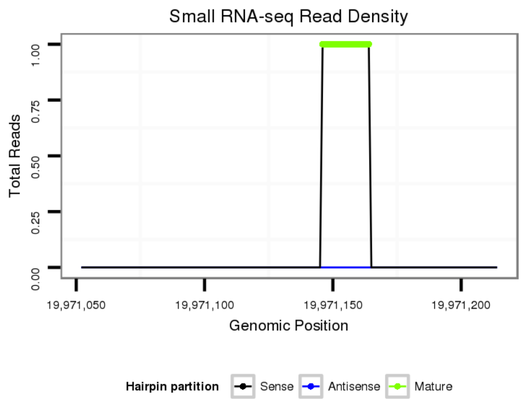
| | | |

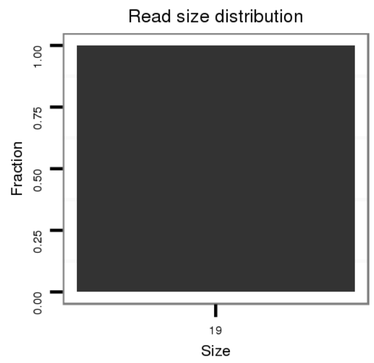
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1373	**scaffold_4929:19971102-19971164 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

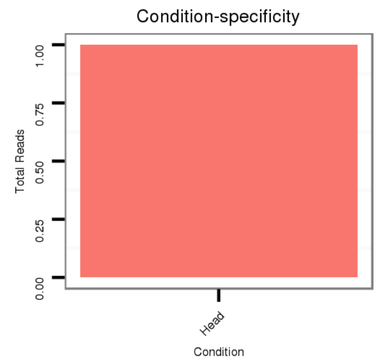
Legend: mature star mismatch in alignment mismatch in read

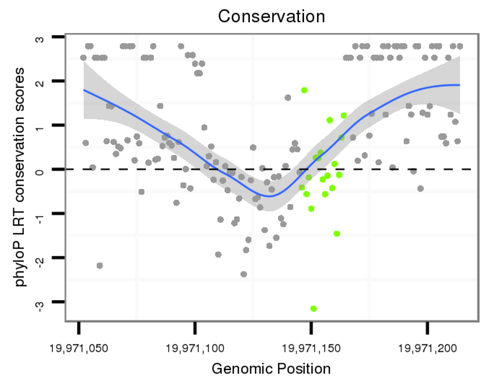
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG10812-in]; CDS [Dere\GG10812-cds]; CDS [Dere\GG10812-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CCTACGCGGGCAACAGCTTCATCTGCCCCGAACTGAAGCCCCTCCTGAAGGTGAGTGCTCCTGAAGGTGAGTGGCTTTCCCTCGGAATTGGGAATTGGCACGGCCAATCTGACCCGATCCCATTCACAGGGCATCGAGTACGCCGACTCGTTCAACACCAATCCCAACAAATGGCTGCT						V108	V060	V107	M055	
************************************..............(((.....((((.(((((..(((.((((.((((((..(((.....)))).)))))))))))..))))....)))))..)))************************************	Read size	# Mismatch	Hit Count	Total Norm	Total	head	head	male body	female body	
....TGACCCGATCCCATTCACAGT.....	21	1	1	12.00	12	9	2	1	0	
....GACCCGATCCCATTCACAG.....	19	0	1	1.00	1	1	0	0	0	

Anti-sense strand reads

GGATGCGCCCGTTGTCGAAGTAGACGGGGCTTGACTTCGGGGAGGACTTCCACTCACCGAAAGGGAGCCTTAACCCTTAACCGTGCCGGTTAGACTGGGCTAGGGTAAGTGTCCCGTAGCTCATGCGGCTGAGCAAGTTGTGGTTAGGGTTGTTTACCGACGA					M055 female body	V107 male body	
************************************..............(((.....((((.(((((..(((.((((.((((((..(((.....)))).)))))))))))..))))....)))))..)))************************************	Read size	# Mismatch	Hit Count	Total Norm	Total			

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4929:19971052-19971214 +	der_1373	CCTACGCGGGCAACAGCTTCATCTGCCCCGAACTGAAGCCCCTCCTGAAGGTGAGTG-----GCT-T----TCCCTCG-------GAATT----------GGG----------A----------ATT-GGCAC-GGCC----------AATCTGACCCGATCCC--ATTCACAGGGCATCGAGTACGCCGACTCGTTCAACACCAATCCCAACAAATGGCTGCT
droYak3	2L:15318007-15318160 -		CCTACGCGGGCAACAGCTTCATCTGCCCCGAACTGAAGCCCCTCCTGAAGGTGAGTG-----GCT-GGCACTAGCATG-------GC----------
droSec2	scaffold_1:238989-239142 -		CCTACGCTGGCAACAGCTTCATCTGCCCCGACCTGAAGCCGCTCCTGAAGGTGAGTG-----GCA-T----GCCCACG-------GCAT---------
droSim2	2rr:3437179-3437332 -		CCTACGCGGGCAACAGCTTCATCTGCCCCGACCTGAAGCCGCTCCTGAAGGTGAGTG-----GCA-T----GCCCACG-------GCC----------
dm3	chr2R:2574809-2574962 -		CCTACGCGGGCAACAGCTTCATCTGCCCCGACCTGAAGCCGCTCCTGAAGGTGAGTG-----GTA-T----TCCCACG-------GCA----------
droEug1	scf7180000409462:3446770-3446919 -		CCTATGCGCGGCAACAGCTTATCTGCCCCGACCTGAAGCCCCTCCTAAAGGTGAGTG-----GCT-T----TCCCAGA-------GC----------
droBia1	scf7180000302292:3577289-3577452 +		CCTATGCGGGGCAACAGCTTCATCTGCCCCGACCTGAAGCCCCTCCTGAAGGTGAGTG-----GCT-T----TCCCAGG-------GCACA----------
droTak1	scf7180000413887:28403-28560 +		CCTATGCGGGGCAACAGCTTCATCTGTCCCGAACTGAAGCCCCTCCTGAAGGTGAGAGCAAGGTGAATT----CCCCGGA-------AAT----------
droEle1	scf7180000491217:440544-440708 +		CCTACGCGGGGCAACAGCTTCATCTGCCCCGACCTGAAGCCCCTCCTGAAGGTGAGTG-----GAT-T----TGCGGGA-------GAAGT----------
droRho1	scf7180000766409:461982-462136 -		CCTATGCGCGGAAACAGCTTCATCTGCCCCGACCTGAAGCCCCTGCTCAAGGTGAGTG-----GCT-T----TCCCAGA-------TTC----------
droFic1	scf7180000453955:727418-727585 +		CCTATGCGCGGCAACAGCTTCATCTGCCCCGACCTGAAGCCGTCCTAAAGGTGAGTG-----GGA-T----TCCAAAA-------GG-GA----------
droKik1	scf7180000302470:137676-137840 -		CCTATGCGGGGCAACAGCTTTATCTGCCCCGACCTGAAGCCGCTCCTGAAGGTGACAC-----------------------------CAGCCCAGCTTCCAAGCATCTCAAAGCCCCTCCT---C----------
droAna3	scaffold_13266:18445008-18445107 +		CCTACGCCGGCAACTCCTTCATTCTGCCCGAGATGCGGGTGTTCT----------
droBip1	scf7180000396568:1541803-1541902 -		CCTACGCTGGCTCTGCCTTCATTGTCCCCGAGTACCGCGACCTGATGA---------
dp5	3:840230-840382 -		CCTATGCGGGCAACAGCTTCATCTGTCCCGAGCTCAAGCCGCTCCTGAAGGTAGGTA-----CTC-C----TATCCCG-------GC----------
droPer2	scaffold_2:1016163-1016315 -		CCTATGCGGGGCAACAGCTTCATCTGTCCCGAGCTCAAGCCGTCCTGAAGGTAGGTA-----CTC-C----TATCCCG-------GC----------
droWil2	scf2_1100000004954:1990464-1990645 +		GTTATGCTGGTAATAGTTCATCTGTCCTGAACTGAACCCTCTTTGAAGGTAAGTG-----GCA-A----AGAAAGA-------AA-CA----------
droVir3	scaffold_12875:15457404-15457573 -		CCTATGCGGGGCAACAGTTCATCTGTCCCGAGCTGAAGCCCCTCTCAAGGTAATAA-----TAT-A----TAATCAG-------------------------------ATATCCGTCTACCT-ATACACA----------
droMoj3	scaffold_6496:8338738-8338945 +		CCTATGCGGGGCAACAGTTCATATGCCCCGACCTGAAGCCGCTCCTAAAGGTACATT-----GAA-T----TGCGTCTCTCTTT---ATATATCTATCTCTTTCCCTCTGCCACCGCCTATCTCTTCAATCAAATGTCGCTCTAAA-----C----------
droGri2	scaffold_15245:12248134-12248233 -		CCTACGCGCGGCAAGTCATTCATTCTGCCCGAGATGCGGGTGTTCT----------

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

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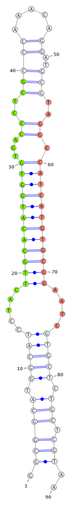
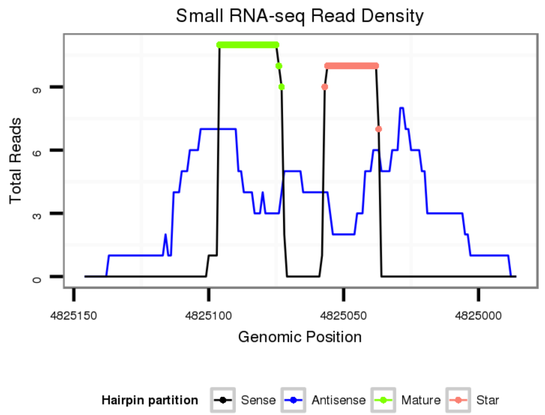
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

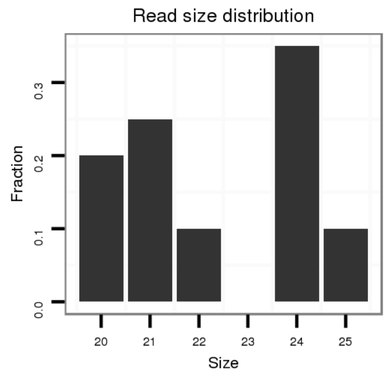
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_98	**scaffold_4770:4825036-4825096 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

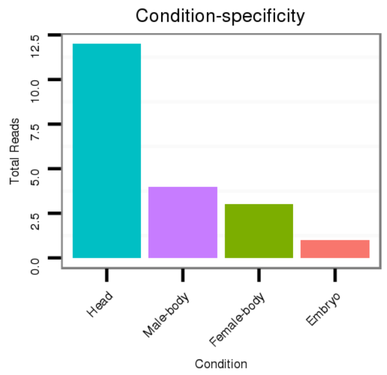
Legend: mature star mismatch in alignment mismatch in read

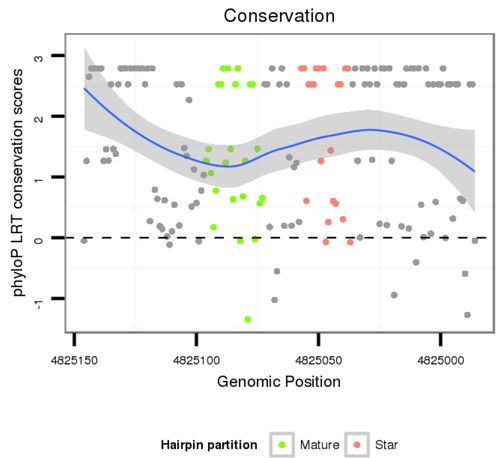
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG24277-in]; Antisense to CDS [Dere\GG15026-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CATTTAATGAGCTTCAAACTTAATTGTTACAACCAGGCGGCATGGCATCCTACTTGCACATGGTGTGACCCTCGCCCAAACAGGATGCGTAGGCCATCATGTGCGGAATCGTGCTCTGCTCGTAAACTCCGGTGAACAGGTGCGCCCAGGGACCCAAGGCG **********.(((((((.(((((.....((((((((((((...((..(((((.....))..)))..))).)))))))))))....)))))..)))..)))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	M055 female body	V107 male body	M057 embryo	V040 embryo
..........TACTTGCACATGGTGTGACCCTCG..........	24	0	1	7.00	7	5	0	2	0	0
..........TAGGCCATCATGTGCGGAATC..........	21	0	1	5.00	5	2	1	1	1	0
..........TAGGCCATCATGTGCGGAAT..........	20	0	1	3.00	3	2	0	1	0	0
..........TACTTGCACATGGTGTGACCCTCGC..........	25	0	1	2.00	2	2	0	0	0	0
..........ATCCTACTTGCACATGGTGTGACCCTC..........	27	0	1	1.00	1	0	0	0	1	0
..........TAGGCCATCATGTGCGGAATCT..........	22	1	1	1.00	1	0	1	0	0	0
..........AGGCCATCATGTGCGGAATC..........	20	0	1	1.00	1	0	1	0	0	0
..........GTAGGCCATCATGTGCGGAATCA..........	23	1	1	1.00	1	1	0	0	0	0
..........GTAGGCCATCATGTGCGGAATC..........	22	0	1	1.00	1	1	0	0	0	0
..........TACTTGCACATGGTGTGACCCT..........	22	0	1	1.00	1	0	1	0	0	0
..........TAGGCCATCATGTGCGGAATCAAA..........	24	3	1	1.00	1	0	1	0	0	0
..........TAGGCCATCATGTGCGGAATCA..........	22	1	1	1.00	1	1	0	0	0	0
..........TACTTGCACATGGTGTGACCCTCGT..........	25	1	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

GTAAATTACTCGAAGTTTGAATTAACAATGTTGGTCCGCCGTACCGTAGGATGAACGTGTACCACACTGGGAGCGGGTTTGTCCTACGCATCCGGTAGTACACGCCTTAGCACGAGACGAGCATTTGAGGCCACTTGTCCACGCGGGTCCCTGGGTTCCGC **********.((((((.(((((.....(((((((((((...((..(((((.....))..)))..))).)))))))))))....)))))..)))..)))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	M057 embryo	M055 female body	V040 embryo	V108 head	GSM1528801 follicle cells	V060 head
..........TAGCACGAGACGAGCATTTG..........	20	0	1	1.00	1	1	0	0	0	0	0	0
..........TTGGTCCGCCGTACCGTAGGATGAACG..........	27	0	1	1.00	1	0	1	0	0	0	0	0
..........ACGCCTTAGCACGAGACGAG..........	20	0	1	1.00	1	1	0	0	0	0	0	0
..........CTGGGAGCGGGTTTGTCCTACGCAT..........	25	0	1	1.00	1	1	0	0	0	0	0	0
..........CGTACCGTAGGATGAACGTGTACC..........	24	0	1	1.00	1	0	1	0	0	0	0	0
..........TCCACGCGGGTCCCTGGGTTC...	21	0	1	1.00	1	1	0	0	0	0	0	0
..........CCGTAGGATGAACGTGTACCACAC..........	24	0	1	1.00	1	0	0	1	0	0	0	0
..........TACCACACTGGGAGCGGGTTTG..........	22	0	1	1.00	1	1	0	0	0	0	0	0
..........CCTTAGCACGAGACGAGCATTTG..........	23	0	1	1.00	1	1	0	0	0	0	0	0
..........GGGTTTGTCCTACGCATC..........	18	0	1	1.00	1	1	0	0	0	0	0	0
..........GTCCGCCGTACCGTAGGATGAACG..........	24	0	1	1.00	1	0	0	1	0	0	0	0
..........GTCCGCCGTACCGTAGGATGAACGTG..........	26	0	1	1.00	1	0	0	0	1	0	0	0
..........CGAGCATTTGAGGCCACTTGTCCACG..........	26	0	1	1.00	1	1	0	0	0	0	0	0
..........TACACGCCTTAGCACGAGACG..........	21	0	1	1.00	1	1	0	0	0	0	0	0
..........CGCCGTACCGTAGGATGAACGTG..........	23	0	1	1.00	1	1	0	0	0	0	0	0
..........CGAGCATTTGAGGCCACTTGTCCA..........	24	0	1	1.00	1	0	1	0	0	0	0	0
..........CGGGTTTGTCCTACGCATCCGGTAG..........	25	0	1	1.00	1	0	1	0	0	0	0	0
..........CGTGTACCACACTGGGAGCGGGTTTGT..........	27	0	1	1.00	1	0	0	0	1	0	0	0
..........CCTTAGCACGAGACGAGCATT..........	21	0	1	1.00	1	0	0	1	0	0	0	0
.....TCGAAGTTTGAATTAACAATGT..........	22	0	1	1.00	1	0	0	1	0	0	0	0
..........AGACGAGCATTTGAGGCCACTTG..........	23	0	1	1.00	1	1	0	0	0	0	0	0
..........GTCCGCCGTACCGTAGGATGAA..........	22	0	1	1.00	1	0	0	1	0	0	0	0
..........CCTACGCATCCGGTAGTACACGCCTTAG..........	28	0	1	1.00	1	0	0	0	0	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4770:4824986-4825146 -	der_98	CATTTAATGAGCTTC-AAACTTAATTGTTACAACCAGGCGGCAT-------GGCAT----------CCTACT---TGCACATGGTGTGACCCTCGCCCAAACAGGATGCGTAGGCCATCATGTGCGGAATCGTGCTCTGCTCGTAAACTCCGGTGAACAGGTGCGCCCAGGGACCCAAGGCG
droYak3	3R:5628934-5629116 +		CATTTAATGAGCTTC-AAACTTAATTGTTACAGCCAGCGGGCAT-------GGCATC----------C---TTGCGCCA----------GCTGCG---TC----------T----------CATCCTACT---TGCACATGGTATGACCCTCGCCCACACAGGATGCGTAGGCCATCAGTGCGGAATCGGTGCTCTGCTCGTAGACTCCGGTGAACAGGTGCGCCCAGGGACCCAACGCG
droSec2	scaffold_38:294461-294643 -		-ATTTAATGAGCTTC-AAACTTAATTGTTACAACCAGGCGGCAT-------GGCAAC----------C---TTACACCA----------TCTGCG---TC----------CC----------CAGCCTACT---TGCACATAGTATGACCGTCGCCCACGCAGGATGCGTAGGCCATCATGTGCGGAATGGTGCTCTGCTCGTAGACTCCGGTGAACAGGTGCGCCCAGGGACCCAACGCG
droSim2	3r:4472126-4472308 -		-ATTTAATGAGCTTC-AAACTTAATTGTTACAACCAGGCGGCAT-------GGCAAC----------C---TTACACCA----------TCTGCG---TC----------CC----------CATCCTACT---TGCACATGGTATGACCGTCGCCCACGCAGGATGCGTAGGCCATCATGTGCGGAATGGTGCTCTGCTCGTAGACTCCGGTGAACAGGTGCGCCCAGGGACCCAACGCG
dm3	chr3R:16830900-16831082 +		-ATTTAATGAGCTTC-AAACTTAATTGTTACAACCAGGCGGCAT-------GGCAAC----------C---TTGCACCA----------TCTGCG---TT----------TC----------CATCCTACT---TGCACATGGTATGACCGTCGCCCAAGCAGGATGCGTAGGCCATCATAGCGGAATGGTGCTCTGTTCGTAGACTCCGGTGAACAGGTGCGCCCAGGGACCCAACGCG
droEug1	scf7180000409542:314116-314299 -		GATTTAATGAGCTTC-AAACTTAATTGTAATGGCCAGGCGGCAT-------GGCATC----------C---TCTC--TA----------GCTTCTCTAG----------CA----------GCTCCTACT---TGCACATGGTCTGCCCTCGCCTAAACACGATGCGTAGGCCATCAGGTGCGGGAATAGTGCTTCTGCTCGTAGACTCCGGTAAACAGGTGCGCCCATGGACCAAGAGCA
droBia1	scf7180000302155:180904-181095 +		GATTTAATGAGCTTC-AAACTTAATTGTAATGGCCAGGAGGCAT-------GACATC----------C---CCA----------TC----CTGCTCCTCC---TCCTCCTC---------CCC----------CTTCCTACT---TGCACATGGTCTGCCCTCGCCCAGGCAGGATGCGTAGGCCATCAGGTGCGGGAATGGTGCTCTGCTCGTAGACCCGGTGAACAGGTGCGCCCAGGGACCATGGGCA
droTak1	scf7180000415750:430814-430987 -		GATTTAATGAGCTTC-AAACTTAATTGTTATGGCCAGGCGTCAT-------GGCATC----------C---TCGCTG----------CT----------CCTCCTACT---GGCACATGGTCTGCCCCTCACCCAAACAGGATGCGTAGGCCATCAGGTGCGGGAATGGTGCTCTGCTCGTAGAGCCCGTGAAGAGGTGCGCCCAGGGACCCAGGGCG
droEle1	scf7180000491080:708716-708899 +		GATTTAATGAGCTTC-AAACTTAATTGTTATGGCCAGGCGGCAT-------GGCATC----------C---CCTCGCCA----------GCGTCT---GC----------GT----------CATCCTACT---TGCACATGGTCTGCCCTGCCCCAACAGGATGCGTAGGCCATCAGCCTGGGGAATGGTGCTCTGCTCGTAGACGCCCAGTGAAGAGGTGCGCCCAGGGACCCAGGCA
droRho1	scf7180000779659:419640-419800 +		TATTTAATGAGCTTC-AAACTTAATTGTTATGGCGAGGCGGCAT-------GGCAT----------CCTACT---TGCACATGGTCTGCCCGCGCCCAAACAGGATGCGTAGGCCATCAGCCTGGGGAATGGTGCTCTGCTCGTAGACTCCGGTGAAGAGGTGCGCCCAGGGACCCAGGGCA
droFic1	scf7180000454096:97038-97267 +		GATTTAATGAGCTTC-AAACTTAATTGTTACGGCCACCCGGCAT-------GGCATATCCTTGCTGGCTTCCCCTGTTT---CCCAT----------TCCCCCTTCTGCTCCTCT---TTCTGTTATCCTGTTCTCCT----------TTTCCTACT---TGCACATGGTGTGCCCCTCACCCAGGCAGGATGGATAGGCCATCAGGTGCGGGAATGGTGCTCTGCTCGTAGAGCCCGGTGAATAAATGGGACCAAGGCCCCAAGGCG
droKik1	scf7180000302809:92048-92227 +		GATTTAATGAGCTTC-AAACTTAATTGTTATTGCCAGGCGGCAT-------GGCATC----------C---CCCC---A----------T----------CCT----------TC----------GATCCTACTTGCTGCACATGGTGTCCCCTCGCCCAACAGGAGCGTAGGCCATCAGGTGCGGGAATGGTGCTCTGCTCGTAGACCCGGTGAAGAGGTGCGACCAGGGACCCAAAGCG
droAna3	scaffold_13340:8084932-8085142 +		GATTTAATGAGCTTCGAAACTTAATTGTTATGGCCGAGCGGCAT-------GGCATAGCAAGGAGGAGTTC---TGCCT---CCAAG----------TC----C---------CGCTGCCTCCTA---------GTC----------CATCCTACGTACTGCACATAGTGAGACCCTCGCCGACCCAGGAGCGTAGGCCATCATGTAGGGAATGGTGTTCTGCTCATAGACCCGGTAAATAGGTGCGACCAGGGACCCACGGCG
droBip1	scf7180000396708:762507-762716 -		GATTTAATGAGCTTCGAAACTTAATTGTTATGGCCGAGCGGCAT-------GGCACGACACGGAGGAGTCC---TGCCT---CCA-G----------AC------C---------TGCTGCCCCCGA---------GTC----------CATCCTACGTGCTGCACATGGTGAGCCCTCGCCCACGCAAGAGCGTAGGCCATCATGTGGGAATGGTGTTCTGCTCGTAGACCCGGTGAACAGGTGCGACCAGGGACCCACGGCG
dp5	2:12606625-12606799 -		GATTTAATGAGCTTC-AAACTTAATTGTTATGGGCAGGCGGCAT-------GCCATC----------C---CCT----------CCTG----------CCA----------C-CTACGTGCTGCACATGGTGTGTCCCTCGCCCAGGCAGGCGGCATAGGCCATCAGGTGCGGGAATGGTGCTCTGCTCGTAGACGCCGGTGAACAGATGCGACCAGGGACCCACACGCA
droPer2	scaffold_0:7860160-7860350 +		GATTTAATGAGCTTC-AAACTTAATTGTTATGGGCAGGCGGCAT-------GCCATC----------C---CGA----------TC----CCTGTTCCTCC---CCTCCTG---------CCA----------C-CTACGTGCTGCACATGGTTGTCCCTCGCCCAGGCAGGCGGCATAGGCCATCAGGTGCGGGAATGGTGCTCTGCTCGTAGACGCCGGTGAACAGATGCGACCAGGGACCCACACGCA
droWil2	scf2_11000000004902:6159250-6159469 +		-ATTTAATGAGCTTC-AAACTTAATTGTTATGAACGCCAGGCATGCTACATTGGCCAC----------A---TGCCACCACCA----------CCTTCT---TC----------ACCTCCTA---------CTCCTTACTTCTTTTGCTTCGATTCTAC-GGCTGCACATGGTGTGACCTTCGCCCAAGCAAGCTGGTATAAGCCATTATTATGGGAATGGTATTCTGCTCATAAATGCCGGTAAACAAGTGGGCCCAAGGCCCAAAGCA
droVir3	scaffold_12855:2330992-2331189 +		GTTTTAATGAGCTAC-AAACTTAATTGTGATGAGGTGCAGACGCA----CGCA----------C---CCA-GGACCAGGGCGCGTGTG-CCCCCTAG----------GCGCTGCTGCACATGGTGAGCCCATCGCCCAGCAAGCCGCTGTAGGCCATCATGTGCGGAATAGTGCTCTGCTCGTAGAGCCGGTAAACAATGCGACCAGGGCCCCATGCA
droMoj3	scaffold_6540:32645705-32645885 +		GTTTTAATGAGCAC-AAACTTAATTGTGATGAATGCAGGCACGCA----GCAGG----------C---GCTC----------AAG-TCCTTTGC----------GAGCCGGGACGCACAGGTGAGCCCATCGCCCAGGCAGGCGCTGTAGGCCATCATGTGCGGGAATGGTGCTCTGCTCGTAGAGCCGGTAAACAAGTGGGACCAGGGACCCGACGCA
droGri2	scaffold_15074:2329135-2329308 +		---TTAATAGGCTAC-AAACTTAATTGTGATGATGTCTCAGTCACGCT-CAAGGATTC----------A---TC----------ATT----------TAGTTTG--GGCTGCAATGGTTAAACCATCGCCGAGACAGGCGCTGTATGCCATCATATGGGGTATGGTGTTCTGCTCATAGACACCGTAAACAAATGGGACCAAGGACCCAGAGCA

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

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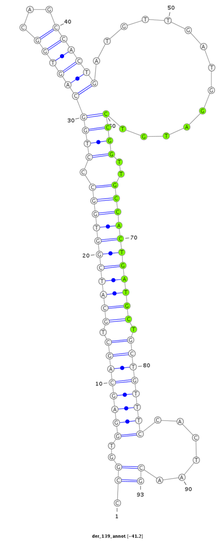
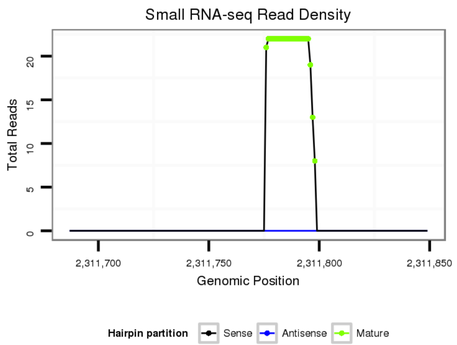
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

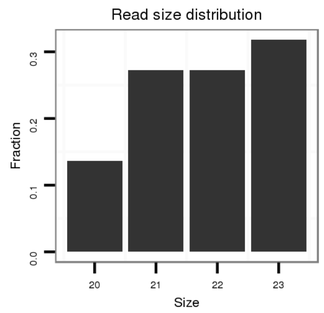
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_139	**scaffold_4784:2311737-2311799 +**	**candidate**	**Canonical miRNA**	**3pUTR**	[View on UCSC Genome Browser (Cornell Mirror)]

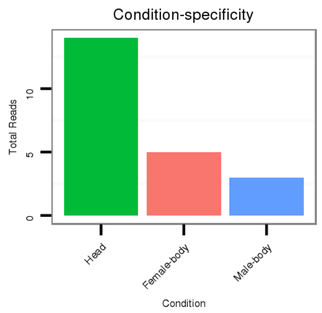
Legend: mature star mismatch in alignment mismatch in read

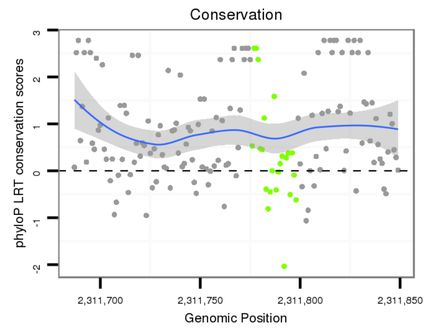
Predicted structure











Show Alternate Folds

Flybase annnotation

utr3 [utr3_plus_3639]

No Repeatable elements found

Sense Strand Reads

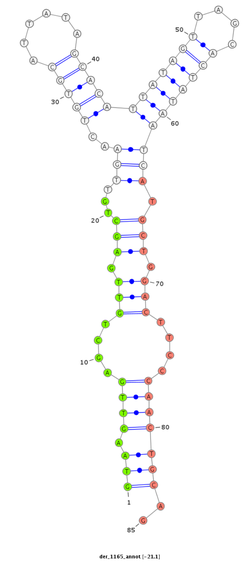
hide 3p reads | show mid mismatch reads

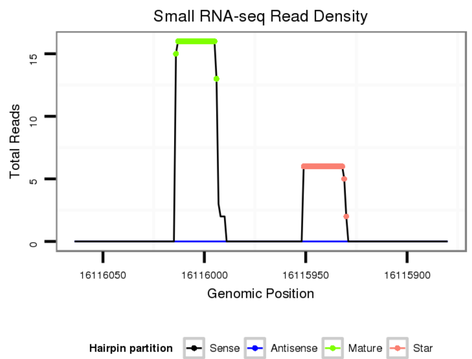
| | | |

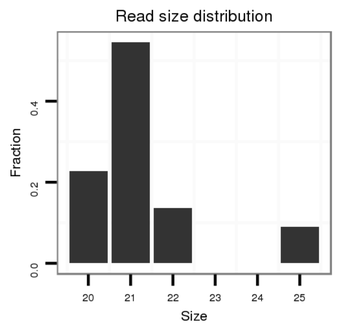
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1165	**scaffold_4845:16115930-16116014 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

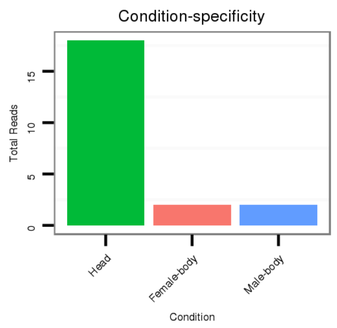
Legend: mature star mismatch in alignment mismatch in read

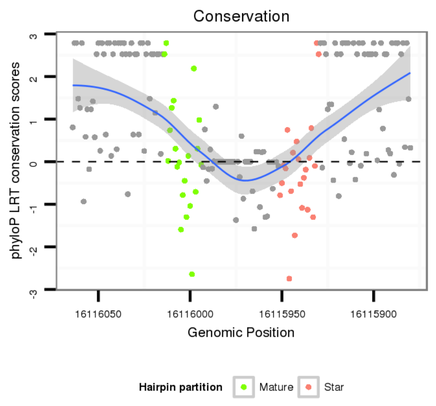
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dere\GG20402-in]; CDS [Dere\GG20402-cds]; CDS [Dere\GG20402-cds]; utr3 [utr3_plus_2380]; utr3 [utr3_plus_2379]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTTTGTGCGGGAGGAGAGCTTCGTTTACTCCGTGCCCTTCGATGCGGGTGGTAAGTTGAGCTGTTGAGCTGTTGAACTGTGCATTATAGCACATTATAGTTAGCACTATAATCATGCTGGACTTCCCAACTGCAAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V107 male body	M055 female body	V060 head
**********(((.((((.....(((.(((...(((..((((((.....)))))(((((((.....)))))))))).)))..)))....)))))))..**********									
.....GTAAGTTGAGCTGTTGAGCTG.....	21	0	1	9.00	9	7	2	0	0
.....ATGCTGGACTTCCCAACTGCA.....	21	0	1	3.00	3	1	0	1	1
.....GTAAGTTGAGCTGTTGAGCT.....	20	0	1	3.00	3	3	0	0	0
.....ATGCTGGACTTCCCAACTGCAG.....	22	0	1	2.00	2	1	0	1	0
.....GTAAGTTGAGCTGTTGAGCTGTTGA.....	25	0	1	2.00	2	2	0	0	0
.....ATGCTGGACTTCCCAACTGC.....	20	0	1	1.00	1	0	0	0	1
.....TGCTGGACTTCCCAACTGCAGA.....	22	1	1	1.00	1	1	0	0	0
.....GTAAGTTGAGCTGTTGAGCTGT.....	22	0	1	1.00	1	1	0	0	0
.....TAAGTTGAGCTGTTGAGCTG.....	20	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

AAAACACGCCCTCCTCTCGAAGCAAATGAGGCACGGGAAGCTACGCCCACCATTCAACTCGACAACTCGACAACTTGACACGTAATATCGTGTAATATCAATCGTGATATTAGTACGACCTGAAGGGTTGACGTCTCTCGTTGAGTCTCTAGGACCACTGGCGGTCGGTACGGCAGAAGGTGTTA	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V040 embryo
**********(((.((((.....(((.(((...(((..((((((.....)))))(((((((.....)))))))))).)))..)))....)))))))..**********							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4845:16115880-16116064 -	der_1165	TTTTGTGCGGGAGGAGAGCTTCGTTTACTCCGTGCCCTTCGATGCGGGTGGTAAGTTGAGCTGT-TG--AGCTGT----------TGAACTGTGCATTATAGCACATTATAGTTAGCACTATAATCATGCTGGAC--------T--TCCC--AACTGCAGAGAGCAACTCAGAGATCCTGGTGACCGCCAGCCATGCCGTCTTCCACAAT
droYak3	2R:7250023-7250187 -		TTTTGTGCGGGAGGAGAGCTTCGTTTACTCCGTGCCCTTCGATGCGGGTGGTAAGTTGAGATGTACAC--------TCATCGTA----------CG----------T----GCTAACACATAATCACATGGAC--------T--TCCC--CACTGCAGAGAGCAACTCAGAGATCCTGGTGACCGCCAGTCATGCCGTCTTCCACAAT
droSec2	scaffold_1:7231178-7231334 +		TTTTGTGCGGGAGGAGAGCTTCGTTTACTCCGTGCCCTTCGATGCGGGTGGTAAGTTCAGAGGTACC--------TCATCGTA----------CAT----------CATTATCTAAATGGA--------T--TCCC--AACTGCAGAAAGCAACTCAGAGATCCTGGTGACCGCCAGTCATGCAGTTTCCACAAT
droSim2	2r:10393092-10393248 +		TTTTGTGCGGGAGGAGAGCTTCGTTTACTCCGTGCCCTTCGATGCGGGTGGTAAGTTGAGAGGTACC--------TCATCGTA----------CAT----------CATAATCTCACTTGAC--------T--TCCC--AACTGCAGAAAGCAACTCAGAGATCCTGGTGACCGCCAGTCATGCCGTTTCCACAAT
dm3	chr2R:9703960-9704116 +		TTTTGTGCGGGAGGAGAGCTTCGTTTACTCCGTGCCCTTCGATGCGGGTGGTAAGTTGGAGGTACC--------TCATCGTA----------CAT----------CATAATCGTAATGGAA--------T--TCCC--AACTGCAGAAAGCAACTCAGAGATCCTGGTGACCGCCAGTCATGCCGTTTCCACAAT
droEug1	scf7180000409462:3150898-3151062 -		TTTTGTGCGGGAGGAGAGCTTCGTGTACTCCGTGCCCTTCGATGCGGGTGGTAAGTTGAGATGTACATTAA----------ATTTAGGAGCAAGATAT----TGATGT----------AT-----TCATT--ATCC--ACCTGCAGAGAGCAACTCAGAGATCCTGGTGACCGCCAGTCATGCCATTTCCACAAT
droBia1	scf7180000302291:432064-432228 -		CTTCGTTACGGAGGAGAGCTTGTTTACTCCGTGCCCTTGACGCGGGTGGTCAGTTGAGGTGTACAA--T---------A----------G---GTTCATGCGCAA----------T-TAACGATAATAT----GCTATT--ATC--TCCTATAGAGAGCAATTCAGAGATCCTGGTGACCGCCAGCCATGCTATTTCCACAAT
droTak1	scf7180000415401:930451-930612 -		TTTTGTACGGGAGGAGAGCTTCGTTTACTCCGTTGCCTTCGATGCGGGTGGTAAGTTGAGATGTAATAT--T---------A----------C---TTTTAAGCTC---TGTAT----------A---A---CC----------TAACA--A-----CATT--TCCC--ACCTGTAGAGAGCAATTCGGAGATCCTGGTGACCGCCAGCCATGCCGTTTCCACAAT
droEle1	scf7180000486779:17993-18148 -		TTTTGTGCGGGAGGAGAGCTTCGTTTACTGAGTGCCCTTCGATGCGGGTGGTAAGTTGACAAAAGCT--------TATTTGTT----------TAA----------C----------AAATTTATAAAGA--A--------T--TTA--TTCCTTAGAGAGCAACTCAGAGATCCTAGTGACGGCCAGTCATGCCGTTTCCACAAT
droRho1	scf7180000779933:15943-16106 +		TTTTGTGCGGGAGGAGAGCTTCGTTTACTGAGTGCCCTTCGATGCGGGTGGTAAGTTGATAAAACT--------TACTTTTC----------AAT----------AATTATTCACAGA--ATATTTTAT--TCCC--ACCTGTAGAGAGCAATTCAGAGATCCTGGTGACGGCCAGTCATGCCGTTTTCACAAT
droFic1	scf7180000454039:518615-518775 +		CTTTGTTAGGGAGGAGAGCTTCGTTTACTCCGTGCCCTTCGATGCGGGTGGTAAGTCCTATAATTTATAT--T----------AT----------TTAAAT--AGGTAT----------T---------A----------CTAATT--A--------T--ATTA--ATCTTATAGAGAGCAATTCGGAGATCCTGGTGACGGCCAGCCAACGCTGTTTCCACAAT
droKik1	scf7180000301798:21372-21638 +		TTTTGTGCGGGACGAAAGCTTCGTCTACTCGTGCCCTTCGATGCGGGTGGTCAGTTGATATC--C---AG--ATTTTAAGAACCGGATCTTAGATAATAAATATCACTTATATGATTCCCGCGGTGTAGCAGATACACAAGCAAATCAATTAAAGAGACGTTCTTAGGCAACCCAAATTAAAAATGTATTACATTTTTTAACCTT----TCCGT----------A---A----------T--CTCC--ATCTGCAGAGAGCAATTCGGAATCCTGGTCAGCGCCAGTCATGCCGTCTTCACACGC
droAna3	scaffold_13266:17005892-17006050 +		TTTTGTACGAGAAGAGAGCTTGTTTACTCGTGCCTTCGATGCGGGTGGTAAGTTAGTCCTATT--AACTATA----------TT----------AAGCA--TAATAT----------T---------A----------ATAATA--A--------T--ATTA--ATTATGCAGAAAGCAAATCGGAGATTTTGGTAACCGCCAGTCATGCCATTTTCATAAC
droBip1	scf7180000396735:253894-254051 +		TTTTGTACGAGAAGAGAGCTTGTTTACTCGTGCCTTCGATGCGGGTGGTCAGATAAAT-TA---A----------CTTATTTTA----------AA----TAATAT----------CAATATAA--------T--ATGAAACATTCAGAAAGCAAATCAGAGATTCGTAGTACCGCCAGTCATGCCATTTTCATAAC
dp5	3:14402220-14402378 -		TTTTGTACGGGCGGAAAGCTTTGTCTACTCCGTGCCCTTCGATGCGGGCGGTATGTTGCGGCGTACC--AGCTATA----------TT----------TTGGACTC----CACATAA----TCG----------TCTC--TTG--TCATTTAGAAAGCAACTCTGAGATCCTTGTTAACTGCCAGTCATGCCATCTTCCATAAT
droPer2	scaffold_4:3203972-3204130 +		TTTTGTACGGGCGGAAAGCTTTGTCTACTCCGTGCCCTTCGATGCGGGCGGTATGTTGCGGCGTAAG--AGCTATA----------TT----------TTGGACTC----CACATAA----TCG----------TCTC--TTG--TCATTTAGAAAGCAACTCTGAGATCCTTGTTAACTGCCAGTCATGCCATCTTCCATAAT
droWil2	scf2_1100000004822:1024908-1025069 -		TTTTATAAAGGGAGGAAAGTTTTGTCTACTCGTGACCCTTCGATGCAGGCGGTAAATATGAT-CTAACTAAGC--CA----------TT----------TTAAGTGCAAA----CTAA-AGTTC----------T---------A----------TTATCT--TTTT--ATTTTCAGAAAGCAACTCGGAATTTTAGTCACTGCCAGTCATGCCATTTTCATAAC
droVir3	scaffold_12875:8365988-8366147 +		TTTTGTGCAAAAGGAGAGCTTCGTCTACTCCGTGCCTTCGATGCAGGCGGTAAGTCTGGC---T-ATCTCT--AT----------TT----------GGAGAATC----TGTA--GTTAACTG----------T-------TCTCTATTA--ACTTGCAGAGAGTGGTTCAGAATTATTGTTACTGCCAGTAACGCCATCTTTCACAAT
droMoj3	scaffold_6496:18852434-18852594 -		TTTTGTGCACAAGGAGAGTTTTGTCTACTCGTGCCCTTCGATGCTGGTTGGTAAGTCTGTT-CACAACTTTATC--AT----------CT----------CTAGGGTC----TGT----TAACTG----------A---------TCTC--TG-GAACTCTTTAGAAAGTGGCTCGGAATCATTGTTAACTGCCAGCAATGCCATTTTCACAAT
droGri2	scaffold_15245:1814916-1815075 +		TTTTGTGCACAAGGAGAGCTTTGTCTACTCGTGCCCTTGATGCTGGAGTGCGTCTTCCGGAA--C--C----------CCCT----------TTAAAAGCAGACTAT----------C---------T---------AAAAAC--------ATA--TTG--TTTGCAGAGAGTGGCTCAGAATAATGGTAACTGCCAGTATGCCATCTTTCACAAT

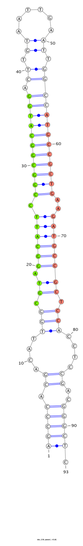
Generated: 09/08/2015 at 07:01 PM

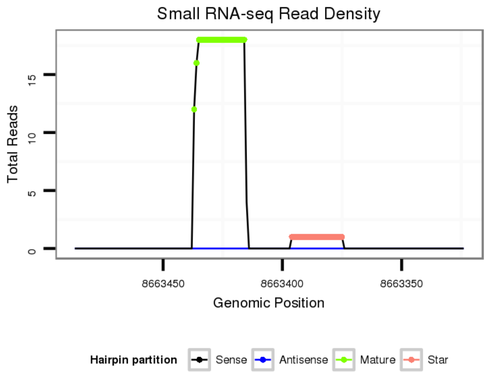
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

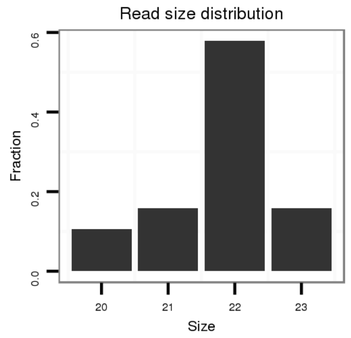
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_150	**scaffold_4929:8663374-8663437 -**	**candidate**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

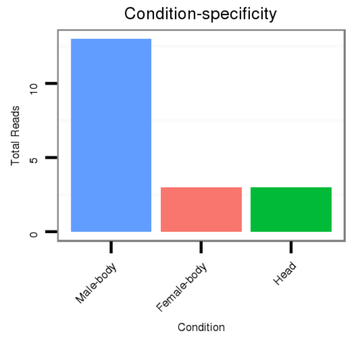
Legend: mature star mismatch in alignment mismatch in read

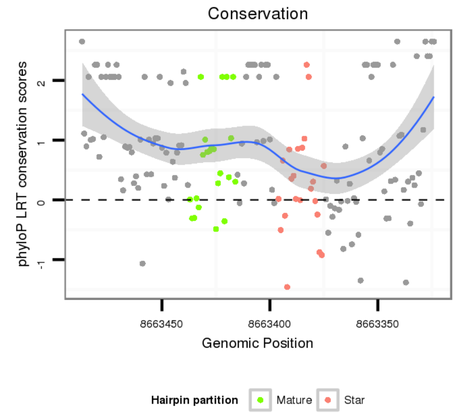
Predicted structure











Show Alternate Folds

Flybase annotation

Antisense to intron [Dere\GG25263-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACCCTAAACCTGACCCACTGGCGGGTGACCAAATTAGCCCACGACATTGGCGTAGGCATTCCGGCGGCATGGACTTGTAATTGAATTGGCCATGCCGCTGAAGATGCCGCTCCACCTCCGACGGGCTCCAAATCGATTGGGTGCACTGCTGGCCAGCGGAGGAT	Read #		Hit	Total		V107	V108	M055
********************************(((((.((.....(((.((.((((((.(((((((((((.((.((.((.....)).)))))))))))))..)))))))).)))....)).)))))).********************************	size	Mismatch	Count	Norm	Total	body		
.....CGTAGGCATTCCGGCGGCATGG.....	22	0	1	9.00	9	7	2	0
.....CGTAGGCATTCCGGCGGCATGGA.....	23	0	1	3.00	3	2	1	0
.....GTAGGCATTCCGGCGGCATGG.....	21	0	1	3.00	3	1	0	2
.....TAGGCATTCCGGCGGCATGG.....	20	0	1	2.00	2	2	0	0
.....ATGCCGCTGAAGATGCCGCTCC.....	22	0	1	1.00	1	0	0	1
.....GTAGGCATTCCGGCGGCATGGA.....	22	0	1	1.00	1	1	0	0
.....ATGCCGCTGAAGATGCCGCTCCTT.....	24	2	1	1.00	1	1	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4929:8663324-8663487 -	der_150	ACCC---------TAAACCTGACCCACTGGCG------GGT-GACCAAATTAGCCCACGACATTG-----GCGTAGGCAT---T----------CCGGC---GGCATGGAC-------TTGTAATTGAATTGGCCAT-----GC----C----------GCTGAAGATGCC-G-CT----------CGACC--------TCC----------GACGG-GCTCCAAATCGATTGGGTGCA----------CTGCTGGCCAGCGGAGGAT
droYak3	2L:18327992-18328160 +		ACCC---------TAAACCTGACCCACTGGCG------GGT-GACCAAATTAGCCCACGACATTGCCTTGGCGTCGGCAT---T----------CCGGA---GGCATGGAC-------TTGTAATTGAATTGGCCAT-----GC----C----------GCGAAGATGCC-G-CT----------CGACC--------TCC----------AACGG-GCTCCAAATCGATTGGGCGCA----------CTGCTGGCCAGCGGAGGAT
droSec2	scaffold_1:3311758-3311921 +		ACCC---------TAAACCAGACCCACTGGCG------GGT-GACCAAATTAGCCCACGACATTG-----GTCTAGGCAT---T----------CCGGA---GGCATGGAC-------TTGTAATTGAATTGGCCAT-----GC----T----------GCCGAAGATGCC-G-CT----------CGACC--------TCC----------AGCGG-GCTCCAAATCGATTGGGTGCA----------CTGCTGGCCAGCGGAGGAT
droSim2	2r:6480697-6480860 +		ACAC---------TAAACCTGACCCACTGGCG------GGT-GACCAAATTAGCCCACGACATTG-----GCCTAGGCAT---T----------CCGGA---GGCATGGAC-------TTGTAATTGAATTGGCCAT-----GC----C----------GCCGAAGATGCC-G-CT----------CGACC--------TCC----------AGCGG-GCTCCAAATCGATTGGGTGCA----------CTGCTGGCCAGCGGAGGAT
dm3	chr2R:5702800-5702963 +		ACCC---------TAAACCTGACCCACTGGCG------GGT-GACCAAATTAGCCCACGACATTG-----GCGTAGGCAT---T----------CCGGC---GGCATGGAC-------TTGTAATTGAATTGGCCAT-----GC----T----------GCCGAAGATGCC-G-CT----------CGACC--------TCC----------AGCGA-GCTCCAAATCGATTGGGCGCA----------CTGCTGGCCAGCGGAGGAT
droEug1	scf7180000409209:464498-464660 -		ACCC---------TAAACCTGACCCACTGGCG------GGT-GACAAATTAGCCCACGACATTG-----GTGTAGGCAT---T----------CCAGA---GGCATGAAC-------TTGTAATTGAATTAGCCAT-----GC----C----------GTTAGCGATGCC-T-CT----------TTACC--------TCC----------AATGG-ATTCTAAATCGATTGGCCTCA----------CTGCTTGCCAGCGGAGGAT
droBia1	scf7180000301506:1003980-1004142 -		ACCC---------TAAACCTGACCCACTGGCG------GGT-GACAAATTAGCCCGCACATTG-----GCCAGGCAT---T----------CCAGA---GACCTGAAC-------TTGTAATTGAATTAGCCAT-----GC----C----------GTTAGCGATGCC-G-CT----------CGCCC--------GGC----------GATGG-GTTCCGAATCGATTGGAGCCA----------CTGCTTGCAGCGGAGGAT
droTak1	scf7180000415870:582528-582691 -		ACCC---------TCAACCTGACCCACTGGCG------GGT-GACAAATTAGCCCACGACATTG-----GCCAGGCAT---T----------CCGGA---GGCCTGAAC-------TTGTAATTGAATTAGCCAT-----GC----C----------GTTAGCGATGCC-G-CC----------CGACC--------GCC----------CAAGG-GTTCCAAATCGATTGGACCCA----------CTGCCCCAAGCGGAGGAT
droEle1	scf7180000491107:1396480-1396652 -		ACCC---------TAAACCTGACCCACTGGCG------GCT-GACAAATTGCCCCACGACATTG-----GCGTTGGCAT---T----------CCGGA---GGCATGAAC-------TTGTAATTGAATTAGCCAT-----GC----C--C-T----------CGACCGACCTCCGAT---GTTGCGATATTCC----------GATGG-GTTCCACATCGATTGGAGCCA----------CTGCTTGCCAGCGGAGGAT
droRho1	scf7180000777217:607313-607480 +		ACCC---------TAAACCTGACCCACTGGCG------GCT-GAACAAATTAGCCCACGACATTG-----GCCAGGCAT---T----------CCGGA---GGCATGAAC-------TTGTAATTGAATTAGCCAT-----GC----C----------GTTAGCGATGCC-GGGA---GCACCTCCGAT---GT--------TCC----------AATGG-GTGCCCAATCGATTGGACAGA----------CTG----CCAGCGGAGGAT
droFic1	scf7180000453858:1027416-1027578 -		ACCC---------TAAACCTGACCCACTGGCG------AGT-CAGTTAGTCAGGT----------A-TCAGGCAT---TGCT----------CCGGA---GCCACAAGTCGTAATTGGTAATTGAATTAGCGC----GAC----C----------GTTAGCGATGCC-G-AT----------GGTCC--------GCA----------AGAGG-AGTCCCAATCGATTGGACGCA----------CTGCCGCCCGCGGAGGAT
droKik1	scf7180000302476:1114776-1114960 +		ACCC---------TAAACCTGACCCAGAGAGA-CACAGAGTGGAACAAATTAGCCCACGACATTG-----GCC---GCAT---T----------CCCCA---GGCATGAAC-------TTGTAATTGAATTAGCCAG-----ACGACGTCCAGGGCGATGGGAGTCGTGGTGCC-TGGA----------CGACC--------TCC----------GATAA-AGCCGGAATCGATTGGACGCA----------CTGCTGGCCAGCAGAGGAT
droAna3	scaffold_13266:12973112-12973286 +		ACCC---------TAAACCTGACCCAGAGACG------AGT-GACCAAATTAGCCCGCACATTG-----GCC-ACGCAT---A----------CCAGA---GGCTGAAC-------TTGTAATTGAATTACTGTGGGAGGCGC---A----------ATTAGCGATGCA-TGCC----------CGAAC--------AGC----------CACACATTAAGAA-AACCTTAATTGATTCTCCA----------TTGATT---GCCAAGGAT
droBip1	scf7180000396730:949892-950066 -		ACCC---------TAAACCTGACCCAGAGACG------ACT-GACCAAATTAGCCCGCACATTG-----GCC-ACAGCAT---A----------CCAGA---GGCTGAAC-------TTGTAATTGAATTACCCAGGGAGGCGC---A----------ATTAGCGATGCA-TGCC----------CGAAA--------TGC----------TGCA----CATTAAGAA-AACCTTAATTGATTCTCCA----------TTGATT----GTAAAGGAT
dp5	3:8775919-8776134 -		ACCC---------TAAACCTGACCCAGAAAGCG------AGA-CACCAAATTAGCCCACGACATTG-----CCCCTTGCATGC--TATGGAATGTACGCAAT---------CTTACTGCCATGC-GG-------TGGTAATGGAATTACGCTG----GC----C----------ATTAGCGATGCC-T-GG----------CGAAG--------TGC----------AGCAG--GCA----GAT-AAGAAGGGCAATTGATTGGCTGCATAACGAATGCATTCTGGGGCACTGCAGCGCTAGGGAGGAT
droPer2	scaffold_4:2660013-2660228 -		ACCC---------TAAACCTGACCCAGAAACG------AGA-CACAAATTAGCCCACGACATTG-----CCCCTTGCATGC--TATGGAATGTACGCAAT---------CTTACTGCCATGC-GG-------TGGTAATGGAGTTACCCTG----GC----C----------ATTAGCGATGCC-T-GG----------CGAAG--------TGC----------AGCAG--GCA----GAT-AAGAATGGGCAATTGATTGGCTGCATAACGAATGCATTCTGGGGCACTGCAGCGCTAGGGAGGAT
droWil2	scf2_11000000004514:3690169-3690393 +		ACCCGAACGGCCTCAAAACGTCACCCACTAATGACAACGAGTGGTTGTGTAGTGTTCGTTCTG-----GAATGTGCGA---T----------CA--CCGACGAGAGTCAAA---GTCATGGTT------GGGTAATTGAATTAGACAT-----TT-GACC----------ATTTGAAATGGTCT--A----------GC----------CTACAAGACCAGAGTGGCAGACTGTGGACAGAGATAAG-ATTTCAAATTGATTGGCGCTACAA----------TTGCATGGTAGGAGGAT
droVir3	scaffold_12875:6037816-6037835 +		AT--TGCATGGTAGGGAGGAT
droMoj3	scaffold_6496:24005606-24005625 -		AT--TGCAGGGTAGGAGGAT

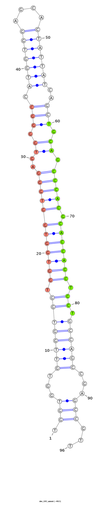
Generated: 09/08/2015 at 07:47 PM

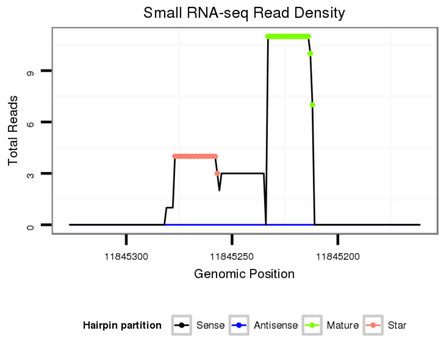
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

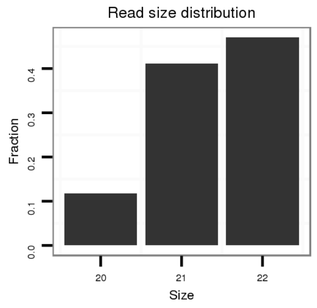
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_192	**scaffold_4784:11845211-11845277 -**	**confident-exception**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser [Cornell Mirror]]

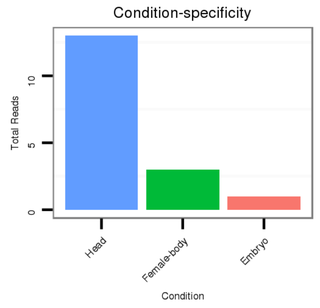
Legend: mature star mismatch in alignment mismatch in read

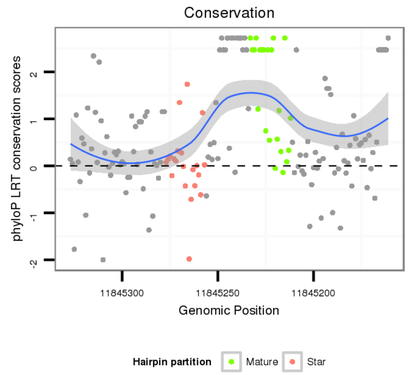
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dere\GG13876-cds]

Repeatable elements

Name	Class	Family	Strand
(CCA)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

						V108	M055	M057	V060
GACGGGGCCGCGGGCGGAGGAGTTCCAGGCGGAGGTGGTGGTGTTGGTGGTGGTGGAGTGGGGCCATGGTGGAGCACTATTATCAGCTGCAGCCCACGCACCACCTCCTGCCAGCCGACGCGTTACCAACGACAGCGACAGCAACAGCGAATTCCGGCGA	Read size	# Mismatch	Hit Count	Total Norm	Total	head	female body	embryo	head
**********.(((...(((((((((.(((((((((((..((.(((.(((((((....)))))))..)))).)).)))))).)))))))).)))))...)))...**********									
..TGCAGCCCACGCACCACCTCCT	22	0	1	7.00	7	5	0	1	1
..TGCAGCCCACGCACCACCTCC	21	0	1	3.00	3	2	1	0	0
..TGGTGGTGGTGGGAGTGGGGC	21	0	1	2.00	2	2	0	0	0
..ATGGTGGAGCACTATTATCAG	21	0	1	2.00	2	1	1	0	0
..GTGGTGGTGGTGGGAGTGGGGCC	26	0	1	1.00	1	1	0	0	0
..TGGTGGTGGTGGGAGTGGGG	20	0	1	1.00	1	1	0	0	0
..CATGGTGGAGCACTATTATCAG	22	0	1	1.00	1	0	1	0	0
..TGCAGCCCACGCACCACCTC	20	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

					V040	V107	M057	M055	V060
CTGCCCCGGCGCCCGCCTCCTCAAGGTCCGCCTCCACCACCACAACCACCACCACCACCCTCACCCCGGTACCACCTCGTGATAATAGTCGACGTCGGGTGCGTGGTGGAGGACGGTCGGCTCGGCAATGGTTGCTGTCGCTGTCGTTGTCGCTTAAGGCCGCT	Read size	# Mismatch	Hit Count	Total Norm	Total	embryo	male body	embryo	female body	head
**********.(((...(((((((((.(((((((((((..((.(((.(((((((....)))))))..)))).)).)))))).)))))))).)))))...)))...**********										
..GTGCAGCCCACGCACCACCTC	20	0	1	1.00	1	1	0	0	0	0

Show Alignment With Reads

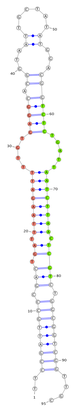
Re-alignment of all predicted orthologs

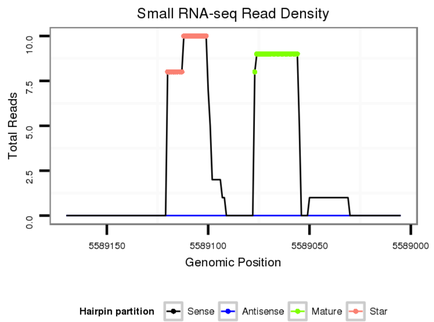
Species	Coordinate	ID	Alignment
droEre2	scaffold_4784:11845161-11845327 -	der_192	GAC----------GGGGCCGCGGGCGGAGGAGTTCC----------AGGCGGAGG---TGGTGGTGTTGGTGGTGGTGG---TGG-----TGG----------GAGTGGGGCCATGGTGGAGCACTATTATCAGCTGCAGCCCACGCACCACCTCCTGCCAGCCG---AGCCGTTACC----------AACG-----AC----------AGCG----------AC----------AGCAACAGC--GAATTCCGGCGA
droYak3	3L:11898767-11898927 -		GAC----------GGGGCCGCGGGCGGAGGAGTTCC----------AGGCGGAGG---TGGTGGTGTTGGTGGTGGTGG---TGG-----TGG----------GAGTGGAGCATGGTGGAGCACTATTATCAGCTGCAGCCCACGCACCACCTCCTGCCAGCCG---AGACGTTGAAGC----------AACG-----AC----------AGCG----------AC----------AGCAACAGC--GAATTCCGGCGA
droSec2	scaffold_0:4046142-4046290 -		GAC----------GGGGCAGCGGGCGGAGGAGTTCC----------AGGCGGAGG---TGGTGGTGTTGGTGGTGGTGG---TGG-----TGGTGGTGGTGGCATTGGCGGTGGGGCCATGGTGGAGCACTATTATCAGCTGCAGCCGCGCACCACCTCCTGCCAGCCG---AGCGTTGCC----------AACG-----AC----------GGCG----------AC----------AGCAACAGC--AAATTCCGGCGA
droSim2	3L:11560985-11561133 -		GAC----------GGGGCAGCGGGCGGAGGAGTTCC----------AGGCGGAGG---TGGTGGTGTTGGTGGTGGTGG---TGG-----TGGTGGTGGTGGCATTGGTGGTGCGGCCATGGTGGAGCACTATTATCAGCTGCAGCCCACGCACCACCTCCTGCCAGCCG---AGCGTTGCC----------AACG-----AC----------GGCG----------AC----------AGCAACAGC--AAATTCCGGCGA
dm3	chr3L:11855964-11856118 -		GAC----------GGGGCAGCGGGCGGAGGAGTTCC----------AGGCGGAGG---TGGTGGTGTTGGTGGTGGTGG---TGG-----CGGTGGTGGTGGCATTGGTGGTGCGGCCATGGTGGAGCACTATTATCAGCTGCAGCCCACGCACCACCTCCTGCCAGCCG---AGCCGTTACC----------AACGACGGGCCAC----------AG----------CAAC----------AC----------AGCAACAGC--AAATTCCGGCGA
droEug1	scf7180000409711:3738190-3738326 -		GAC----------GGGGCAATGGGCCGGAGGAGTTCC----------AGGCGGAGG---TGGTGGTGTTGGTGGTGGTGG---TGG-----CGG----------GAGTGGAGCACTATTATCAGCTGCAGCCCACGCACCACCTCCTGCCAGCGG---AGCCGAAGAGC----------AACG-----AC----------AGCA----------AC----------AGCAGCAGGA----ACAACAACGAAACAGC--AAATTCCGGCGA
droBia1	scf7180000302428:4093736-4093899 -		GAC----------GGGGCGCGGGCGGAGGAGTCCAGGCGGAGG---TGGTGGTGCGCCATGGTGGAGCACTATTATCAGCTGCAGCCCACGCACCACCTCCTGCCAGCCG---AGCCGTTACC----------AACG-----AC----------AGCA----------AC----------CACAACAACACAGCG--GAATCCGGCGA
droTak1	scf7180000415392:274043-274188 -		GAC----------GGGGCGTGGGCGGAGGAGTCCAGGCGGAGG---TGGTGGTGCGCCATGGTGGAGCACTATTATCAGCTGCAGCCCACGCACCACCTCCTGCCAGCCG---AGCCGTTACC----------AACG-----AC----------AGCA----------AC----------AAACAACAACAGC--GAATCCGGCGA
droEle1	scf7180000491193:3751946-3752104 -		GAC----------GGGGCAGCGGGCGGAGGAGTCCAGGCGGAGG---TGGTGGTGCGCCATGGTGGAGCACTATTATCAGCTGCAGCCCACGCACCACCTCCTGCCAGCCG---AGCCGTTACC----------AACG-----AC----------AGCA----------AC----------CAGCAACAACAGC--GGATCCGGCGA
droPic1	scf7180000454113:2811082-2811314 +		GAC----------GGGGCAGCGGGCGGAGGAGTTCCAGGCGGAGG---TGGTGGTGCGCCATGGTGGAGCACTATTATCAGCTGCAGCCCACGCACCACCTCCTGCCAGCCG---AGCCGTTACC----------AACG-----AC----------AGCA----------AC----------AGCAGGAGTAGCAACAACAGGAGGTGGAGGAGGAGGAGTAGGAGTAGGAGGAGCAACG----------AGCAGGAGAATAACCGGCGA
droKik1	scf7180000302391:963291-963424 +		GAC----------GGGGCGTGGGCGGAGGAGTCCAGGCGGAGG---TGGTGGTGCGCCATGGTGGAGCACTATTATCAGCTGCAGCCCACGCACCACCTCCTGCCAGCCG---AGCCGTTACC----------AACG-----AC----------AGCA----------AC----------AACACCAACAACAGC--GAATCCGGCGA
droAna3	scaffold_13337:6112744-6112919 -		CCGTCGGCACCGGAGGGGGCGTGGGAGGAGCCAGGCGGAGG---TGGTGGTGCGCCATGGTGGAGCACTATTATCAGCTGCAGCCCACGGATGA

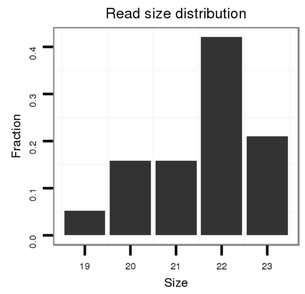
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_103	**scaffold_4770:5589055-5589120 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

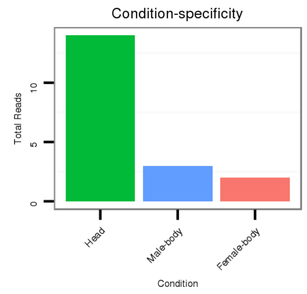
Legend: mature star mismatch in alignment mismatch in read

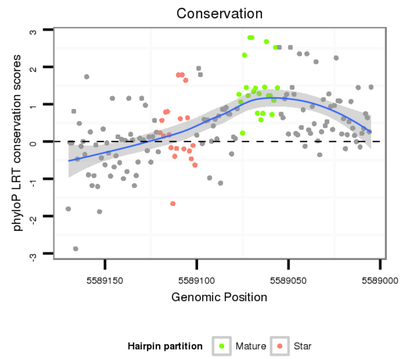
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dere\GG23812-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GAAAGATACCTATACTGCCTATTAAAAGCGTTATTTTCCGATTGCCCGACTGATTTAAGATTTTGTGAGGCACGGTAATTGCTATATGGACGGTCTCTGATTAATCTTAACTCGTCTGGCGGTCGGTTGCTCTGTCACCCGATCATTCGTTCATTCGCTGGCTGAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V060 head	V107 male body	M055 female body	V040 embryo	M057 embryo
**********..(((((((((.(((.((.((((((((....((((((.((....((.....))...)))))))).....))))))).)))))).....))))))))....**********											
....TCTCTGATTAATCTTAACTCGT....	22	0	1	4.00	4	3	0	1	0	0	0
....TCTCTGATTAATCTTAACTCGTC....	23	0	1	4.00	4	2	1	0	1	0	0
....TGATTTAAGATTTTGTGAGG....	20	0	1	3.00	3	3	0	0	0	0	0
....TGATTTAAGATTTTGTGAGGCA....	22	0	1	3.00	3	1	1	0	1	0	0
....TGATTTAAGATTTTGTGAGGC....	21	0	1	2.00	2	2	0	0	0	0	0
....GATTTTGTGAGGCACGGTAAT....	21	0	1	1.00	1	0	0	1	0	0	0
....GATTTTGTGAGGCACGGTA....	19	0	1	1.00	1	0	0	1	0	0	0
....TCTGATTAATCTTAACTCGTCA....	22	1	1	1.00	1	0	1	0	0	0	0
....GGTCGGTTGCTCTGTCACCC....	20	0	1	1.00	1	0	0	0	0	0	1
....CTCTGATTAATCTTAACTCGTC....	22	0	1	1.00	1	1	0	0	0	0	0

Anti-sense strand reads

CTTTCTATGGATATGACGGATAATTTTCGCAATAAAAGGCTAACGGGCTGACTAAATTCTAAAACACTCGGTGCCATTAACGATATACCTGCCAGAGACTAATTAGAATTGAGCAGACCGCCAGCCAACGAGACAGTGGGCTAGTAAGCAAGTAAGCGACCGACTA	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	M055 female body	M057 embryo	V108 head
**********..((((((((((.(((.((.((((((((....((((((.((....((.....))...)))))))).....))))))).)))))).....))))))))....**********									
....TCTCTGATTAATCTTAACTCGTC....	22	0	1	4.00	4	3	0	1	0
....TCTCTGATTAATCTTAACTCGTC....	23	0	1	4.00	4	2	1	0	1
....TGATTTAAGATTTTGTGAGG....	20	0	1	3.00	3	3	0	0	0
....TGATTTAAGATTTTGTGAGGCA....	22	0	1	3.00	3	1	1	0	1
....TGATTTAAGATTTTGTGAGGC....	21	0	1	2.00	2	2	0	0	0
....GATTTTGTGAGGCACGGTAAT....	21	0	1	1.00	1	0	0	1	0
....GATTTTGTGAGGCACGGTA....	19	0	1	1.00	1	0	0	1	0
....TCTGATTAATCTTAACTCGTCA....	22	1	1	1.00	1	0	1	0	0
....GGTCGGTTGCTCTGTCACCC....	20	0	1	1.00	1	0	0	0	1
....CTCTGATTAATCTTAACTCGTC....	22	0	1	1.00	1	1	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4770:5589005-5589170 -	der_103	GA--------AAGATACCT--ATACTG----------CC-TAT----------TAAAAGCGTTATTTTCCGATT----------G-CCCGACTGATTTAAGATTTTGTGAGGCACGGTAATTGCTATATGGA--CG----------GTCTCTGATTAATCTTA---ACTC----GTCTGGCGGTCGGTTGC-------TCTGTCA-CCCGATCATTCGTTC----------ATTC-GCTGGCTGAT
droYak3	3R:4867738-4867893 +		GA--------AAGATACCT--ATACTA----------CC-TAT----------TA----------AT-----------AATATCCATTACGACTGATTTAAGATTTTGTGAGGCACGGTAATTGCTATATGGA--CG----------GGTCTCTGATTAATCTTA---ACTC----GTCTGGCGGTCGGTTGC-------TCTGTCA-CCCGATCATTCGTTC----------ATTC-GCTGGCTGAT
droSec2	scaffold_27:645129-645278 -		GA--------AAGATACCT--ATACTA----------TC-TAT----------TA----------AT-----------AATATCCATTACGACTGATTTAAGATTTTGTGAGGCACGGTAATTGCTATATGGA--CG----------GGTCTCTGATTAATCTTA---ACTC----GTCTGGCGGTCGGTTGC-------TCTGTCA-CCCGATCATTCGTTC----------ATTC-GCTGGCTGAT
droSim2	3r:5212217-5212366 -		GA--------AAGATACCT--ATACTA----------TC-TAT----------TA----------AT-----------AATATCGACTGATTTACGATTTTGTGAGGCACGGTAATTGCTATATGGA--CG----------GGTCTCTGATTAATCTTA---ACTC----GTCTGGCGGTCGGTTGC-------TCTGTCA-CCCGATCATTCGTTC----------ATTC-GCTGGCTGAT
dm3	chr3R:16087405-16087554 +		GA--------AAGATACCT--ATACTA----------TC-TAT----------TA----------AT-----------AATATCGACTGATTAAAATTTTGTGAGGCACGGTAATTGCTATATGGA--CG----------GGTCTCTGATTAATCTTA---ACTC----GTCTGGCGGTCGGTTGC-------TCTGTCA-CCCGATCATTCGTTT----------ATTC-GCTGGCTGAT
droEug1	scf7180000409801:2408921-2409095 +		GA--------AACC-TTT--GAGCA----------CC-TAT----------CTCAATTTTCTATAGCTAATCTATT----------TTCATCTATTTTTGACTGATTTAAGCGTTGTTCGACAGTTATGCTATATGGA--CG----------GGTCTCTGATTAATCTTA---ACTC----GTCTGGCGGTCGGTTGC-------TCTGTCG-TCCGATCATTCGTTC----------ATTC-GCTGGCTGAT
droBia1	scf7180000302402:1879933-1880096 +		CA--------CAGATATTT--TTGCTG----------AAATCACT----CC-TAT----------ATCAACAGCAA----------CACTATTTTTGATGATTTCGCTTTTGCGGCACGTTATGCTATATGGA--CG----------GGCTCTGATTAATCTTA---ACTC----GTCTGGCGGTCGGTTGC-------TCTGTCG-TCCGATCATTCGTTC----------ACTC-GCTGGCTGAT
droTak1	scf7180000415013:21245-21412 +		TC--------CAGTTGTC--ATACTA----------CA-TAA----T----------TAAATAAT----------AACTATTT----------TTCTCTATTTTGACTGTTTTGCTTTTGCTTGTACAGTTATGCTATATGGA--CG----------GGCTCTGATTAATCTTA---ACTC----GTCTGGCGGTCGGTTGC-------TCTGTCG-TCCGATCATTCGTTC----------ATTC-GCTGGCTGAT
droEle1	scf7180000491008:829305-829478 -		CA--------ACAATTTT--AAATTA----------T-TAT----------AATTTTTTATAAGGAAGGGATAT---------G-------GTTCGTCTATTTTGCTGAGTTAAGATTTAGTTGTACAGTTATGCTATATGGC--CG----------GGTCTCTGATTAATCTTA---ACTC----GACTGGCGGTCGGTTGC-------TCTGCTGTTGCGATCATTCGTTC----------ATTC-GCTGGCTGAT
droRho1	scf7180000777229:5818-6016 -		AA--------TAAATATT--GTTCAG----------TTTGTGCAGACATTTTGTTAAATAT----------CCAAATTTTAAAAACCATAACGATGT----------GTCATCTATTTTGCTGATTTACTGTTTCGTTGAACACGTTATGCTATATGGA--CG----------GGCTCTCTGATTAATCTTA---ACTC----GACTGGCGGTCGGTTGC-------TCTGTCG-CCCGATCATTCGCTC----------ATTC-GCTGGCTGAT
droFic1	scf7180000454126:1115585-1115832 +		GA--------AAGATACAATGCATTCTGCAAAATAGAAAAAAAAGAAACGTAAAGCTTTTGTGTCG----------TTTGTT----------AAATTTTGTCTTTAATAATTCTACCATTAATTCCAACAATAACAACCCTACCATTTTAATCTATTTTGATGATTTAAGATTTTGTGGGCACGTTATGCTATATGGA--CG----------GGCTCTCTGATTAATCTTA---ACTC----GTCTGGCGGTCGGTTGC-------TCTGTCG-ACCGATCATTCGTTC----------ACTC-GCTGGCTGAT
droKik1	scf7180000302650:12996-13195 +		GTTCAATTCGAAATG----TTATGG----------ATATCTGTTTTAA----TAT----------TCAATTTTATCTTTAA----------TTTTAC-GTTGACTGATTTAAATTTTGTTAGGCACGTTCC-GCTATATAGTCTCG----------GGTCTCTGATTAATCTTA---ACTC----GTCTGGCGGTCGGTTGC-------TGGTA-GTTCGATCGTC----------ATTC-GCTGGCTGAT
droAna3	scaffold_13340:2633958-2634018 +		--GCTCTCTGATTAATCTTA---ACTC----GTCTGGCGGTCG----------A-CCGAT----GCGCTC----------ATTCCCTGCTTGAT
droBip1	scf7180000396712:1705272-1705330 -		--TCTCTGATTAATCTTA---ACTC----GTCTGGCGGTCG----------A-CCGAT----GCGCTC----------ATTCCGTTATTGAT
dp5	2:27601444-27601500 -		--TCTCTGATTAATCTTA---ACTC----GTCTGGCGGTCG----------A-CCGAT----GCGCTC----------CTTC-GTTGGGTGCT
droPer2	scaffold_6:2922995-2923051 -		--TCTCTGATTAATCTTA---ACTC----GTCTGGCGGTCG----------A-CCGAT----GCGCTC----------CTTC-GTTGGGTGCT
droWil2	scf2_1100000004902:10748670-10748729 -		--GTCTGATTAACTCTTA---ACTC----GTCGGTTGTCGGTTGC-------TCTGTCG-TTTCGTCGTT----------TTTCGTGATGAT
droVir3	scaffold_13042:3486084-3486260 -		TA--------TTTTCG----------CC-GAT----------AAACAAGTTTTTTCGAAATT----------CCGATAAACAGTTGCGGATTTTCGAAAACGTGAAAGCAGTCGTGGTTCCGT----------TTGTCAACAATCAATCATT---TCAGTCCGTCAATTGTCAACAA-TCAGTCAGAGTAAGTCTGTCC-GTCACTCAGT
droMoj3	scaffold_6496:13454010-13454212 -		GA--------AAGAA-TAT--GTACA----------A----------TA-TAA----TAAATTCTTGATTGAGTTTGAT----------AGGCAAGCTAAATT----------TATGTAAGCTTGACTGATTCGGAA-------AGTAGAT-------ATATGGA--TTAGTAGATTCCTTATCAGATCAATGGTGTAAGCTAATCGGTCGTTTTGTGA----GTCA-A-GTCGTCATTTTGCCTGTCGTCGTCGTC----TTTGTCTCC
droGri2	scaffold_14853:9413603-9413697 -		GC--------AAGAT----TA-----------CC-TAT----------AGTAGATGGA--GC----------TCGTGATTAATCC-AGC---GTT----GTCAATTAGTCGTCAA---TCAGTCATCAATT---AGTTCGTGA----------ATGAGTTCGTCAT

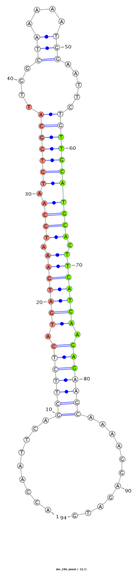
Generated: 09/08/2015 at 07:47 PM

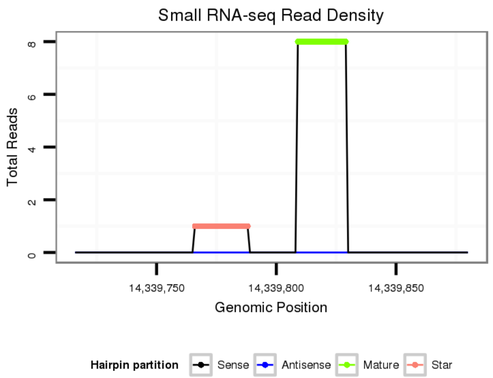
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

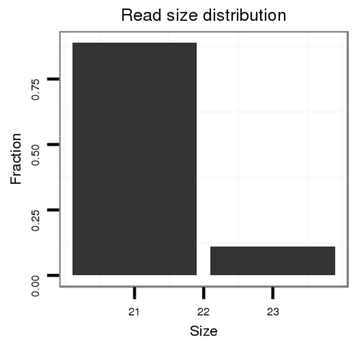
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_106	**scaffold_4784:14339766-14339830 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

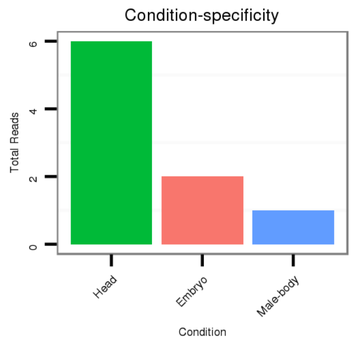
Legend: mature star mismatch in alignment mismatch in read

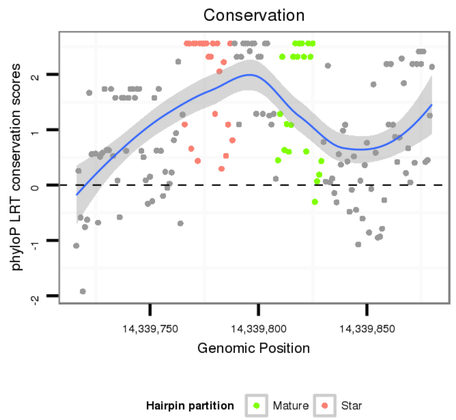
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG15682-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

										V108	V040	V107
AAAGCCAAAGTGTATTATCAGCCAGAACAATGGCAACCAATTCAGCTTCTCATGATGAAATGCAATGTGGCATTGGCTAAAAATGGAATTCTGTTGCATGCACTTCATCAAGAGAAGCAAAAGGAGATGCGGGAGAAGAATCCCTGACTGACTGGCTGACAGCTG	Read size	# Mismatch	Hit Count	Total Norm	Total	head	embryo	male body
************************************.........(((((((.(((((((.((((.(((((((....(((....)))).....)))))))))).)))))))..))))))).....**********************************												
..........TTGCATGCACTTCATCAAGAG..	21	0	1	8.00	8	5	2	1				
..........TTGCATGCACTTCATCAAGAGT.	22	1	1	2.00	2	1	0	1				
..................CATGATGAAATGCAATGTGGCAT..	23	0	1	1.00	1	1	0	0				

Anti-sense strand reads

						V060	M057	M055
TTTCGGTTTCACATAATAGTCGGTCTTGTTACCGTTGGTTAAGTCGAAGAGTACTACTTTACGTTACACCGTAACCGATTTTTACCTTAAGACAACGTACGTGAAGTAGTTCTCTTCGTTTTCCTCTACGCCCTCTTCTTAGGGACTGACTGACCGACTGTCGAC	Read size	# Mismatch	Hit Count	Total Norm	Total	head	embryo	female body
************************************.........(((((((.(((((((.((((.(((((((....(((....))).....)))))))))).)))))))..))))))).....**********************************								

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4784:14339716-14339880 +	der_106	AAAGC---------CAAA-GTGTATTAT--CAGCCAGAACAATGGCAACCAATTCAG----------CTTC----------TCATGATGAAATG---CAATGTGGCATTGGCTAAAAATGGAATTCTGTTGCATGCACTTCATCAA----GAG--AAGCAAA----------AGGAGATG----------CGGGAGAA---G----------AATCCCTGACTGACTGGCTGAC-AGCTG
droYak3	3L:14448054-14448229 +		AAAGCCAAAGAGCTAAA-GATATCCAT--CAACCAGAACAATGGCAACAAATGCAG----------CTTCTT----------CTCATAATGAAATG---CAATGTGGCATTGGCTAAAAATGGAATTCTGTTGCATGCACTTCATCAA----GAG--AAGCAAA----------AGGAGATG----------AGGGAGAA---G----------AGTCCCTGACTGACTGGCTGAC-AGCTG
droSec2	scaffold_0:6494510-6494677 +		AAAGC---------TAAA-GATATTAT--CAACCAGAACAATGCAAACAAATGCAG----------CTTCTT----------CTCATAATGAAATG---CAATGGGTATTGGCTAAAAATGGAATTCTGCTGCATGCACTTCATCA----GAG--AAGCAAA----------AGGAGATG----------AGGGCGAA---G----------AACCCTGACTGACTGGCTGAC-AGCTG
droSim2	3L:14019249-14019416 +		AAAGC---------TAAA-GATATTAT--CAACCAGAACAATGGCAACAAATGCAG----------CTTCTT----------CTCATAATGAAATG---CAATGGGTATTGGCTAAAAATGGAATTCTGCTGCATGCACTTCATCAA----GAG--AAGCAAA----------AGGAGATG----------AGGGCGAA---G----------AACACCTGACAGACTGGCTGAC-AGCTG
dm3	chr3L:14357480-14357647 +		AAAGC---------TAAA-GATATTAT--CAACCAGAACAATGGCAAAAATGTG----------CTTCTT----------CTCATAATGAAATG---CAATGAGACATTGGCTAAAAATGGAATTCTGCTGCATGCACTTCATCAA----GAG--AAGCAAA----------AGGAGATG----------AGGGAGAA---G----------AACCCTGACTGACTGGCTGAC-AGCTG
droEug1	scf7180000409456:579299-579476 +		GAAAC---------GAAATTGGTATTAC--CAACCAGAACAAAGGCAACAATAGCAG----------CTTCTT----------CGTCATAATCAAATGTGGCAATGTGACATTGGCTAAAAATGGAATTCAACTGCTGCACTTCATCAC----GAG--AAGCAGT----------GAAA-ACGAGCTG----------TGGC-AG-AGG---AGCAAGAG---G----------AATCCCTGA--------CTGAC-AGCTG
droBia1	scf7180000302428:5533249-5533419 -		GATTC---------CAAA-TGTATTAC--CACCAGAACAAAGGCAGCAAAATGCAG----------CTTTT----------CTTCATAATCAAATG---CAATGTGGCACTGGCTAAAAATGGAATTCTGCTGCTGCACTTCATCAC----GAGGGCAGCAA----------AGGAGATG----------GAGGAGCC---G----------GGGCCCTGACTGACTGGCTGAC-AGCTG
droTak1	scf7180000415135:7600-7762 +		AAATC---------CAAA-TGTATTAC--CACCAGAACAAAGAATAGCAAATGCAG----------CTTCTT----------CTTCATAATCAAATG---CAATGTGGCATTGGCTAAAAAGGAATTCTGCTGCTGCACTTCGTCAA----GAG--AAGCAAG----------AGGAGACA----------GAGGAGC---G----------GGGCCCTGACTGACTGGCTGAC-AGCTG
droEle1	scf7180000491199:1471074-1471251 +		AATGCGACTCGATCTCAAA-TGAATTAC--CAACCAGAACAAAGGAAAGCAAATGCAG----------CTTCTT----------CTGCATTATCAAATG---CAATGTGGCATTGGCTAAAAATGGAATTCTGCTGCTGCACTTCGTCAA----CGA--AAGCAAA----------AGGAGCGCA----------AAGGAGAA---G----------AAGCCCTGACTGACTGGCTGAC-AGCTG
droRho1	scf7180000769112:1-168 -		GAATT---------TAAA-TGCAATTAC--CAGCCAGAACAAAGGAAGCAAATGCAG----------CTTTTT----------CTTCATAATCAAATG---CATTGTGGCATTGGCTAAAAATGGAATTCTGCCGTCTGCACTTCGTCAA----CGC--AAGCGTAT----------TGGAGCGC---G----------AGGGAGCA---G----------AAGCCCTGACTGACTGGCTGAC-AGCTT-
droFic1	scf7180000453784:697374-697542 +		GAACT---------CAAA-TTGTATTAC--CACCAGAACAAAGGCAACAAAGCAG----------CTTCTT----------CGTCATAATGAAATG---CAATGTGGCATTGGCTAAAAATGGAATTCTGCATGCCAGCACTTCATCAA----AGG--AAGCAACA----------AGGAGCGG---G----------AGGGAGAA---G----------CCTTATGTGACTGACTGGCTGAC-AGCTG
droKik1	scf7180000302441:406626-406819 +		CATTAC---------CAAA-TGGTATTACGCCCAGCCAGAACAAAGGCAGCAAATGCGT----------GGGCTTCGTCC----GGCCTCATTATCAAATG---CAATGTGGCATTGGCTAAAAATGGAATTCTGCTGCTGCACTTCATCAA----GCG--AAGAATA----------AGGCCAAAG----------CAGGAGGAGGAGG-AGGAG-GTGGAGCG---G----------AAGCCCTGATGACTGACTGAC-AGCTG
droAna3	scaffold_13337:4711148-4711367 -		GTGCA---------CAAA-TGTATTAC--CAACCAGAACAAAAGCAGCAAAA----TGCTGCCTTTGAATCTGCTTGGCCGGGCTGGGGTTCATAATCAAATG---CAATGTGGCATTGGCTAAAAATGGAATTCTGCTGCTGCACTTCATCATTCAAGAG--GGCGCAACTGCAGAGGCTCCTCCAGCAAGGGCA-AGGAGCTG----------GGCAGCAGAGAAGTG----------C----------AAGTCCTGACTGA----CTGAC-AGCTG
droBip1	scf7180000396371:39976-40184 -		C-----------CACCTGTGTATTAC--CAGCCAGAACAAAAGCAGCAAATGTAACTGCTGG----------CTTCTG----------GGGTTCATAATCAAATG---CAATGTGGCATTGGCTAAAAATGGAATTCTGCTGCTGCACTTCATCATTCAAGAG--GAGCAACTGGTAAAGT---TCCAGCCAGGGCA-AGGAGCTG----------GGGA-AG-CTG---GGGAAGGAGAAGTG----------C----------AAGTCCTGACTGA----CTGAC-AGCTG
dp5	XR_group6:7035446-7035603 +		C-----------CA----C---------C---TCATAATCAAATG---CAATGTGGCATTGGCTAAAAATGGAATTCTGCTGCTGCACTTCATCAGA---GATG--------C---CAGGGAAAAGG---CTG----------GGG---AG--TGGGAC-----G---TGGGACTGTGACTGGGGGCAGCAAGAAGGTAAAGCTGGACTGTGACTGACTGACAGAC-AGCTG
droPer2	scaffold_41:399222-399379 +		C-----------CA----C---------C---TCATAATCAAATG---CAATGTGGCATTGGCTAAAAATGGAATTCTGCTGCTGCACTTCATCAGA---GATG--------C---CAGGGAAAAGG---CTG----------GGG---AG--TGGGAC-----G---TGGGACTGGGACTGGGGGCAGCAAGAAGGTAAAGCTGGACTGTGACTGACTGACAGAC-AGCTG
droVir3	scaffold_13049:21981456-21981583 -		CGGT----------CA----C---------C----------------------TTGG----------CTTGG----------GTTCATAATCAAATG---CAATG--GCA-TGACTAAAAATGGAATTCTTCTGCTGCTGCACTTCATCAA----CAT--GGGGGGGC----------CCCAAATG----------ACTCAAAA---G----------AGGCCAGACAAACGGACAGGACTAAATG
droMoj3	scaffold_6680:16541312-16541469 -		T-----------CA----C---------C----------------------TGGG----------TTTGG----------GTTCATAATCAAATG---CAAT--GGCA-TGACTAAAAATGGAATTCTGCTGCTGCACTTCATCAA----CAT--GGGGGGGC----------CCCAAATGACGCAAAGGACAAACACAGGCAGATGGAGAGAGAG--AGAGAGAGCG---G----AGAGGCAGAGAGGGCGACA----------AG-------------------GCTG
droGri2	scaffold_15110:21580113-21580219 +		C-----------CA----C---------C--TCATAATCAAATG---CAAT--GGCA-TGACTAA-CAATGGAATCTTCTGCTGCTACACTTCATCAA----CAT--GGGGGGGC----------CCCAAATG----------ACTC----G---AAATATCTGTTGAACACAGCTGAC-AGAC-

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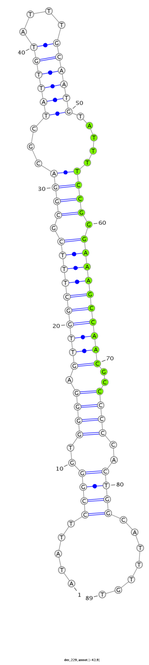
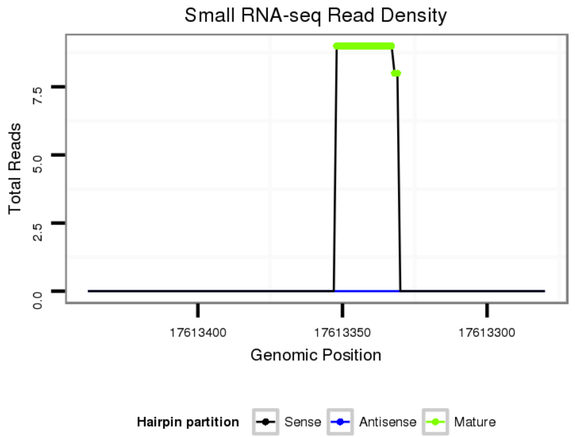
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

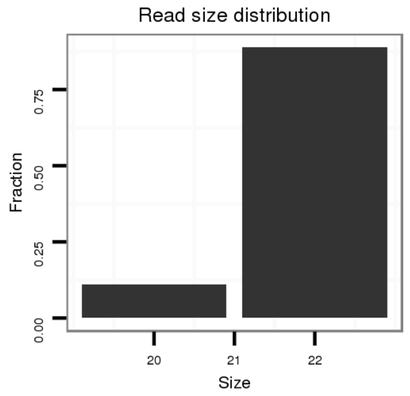
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_229	**scaffold_4690:17613330-17613388 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

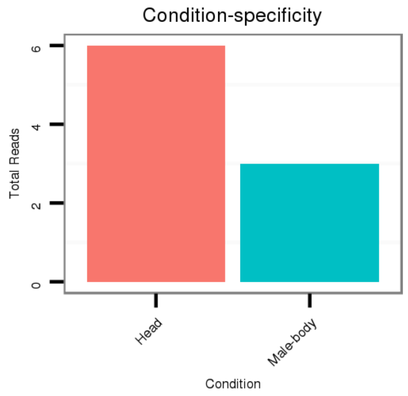
Legend: mature star mismatch in alignment mismatch in read

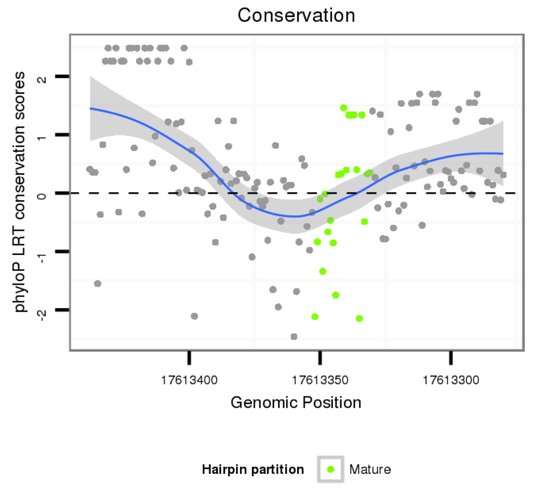
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG17550-in]; CDS [Dere\GG17550-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TACACCGTGGAGGCCTACTCCAGTACGTATACGTGATATTCCGGGTGGGGAGTTGGCTTTCGCGGACGCTATTGTATTTGCAATGTATTTTCCGGGAAAGCCAACGCCCCCCACTGGCATTTGTCGTGTTGTGTAATCAGTAATCCCGAGATGAGCACC	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	V108 head	V107 male body	V040 embryo
**********.....((((..((((.((((((((((.((((...((((((....))))))).....)))).)))))))))..))))..))))).....**********									
.....ATTTTCCGGGAAAGCCAACGCC.....	22	0	1	8.00	8	0	5	3	0
.....ATTTTCCGGGAAAGCCAACGCCA.....	23	1	1	1.00	1	0	0	1	0
.....ATTTTCCGGGAAAGCCAACG.....	20	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

ATGTGGCACCTCCGGATGAGGTCATGCATATGCACTATAAGGCCCACCCCTCAACCGAAAGCGCCTGCGATAACATAAACGTTACATAAAAGGCCCTTTCGGTTGCGGGGGGTGACCGTAAACAGCACAACACATTAGTCATTAGGGCTCTACTCGTGG	Read size	# Mismatch	Hit Count	Total Norm	Total	V060 head
**********.....((((..((((.((((((((((.((((...((((((....))))))).....)))).)))))))))..))))..))))).....**********						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4690:17613280-17613438 -	der_229	TACACC--GTGGAGGCCTACTCCAGTACGTATAC---GTGATATTCC------GGGTGGGGAGTTGGCTTTCGC-----GGACGCTATTGTATTT--GC---------------A---------------ATGTATTT-TCCGGGAAAG--CCAACG--CCCCCA----------CTGGCATTTGTCGTGT---T-GTGT--AATCAGTAAT--C---------CCGAGATGAGCACC
droYak3	X:20253967-20254125 -		TACACC--GTGGAGGCCTACTCCAGTACGTATAC---GTAATATTCC------GGGTGGGGGATTGGCTTTCGT-----GGAGACCATACCACCC--AC---------------------T---------CCAAC-TCCTCGAAAG--CCAGCG--CCCC-CA----------TTCGTTGCCATTCGTTGTGT---T-GTGT--AATCAGTAAT--C---------CCGAGATGAGCACC
droSec2	scaffold_8:3390427-3390578 -		TACACC--GTGGAGGCCTACTCCAGTACGTATAC---GTAATATTCC------GGGTGGGGGTTGGCTTTCGT-----GGAGACCGTACCACCC--AC---------------------------TACTC-TCGGGGAAAG--CCACCA--CCC--CA----------CGGCCATTTGTTGTGT---T-GTGT--AATCAGTACT--C---------CTGAAATGAGCACC
droSim2	x:19815304-19815455 -		TACACC--GTGGAGGCCTACTCCAGTACGTATAC---GTAATATTCC-------GCGTGGGGGTTGGCTTTCGT-----GGAGACCGTTCCACCC--AC---------------------------TACTC-TCCGGGAAAG--CCACCA--CCC--CA----------CGGCCATTTGTTGTGT---T-GTGT--AATCAGTACT--C---------CTGAAATGAGCACC
dm3	chrX:21082584-21082735 -		TACTCC--GTGGAGGCCTACTCCAGTACGTATAC---GTAATATTCC-------AGGTGGGGGTTGGCTTTCGT-----GGAGACCTTACCACCA--AC---------------------------TATTC-TCCTAGAAAG--CCATCA--CCC--CA----------CTGCCATTTGTTGTGT---T-GTGT--AATCAGTACT--C---------CTGAAATGAGCACC
droEug1	scf7180000408193:405125-405277 +		TACACC--GTGGAGGCCTACTCCAGTACGTATAC---GTGATGTTCC------GGGTGCCGCG--TGGCCTTCGA-----GGAGAACATGCCACCC--TT---------------------G---------TCTTC-TCCTGGAAGG--CCAACG--CACT-CG----------CTGCTTATGTGTTGTAT---T-GTGT--AATCAGTAAT--C---------CCGAGATGAGCACC
droBia1	scf7180000302187:449653-449811 +		TACTCC--GTGGAGGCCTACTCCAGTACGTATGC---GTGGTGTTGC------GGGTGGGG---TGGGTCTCCTGCCCAGGGACAACC-------T--GT---------------------G---------TGTTCCGTCCTCGAAAGACCGCCCCTCCC--CA----------CAGTGTTATGTGTTGTGT--TTCGTGT--AACCTATAAT--C---------CCGAGATAAGCATC
droTak1	scf7180000415158:365523-365617 +		TACACC--GTGGAGGCCTACTCCAGTACGTATAC---GTGATATTCC-------[-----------]-----[-----------]--C---------------------------TTGTTATGTGTTGTAT--CT-GTGT--ATCAAGTAAT-CC---------CCGAGATGAGAGTT
droEle1	scf7180000490214:835681-835823 +		TACACC--GTGGAGGCCTACTCCAGTACGTATAC---GTGATATTCC-------GGGCGGCGGG--GGCTTTCGG-----GGTGAAC--------T--GC---------------------------CATTT-TCCTTTAAAG--CCACCG--CCCC--C----------CTGTTATTTGTTGTAT---T-GTGT--AATCAGTAAC--C---------CCGAGATGAACACC
droRho1	scf7180000780082:142090-142248 +		TACAAC--GTGGAGGCCTACTCCAGTACGTATAC---GTGATATTCC-------GGGCGGCGGG--GGCTTTCGG-----GGAAACCATACCACCC--CA---------------------------ACCATCTCCCCTGGAAAG--CCACCG--CCCC-CG----------TTGT---TTGTTTGTTGTAT---T-GTGT--AATCAGTAATTCC---------CCGAGATGAACACC
droFic1	scf7180000454077:536625-536778 -		TACTCC--GTGGAGGCCTACTCGAGTACGTATAC---TTGATATTTGATATTGCGGGCGGCGGG--GGCTTTCG-----[----------]C---A--AC---------------------TCTTTCTTCTCCC----CA--TGGAGGAAAG--CCACCG--CCCC-CA----------CAGTTGTTTGTTGTGT---T-GTGT--GATCAGTAAT--C---------CCGAGATGAGCACC
droKik1	scf7180000302395:448686-448834 -		CTCCAC--GTGGATGCATACTCCAGTACGTATAC---GTGATATTCG-------GAGACCAGGA--CGCTGCTGG-----CAGTTC---------T--GTCTTCGTTTATTATGATTATTGTTTCCTCCTTCGCCT----C---[----------]-------[-------]----------GTGA---A-CTGT--[-------]AAATCCCCCCTTAAAAATATCAACCGA[------]AATC
droAna3	scaffold_13334:1155870-1155910 +		TACCAC--GTGGATGCCTACTCCAGTCGTATAC---TTGATATTC-[----------]-----[----------]--C---------------------------[-------]----------[-------]----------
droBip1	scf7180000395922:51108-51149 -		TACACC--GTGGATGCCTACTCCAGTCGTATAC---TTGATATTTC-[----------]-----[----------]--C---------------------------[-------]----------[-------]----------
dp5	XL_groupla:9146026-9146171 +		[------]--GTGGAGGCATACTCCAGTACGTATACACGCGATGTGCC------AGCTGCA[----------]-----[---------]CCCCCGCGC---------------------------[-------]----------[-------]----------
droWil2	scf2_1100000004515:69826-69862 -		AATCAA--GTGGATGCCTATTCCAGTGCGTATAC---GTAAT[-----]------[----------]-----[----------]--C---------------------------[-------]----------[-------]----------
droGri2	scaffold_15203:11211927-11211967 +		TCAGCCATGTGGATGCCTATTCCAGTAAGTATAC---GTAATAT[---]------[----------]-----[----------]--C---------------------------[-------]----------[-------]----------

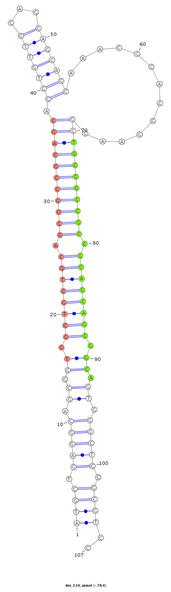
Generated: 09/08/2015 at 07:48 PM

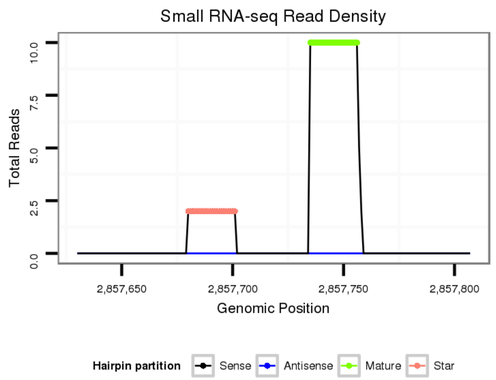
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

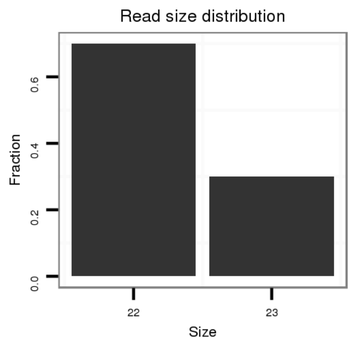
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_134	**scaffold_4690:2857680-2857757 +**	**candidate**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

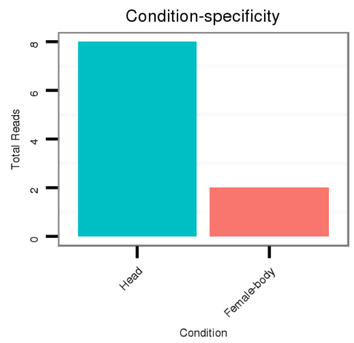
Legend: mature star mismatch in alignment mismatch in read

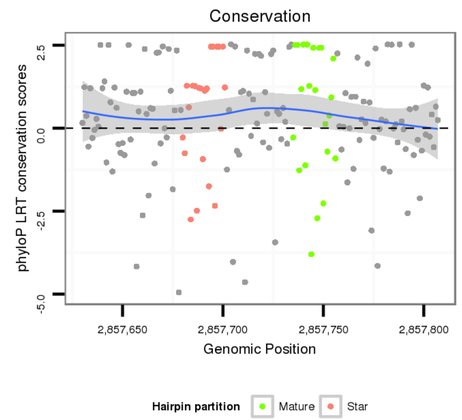
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dere\GG18769-cds]

Repeatable elements

Name	Class	Family	Strand
(CAG)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

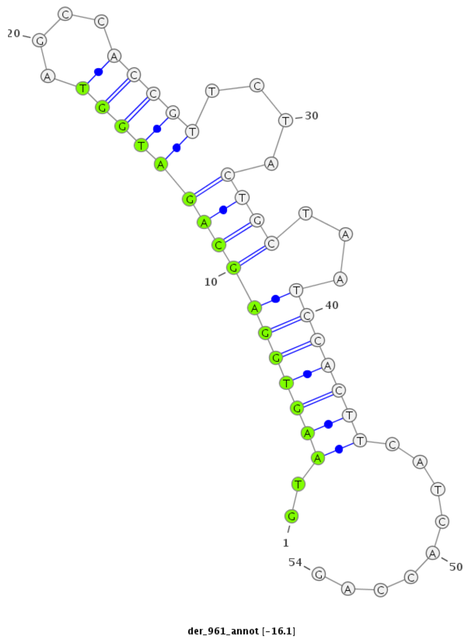
hide 3p reads | show mid mismatch reads

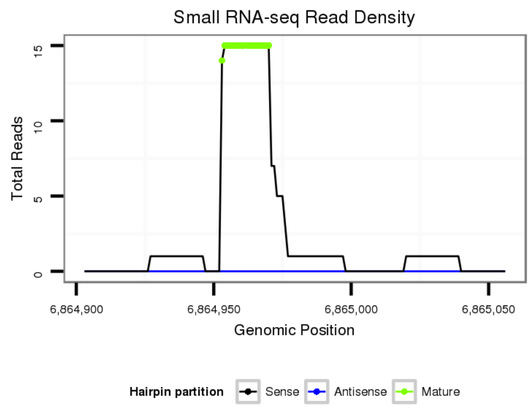
| | | |

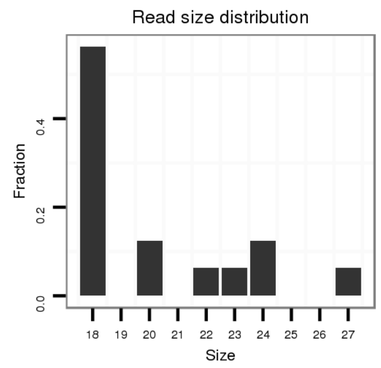
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_961	**scaffold_4820:6864953-6865006 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

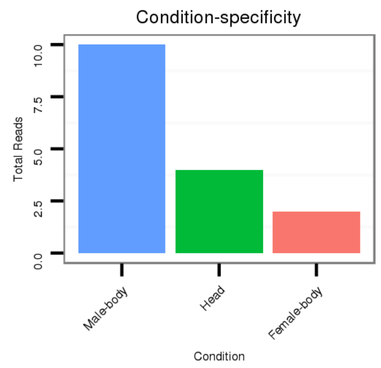
Legend: mature star mismatch in alignment mismatch in read

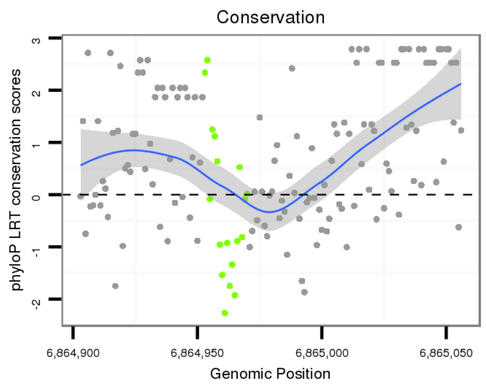
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG12249-in]; CDS [Dere\GG12249-cds]; CDS [Dere\GG12249-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTCTTTTTGAGGTCTCCCGCCAACACCAGTGTCACGCTCCTAACGCCTAGGTAAGTGGAGCAGATGGTAGCCACCGTTCTACTGCTAATCCACTTCATCACCAGGGTACATGACAACTCCCGTTCCGGATTCAACCAGTGGCCCTTCATGTCTG	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	V108 head	GSM1528801 follicle cells	M055 female body	M057 embryo	V040 embryo
**********..((((((((((((((((((....))))))....))))...)))))))).....**********												
.....GTAAGTGGAGCAGATGGT.....	18	0	1	9.00	9	8	1	0	0	0	0
.....AGTGTCACGCTCCTAACGCCTAGGAT.....	26	2	1	4.00	4	0	0	4	0	0	0
.....GTAAGTGGAGCAGATGGTAGCCAC.....	24	0	1	2.00	2	1	1	0	0	0	0
.....GTAAGTGGAGCAGATGGTAG.....	20	0	1	2.00	2	0	2	0	0	0	0
.....GTAAGTGGAGCAGATGGTAGCCA.....	23	0	1	1.00	1	1	0	0	0	0	0
.....AGTGTCACGCTCCTAACGCCC.....	21	1	1	1.00	1	0	0	0	1	0	0
.....ACCAGTGTCACGCTCCTAAC.....	20	0	1	1.00	1	0	1	0	0	0	0
.....TAAGTGGAGCAGATGGTAGCCA.....	22	0	1	1.00	1	0	0	0	1	0	0
.....AGCCACCGTTCTACTGCTAATCCACTT.....	27	0	1	1.00	1	0	0	0	1	0	0
.....TCCGTTCCGGATTCAACCA.....	20	0	1	1.00	1	0	0	0	0	1	0

Anti-sense strand reads

GAGAAAAACTCCAGAGGGCGGTTGTGGTCACAGTGCGAGGATTGCGGATCCATTCACCTCGTCTACCATCGGTGGCAAGATGACGATTAGGTGAAGTAGTGGTCCCATGTACTGTTGAGGGCAAGGCCTAAGTTGGTCACCGGGAAGTACAGAC	Read size	# Mismatch	Hit Count	Total Norm	Total	V040 embryo	V060 head	M055 female body
**********..((((((((((((((((....))))))....))))...)))))))).....**********								

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4820:6864903-6865056 +	der_961	CTCTTTTTGAGGTCTCCCGCCAACACCAGTGTCACGCTCCTAACGCCTAGGTAAGTGGA----------GCAGA----------TGGTAGCCA-----CCGTTC----------TAC-----TGCTAATCC--A----CT----------TCATCACCAGGGTACATGACAACTCCCGTTCCGGATTCAACCAGTGGCCCTTCATGTCTG
droYak3	3R:25310971-25311129 +		CTCTTTTTGAGATCGCCGCCAACACCAGTGTCACGCTCCTAACGCCTAGGTAAGTGGA----------GCAGA----------TGGTAGCCACCGCACCGAAC----------TCC-----TGCTAATCC--A----CT----------TGTTCACCAGGGTACATGACAACTCCCGTTCCGGATTCAACCAGTGGCCCTTCATGTCTG
droSec2	scaffold_33:436113-436266 -		CTCTTTTTGAGGTCTCCCGCAAACACCAGTGTCACGCTCCTAACGCCTAGGTAAGTGGC----------GCAGA----------TGGTAACCA-----CCGAAC----------TCC-----TGCTAATTC--C----CT----------CCATCAACAGGATACATGACAACTCTCGTTCCGGATTAAACCAGTGGCCCTTCATGTCTG
droSim2	3r:20692631-20692784 -		CTCTTTTTGAGGTCTCCCGCAAACACCAGTGTCACGCTCCTAACGCCTAGGTAAGTGGC----------GCAGA----------TGGTAACCA-----CCGAAC----------TCC-----TGCTAATTC--C----CT----------CCATCAACAGGATACATGACAACTCTCGTTCCGGATTCAACCAGTGGCCCTTTATGTCTG
dm3	chr3R:21182015-21182168 -		CTCTTTTTGAGGTCTCCCGCAAACACCAGTGTCACGCTCCTAACGCCTAGGTAAGTGGC----------GCAGA----------TGGTAACCA-----CCGAAC----------TCC-----TGCTAATTC--C----CT----------CCATCAACAGGATACATGACAACTCTCGTTCCGGATTCAATCAATGGCCCTTCATGTCTG
droEug1	scf7180000409692:196170-196325 +		TTGTTCCTGAGGTCTCCCGCCAACACCAGTGTCACTCTCTAACGCCAAGGTAAGTCAT----------GTCCC----------TGGTAACC-----GAAAC----------TTT-----CACTAATTC--CAAAACT----------TGTTCACCAGGATACATGACAACTCCCGTTCTGGTTTCAACCAATGGCCTTCATGTCTG
droBia1	scf7180000302136:2002022-2002178 -		CTGTACTTGAGGTCGCCGCCAACACCAGTGTCACGCTCTAACGCCCAGGTCAGATCA----------GCAGT----------CCTGGCT-TAAA-TAAAC----------TTT-----CACTAACA--C----CT----------TATCACCAGGGTCCAGACAACTCCCGTTCCGGTTTCAACCAGTGGCCCTTCATGTCGG
droTak1	scf7180000415257:18806-18879 -		----------GCTAATCA--C----CT----------T----------GTTTCACCCAGGATACATGACAACTCCCGTTCCGGTTTCAACCAGTGGCCCTTCATGTCGG
droEle1	scf7180000491212:555912-556131 -		CTGTTCTTAAGGTCACCGCCAACACCAGTGTCACGCTCCTAACGCCTAGGTAAGTGGTCTCTATATAGCACTGTGTAACATTCCTAGGGTGTTAAACAGTGCTT----------C---GCAACT-----T--C----GAACTTACGATTCTGAAAATACACTTT----TCTAACA--C----CT----------AATCGTAATTT----------ATTCACCAGGGTGCATGACAACTCCCGTTCCGGTTTCAACCAGTGGCCTTTCATGTCGG
droRho1	scf7180000779365:58341-58499 +		ATCTTCTTGAGGTCACCCGCCAACACCAGTGTCACATCCTAACACCCAGGTAAGTAGA----------GCTCT----------CAGTGGCCC-----CAAAAC----------TTT-----CACTTATTTATCGTAA--C----------A-C----------ATTTCGCCAGGATACACGACAACTCGCGCTCCGGTTTCAACCAGTGGCCCTTCATGTCGG
droFic1	scf7180000454055:1099640-1099798 -		ATCTACTTCGCATCACGCCAACACCAGTGTTACGCTCCTCAGTCCTAGGTAAATTAC----------TCATTATTTAAGGC----------CTT-----GCTTT-----CCCTAATAA--C----CC----------AATGTTATTT----------AATCCATTAGGATCCACGACAATCCCCGTCCGGCTTCAACCAGTGGCCCTTCATGTCGG
droKik1	scf7180000302355:1327776-1327853 +		GAATTCTCCCTCCTATTCCCT----------CTA-CAATCA--C----CT----------TA--CAATCA--C----CT----------TA--CAATCA--C----CT----------TA--CAATCA--C----CT----------TA--CAATCA--C----CT----------TA--CACACAGAATCCATGACAATTCCCGTTCCGGCTTCAACCAGTGGCCCTTCATGTCGG
droAna3	scaffold_13340:9287362-9287520 +		CTGTATCTCCGGTCTCCAGCCAACAGTAGCGTTACCGTGCTCACATCCAGGTCAGTTCT----------TATT-----AGT----------TCTTTG--ACCTAAATGCCC----------TAC-----TAATGACCC--G----AT----------TCGCGTCCAGACTCCAGGACAATTCGCGTTCCGGATTCAACCAGTGGCCATTTATGTCAG
droBip1	scf7180000396712:444030-444185 +		CTGTATCTCAGGTCTCCAGCCAACACCAGTGTGACACGTGCTCACGTCCAGGTAGTCCT----------CCTTT-----GGT----------CTCCA--ATCGAACTGCAC----------TAC-----TAATGACA--G----CA----------T-CGTTCCAGACTTCAGATAATACTCCGCTCCGGATTCAACCAGTGGCCCTTCATGTCAG
dp5	2:27536765-27536929 +		CTGTACTTGAGGTCGCGCCAACACCAGTGTGACGTTGCTGACGCCCGGTAACATTT----------TGCCCTGAGAGGTC----------CT----------GCTTGCCCCCACTTATG--C----CC----------CCCCACTCTAATCTCCCGGCAGTGTCATGACAACTCGCGCAGGGCTTCAATCAGTGGCCCTTCATGTCGG
droPer2	scaffold_6:2856420-2856583 +		CTGTACTTGAGGTCGCGCCAACACCAGTGTGACGCTGCTGACGCCCGGTAACATTT----------TGCCCTGAGAGGTC----------CT----------GCTTGCCCCCACTTAC--C----CC----------CCCCACTCTAATCTCCCGGCAGTGTCATGACAACTCGCGCAGGGCTTCAATCAGTGGCCCTTCATGTCGG
droWil2	scf2_1100000004902:6929440-6929599 +		TTGTATTTTAAAGTCTCCAGCCAACACTAAGGTCACACGTGCTCACACCAGGGTAAGTGCAG----------AGAGAATA----------TAGAA----C----AG----------TCC-----TTCAGATGTGTAATATCAT----------TTCACTCTCCAGAATTCATGACAATCTCCGTTCCGGCCTTCAATCAATGGCCCTTCATGTCGG
droVir3	scaffold_12822:3383978-3384139 +	dvi_2702	CTCTTCCGTCACCTCGCGAATGGGCACCAA----------GTCAGTTGT----------TTCTT-----ATATATATTAAAGT-----GAA----AGCAAC----------CCT----TGATAATTG--T----CT----------TTGTTAGATCCATGATTCTGTCACGACGCGCCAATCGATGATCAGCATCGCGATGGTTTCACGAAATGGCCCTTCATGACCA
droMoj3	scaffold_6540:16703849-16704008 +		CTCTTCCGTCACCTCCCCATGGGCACCAA----------GTAAGTGTT----------AGTCT-----AGATC---TCAAGT-----GGA----AGCAG----------T--T----TTATACTTC--A----TT----------CCGCATGCTAGATCCATGATTCTGTCGCGACGCGCTAACGACGATGATCATCGCGATGGCTTCACGCAATGGCCCTTCATGACCA
droGri2	scaffold_14906:1022611-1022775 +		CTGTTTTCTCACTTCTCCCATGGGCACCAA----------GTCAGTGGA----------AGTAATA-----C---TCTACT-----T--T----AGAATAA----------C----CAAT-ATTTCACATTA--T----------ACCTTCGCATCCAGATCCATGATTTTGTCGCGTCGTGCCAATCGATGATCATCGCGACGGTTTCACGCAATGGCCCTTCATGACCA

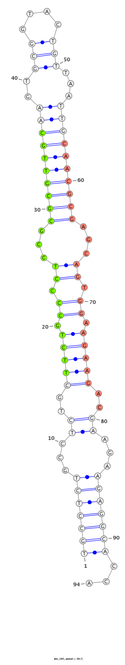
Generated: 09/08/2015 at 07:01 PM

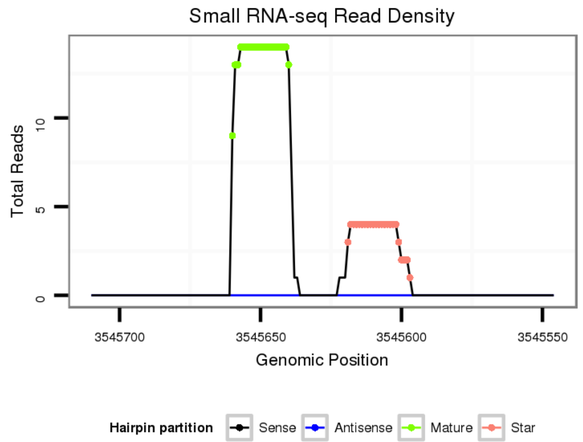
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	0
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

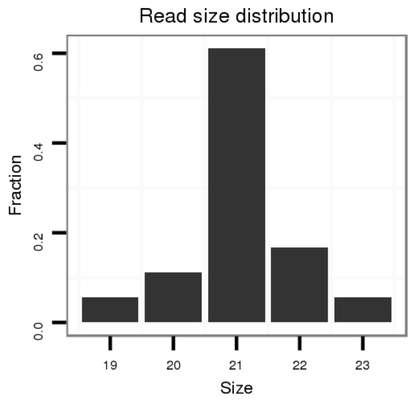
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_105	**scaffold_4690:3545596-3545660 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

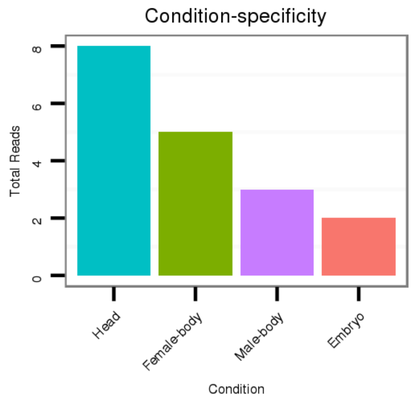
Legend: mature star mismatch in alignment mismatch in read

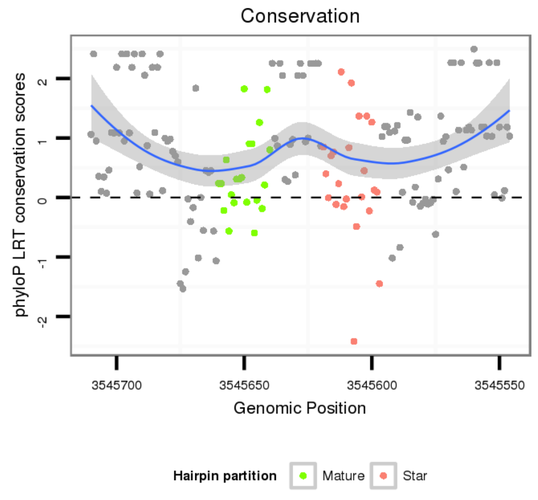
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTCGAGTTAACTTCTACTTTTCCGCTCTTCCGCTCTGCCTCTGCCTCTGCTTCTTGCCCCTCCGCGCGTTGCAAGTGCGGTACTGTTAATTGCAACGCGAGCAGTGGAAGAAGACGAAGAAGAGGCACCACCATCAGCGGCGGCGTCATTAATTAAGCGCCACTAG **********(((((((...((..((((((.((.((...((((((((((..(((....)))...))))))))))...))).)).)))))..))...)))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	V108 head	V107 male body	M057 embryo	V040 embryo	V060 head
.....TTCTGCCCCTCCGCGCGTTGC.....	21	0	1	5.00	5	1	3	0	0	0	1
.....TCTGCCCCTCCGCGCGTTGCA.....	21	0	1	3.00	3	1	0	1	1	0	0
.....TTCTGCCCCTCCGCGCGTTGCA.....	22	0	1	3.00	3	1	1	1	0	0	0
.....TTCTGCCCCTCCGCGCGTTG.....	20	0	1	1.00	1	1	0	0	0	0	0
.....CAACGCGAGCAGTGGAAGAAGAC.....	23	0	1	1.00	1	0	0	0	0	1	0
.....TTGCAACGCGAGCAGTGGAAG.....	21	0	1	1.00	1	0	1	0	0	0	0
.....AACGCGAGCAGTGGAAGAAGA.....	21	0	1	1.00	1	0	1	0	0	0	0
.....CAACGCGAGCAGTGGAAGA.....	19	0	1	1.00	1	0	0	1	0	0	0
.....TCTGCCCCTCCGCGCGTTGCAAA.	23	1	1	1.00	1	0	0	0	1	0	0
.....TGCCCCTCCGCGCGTTGCAAG.....	21	0	1	1.00	1	1	0	0	0	0	0
.....TCTGCCCCTCCGCGCGTTGC.....	20	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

CAGCTCAATTGAAGATGAAAAGGCGAGAAGGCGAGACGGAGACGGAGACGAAGACGGGGAGGCGCGCAACGTTCACGCCATGACAATTAACGTTGCGCTCGTCACCTTCTTCTGCTTCTTCTCCGTGGTGGTAGTCGCCGCCGCAGTAATTAATTCGCGGTGATC **********(((((((...((..((((((.((.((...((((((((((..(((....)))...))))))))))...))).)).)))))..))...)))))))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V040 embryo	V108 head

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4690:3545546-3545710 -	der_105	GTCG---AGTT-AACTTCTACTTTTCCGCTCTTCCGCTCT--G----------CCTCTGCCTCTGCTTCTGCCCCT---CC------GCGCGTTGCAA--GTGCGGT----------ACTGTTAATTGCAACGCGAGCAGTGGAAGAAG--------ACGAAG----------AAGA----------GGCAC------CACCATCAGCGGCGGCGTCA--TTAATTAAGCGCCACTAG
droYak3	X:15044320-15044493 -		GTCG---AGTT-AACTTCTACTTTTCCGCTCTGCCGCTGCTTCTGCTCTC----------GTCT------GTTCTGCC---CCCC------GCGTGTTGCAA--GTGCGGT----------ACTGTTAATTGCAACGGCAGCAGCAGCAGCAG--------AAGAAGAAGA----AGTAGAAGA----------AG------CACCACTATCGGCGGCGTCA--TTAATTAAGCGCCACTAG
droSec2	scaffold_36:329779-329963 +		GTCG---AGTT-AACTTCTACTTTTCCGCTCTTCCGCTCTACTCCGCTCTTCTTCACTCTTCTTCTCGCT----------T---GTTGTCCTCGCC------GCGCGTTGCAA--GTGCGAT----------ACTGTTAATTGCACGCGAGCAGTGGAAGAAG--------ACGAAGAAGAAG-------AAGA----------AG------CACCACGCATCGGCGGCGTCA--TTAATTAAGCGCCACTAG
droSim2	X:11035839-11036026 +		GTCG---AGTT-AACTTCTACTTTTCCGCTCTTCCGCTCTACTCCGCTCTTCTTCACTCTTCTTCTCGCT----------T---GTTGTCCTCGCGT------GCTCGTTGCAA--GTGCGGT----------ACTGTTAATTGCACGCGAGCAGTGGAAGAAG--------ACGAAGAAGA-----AGAAGAAGA----------AG------CACCACGCATCGGCGGCGTCA--TTAATTAAGCGCCACTAG
dm3	chrX:11653981-11654158 +	dme_389	GTCG---AGTT-AACTTCTACTTTTCCGCTCTTCCGCTCTACACCTCGCTTCTTCACTCTTCC------------T---GTTCACCTCGCC------GCGCGTTGCAA--GTGCGGT----------ACTGTTAATTGCACGCGAGCAGTGGATGAAG--------ACGAAGAAGAAG-------CAGC----------AC------CACCACGCATCGGCGGCGTCA--TTAATTAAGCGCCACTAG
droEug1	scf7180000409528:2770-2909 -		GTCG---AGTT-AACTTCTACTTTTCCGCTCTTCCGCTGC-C----------T-TTT----------CC---CGCCGCTT---CCCGCAA--GTGGTGT----------CCTGTTAATTGCAGCGGCAGTAGAAGAAG---------------AAG-------TAGC----------AG------CACCAGCTTCGGCGGCGTCA--TTAATTAAGCGCCACTAG
droBia1	scf7180000298389:1446042-1446153 +		GTCG---AGTT-AACTTCTACTTTTCCGCTCTTCCGCTCC-T----------GTG----------CC---CGCCGC----CCCTGCAA--GTGCGGT----------ACTGTTAATTGCAGCGGCAGAAGAA---------------------------------------GCGGCGTCA--TTAATTAAGCGCCACTAG
droTak1	scf7180000414375:233299-233442 -		GTCG---AGTT-AACTTCTACTTTTCCGCTCTTCCGCTCT--T----------GTGGTC-T-TCTT---TTCC---GCGCGC----CCCTGCAA--GTGCGGT----------ACTGTTAATTGCAGCGGCAGAAGGAGAAG---------------AAGA----------AG------CACCACATCGGCGGCGTCA--TTAATTAAGCGCCACTAG
droEle1	scf7180000491023:521360-521490 -		GTCG---AGTT-AACTTCTACTTTTCCGCTCTTCCGCTCG-T----------CGCT-TCT----------CC---CGCCGC----CCCTGCAA--GTGCGGT----------ACTGTTAATTGCAGCGGTCAGAAGTGGAAGAAG--------------------------CGGCAGCGGCGGCGTCA--TTAATTAAGCGCCACTAG
droRho1	scf7180000777256:11279-11422 -		GTCG---AGTT-AACTTCTACTTTTCCGCTCTTCCGCTCT--T----------CCTT----------CC---CGCCGC----CCCTGCAA--GTGCGGT----------ACTGTTAATTGCAGCGGCAGAAGTGGCAGAAG--------AAGAAGCATC----------AGCAG-----AAGCAGCAGCGGCGGCGTCA--TTAATTAAGCGCCACTAG
droFic1	scf7180000453277:112072-112248 +		GTCG---AGTT-AACTTCTACTTTTCCGCTCTTCCGCTCG-C----------GTTTT----------CC---CGCCGC----CCCTGCAA--GTGCGGT----------ACTGTTAATTGCAGCGGCACAAGAAGAAGAAGCATATGATGATGAAGAAGA--AGAAGAA--GAAGTTGAAAAAGA--AGCAG-----AAGTAGAAGCGGCGGCGTCA--TTAATTAAGCGCCACTAG
droKik1	scf7180000302544:479366-479455 +		GTCGCCGGGGCC-AACTTCTACTTTTCCGCTCTTCGGC---C----------------------------------C---C------CCCTGCAAGTGTGCGGT----------ACTGTTAATTGCAG--CGGCGTCA--TTAATTAAGCGCCAGCAG
droAna3	scaffold_13417:1400265-1400413 +		GTCG---TGGT-AACTTCTACTTCTTCCGCTCTTCCG----C----------------------------------C---C------CCCCAG--GTGAGGC----------ACTGTTAATTGCGGCGGCACAAGCTGAAGCACCAGCTGGGGCAGAAG----------CAGA--------AGCACGAGCAGCGAGAAAGGCAGAGAAGGCTTCA--TTAATTAAGCGCCAGTAG
droBip1	scf7180000395647:15872-16016 +		GTCG---TGGT-AACTTCTACTTTTCCGCTCTTCCG----C----------------------------------C---C------CCCCAG--GTGAGGT----------ACTGTTAATTGTGGCGGCACAAGAAGAAGAAG--------CAAGCACA--AGCAGAA--GCACGGGA-AAAGCACGAGCATGTGCAA--------GAAGAAGGCTTCA--TTAATTAAGCGCCAGTAG
dp5	XL_group1a:2270644-2270762 -		GTCC---AACT-AACTTCTACTTTTCCTCTCTTCCGTTCT--T----------CCACT----------TG---TGCAGCT---CCCCGCAGCAAGCGTGCGGT----------ACTGTTAATTGCAGCGGCAGCAGTA--------------------------------GCAGGATCA--TTAATTAAGCTCCATCAG
droPer2	scaffold_28:706492-706610 -		GTCC---AACT-AACTTCTACTTTTCCTCTCTTCCGTTCT--T----------CCACT----------TG---TGCAGCT---CCCCGCAGCAAGCGTGCGGT----------ACTGTTAATTGCAGCGGCAGAGGTA--------------------------------GCAGGATCA--TTAATTAAGCGCCATCAG
droWil2	scf2_1100000004590:372748-372777 +		G---C----CCCC-------------------------C---C----------------------------------C---C------CCCCGC----------ACTGTTAATTGCAGCGGCAGCAGTA--------------------------------GCGGGATGGACTTAATTAAGCGTCATTAG
droVir3	scaffold_12928:2241911-2241958 -		GTTT---GGTT-AACTTTACTCATCCACCTCCCGCTCT--C----------TCTCT----------GT---CTCT------CCCCCC----------ACTGTTAATTGCAGCGGCAGCAGTA--------------------------------GCAGGATCA--TTAATTAAGCGCCATCAG
droGri2	scaffold_15081:164605-164739 +		CTCT---GCTGCTGCCTCTGCTGCT-GCCTCTCGCTGC--T--G----------CCGCT----------GC---TGCTGCTGAAGCACGTTGAAA--ATGTTGTAACTTTGCAGCTTATCCTGGAATTAGGTAAGCAACAGCA--------------------------------GCAGCGGCC--GCCA--GGACGCAGCGAAGA

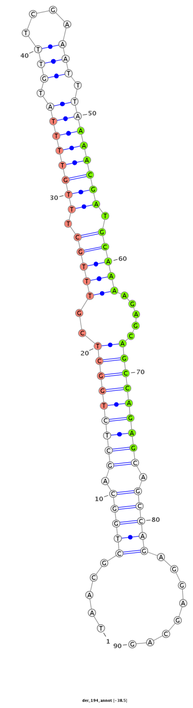
Generated: 09/08/2015 at 09:53 PM

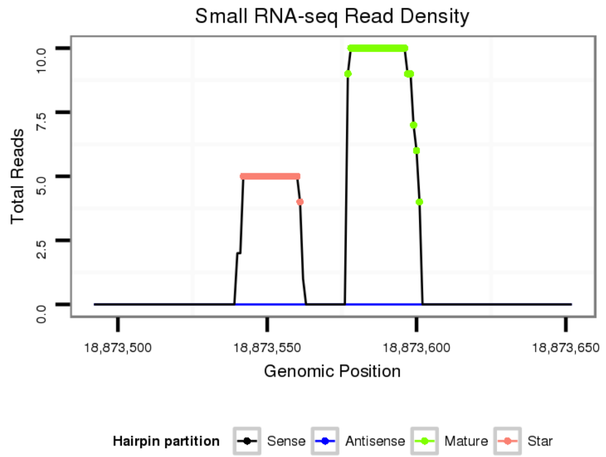
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	0
rescue.known	0
rescue.confident	0
rescue.candidate	2

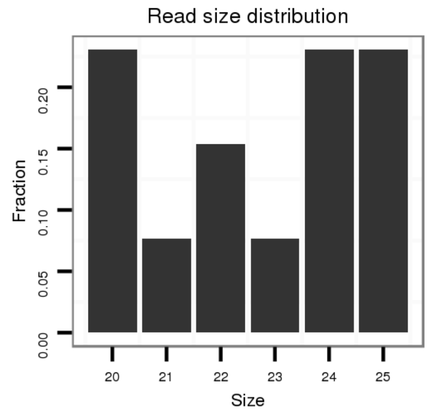
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_194	**scaffold_4929:18873542-18873602 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

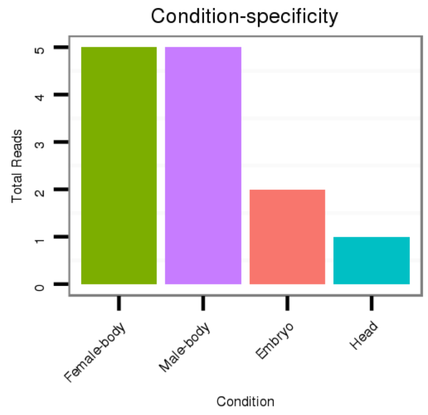
Legend: mature star mismatch in alignment mismatch in read

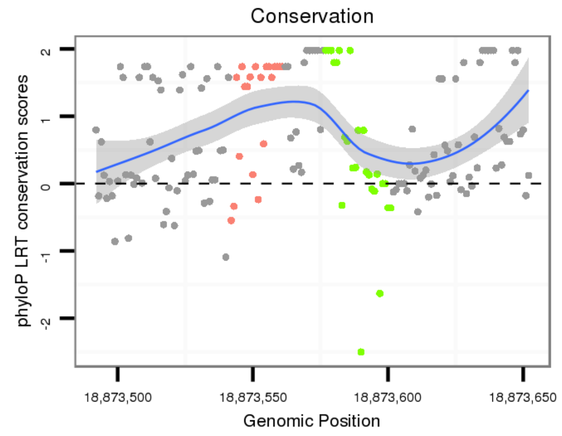
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG10703-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGTTTTCCGTGCGAGCCCAAACCTCAGCGCCCTCTTAACGCTGGCAGCTCTGGCTCGTTTGCTTTGTTTTATGTTTCGAAATTTAAAACGATGCAAAAGAGCAGCCAGAGCAGCCAGAGGAGCAGCAGCTCGCGAGGAGGCTGATAATAGGGGCAGAAACA	Read size	# Mismatch	Hit Count	Total Norm	Total		V107 male body	M055 female body	V108 head	V040 embryo	M057 embryo	V060 head
.....	25	0	1	3.00	3	3	0	0	0	0	0	0
.....	24	0	1	2.00	2	0	0	0	0	1	1	0
.....	20	0	1	2.00	2	0	2	0	0	0	0	0
.....	26	1	1	2.00	2	2	0	0	0	0	0	0
.....	22	0	1	2.00	2	2	0	0	0	0	0	0
.....	23	0	1	1.00	1	0	0	1	0	0	0	0
.....	21	0	1	1.00	1	0	1	0	0	0	0	0
.....	24	0	1	1.00	1	0	1	0	0	0	0	0
.....	21	0	1	1.00	1	0	0	1	0	0	0	0
.....	20	0	1	1.00	1	0	1	0	0	0	0	0
.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....	22	1	1	1.00	1	1	0	0	0	0	0	0

Anti-sense strand reads

ACAAAAGGCACGCTCGGGTTTGGAGTCGCGGGAGAATTGCGACCGTCGAGACCGAGCAAACGAAACAAAATACAAAGCTTTAAATTTTGCTACGTTTTCTCGTCGGTCTCGTCGGTCTCCTCGTCGTCGAGCGCTCCTCCGACTATTATCCCCGTCTTTGT	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	V107 male body	V108 head
.....	25	0	1	3.00	3	3	0	0
.....	24	0	1	2.00	2	0	0	0
.....	20	0	1	2.00	2	0	2	0
.....	26	1	1	2.00	2	2	0	0
.....	22	0	1	2.00	2	2	0	0
.....	23	0	1	1.00	1	0	0	1
.....	21	0	1	1.00	1	0	1	0
.....	24	0	1	1.00	1	0	1	0
.....	21	0	1	1.00	1	0	0	1
.....	20	0	1	1.00	1	0	1	0
.....	22	0	1	1.00	1	1	0	0
.....	22	1	1	1.00	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4929:18873492-18873652 +	der_194	TGTTT---TCC--GTGCG--AGCCCAAA---CCTCAGC-GCCCTCTTA------ACGC--TGGCAGCTCTGGCT----------CGTTTGC--TTTGTTTTATGTTTCGAAATTTAAAACGATGCAAAAGAGCAGCCAGAGCAGCCAG---AG--GAGCAGCAGCTCGCGAGGAGG-CTGATAATAGGGGCAGAAACA--
droYak3	2L:16408027-16408178 -		TGTTT---TTC--GTGTG--AGCCCAAA---CCTCAGC-GCCCTCTTA------ATGC--TGGCAGCGCCGGCT----------CGTTTAC--TTTGTTTTATGTTTCGAAATTTAAAACGATCAAAACAGCAGCC---------AA---AG--AAGCAGCGCTCGTGAGGAGT-CTGATAATAAAGGCAGAAATA--
droSec2	scaffold_1:1390695-1390839 -		TGTTC---TTC--GTGTG--AGCCCAAA---CC-----T----TCTTG------ATGCCTGGCAGCGCTGGCT----------CGTTTGC--TTTGTTTTATGTTTCGAAATTCAAAACGATGCAAAAGAGCAGCC---------CA---AG--GAGCAGCAGCTCGTGAGGAGT-TTGATAATAAAGGCAGATATA--
droSim2	2r:4576533-4576679 -		TGTTC---TTC--GTGTGAGAGCCCAAA---CC-----T----TCTTG------ATGCCTGGCAGCTCTGGCT----------CGTTTGC--TTTGTTTTATGTTTCGAAATTCAAAACGATGCAAAAGAGCAGCC---------CA---AG--GAGCAGCAGCTCGTGAGGAGT-CTGATAATAAAGGCAGATATA--
dm3	chr2R:3743728-3743870 -		TGTTC---TTC--GTGTG--AGCCCAAA---CC-----T----TCTTA------ATGC--TGGCAGCTCTGGCT----------CGTTTAC--TTTGTTTTATGTTTCGAAATTCAAAACGATGCAAAAGAGCAGCC---------CA---AG--AAGCAGCAGCTCGTGAGGAGT-CTGATAATAAAAGCAGATATA--
droEug1	scf7180000409672:5768306-5768459 -		TTTT-----TCC--CTGTA-AACCCCAAA---CCTCAGC-GTCCTCTTA------ATGT--TACCAGCGCCGGCT----------CGTTTAC--TTTGTTTTATGTTTCGAAATTTAAAACGAAGCAAATAGCAAA---------GA---AG--AAGCGGCGCTCATGATTGAGT-CTGATAATAAAGGCAGATATTTC
droBia1	scf7180000301506:574429-574584 +		TCTTTTCCTTG--GTGTG--TGCCCAAA---GTTCGCC-ATACTCCTATATATAA----C--CCCAGCTCTGGCT----------CGTTTAC--TTTGTTTTATGTTTCGAAATTTAAAACGATGCAAGATAGCAGCG---------CA---GG--AAGCGACGCTCGTGATGCGT-CTGATAATAAGGCAGATATT--
droTak1	scf7180000415870:91582-91733 +		TTTT-----CC--ATGTG--ACCCAAA---CCTCAGC-GTACTCTTTATGTAA---C--TTCAGAGCCGGCT----------CGTTTAC--TTTGTTTTATGTTGAGAAATTTAAAACGATGCAAAATAGCAGCA---------GA---ATCAGAGCAGCAGCTCGTGTGAGT-CTGATAATAAGGCAGATATT--
droEle1	scf7180000491343:12399-12550 +		TGTTTGC-CGA--GTGTC--AGCCCAAA---CCTCAGA-GCACTCTTA------ATGT--TACCAGCTCTGGCT----------CGTTTAC--TTTGTTTTATGTCTAGAAATTTAAAACGACGCAAAACAGCAACA---------GA---AG--GGCGCGCAGCTCGTGAGGAGT-CTGATAATAAGGCAGATATT--
droRho1	scf7180000780226:193004-193156 -		TTTTT---CGA--GTGTTT-AAGTCCAAA---CCTCAGA-GCACTCTTA------ATGT--TACCAGCTCTTGCT----------CGTTTAC--TTTGTTTTATGTCTAGAAATTTAAAACGAAGCAAAAGAGCGGCA---------GA---AG--GAGCAGCAGCTCGTGATGAGG-CTGATAATAAGGCAGATATT--
droFic1	scf7180000453215:467858-467999 +		TTCC-----CGT--GTGTG--ATTCCAAG---CC-----T----CGTA------GTGC--TACAATCCCCGCT----------CGTTTAC--TTTGTTTTATGGTACGAAATTTAAAACGACGCAAAAGAGCAGCT---------GA---AG--GAGCAGCAGCTCGTGATGGTCGCGATAATAAGGCAGATATT--
droKik1	scf7180000302471:368570-368739 -		ATTTC---TCCCTGTGCA--TGCCCAAA---CCTCGACGCACTCTTA------ATGT--TACCAGCTCTTGCTGTTGATGCTG----CTGGTGCTTTGTTTTATATTTCGAAATTTAAAACGATGCAAAATAGCGAAG--GATG---GAAGCAA--GACTACGCAGCTCTTGATGAAC-CTGATAATAAGGCAGATTTCA--
droAna3	scaffold_13266:16077159-16077312 -		TTTCC---TCT--GTGTA--AGCCCAAAAAACTCCTTGGGCCTTTA------ATGT--TCTAGCTCTTGGTCCTGCCGCCGTCGTATAC--TTTGTTTTATGTTTCGAAATTTAAAACGATGCACAATAGCC-TG---------GA---AG--GCGC-----------CGCCT-CCGATAATAAGCCAGATACT--
droBip1	scf7180000396567:561910-562057 +		TTTC---TCCCTGTGTA--AGCCCAAAAAAGTTCGTTGGGCCTTTA------ATGT--TCTAGCTCTTGGTCCTGCTGCCGTCGTATAC--TTTGTTTTATGTTTCGAAATTTAAAACGATGCACGAGATAGCA----TG---GA---AG--GCGC-----------TGCCT-CTGATAATGAAGGCAGATTATT--
dp5	4:13447513-13447093 +		T--GTTTCGAAATTTAAAACGATCAAAAGTGAAAGCC---------GG---AGCTGCATAGAAGCATGAGATGCGT-CTGATAATGAGGGAAGATA----
droPer2	scaffold_2:8172986-8173066 -		T--GCTTCGAAATTTAAAACGATCAAAAGTGAAAGCC---------GG---AGCTGCATAGAAGCATGAGATGCGT-CTGATAATGAGGGAAGATA----

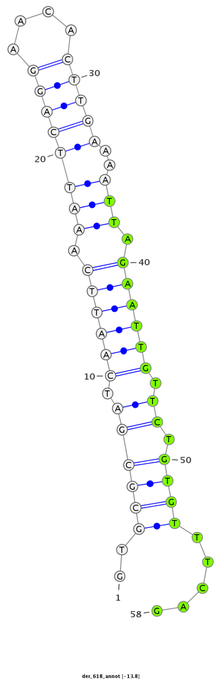
Generated: 09/08/2015 at 07:48 PM

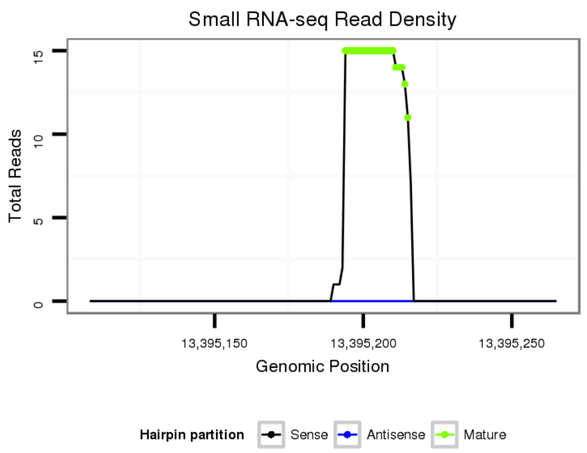
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

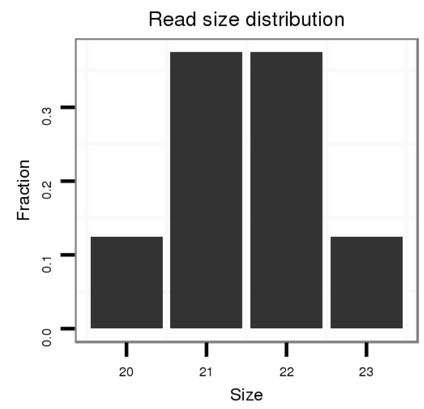
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_618	**scaffold_4770:13395158-13395215 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

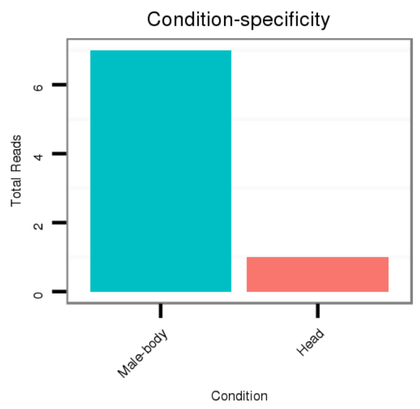
Legend: mature star mismatch in alignment mismatch in read

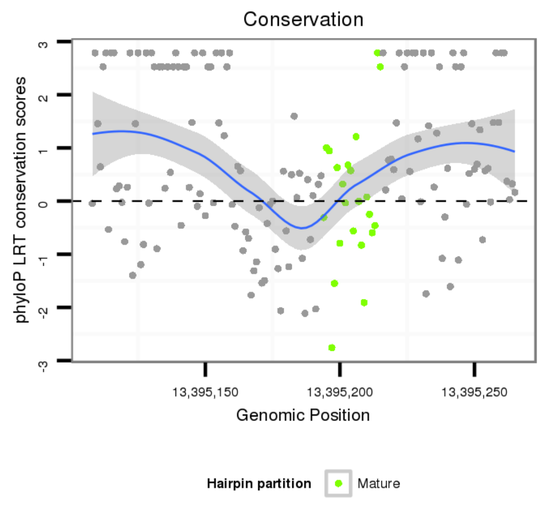
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG17132-in]; CDS [Dere\GG17132-cds]; CDS [Dere\GG17132-cds]; utr5 [utr5_minus_8733]; utr5 [utr5_minus_8734]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

TAAGGACAAAACGGTGTTTATAACCGGAGGCACAGGATTACTGGGCAAAGGTGCGCGATCAATTCAAATTCAGGAACACTTGAAAATTAGAATTGTTCTGTGTTTCAGTGGTCATTGAAAAGCTGTTGCGGGCGACGGATGTGAAACGTATATATTTC	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	V108 head	V040 embryo
**********..(((((((.(((((((.(((((((((....))))))..))))..)))))))..)).)))).....**********								
.....TTAGAATTGTTCTGTGTTTCAGT.....	23	0	1	7.00	7	6	1	0
.....TTAGAATTGTTCTGTGTTTCAG.....	22	0	1	3.00	3	3	0	0
.....TTAGAATTGTTCTGTGTTTCAGA.....	23	1	1	2.00	2	2	0	0
.....TTAGAATTGTTCTGTGTTTCA.....	21	0	1	2.00	2	2	0	0
.....AAAATTAGAATTGTTCTGTGT.....	21	0	1	1.00	1	0	1	0
.....TTAGAATTGTTCTGTGTTTCAGTA.....	24	1	1	1.00	1	1	0	0
.....ATTAGAATTGTTCTGTGTTTCAGA.....	24	1	1	1.00	1	1	0	0
.....TTAGAATTGTTCTGTGTTTC.....	20	0	1	1.00	1	1	0	0
.....ATTAGAATTGTTCTGTGTTTCAG.....	23	0	1	1.00	1	1	0	0

Anti-sense strand reads

ATTCCTGTTTTGCCACAAATATTGGCCTCCGTGTCCTAATGACCCGTTTCCACGCGCTAGTTAAGTTTAAGTCCTTGTGAACTTTTAATCTTAACAAGACACAAAGTCACCAGTAACTTTTCGACAACGCCCGCTGCCTACACTTTGCATATATAAAG	Read size	# Mismatch	Hit Count	Total Norm	Total
**********..(((((((.(((((((.(((((((((....))))))..))))..)))))))..)).)))).....**********					

No data available in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4770:13395108-13395265 +	der_618	TAAGGACAAAACGGTGTTTATAACCGGAGGCACAGGATTACTGGGCAAAGGTGCGCGATCAATTC----------AAAT----------TCAGGAACACTT----------G----AAAATTA---G----------AATTGTTCTG--------T---GTTTCAGTGGTCATTGAAAAGCTGTTGCGGGCGACGGATGTGAAACGTATATATTTC
droYak3	3R:12547593-12547747 -		TAAGGACAAAACGGTTTTTATAACCGGAGGCACAGGATTACTGGGCAAAGGTGCGCGATCAATTC----------AAAT----------TCA---ACACGT----------G----ATAATTA---T----------GATTCTTCTG--------T---GTTTCAGTGGTCATAGAAAAGCTGTTGCGGGCGACGGATGTGAAGCGTATATATTTC
droSec2	scaffold_5907:1171-1343 +		CAAGGATAAAACGGTGTTTATGACCGGAGGCACAGGATTACTGCGCAAAGGTGCGCGATCAATTAC-CCAAAAAA---T----------TAAGAACATA---------AAAA--AA---AATTA---G----------AATTGTTCTGCCCTAAA-A---ATTTCAGTGGTCGTAGAAAAGCTATTGCGGGCAACGGATGTGAAACGTATATATTTC
droSim2	3r:12890283-12890454 +		CAAGGATAAAACGGTGTTTATAACCGGAGGCACAGGATTACTCGGCAAAGGTGCGCGATAGATTACTCAAAAAAA---T----------TGAAGAACATTT----------A----AAAATA---T----------AATGGTTCTGCCCTAAA-A---ATTTCAGTGGTCGTAGAAAAGCTATTGCGGGCAACGGATGTGAAACGTATATATTTC
dm3	chr3R:8221496-8221665 -		TAAGGACAAAACGGTGTTTATAACCGGAGGCACAGGATTACTCGGCAAAGGTGCGCGCGTGCGATTA----------TTATCCAAT----------AGAAGAACATTT----------A----TAAATA---T----------TTTTGTTTTGCCCTAAA-T---ATTACAGTGGTCGTAGAAAAGCTATTAAGGGCGACGGATGTGAAACGTATATACTTC
droEug1	scf7180000409615:472810-472978 -		TAAGGATAAAACAATTTTTATAACCGGAGGCACAGGATTACTGGGCAAAGGTGTGGTATTAAATA----------AAAA----------CCAAAAACATGT----------GTTA---TAATA---T----------CATTGTTCTGCCTTTAA-AAAAATGTTAGTGATCATTGAAAAGCTATTGCGATCGACGGAACTGAAACGTGTATATTTT
droBia1	scf7180000302155:80529-80695 +		TAAGGACAAAACAGTTTCTTAACCGGAGGCACAGGATTGCTGGGAAAAGGTGCGGAGTGAATTT--GAAAATAA---G----------CGGA---------------------AAAAG--AA---TATTA---G----------TACTATTCTGGACGGTACA---CTTTCAGTGATCATAGAAAAGTTGTTGCGGTCGACAGATGTGAAACCCATATACATG
droTak1	scf7180000415366:314002-314163 +		TAAGGACAAAACAGTTTTAATAACCGGAGGCACAGGATTGCTGGGCAAAGGTGCGGAACGTGAA---A--AAAA----------------------CGAAAG--GACATTATTA---T----------CATTGTTCTGCCCTCAAAT---CTTTTAGTGACCATTGAAAAGCTATTGCGGTCGACGGATGTGAAACGTATATATTTC
droEle1	scf7180000490731:41861-42040 +		CAAGGACAAAACAGTGTTTATAACTGGAGGCACAGGATTTCTAGGCAAAGGTGCGCCATTTTCC---AAAAAAA---A----------GAAAAAAATC-AATTTCAACCAAAG--GA---TAATA---G----------CAGTGTTTTATCCAAAA-A---TTTGCAGTGATCATAGAAAAGTTATTGCGCAGCTAGAGATGTGAACGTGTATATATTTC
droRho1	scf7180000779237:6241-6408 -		TAAGGACAAAACAGTTTTCATAACCGGAGGCACAGGATTTCTAGGCAAAGGTTCGCCACATATCC---A--AAA----A----------TC----------ATTGTCAACAAAAG--GA---TAATA---G----------CAATGTTTTGTCCCACA-A---ATTACAGTGATCATAGAAAAGCTATTGCGGGTAACCGATGTGGAACGTATATATTTC
droFic1	scf7180000453812:858734-858904 +		TAAGGATAAAACGGTTTCGTAACCGGAGGCACGGGATATCCTGGGCAAAGGTGTGGTATGTATA---A--AAA----T----------GAAGAAC----AATTTTGACCAAAG--GA---TAATA---A----------CAGTGTTTTGCAAAAAAA---CTTTCAGTGATTATTGAAAAGCTGTTGCGATCGACGAGAAGTGAAACGTATTTATTTC
droKik1	scf7180000302475:94622-94781 -		CAAAGACAAGGTCGTGTTTCTAACAGCCGCACCGGATTTTTGGGAAGAGGTATGCGTCCCGTGC---A--GAT----TCATT----------TCAGT---CCTT----------G----GGATTCA---T----------AATTCTACTG--------C---CCCCTAGTCATTATTGAAAAGCTGTTGCGAGCTACGGATGTGAAACCCATATACGCC
droAna3	scaffold_13340:7435954-7436116 -		TAAGGATAAAGTGGTGTTCATGACTGGAGCCACCGGTTTCTAGGAAAAGGTTATTAGCCACATA---A--CGC----TTTGTT----------TCAAAAACAATT----------T----AA-ATTA---A----------TTTAGT----------GATA-T---ATTTTAGTGATTATTGAGAAACTTTTGCGATCTACCGAAGTGAAACGAATATATTCC
droBip1	scf7180000396708:1411563-1411723 +		TAAGGATAAGGTGGTTTTTTGACAGGAGGCACGGTTTTTAGGAAAAGGTTAATAACCAATCT----------TATACTTGT----------GAATTA---ACTT----------T----AT-AT----T----------TATGCATACACTTATA-T---ATTTTAGTCATTATTGAAAACTGTTGCGGTCTACCGATGTCAAGGAAATATATACC
dp5	2:5450559-5450716 -		TAGGGACAAGACGATATTCGTAACTGGCGGCACTGGATTTTGGGCAAAGGTGCGGTGCAAGGA----------CTGGA-----TGGAAACATGAG----------T----AACC----------T----TATTATACCTTTTC-A---TTTTCAGTGATTATTGAAAAATCCTACGAGCGACAGATCCAAAGAAAATATATTTC
droPer2	scaffold_19:1166761-1166918 -		TAGGGACAAGACGATATTCGTAACTGGCGGCACTGGATTTTGGGCAAAGGTGCGGTGCAAGGA----------CTGGA-----TGGAAACAAGAG----------T----AACC----------T----CATTGTACCTTTTC-A---TTTTCAGTGATTATTGAAAAATCTTACGAGCGACAGATCCAAAGAAAATATATTTC
droWil2	scf2_1100000004902:5365501-5365657 -		CAAAGATAAAGAACATTCTTATAACGGTGGCACGGGATTGTAGGCAAAGGTGTGTATTAACTT--CAAAAAAT---C----------TATG----------CAACG--AA----TTA---T----------CATTGT----GATT-A---TCGTTAGTATCCATTGAGAAATTATTACGCACACGGAGGTGAAACACATATATACC
droVir3	scaffold_13047:18246703-18246865 -		CAAGGATAAGGGGTGTTCCTTACAGGCGGCACCGGCTTCTTTGGCAAAAGTAAGTTGGCAAAC----------GCGAT-----CGT-GACTTGAA----------T----AATTGAATACC----T----------TTACGAATTCATTGT-------T---ACGCAGTTATTATTGAGAAACTGTTGCGCGTCACGGAGGTGCGCCAAATATATTTG
droMoj3	scaffold_6540:13477660-13477823 +		CAAGGATAAGGGGTGTTTGTCACTGGCGGCACTGGATTCTTTGGCAAAAGTAAGTTGGCAAAC----------GCGAT-----CGT-GACTTGAA----------T----AATTGATTACC----T----------TTACGAACTGATTT----T---G---TACGCAGTTATTATTGAGAAACTGTTGCGTGTTACGGAGGTGCCTCAAATATATTTG
droGri2	scaffold_15074:6440447-6440627 +		CAAGGATAAAGGCGTCTTCCTCACAGGCGGCACTGGTTCTTTGGTAAAAGTAAGTTGAACGT----------GACTTGAATTTATTATTGG----------CTGC---TGTTGTTGTTGTTTTACTAACGAATTGATTG--------T---CCGCTAGTTATTATTGAGAAACTGTTGCGCGTCACAGAGGTGCCTCAAATATATTTG

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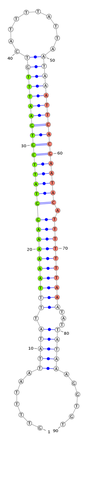
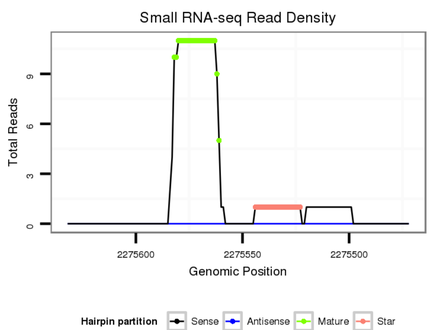
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

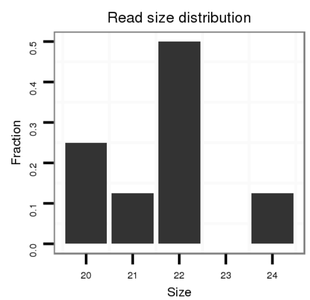
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_196	**scaffold_4845:2275522-2275582 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

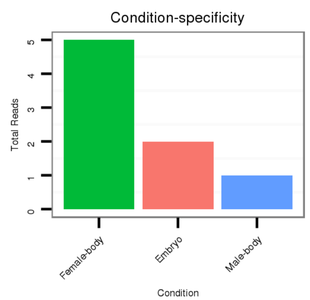
Legend: mature star mismatch in alignment mismatch in read

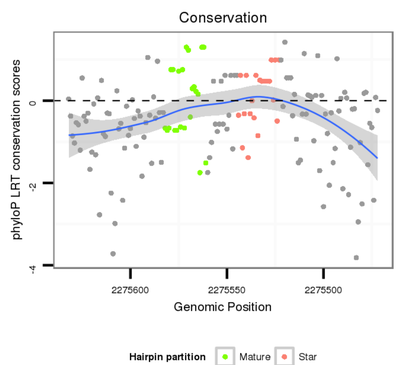
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dere\GG21362-in]

Repeatable elements

Name	Class	Family	Strand
AT_rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CATATATTAAATGCCTATGATTCGGACATCAATACGTTTTAATTATATTTTAAAAAAGGTATTCGTGAATTTGTCATTTTATTAATAAATTCACGAATACATTTTTTTAAATATTATAAAGGTGTTGCATGAGCATTTGAAACATTATTCTGGAAGTAAAA	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	M057 embryo	V107 male body
..........TAAAAAAGGTATTCGTGAATTT..........	22	0	1	3.00	3	3	0	0
..........TTTAAAAAAGGTATTCGTGAATT..........	23	0	1	2.00	2	1	0	1
..........ATTATAAAGGTGTTGCATGAGC..........	22	0	1	1.00	1	0	1	0
..........TAAAAAAGGTATTCGTGAATT..........	21	0	1	1.00	1	1	0	0
..........AAAAAGGTATTCGTGAATTT..........	20	0	1	1.00	1	1	0	0
..........TTAAAAAAGGTATTCGTGAATT..........	22	0	1	1.00	1	1	0	0
..........ATTCACGAATACATTTTTTTAA..........	22	0	1	1.00	1	0	1	0
..........TTAAAAAAGGTATTCGTGAAT..........	21	0	1	1.00	1	0	0	1
..........TAAAAAAGGTATTCGTGAATTTGT..........	24	0	1	1.00	1	0	1	0
..........TAAAAAAGGTATTCGTGAAT..........	20	0	1	1.00	1	0	0	1
..........TTAAAAAAGGTATTCGTGAATG..........	22	1	1	1.00	1	0	1	0

Anti-sense strand reads

GTATATAATTTACGGATACTAAGCCTGTAGTTATGCAAAATTAATATAAAATTTTTTCCATAAGCACTTAAACAGTAAAATAATTATTTAAGTGCTTATGTAAAAAAATTTATAATATTTCCACAACGTACTCGTAAACTTTGTAATAAGACCTTCATTTT	Read size	# Mismatch	Hit Count	Total Norm	Total	V060 head
.....((((((.((((((((((((((((((((((((((.....)))))))))))))))))))))))))).)))))))))...)))))).....**********	22	0	1	3.00	3	3

Show Alignment With Reads

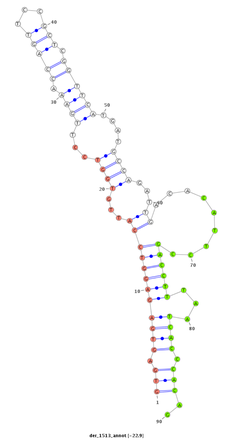
Re-alignment of all predicted orthologs

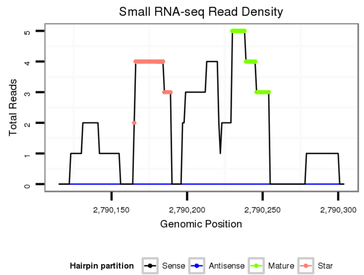
Species	Coordinate	ID	Alignment
droEre2	scaffold_4845:2275472-2275632 -	der_196	CATATATTAAAT--------GCC----------TA---TGATTCGGACATCAAT----------ACGTTTTAATTA---------TATTT----------TAAAAAGGTATTCGTGAATT----------TGTCATTTTATTAATAAATTCACGAAT----------ACATTTTTTTAAATATTATA-AAGGTGTTGCATGAGCATTTGAAA---C----------ATTATTCTGGAAGTAAAA
droYak3	v2_chrUn_4937:71-222 -		CGGGTATTAAAA----------CCGGTCGTT---TGTTTTATAAT----------AGT-------TTGTTGTTAA-AAAGAATAAT-TGATAATTCA----------TAAATTAAATTAAGATATTATTAGCAT----------TTTCTTAAGTACTTAAACTCGCGG----------TGCTAATTACAAAATATCAATTCGCAAG-TGAA
droSec2	scaffold_30:289323-289516 +		CAAATTTTATGT----------TGATCCTATA---ACGAAAGTTTA----------AAAACACAATAT-------TTAATTTGTATTAAATCGAAAGTTCATTTGGTTAGTTCAATTTGTAAAGCATTTTCGTTTATTAATTGTTAG

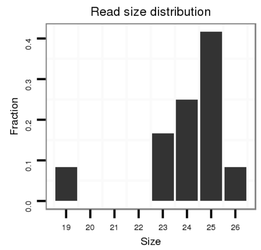
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1513	**scaffold_4929:2790165-2790254 +**	**Known Ortholog**	**MiRNA**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

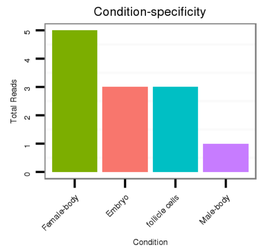
Legend: mature star mismatch in alignment mismatch in read

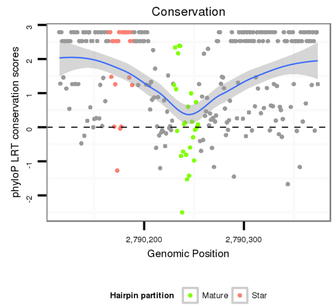
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dere\GG24877-in]; utr5 [utr5_plus_362]; CDS [Dere\GG24877-cds]; CDS [Dere\GG24877-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

```
CTGGAGCTGATAGACAATCCAGCGGTTCTATTTTTAGACGAGCCCACAACGTGAGTGACATTCCGACCTTTAATCACCCACAGCGGATTGGACAGCTCCTCCTCCTTCGACACCATCCAGCTGCTGCGCGGCC
**********************************************(((.(((((((((((((...((((...((((.((((((..))).)))))))...)))))...))))).........)))))))...)))))..)))..**********************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	V107 male body	GSM1528801 follicle cells	M057 embryo	V060 head	V108 head
25	0	1	3.00	3	0	0	3	0	0	0
25	0	1	2.00	2	2	0	0	0	0	0
24	0	1	2.00	2	0	0	0	2	0	0
19	0	1	1.00	1	1	0	0	0	0	0
23	1	1	1.00	1	1	0	0	0	0	0
23	0	1	1.00	1	1	0	0	0	0	0
25	0	1	1.00	1	0	1	0	0	0	0
26	0	1	1.00	1	0	0	0	1	0	0
24	1	1	1.00	1	0	0	0	0	0	0
22	0	1	1.00	1	1	0	0	0	0	0
24	1	1	1.00	1	0	0	0	0	1	0
23	0	1	1.00	1	0	1	0	0	0	0
24	0	1	1.00	1	1	0	0	0	0	0
19	0	1	1.00	1	0	1	0	0	0	0

Anti-sense strand reads

```
GACCTCGACTATCTGTTAGGTCGCCAAGATAAAAATCTGCTCGGGTGTTGCACTCACTCTCCAGGTAACACCAGGAACTTTGGTCAAGGCGAGCCAAGTACTACGGTCTAACTGTGTAAGGCTGGAAATTAGTGGGTGTCGCCTAACCTGTCGAGGAGGAGGAAGCTGTGGTAGGTCGACGACGCGCGG
**************************************************(((.(((((((((((...((((...((((.((((((..))).)))))))...)))))...))))).........)))))))...)))))..)))..**************************************************
```

Read size	# Mismatch	Hit Count	Total Norm	Total	V040 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4929:2790080-2790339 +	der_1513	TGAGTGGCGGCCAGAAGAAGCGTCTGTCCATCGCCCTGGAGCTGATAGACAATCCAGCGGTCTATTTTTAGACG
droYak3	2L:2732641-2732903 +	dya_176	TGAGTGGCGGCCAGAAGAAGCGTGTCCATCGCCCTGGAGCTGATAGACAATCCAGCGGTGTATTTTTAGACG
droSec2	scaffold_5:903565-903828 +		TGAGTGGCGGCCAGAAGAAGCGTGTCCATCGCCCTGAGCTGATAGACAATCCAGCGTGTATTTTTAGACG
droSim2	2L:2625098-2625361 +		TGAGTGGCGGCCAGAAGAAGCGTGTCCATCGCCCTGAGCTGATAGACAATCCAGCGTGTATTTTTAGACG
dm3	Chr2L:2737483-2737746 +	dme-mir-4914	TGAGTGGCGGCCAGAAGAAGCGTGTCCATCGCCCTGGACTGATAGACAATCCAGCGTGTATTTTTAGACG
droEug1	scf7180000409554:3374544-3374813 -		TGAGTGGCGGCCAGAAGAAGCGTGTCCATCGCCGTGAGCTGATAGACAATCCAGCGTGTATTTTTAGACG
droBia1	scf7180000302188:1736337-1736614 +		TGAGTGGCGGCCAGAAGAAGCGTGTCCATCGCCCTGGAGCTGATAGACAACCCAGTGGTGTATTTTTAGACG
droTak1	scf7180000415705:481657-481929 +		TGAGTGGCGGCCAGAAGAAGCGTGTCCATCGCCCTGGAGCTGATAGACAATCCAGCGGTGTATTTTTAGACG
droEle1	scf7180000491273:444333-444600 -		TGAGTGGCGGCCAGAAGAAGCGTGTCCATCGCCATGGAGCTGATAGACAATCCAGCGGTGTATTTTTAGACG
droRho1	scf7180000766156:89853-90117 -		TGAGTGGCGGCCAGAAGAAGCGTGTCCATCGCCATGGAGCTGATAGACAATCCAGCGGTGTATTTTTAGACG
droFic1	scf7180000453924:665372-665645 +		TGAGTGGCGGCCAGAAGAAGCGTGTCCATCGCCCTGGACTGATAGACAATCCAGCGTGTATTTTTAGACG
droKik1	scf7180000302473:48832-49088 -		TGAGTGGCGGCCAGAAGAAGCGTCTGTCCATCGCCCTGGAGCTGATAGACAATCCAGCGTGTATTTTTAGACG
droAna3	scaffold_12984:201875-202183 +		TGAGTGGCGGCCAGAAGAAGCGTGTCCATCGCCCTGGAGCTGATAGACAATCCAGCGTGTATTTTTAGACG
droBip1	scf7180000396574:339941-340243 +		TGAGTGGCGGCCAGAAGAAGCGTGTCCATCGCCCTGGAGCTGATAGACAATCCAGCGTGTATTTTTAGACG
dp5	4_group4:2073834-2074130 +		TGAGTGGCGGCCAGAAGAAGCGTGTCCATCGCCCTGGAGCTGATAGACAATCCAGCGTGTATTTTTAGACG
droPer2	scaffold_101:1078918-1079214 +		TGAGTGGCGGCCAGAAGAAGCGTGTCCATCGCCCTGGAGCTGATAGACAATCCAGCGTGTATTTTTAGACG
droMil2	scf2_1100000004585:1508853-1509091 +		TGAGTGGCGGCAAAAGAACGTCTGTCCATCGCCCTGGACTGATAGACAATCCAGCGGTGTATTTTTAGACG
droVir3	scaffold_12963:11356814-11357067 +		TGAGTGGCGGCCAGAAGAAGCGTGTCCATCGCCCTGGAGCTGATAGACAATCCAGCGGTGTATTTTTAGACG
droMoj3	scaffold_6500:20105650-20105884 +		TGAGTGGCGGCCAGAAAAGCGTGTCCATCGCCCTGGAGCTGATAGACAATCCAGCGGTGTATTTTTAGACG
droGri2	scaffold_15252:5474290-5474553 +		TGAGTGGCGGCCAGAAGAAGCGTCTGTCCATCGCCCTGAGCTGATAGACAATCCAGCGTGTATTTTTGGACG

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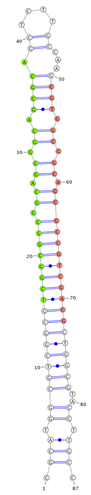
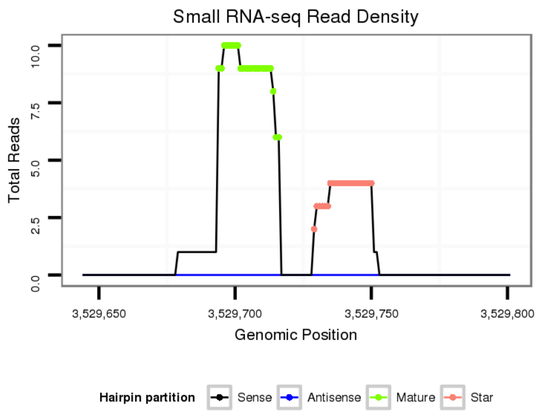
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.prec	1
crit.uni	1
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	1
rescue.confident	1
rescue.candidate	1

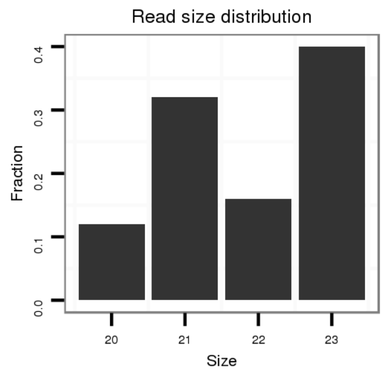
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_101	**scaffold_4784:3529694-3529751 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

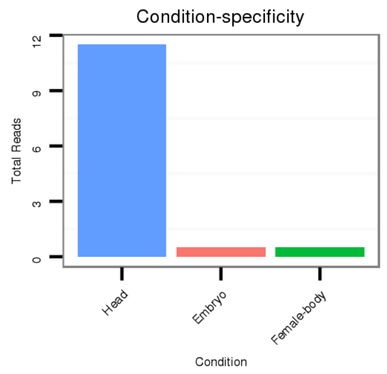
Legend: mature star mismatch in alignment mismatch in read

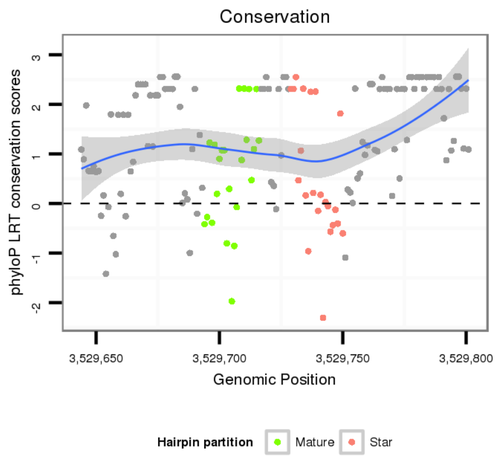
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GCTGCTGCTTTCGTGGGCAGCGGAAAATCTGCTTCCGCATGGCGTCGGCGTCGGCGCAGCGGCAGCGCAGCTCTTGCCAAGCGTGGCGGCAGCGCCGTCGACGCTGGCGTACCTTGCCAGGCGGCGCGAAAGAAAGTAAACAGGCGGAATGCGC	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	M057 embryo	V060 head	M055 female body	V107 male body
**********.(((.((((((((((((((((((.((.((.((.((((.((....)).)...)))).)).)).)).))))))))))))))..)).)))..**********										
.....TCGGCGGCGGCAGCGGCAGCGCA.....	23	0	1	5.00	5	5	0	0	0	0
.....TCGGCGGCGGCAGCGGCAGCG.....	21	0	2	2.00	4	3	0	0	1	0
.....TCGGCGGCGGCAGCGGCAGC.....	20	0	2	1.50	3	2	1	0	0	0
.....CGTGGCGGCAGCGCCGTCGACT.....	22	1	1	1.00	1	0	0	0	1	0
.....CGCATGGCGTCGGCGTCGGCGGC.....	23	0	1	1.00	1	0	0	1	0	0
.....GGCGGCGGCAGCGGCAGCGCA.....	21	0	1	1.00	1	1	0	0	0	0
.....GTGGCGGCAGCGCCGTCGACG.....	21	0	1	1.00	1	1	0	0	0	0
.....GGCAGCGCCGTCGACGCT.....	18	0	1	1.00	1	0	1	0	0	0
.....TCGGCGGCGGCAGCGGCAGCGCAA.....	24	1	1	1.00	1	0	0	0	0	1
.....CGTGGCGGCAGCGCCGTCGACGG.....	23	1	1	1.00	1	0	0	1	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4784:3529644-3529801 +	der_101	GCTG-----CTGCTTTCGTGGG----------C------AGCGGAAAATCT----------GCTTCCGCAT-GGCGTCGGCGTCGGCGCAGCGGCAGCGCAGCTCTTGCCAAGCGTGGCGGCAGCGCCGTCGACGCT----------G----------GCGTACCTTGC--CAGGCGG-----CGCGAAAGAAAGTAAACAGGCG--GAATGCGC---
droYak3	3L:8418534-8418685 -		GCTG-----CTGCTTTCGTGGG----------C------AGCGGAAAATCT----------GCTTCCGCAT-GGCGTCGCGTTG------GCGTCGGCAGCGCAGCTCGCCAAGCGTGGCGACAGCGACGTCGACGTC----------G----------GCGAACTTGC--CAGGCGG-----CGCGAAAGAAAGTAAACAGGCG--GAATGCGC---
droSec2	scaffold_0:127869-128014 -		GCTG-----CTGCTTTCGTCGG----------C------AGCGGAAAATCT----------GCTTCCGCAT-GACGTCG----------GCGTTCGGCAGCGCAGCTCGCCAAGCGTGGCGGCAGCGACGTCGACGTC----------G----------GCGAACTTGC--CAGGCGG-----CGCGAAAGAAAGTAAACAGGCG--GAATGAGC---
droSim2	3L:7652565-7652710 -		GCTG-----CTGCTTTCGTGGG----------C------AGCGGAAAATCT----------GCTTCCGCAT-GACGTCG----------GCGTCGGCAGCGCAGCTCGCCAAGCGTGGCGGCAGCGACGTCGACGTC----------G----------GCGAACTTGC--CAGGCGG-----CGCGAAAGAAAGTAAACAGGCG--GAATGCGC---
dm3	chr3L:7821407-7821552 -		GCTG-----CTGCTTTCGTGGG----------C------AGCGGAAAATCT----------GCTTCCGCAT-GACGTCG----------GCATCGGCAGCGCAGCTCGCCAAGCGTGGCGGCAGCGACGTCGACGTC----------G----------GCGAACTTGC--CAGGCGG-----CACGAAAGAAAGTAAACAGGCG--GAATGCGC---
droEug1	scf7180000409524:818254-818403 +		GCTG-----CTGCTTTCGTGG----------C------AGCGGAAAATCT----------GCTTCCGCATTGACGCTG----------GCTTTGGCTGCGCAGCTCGCCAAGCGTGGCAGCAGCGACGCAAGCGTCAGC----------G----------GCGAACTTTGC--CAGGCTG-----CGCGAAAGAAAGTAAACAGGCG--GAATGCGC---
droBia1	scf7180000302428:2919007-2919164 -		GCTG-----CTGCTTTCGCGGG----------C------AGCGGAAAACT----------GCTTCCGCATTGACGCCGGCGCGGCGGCGGCGCTGGCAGCGCAGCTCGCCAAGCGTGGCGCAGTGCGCCGCTGCGAGG----------G----------GCGAACTTTGC--CAGGCTG-----CGCGAAAGAAAGTAAACAGCG--GAATGCGC---
droTak1	scf7180000415352:150876-151028 -		GCTG-----CTGCTTTCGCCGG----------C------AGCGGAAAATCT----------GCTTCCGCATTGACGTCG----------GCGTCGGCAGCGCAGCTCGCCAAGCGTGGCGCAGGTGACGTCGACGCC----------G------ACAGAG----------GCGAACTTGC--CAGGCTG-----CGCGAAAGAAAGTAAACAGGCG--GAATGCGC---
droEle1	scf7180000491193:3099792-3099944 -		GCTG-----CTGCTTTCGGTCGG----------C------AGCGGAAAATCT----------GCTTCCGCATAGACGTCG----------AGGTCGGCAGCACAGCTCGCCAAGCGTGGCGACAGCGAGCTTGACGTC----------G------GCAGAG----------GCGAACTTGC--CAGGCGG-----CGCGAAAGAAAGTAAACAGGCG--GAATGCGC---
droRho1	scf7180000779699:6200-6361 +		GCTG-----CTGCTTTCGGTCGG----------C------AGCGGAAAATCT----------GCTTCCGCATTGACGTCG----------GCGTCGGCAGAGCAGCTCGCCAACAGCGTGGCGGCAGCGCCGTCGACGTC----------GACGTCGGCAGAA----------GCGAACTTGC--CAGGCGA-----CGCGAAAGAAAGTAAACAGGCG--GAATGCGACAAA
droFic1	scf7180000454065:148677-148847 -		GCTG-----CTGCTTTCGCGG----------C------GGCGGAAAATCT----------GCTTCCGCATTGACGCGG----------GCGTCGGCAGCGCAGCTCGCCAAGCGTGGCGGCAGCGAACGCAACGTCAGCGACGACGTCGACGGCGACAGAA----------GCGAACTTGC--CAGGCGG-----CGCGGAAGAAAGTAAACAGGCG--GAATGCGC---
droKik1	scf7180000302274:151768-151914 -		GCTGCGCCCGCTGCCGGCGTCGA----------C------AGCGGAAAATCA----------GCTTCCGCATT-----CG----------AGCACGGCAGCGCGGCGCTGCCGCCAAGCGTGGCGGCAGTGGCGGTCGGCAGC----------G----------ACGAACTTGC--CAGGCTG-----CGCGAAAGAAAGTAAACAGGCG--GAATGCGC---
droAna3	scaffold_13337:10615285-10615441 -		GCTG-----CTGCTGCCGGCGGCC----------ACGCTGG----------C------TGTTGAAAATCT----------GCTTCCGCATTGACGTCGACGCGGCG-----TTCGGCAGCGCAGCTCGCCAAGCGTTAGAATGA----------G----------AG--CAGCG----------CCGAACTTTGC--CAGGCTG-----CGCGAAAGAAAGTAAACAGGCG--GAATGCGC---
droBip1	scf7180000396569:754758-754915 +		GCTG-----CTGCTGCCGGCGGCC----------ACGCTGG----------C------CGTTGAAAATCT----------GCTTCCGCATTGACGTCGACGCGGACG-----TGCGGCAGAGCAGCTCGCCAGCGAAGCGTGGCTG----------G----------GCAGAAG--CAGCG----------ACGAACTTTGC--CAGGCTG-----CGCGAAAGAAAGTAAACAGGCG--AAATGCGC---
dp5	XR_group8:1666487-1666722 +		GCTG-----CTGCTGCCGCTGACGCTTTCGCTTACGCTTACGCTAGCTTTGGCGCTGGCGTCGCTGCTGCTGCCTGCATGCGCGTCGGAAAATCTA----------CGCTTCCGCATC-TAGT----------GCAGCGGCAGCGCAGCTCGCCAGCAGCGAAGCGTGGCGA-AGCGC-----ACG------------G---AAGGCAGAAAGACAGAGATGGAACGCCGACCCGAAGTTTGCG--CAGGCTGCGGCTGCAGCGAAAGAAAGTAAACAGGCGGAGAATGCGC---
droPer2	scaffold_24:1378167-1378231 -		CGTC-----ACAGTTGCGCC--ATCGAGAGCG----------GCGCTGGCA----------GCGCAGCAACCGCGGAGAGC----------G----------AC---------------------------GCATCGC---
droVir3	scaffold_13049:20621261-20621393 -		G---GAAAATCTAA-AACAAGCATCGCTTCCGCATG-C-ACGCAGAGAG-----CGACAGCGACAGCGCAGCTCATGCGAAGCGTAGCGACAGCTAGA--------G----------GCAAGCTTTGCGCGAGGCTG-----CGCGAAAGAAAGTAAACAG-TG--GAATGCGC---
droMoj3	scaffold_6680:8329690-8329798 -		GC---TTCCGCAT-GCAGTCGC----------CTGCGCAGAGCGCAGCTCATGCGAAGCGTAGCGACAGCTTT--------T----------G----------ACGAACTTTGCGCGAGGCTG-----CGCGAAAGAAAGTAAACAG-TG--GAATGCGC---
droGri2	scaffold_15106:69182-69330 -		G---TGGAAAATCTAAAAACCAGCATCGCTTCCGCATG-C-ACGCAGAGAGTCAGCGGCAGCGGCAGCGCAGCTCACAGCGAAGCGTAGCGGCAGTGTTTTTTGCAC----------C----------ACACAC---AG--CAGGCTG---TCCGCGAAAGAAAGTAAACAG-CG--GAATGCGC---

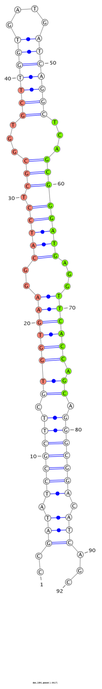
Generated: 09/08/2015 at 07:49 PM

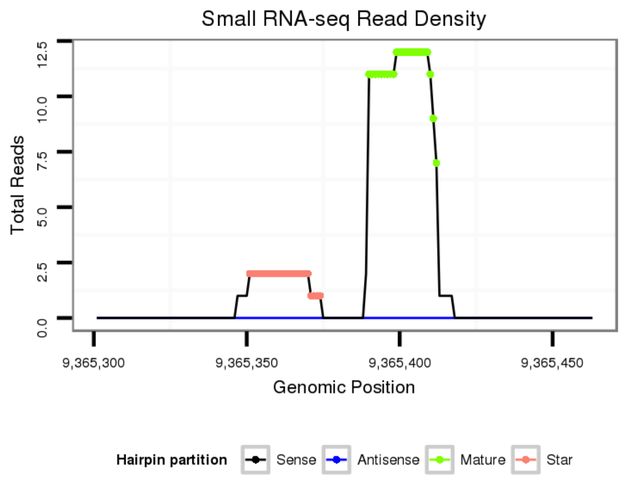
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

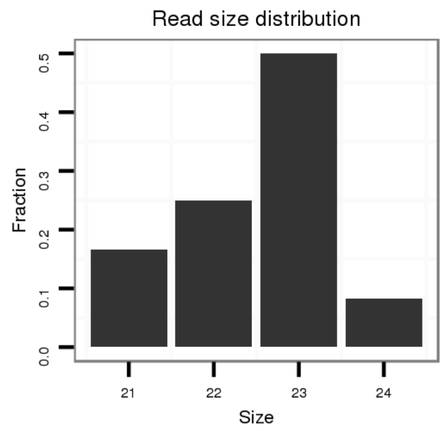
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_104	**scaffold_4690:9365351-9365413 +**	**candidate**	**Canonical miRNA**	**antisense_to_CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

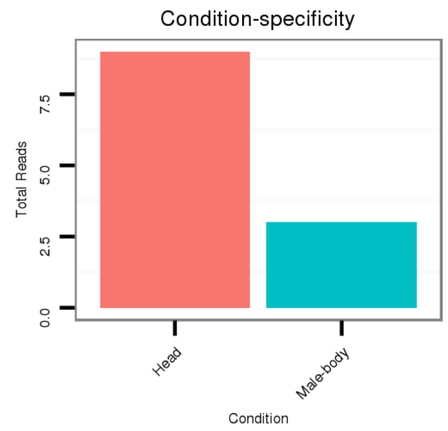
Legend: mature star mismatch in alignment mismatch in read

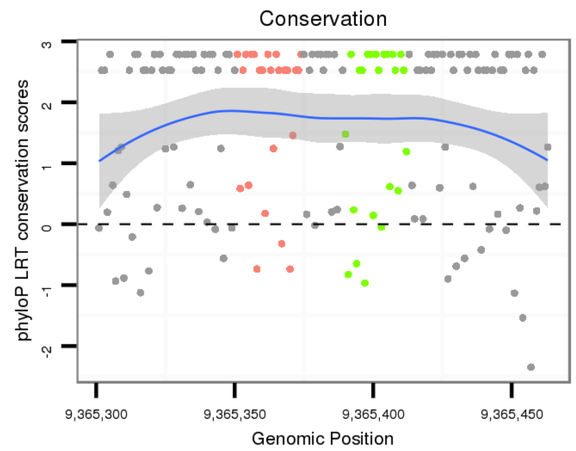
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to CDS [Dere\GG18070-cds]; utr3 [utr3_plus_8609]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CGGCAGTGCAGCGAAACCAGTCTCCGCCTTGATCACCGATATCCGCTTCGTGGTGAAGGCATCCTCGCGGTGCTTGGTGATGATCAGGCTCAGCGGGATGAGGTTCACCAGCAGGGCGGACATCAGCACGATGGACTGGGCGGTGCCGTAGAGGGTGCGCAGG	Read size	# Mismatch	Hit Count	Total Norm		V108 head	V107 male	M055 female body
**********************************..(((.(((((((.(((((((..(((((.(((...(((((((....)))))))...)))))))...)))))).)).)))))))...**********	**size**	**Mismatch**	**Count**	**Norm**	**Total**		**male**	**body**
.....TCAGCGGGATGAGGTTCACCAGC.....	23	0	1	6.00	6	3	3	0
.....TCAGCGGGATGAGGTTCACCAG.....	22	0	1	2.00	2	2	0	0
.....TGAGGTTCACCAGCAGGGC.....	19	0	1	1.00	1	0	1	0
.....TCAGCGGGATGAGGTTCACCA.....	21	0	1	1.00	1	1	0	0
.....CTCAGCGGGATGAGGTTCACCA.....	22	0	1	1.00	1	1	0	0
.....TGGTGAAGGCATCCTCGCGGTGCT.....	24	0	1	1.00	1	1	0	0
.....TTCGTGGTGAAGGCATCCTCGCGG.....	24	0	1	1.00	1	0	0	1
.....CTCAGCGGGATGAGGTTCACC.....	21	0	1	1.00	1	1	0	0

Anti-sense strand reads

GCCGTCACGTCGCTTTGGTCAGAGGCGGAACTAGTGGCTATAGGCGAAGCACCACTTCCGTAGGAGCGCCACGAACCACTACTAGTCCGAGTCGCCCTACTCCAAGTGGTCGTCCCGCCTGTAGTCGTGCTACCTGACCCGCCACGGCATCTCCCACGCGTCC	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	V040 embryo
**********************************..(((.(((((((.(((((((..(((((.(((...(((((((....)))))))...)))))))...)))))).)).)))))))...**********							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4690:9365301-9365463 +	der_104	CGGCAGTGCAGCGAA------ACCAGTCTCCGCCTTGATCACCGATATCCGCTTCGTGGTGAAGGCATCCTCGCGGTGCTTGGTGATGATCAGGCTCAGCGGGATGAGGTTCACCAGCAGGGCGGACATCAGCACGATGGACTGGGCGGTGCCGTAGAGGGTGCGCAGG
droYak3	X:17693365-17693527 +		CGGCAGTGGCGGCGAA------TCCGGTCTCCGCCTTGATCACCGATATCCGCTTGTGGTGAAGGCATCCTCGCGATGCTTGGTGATGATCAGGCTCAGCGGGATGAGGTTCACCAGCAGGGCGGACATCAGCACGATGGACTGGGCGGTGCCGTAGAGGGTGCGCAGG
droSec2	scaffold_8:1398896-1399058 +		CGGCAGTGCAGCAAA------TCCGGTCTCCGCCTTGATCACCGATATCCGCTTCGTGGTGAAGGCATCCTCGCGAATGCTTGGTAATGATCAGGCTCAGCGGCAATGAGGTTCACCAGCAGGGCGGACATCAGCACGATGGACTGGGCGGTGCCGTACAGGGTGCGCAGG
droSim2	x:18005391-18005553 +		CGGCAGTGCAGCAAA------TCCGGTCTCCGCCTTGATCACCGATATCCGCTTCGTGGTGAAGGCATCCTCGCGAATGCTTGGTAATGATCAGGCTCAGCGGGATGAGGTTCACCAGCAGGGCGGACATCAGCACGATGGACTGGGCGGTGCCGTACAGGGTGCGCAGG
dm3	chrX:19104069-19104231 +		CGGCAGTGCAGCGAA------TCCGGTTTCCGCCTTGATCACCGATATCCGCTTCGTGGTGAAGGCATCCTCGCGAATGCTTGGTAATGATCAGGCTCAGCGGGATGAGGTTCACCAGCAGGGCGGACATCAGTACGATGGACTGGGCGGTGCCGTACAAAGGTGCGCAGG
droEug1	scf7180000409089:11271-11433 -		CGGAAGTGCAGCAAA------TCCGTTCCGCCTTAATCACCGATATCCGTTTCGTGGTGAAGGCATCCTCACGAATGCTTGGTGATGATAAGGCTGAGCGGGATTAGGTTCACTAGCAGGGCGGACATCAGCACAATCGACTGAGCGGTGCCGTAGAGAGTTCGAAGG
droBia1	scf7180000302069:1477729-1477891 -		CGGAAGTGGCGGCGAA------TCCGGTCTCCGCCTTGATCACTGATATCCGCTTCGTGGTGAATGGCTCCTCGCGGTGCTTGGTAATGATCAAGCTTAGTGGGGATGAGGTTCACCAGCAGGGCGACATCAGCACGATAGACTGGGCGGTCCCATAGAGAGTGCGCAGG
droTak1	scf7180000415281:108311-108473 +		GGGAAGAGGCGGCGAA------TCCGTCTCCGCCTTGATCACCGATATCCGTTTCGTGGTGAAGGCGTCCTCGCGATGCTTCGTGATGATCAGGCTCAGCGGTATGAGATTCACCAGCAGGGCGGACATTAGCACGATGGACTGGGCAGTGCCGTACAGCGTTCGCAGG
droEle1	scf7180000490751:705893-706055 +		CGGCAGTGGCGGCAAA------GCCCGTCTCCGCCTTGATCACCGAAATCCGCTTCGTGGTGAAGGGGTCCTCGCGGTGCTTGGTGATGATCAGGCCCAACGGGATGAGGTTGACCAGCAGGGCGGACATCAGCACGATCGACTGGGCGGTGCCGTAGAGGGTCCTCAGG
droRho1	scf7180000778091:323295-323457 +		CGGCAGAGGCCCCGAA------TCCGGTCTCCGCCTTGATCACCGATATCCGCTTCGTGGTGAACGGCTCCTCGCGGTGCTTGGTGATGATCAGGCTCAGCGGGATGAGGTTCACCAGCAGGGCGGACATCAGCACGATCGACTGGGCGGTGCCGTAGAGGGTGCGCAGG
droFic1	scf7180000451789:124101-124263 +		CGGCAGTGGTGCGAA------TCCTGTCTCCGCCTTGATCACCGAAATCCGCTTCGTGGTGAAGGCATCCTCGCGGTGCTTCGTGATGATCAGGCTCAGCGGGATGAGGTTCACCAGCAGCGCGGACATCAGTACAATCGACTGGGCGGTGCCGTACGAAAGTCCTCAGG
droKik1	scf7180000302234:7108-7270 -		CGGCAAAGCAGCGAA------ACCCGTCTCCGCCTTAATTACCGACATCGCTTTGGTGGTAAGGCATCCTCCCGATGCTTGGTGATGATCAGGCTTAGCGGTATGAGATTCACCAGCAGGGCGGACATCAGGACTATCGACTGGGCGGTGCCATACAGAGTGTCCGAAGG
droAna3	scaffold_12903:627287-627449 -		GGGCAGAGGCGGCGAA------ACGTGTTTCCGCCTTGATCACCGATATCGTTTCGTGGTGAAGGCGTCCTCCCGGTGCTTGGTGATGATCAGACTCAACGGTATCAGGTTCACCAGCAGGGCGGACATCAGCACTATGGACTGGGCTGTTCCGTACGAGAGTTCTCAGG
droBip1	scf7180000395916:89921-90083 +		AGGCAGAGCAGCGAA------TCCTGTTTCCGCCTTGATCACCGATATCCTCTTTGTGGTGAAGGCATCTTCCCGATGCTTGGTGATGATCAAACTCAGAGGGATCAGGTTCACCAGCAGGGCCGACATCAGCACTATGGATTGGGCTGTTCCATAAGAGTTCTCAAG
dp5	XL_group1e:8304645-8304807 +		CGGCAGGGGCGGCAAA------CCCGTCTCCGCCTTGATCACCGATATTCGTTTGGTTGTGAAAGCATCCTCCCGGTGCTTGGTGATGATCAGGCTGAGGGGATGAGGTTCACCAGCAGGGCGGACATCAGGACGATGGACTGGGCGGTGCCATAGAGGGTGCGCAGG
droPer2	scaffold_13:261324-261486 -		CGGCAGGGGCGGCAAA------CCCGTCTCCGCCTTGATCACCGATATTCGTTTGGTTGTGAAAGCATCCTCCCGGTGCTTGGTGATGATCAGGCTGAGCGGGATGAGGTTCACCAGCAGGGCGGACATCAGGACGATGGACTGAGCGGTGCCATAGAGGGTGCGCAGG
droWil2	scf2_1100000004515:2991063-2991231 +		CGGCAGATTACGAAAGCCCAGTCCGGTCTCCGCTTTAATACCGATATTCGCTTGGTGGTAAATGCATCCTCGCGATGCTTTGTTATGATCAAGCTTAGAGGTATGAGATTCACGAGCAATGGCGACATCAACACTATGGATTGAGCGTGCCATATAAGGGTACGCAAA
droVir3	scaffold_12970:9352527-9352689 +		TGGCAATGCACCGAA------ACCAGTCTGAGCCTTGATCACGGATATCCGCTTGGTGGTAAATGCATCCTCCCGGATGCTTGGTGATGATCAGGCTCAGTGGAATGAGATTCACCAGCATTGGCCGACATCGAGCACAATGGACTGAGCAGTGCCGTACAGAGTGCGCAGG
droMoj3	scaffold_6308:1380839-1381001 -		TGGCAGCGCACCGAA------GCCGTCTCCGCCTTGATTACTGAGATCCGTTTGGTTGTGAACGCATCCTCGCGATGCTTGGTGATGATCAGGCTGAGCGGTATGAGATTCACCAGCAATTGGCCGACATCAGCACAATGGACTGCGCGGTGCCATACAGGGTGCGCAGG
droGri2	scaffold_15203:2032604-2032766 -		TGGCAGCGCACCGAA------ACCGGTCTCCGCCTTGATCACCGATATGCGCTTGGTGGTAAGGCATCCTCGCGACGCTTGGTAATGATAAGGCTCAATGGTATCAGGTTTACCAGCATCGGCGACATCAGGACTATCGACTGTGCGGTCCCATACAGAATGTCCGCAGG

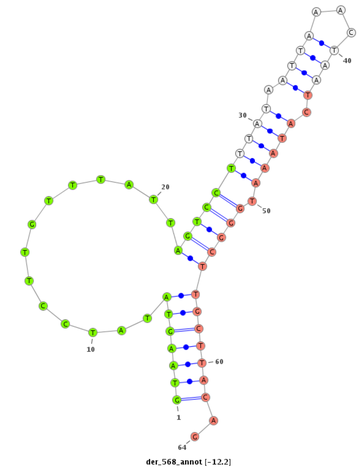
Generated: 09/08/2015 at 07:49 PM

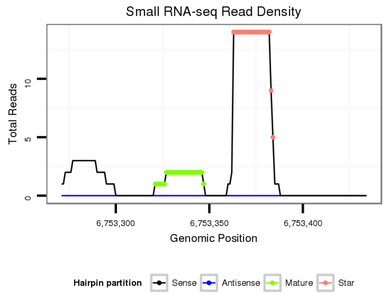
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

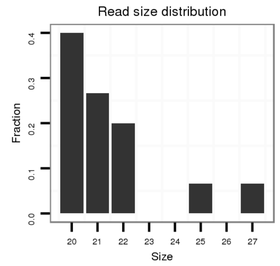
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_568	**scaffold_4770:6753321-6753384 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

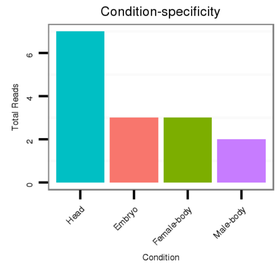
Legend: mature star mismatch in alignment mismatch in read

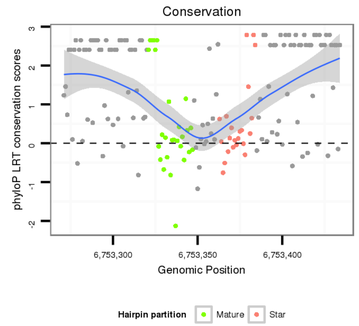
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG16197-in]; CDS [Dere\GG16197-cds]; CDS [Dere\GG16197-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GAAGCCGTAGTGGGTGACTTTGGTCTAGCCGCAAAAATACCAGTCAAATCGTAAGTATATCCTTGTTTATTAGTCCTTTATAATTAAACTAATCATAAATGGGCTTGCTTACAGCAGAAAATCACGCCTTGAGACAGTCGGCTCTCCGTATTGGGTTAGTCCGG	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	M055 female body	V107 male body	M057 embryo	V040 embryo
(((((((.............(((((((((.(((.(...)))).)))))).)))))))))..										
.....TCATAAATGGGCTTGCTTAC.....	20	0	1	5.00	5	4	0	1	0	0
.....TCATAAATGGGCTTGCTTACAG.....	22	0	1	3.00	3	1	0	0	0	2
.....TAATCATAAATGGGCTTGCTTACAG.....	25	0	1	1.00	1	1	0	0	0	0
.....GTAAGTATATCCTTGTTTATTAGTCCT.....	27	0	1	1.00	1	0	1	0	0	0
.....ATATCCTTGTTTATTAGTCC.....	20	0	1	1.00	1	0	0	0	1	0
.....TCATAAATGGGCTTGCTTAA.....	20	1	1	1.00	1	0	1	0	0	0
.....CATAAATGGGCTTGCTTACAGA.....	22	1	1	1.00	1	0	1	0	0	0
..AGCCGTAGTGGGTGACTTTGGT.....	22	0	1	1.00	1	0	0	1	0	0
.....ATCATAAATGGGCTTGCTTACAGCAG.....	26	0	1	1.00	1	1	0	0	0	0
......GTAGTGGGTGACTTTGGTCTAGC.....	23	0	1	1.00	1	0	0	0	1	0
GAAGCCGTAGTGGGTGACT.....	19	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4770:6753271-6753434 +	der_568	GAAGCCGTAGTGGGTGACTTTGGTCTAGCCGCAAAAATACCAGTCAAATCGTAAGTATA----TCC----------TT-GTTTA----------TTAG---TCC-
droYak3	3R:3534515-3554706 -		GAAGCGTAGTGGGTGACTTTGGTCTAGCCGCAAAGATACCAGTCAAGCGTAAGTATA----ACC----------T-GTGTAA----------CAACTATAACAGCGTA----------****
droSec2	scaffold_77:62623-62795 +		GAAGCGTAGTGGGTGACTTTGGTCTAGCCGCAAAGATACCAGTCAAATCGTAAGTATA----TCC----------T-GTGTAA----------ACA----CCTTGTAG
droSim2	3r:6381674-6381846 +	dsi_27342	GAAGCGTAGTGGGTGACTTTGGTCTAGCCGCAAAGATACCAGTCAAATCGTAAGTATA----TCC----------T-GTGTAA----------ACA----TCTTGTAA
dm3	chr3R:14875745-14875917 -		GAAGCGTAGTGGGTGACTTTGGTCTAGCCGCAAAGATACCAGTCAAATCGTAAGTATA----TCT----------T-GTGTAC----------ACA----AAGGTAA
droEug1	scf1800004098804:1117128-1117293 -		GAAGCCGTAGTGGGTGACTTTGGTCTAGCCGCAAGATACCAGTTAAATCGTAAGTCGTA----TCC----------T-GTGTAA----------****
droBia1	scf1800003024026:628969-629161 -		GAAGCCGTTGTGGGTGACTTTGGTCTAGCCGCAAAGATACCAGTCAAATCGTAAGTCGTA----CGC----------T-GTGTAA----------CCAAAATATCAG
droTak1	scf1800004152563:371641-371868 -		GAAGCCGTGTGGGTGACTTTGGTCTAGCCGCAAAGATACCAGTCAAATCGTAAGTGTG----TCC----------T-GTTTAA----------CTTGA------TTTCATTA----TAACAAAA----GCTC----------GTTT------****
droEle1	scf1800004909094:632333-632516 -		GAAGCCGTCGTAGGTGACTTTGGTCTAGCCGCAAAGATACCAGTCAAATCGTAAGTCGTA----TCC----------CC-GTTTAA----------CTGAATATCAGCTTA----------****
droRho1	scf1800007799904:529841-530082 -		GAAGCCGTCGTGGGTGACTTTGGTCTAGCCGCAAAGATACCAGTCAAATCGTAAGTCGTA----CGC----------T-GTGTAA----------CTAAAATATCAGCTTAGTGTTACTTG----------****
droFic1	scf1800004534812:163355-163654 +		GAAGCCGTGTGGGTGACTTTGGTCTAGCCGCAAAGATACCAGTCAAATCGTAAGTCGTA----CA-TT----------TC-GTCTAA----------CTAAATATCAGCTTTGAATT----TTA----AATTTAAAACAACACATTCGAAAAGAACACAAATCTTTAGTTTATA---ATG-GT-
droKik1	scf1800003000058:216073-216233 +		GAAGCCGTTGTGGGTGACTTTGGTCTGCCGCAAAGATACCAGTAAAACGTAAGTGGC----TCC----------CT-ACAACA----------C****
droAna3	scaffold_13340:17511945-17512108 -		GAAGCCGTCGTGGGTGACTTTGGTCTAGCCGCAAAGATACCAGTTAAATCGTAAGTGCC----TCT----------TAAAGTGTA----------****
droBip1	scf1800003967216:420269-420427 +		GAAGCCGTCGTGGGTGACTTTGGTCTAGCCGCAAAGATACCAGTTAAATCGTAAGTCGTA----CA--GACTTTGAAACTCCAATGGCCTATTCGT----
dp5	2:6806590-6806758 -		GAAGCCGTCGTGGGTGACTTTGGTCTAGCCGCAAAGATACCAGTCAAATCGTAAGTCGTA----TCC----------TT-GTCT----------A----------GCATCGTCCGTGG----GGA----------AA----CTGA----------****
droPer2	scaffold_0:644123-644291 -		GAAGCCGTCGTGGGTGACTTTGGTCTAGCCGCAAAGATACCAGTCAAATCGTAAGTCGTA----TCC----------TT-GTCT----------A----------GCATCGTCCTGTGC----GGA----------AA----CTGA----------****
droWil2	scf2_1100000004943:2102371-2102529 +		GAAGCCGTTGTGGGTGATTTGGTCTAGCCGCAAAAATACCGTTAAATCGTAAGTCCA----ATT----------T-GTCTACA----------****
droVir3	scaffold_12822:19337-19622 -	dvi_2253	GAAGCGTGTGTTGGTGATTTGGTCTGCCGCTAAAATACCAGTCAATCGTAAGTATA----TCT----------TCTACAGTTTCTATTTATATAGA------TTTAATTT----TTA----TGCTCAATACATTTCCAAACAAAGAATATGTTTAAGTACAC----ATG-GTGTTCTATTTA
droMoj3	scaffold_6540:32675245-32675409 -		GAAGCGTGTGTGGCGACTTTGGTCTAGCCGCTAAGATACCAGTCAAATCGTAAGTTCCTAAGTTCG----TTCCACG----------T-GTCTAC
droGri2	scaffold_15074:3719388-3719475 +		TTC----------****

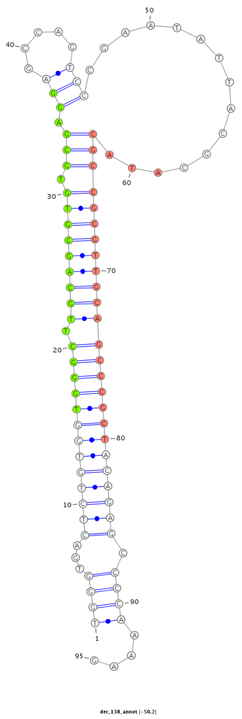
Generated: 09/08/2015 at 10:32 PM

	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tpto3	1
crit.uri	1
crit.back	1
rescue.mid	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

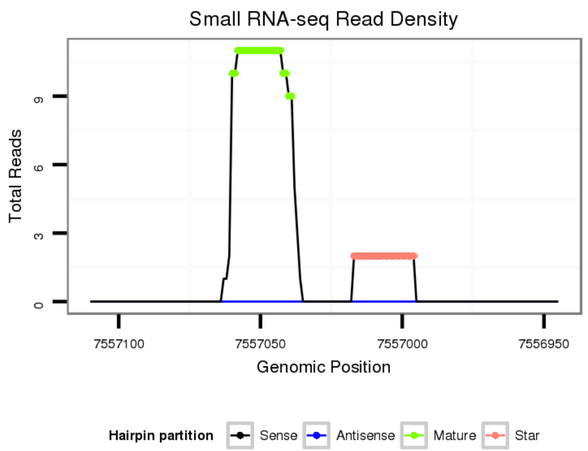
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_138	**scaffold_4820:7556995-7557060 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

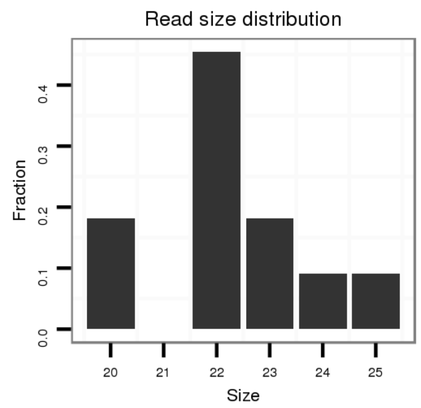
Legend: mature star mismatch in alignment mismatch in read

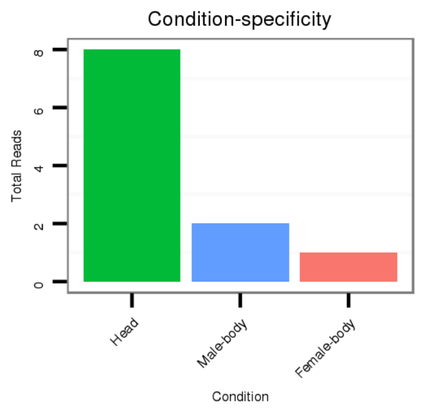
Predicted structure

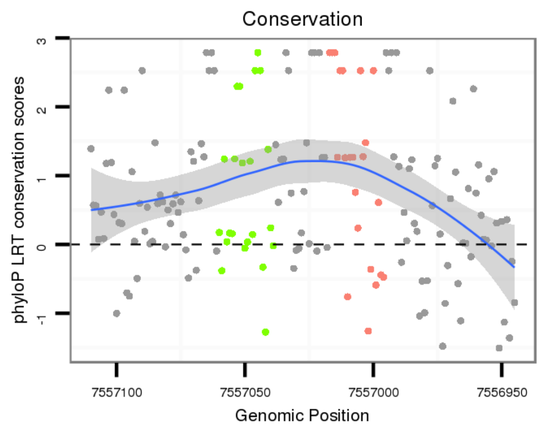


Show Alternate Folds









Flybase annnotation

intron [Dere\GG11309-in]; utr3 [utr3_plus_6709]; utr5 [utr5_plus_12038]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACACATACACGCACGCGCGATCGGTTGTGCCTGTGTGGGTGACTCTGTGGTGGGCTTGCAGCGTGTGCGAGGAGCCAGTCCCGAATATTACGCATACGCCGCGTTGCAGCCCGCTACAGAGCCCCAAAAGCAGGCACTTTCGATACGCCACAATATTTACGAACAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V107 male body	M055 female body	V060 head
**********(((((...(((((((((((((.(((((((((.(((.(((.....))).............)))))))))))))))))))))).)))))....**********									
..........TGGGCTTGCAGCGTGTGCGAGG..........	22	0	1	3.00	3	3	0	0	0
..........TGGGCTTGCAGCGTGTGCGAGGA.........	23	0	1	2.00	2	2	0	0	0
..........ATACGCCGCGTTGCAGCCCGCT..........	22	0	1	2.00	2	2	0	0	0
..........GGCTTGCAGCGTGTGCGAGG..........	20	0	1	1.00	1	0	0	1	0
..........GTGGGCTTGCAGCGTGTGCGAGGAG......	25	0	1	1.00	1	0	1	0	0
..........TGGGCTTGCAGCGTGTGCGA..........	20	0	1	1.00	1	1	0	0	0
.........TGGTGGGCTTGCAGCGTGTGC..........	21	0	1	1.00	1	1	0	0	0
..........TGGGCTTGCAGCGTGTGCGAGGAGC.....	25	0	1	1.00	1	0	1	0	0
..........TGGGCTTGCAGCGTGTGCGAGGAG......	24	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

TGTGTATGTGCGTGCGCGCTAGCCAACACGGACACACCCACTGAGACACCACCCGAACGTCGCACACGCTCCTCGGTCAGGGCTTATAATGCGTATGCGGCGCAACGTCGGGCGATGTCTCGGGGTTTTCGTCCGTGAAAGCTATGCGGTGTTATAAATGCTTGTT	Read size	# Mismatch	Hit Count	Total Norm	Total	GSM1528801 follicle cells
**********(((((...(((((((((((((.(((((((((.(((.(((.....))).............)))))))))))))))))))))).)))))....**********						

Show Alignment With Reads

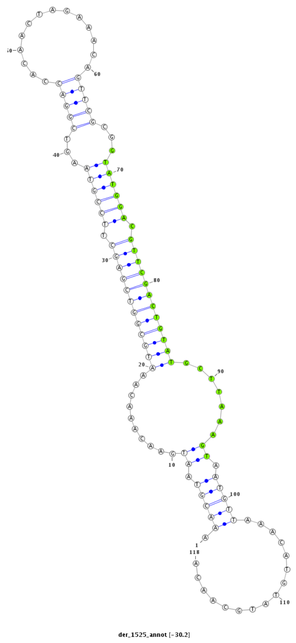
Re-alignment of all predicted orthologs

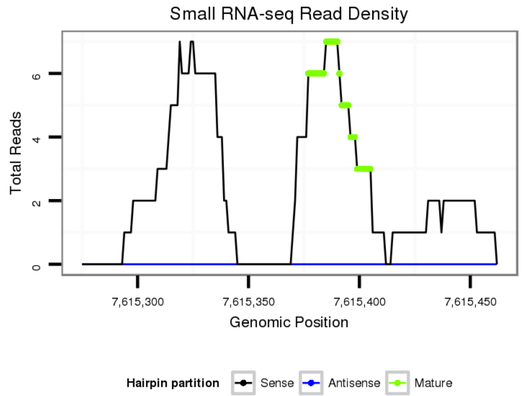
Species	Coordinate	ID	Alignment
droEre2	scaffold_4820:7556945-7557110 -	der_138	AC-------ACATACACGCACG---------C-GCGATCG-GTTG------TGCCTG--T---GT--GGGTGACTCTGTGGTGGG--CTTGCAGCGTGTG--CGA-GGAGCCAGTCC-C--GA-ATATTACG-------------CATACGCCGCGTTGCAGCCCGCTACAGAGCCCC-AAA-------AGCAGGCACTTTCGAT-A-CGCCA-CAA-TATTT----AC-----GA-----AC--AA
droYak3	3R:25995681-25995856 -		AC-------ACATACACTCACG---------C-GCGATCG-GTTG------TGCCTG--T-GTGT--GGGTGACTCTGTGGTCGG--TTTGCAGTGTGTG--CGA-GAAGCCAGTCC-C--GA-ATATTACG-------------CATACGCCGCGTTGCAGCCTGTCACAGAGCCCCGAAA------ACCAGGCATCGGCGAT-A-CGCCA-CAA-TATTT----AC-----GATCGATACAAGT
droSec2	scaffold_0:20835551-20835718 +		AC-------ACATACACTCACG---------C-GCGATCG-GTTG------TGCCTG--T-GTGT--GGGTGACTCTGTGATGGG--TTTGCAGTGTGTG--CGA-GAAGCCAGTCC-C--GA-ATATTACG-------------CATACGCCGCGTTGCAGCCTGCTACAGAGCCCC-AAA------GCCAGGCACTTCGAG-A-CGCCA-CAA-GATTT----AC-----GA-----AC--AT
droSim2	3r:20018721-20018890 +		AC-------ACATACACTCACG---------C-GCGATCG-GTTG------TGCCTG--T-GTGT--GGGTGACTCTGTGATGGG--TTTGCAGTGTGTGTGCGA-GAAGCCAGTTT-C--GA-ATATTACG-------------CATACGCCGCGTTGCAGCCTGCTACAGAGCCCC-AAA------ACCAGGCACTTCGAG-A-CGCCA-CAA-GATTT----AC-----GA-----AC--AT
dm3	chr3R:20501078-20501245 +		AC-------ACATACACTGCACG---------C-GCGATCG-ATTG------TGCCTG--T-GTGT--GGATGACTCTGTGATGGG--TTTGCAGTGTGTG--TGA-GAAGCCAGTCC-C--GA-ATATTACG-------------CATACGCCACGTTGCAGCCTACTACAGAGCCCC-AAA------GCCAGGCACTTCGAT-A-CGCCA-CAA-GATTT----AC-----GA-----AC--AT
droEug1	scf7180000409881:226106-226278 +		AC-------TCATACAAATACTT--------A-GGTATGTT-ATAT------TGCCTG--T-GTGT--GGGTGTCTCTGTGATGGGC-TTTGCAGTGTGTGTGCAA-GGAGCCAGTCC-A--GATTTATTACG-------------CATACGCCACGTTGCATCCCGACACAGAGCCCCAAAA------GCCAGGCACTCTCGAT-A-GCGTA-CAC-TATAT----AC-----CC-----AA--AG
droBia1	scf7180000302402:4281300-4281465 +		AC-------ACATACCAACACG---------AGGGGATCG-GTTG------TGCCCG--T-GTGT--GGGTGTATCTGTGGCGGG--TTGCAATGTGTG--CGA-GGAGCCAGTCA--C--GA-ATATTCACG-------------CATACGCAGCGTTGTG-CCCGCTACAGAGCCCC-AAA-------ACAGGCACTTTCGAC-A-CCCCA-CAC-TATAT----AA-----GT-----T--AT
droTak1	scf7180000415310:638535-638703 -		AC-------ACATACAC--ACG---------A-GGGATCG-GTTG------TGCCTG--T-GTGT--GGGTGAGCTGTGTGGCGGG--TTTGCAGTGTGTG--CAA-GGAGCCAGTCA-C--GA-ATATTCAAG-------------CATACGCCGCGTTGCAACCTGCTACAGAGCCCCAAAA------ACCGGGCACTTCCGAGTTGCCCACACC-TATACAT--AT-----GT-----AC--T
droEle1	scf7180000491194:558384-558545 +		AC-------ATATACACACACG---------C-GGAATGG-GTTG------TGCCTGAGTG-TGC--GGATGACTCTGTGACGGGC-TTTGCAGTGTGTGTGCGA-GGAGCCAGTCC-C--AA-ATATTCACG-------------CATACGCCGCGTTGCAACCCGTACAGAGCCC--AAA------ACCAGGCACTTCCGAT-G-CCCCA-CAC-TAT---------------------
droRho1	scf7180000779488:600102-600274 +		ACTCGATTTACATACAC--ACG---------C-GGATGG-GTTG------TGCCTG--T-GTGT--GGGTGACTCTGTGGCGGG--TTTGCAGTGTGTGTGCAA-GGAGCCAGTCC-C--GA-ATATTCACG-------------CATACGCCGCGTTGCAGCCCGCTACAGAGCCC--AAA------ACCGGCACTCCGAT-T-CGCCA-CAC-AATATGTTTAT-----G--------
droFic1	scf7180000454106:1811234-1811401 -		AC-------ACATACAC--ACG---------C-G-GATCGGGTTG------TAACTG--T-GTGT--GGGTGACTCTGTGATGGGTTTTTGCAATGTGTG--CGA-GGAGCCAGTCC-C--GA-AATTCACG-------------CATACGCCGCGTTGCA-CCCGCCACAGAGCCCCGAAA------ACCAGTACTTCCGGATT-CCCTA-CAC-TGTA-----C---A-A-----AT--AT
droKik1	scf7180000302388:1695905-1696064 -		AA-------------------T---------T-GGGATCG-GTTG------TGCCTGCTTG-GGT--GAGTGCCTCTGTGACATG--GTTGCAACGCGTG--CTACAGAGCCAGTAGCAA--AAAAAATTACG-------------CATACGCCGCGTTGCATTCTGGCACAGAGACCG-CC------TGTGCGGCACGCCGAA-T-CCCTA-CAC-TATAT----CT-----GC-----AC--AT
droAna3	scaffold_13340:4674258-4674421 -		AC-------ACCTGCACACCC---------G-GGAATCAGGCTG-------TGCCTG--T-GTCT--GTGTGACTTGTGACCG--------TGCGTG--CCATGTGCACAGACC-A--GAAATATTACG-------------CATACGCCTGGTGGCACGCCGCTACAAGTCTG-CAG-------ACAGGGCACACCTGAT-A-CCCTA-CAC-TTGTATTTA-------T-----AT--TA
droBip1	scf7180000396359:515961-516108 +		---------------------

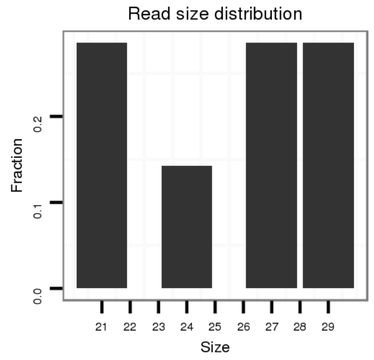
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1525	**scaffold_4770:7615325-7615412 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

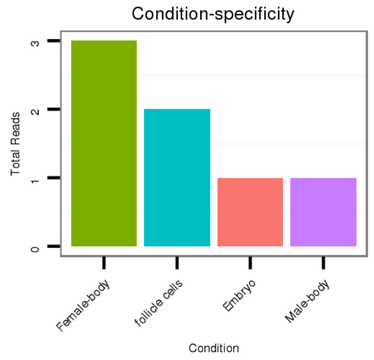
Legend: nature star mismatch in alignment mismatch in read

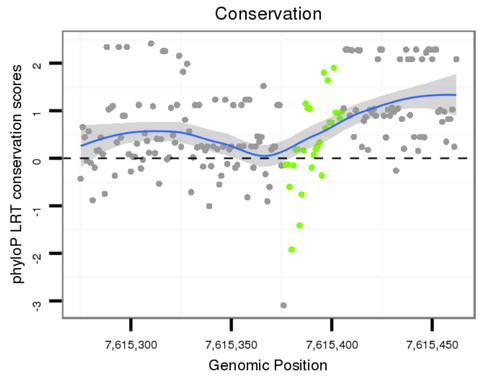
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAGTAAAGAAAACAAAACCAAGCAACAAAAAACAGTAAACGTAATGAACAAACAAATGCGGTCGAGCTTCCGTAAGTCGGACCACAACTAGAAACGTTCGCGGTATGGACGTTCGACTGTATGCTTAAAGTAATGTTAAACATGTATGCAACAAGTTTAGTGAGCCTTGTGTTTAGTTTAGTTGTTGC	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	V108 head	V040 embryo	GSM1528801 follicle cells	V107 male body	M057 embryo	V060 head
**********.(((((.((.........(((((((((((.(((((((...(((((.............)))))...)))))))..)))))))))))).....)).)))))..............**********												
.....GTATGGACGTTCGACTGTATGCTTAAAGT.....	29	0	1	2.00	2	0	0	0	2	0	0	0
.....GAACAAACAAATGCGGTCGA.....	20	0	1	2.00	2	0	1	0	0	1	0	0
.....AACAAAAACAGTAAACGTAATGAACAAA.....	28	0	1	1.00	1	0	0	1	0	0	0	0
.....TAATGAACAAACAAATGCGGTCGAGC.....	26	0	1	1.00	1	1	0	0	0	0	0	0
.....AAGCAACAAAAACAGTAAACGTAATG.....	26	0	1	1.00	1	0	0	0	0	0	0	0
.....TCGCGGTATGGACGTTCGACTGTATGC.....	27	0	1	1.00	1	1	0	0	0	0	0	0
.....CATGTATGCAACAAGTTTAGTG.....	22	0	1	1.00	1	0	0	1	0	0	0	0
.....AACAAATGCGGTCGAGCTTCC.....	21	0	1	1.00	1	0	0	0	0	0	0	1
.....GTTCGACTGTATGCTTAAAGTAATGTT.....	27	0	1	1.00	1	0	0	0	0	0	1	0
.....TTAGTGAGCCTTGTGTTTAGTT.....	22	0	1	1.00	1	1	0	0	0	0	0	0
.....TAAACGTAATGAACAAACAAATGCGGT.....	27	0	1	1.00	1	1	0	0	0	0	0	0
.....TTCGCGGTATGGACGTTCGAC.....	21	0	1	1.00	1	1	0	0	0	0	0	0
.....GCCTTGTGTTTAGTTTAGTTGTTG.	24	0	1	1.00	1	0	1	0	0	0	0	0
.....GTTCGCGGTATGGACGTTCGA.....	21	0	1	1.00	1	0	0	0	0	1	0	0
.....GTAATGAACAAACAAATGCGGT.....	22	0	1	1.00	1	0	1	0	0	0	0	0
.....TCGCGGTATGGACGTTCGACTGTA.....	24	0	1	1.00	1	1	0	0	0	0	0	0

Anti-sense strand reads

TTCATTTCTTTTGTTTTGGTTCGTTGTTTTTGTCATTTGCATTACTTGTTTGTTTACGCCAGCTCGAAGGCATTCAGCCTGGTGTTGATCTTTGTCAAGCGCCATACCTGCAAGCTGACATACGAATTTCATTACAATTTGTACATACGTTGTTCAAATCACTCGGAACACAAATCAAATCAACAACG	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body
**********.(((((.((.........(((((((((((.(((((((...(((((.............)))))...)))))))..)))))))))))).....)).)))))..............**********						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4770:7615275-7615462 +	der_1525	AAGTAA---AGAAAACA----------AAACCAA--------GCAA-C-----AAA----AACAGT-AAACGTAATGAACAAACAAATGCGGTCGAGCTTCCGTAAGTCGGACCACAACTAGAAAC----------AGTTCGCGGTATGGA-CGTTCGACTGTATGCTTAAA-GTAATGTTAAACATG---------TATGCAACAAGTTTAGTGAGCCTTGTGTTTAGTTTAGTTGTTGC----------
droYak3	3R:2621986-2622173 -	dya_132	AAGTGA---AGAAAACA----------AAACCAA--------GCAA-C-----AAA----AACAGT-AATCGTAATGAACAAACAAATGCGGCCGAGCTTCGTAAGTCGGACAAGAACTAGAAT-----------------------TAGTTCGTCTTATGGA-CGTTCGACTGTATGCTTAAA-GTAATGTTAAACATG---------TATGCAACAAGATTAGTGAGCCTTGTGTTTAGTTTAGTTGTTGC----------
droSec2	scaffold_12:131808-131988 +	dse_1848	AAGTAA---TGAAAACA----------AAACCAA--------GCAA-C-----AAA----AACAGT-AATCGTAATGAACAAACAAATGCGGTCGAACATGATGAAGTCGAACTAGAATCTACGAAT-----------------------ATAGTTCGCCTTGCCGGA-CGTTCGACTGTCGTGCTTAAA-GTAAT--------G---------TATGCAACAAGTTTAGTGAGCCTTGTGTTTAGTTTAGTTGTTGC----------
droSim2	3r:7258340-7258529 +	dsi_32443	AAGTAA---TGAAAACA----------AAACCAA--------GCAA-C-----AAA----AACAGT-AATCGTAATGAACAAACAAATGCGGTCGAGCATCAGTAAGTCGAACTAGAATCGTAACGAT-----------------------ATAGTTCGCCTTGCCGGA-CGTTCGACTGTCGTGCTTAAA-GTAATGTTAAACATG---------TATGCAACAAGTTTAGTGAGCCTTGTGTTTAGTTTAGTTGTTGC----------
dm3	chr3R:14020069-14020263 -	dme_386	ATGTAA---TGAAAACA----------AAACCAA--------GCAA-C-----AAA----AACTGT-AATCGTAATGAACAAACAAATGCGGTCGAGATATTCGTAAGTCGGACTAGAATCTA-----------------------TGTAACGAATATAGTTCGCCTTGCCGGA-CATTCGACTGTTGCTTAAA-GTAATGTTAAACATG---------TATGCAACAAGTTTAGTGAGCCTTGTGTTTAGTTTAGTTGTTGC----------
droEug1	scf7180000409246:369734-369961 -		AAGTAA---AAAAGGA----------AAACTAA--------GCAA-C-----AAA----AGCAGT-AATCGTAATGAACAAACAAATGCAGTTGAACTTCGTAAAACGAACTACAATTAGAAGTAAAAGTAAAAGTTATAAATGAACTTGAAGTTCTGCTTGTGGTTCGAATTAGAGA-CGTTCGACTGTCGTACTTAAATGTAATGTTAAACATG---------TATGCAACAAGTTCAGTGAGCCTTGTGATTAGTTTCGTTGTTGC----------
droBia1	scf7180000299102:1950377-1950601 +		AAGTAA---AGAAAACA----------AAACCAA--------GCAGGC-----AAA----AAAAGT-AATTGTAATGAACAAACGAGCACATCGAACTTCGTATGTCAACGTACGAACTAGAAATACGAGCAAAATCTGTAAAGAAACTTGAAGTTCTCTTTTTGATTCGACTCACGA-TATTCGACTGCA---CTAAA-GTAATATAAAACATG---------TATGCAACAAGTTTAGTGAGCCTTGTGTTTAGTTTAGTTGTTGC----------
droTak1	scf7180000414450:147920-148092 -		AA--CAGTTTAATTTGTTTACGTCCAACGACAACTAGAAATACAAGTAAAATCTTTGAAAGAACTTGGAGTTCTATTTGTAGTTCGATTTACAG-----------------------A--AATGTTAAACATG---------TATGCAACAAGTTTAGTGAGCCTTGTGTTTAGTTTAGTTGTTGC----------
droEle1	scf7180000491008:2241877-2242100 +		AAGTAA---AAACAAAA----------AGAAAATCCAA--------GCAGC-----AAA----AACAGT-AATGTCAATTAACAACAAAACACAGTCGATCTTCGTACAAGTCGAACAAGAACTAGAATCACAAGTTAAAT--------AACTTGAAGTTCTGTTTATGGACGCAACATGTACATTTCGACTGTATACTTAAA-TAAATGTAAAAATG---------TATGCAACAAGTTAGGTGAGCCTTGCGTTTAGTTTAGTTGTTGC----------
droRho1	scf7180000778633:31134-31363 -		AAGTAA---AGAAAACA----------AAAACCAA--------GCAAGC-----AAAAA----AACAGT-AATGCCAATGAACAACAAACACAGTCGGTCTTCGTAAGTCGAACAAAACTGGAAATACAAGTACACAATTACAAAGCTAAATAGAAGTGATGTTTATGGTTCGAGATATAGTTAGTTCGACAGTATACTTAAA-GTCATGTTAAACATG---------TATGCAACAAGTTAAGTAAGCCGTGTGTTAGTTTAGTTGTTGC----------
droFic1	scf7180000453800:497454-497679 -		AAGTAA---TGAAAACA----------AAACCAA--------GCAA-A-----CAA----AGCAGT-AATCGTAAAGAACAACAAACACAGTCGAACTTCGTAAGTCGAACAAAAGAAAAGCAAGTAATATCTCGAAAC-AACTTAAAGTTCTCATTTTAGTTCGAGATGCTAGA-TCGTTCGACTGTATACTTAAA-GTAATGTTAAACATG---------TATGCAACAAGTTTAGTGAGCCTTGTGTTTAGTTTAGTTGTTGC----------
droKik1	scf7180000302809:267110-267248 +		AGAGAA---GGTTGACA----------AAACACAGCAGCAAAGCAA-GAGCAACAG---AGCAGT-AATGTAAATGACAACAAAT--TATACTTAAA-GTAATGTTAAACATG---------TACGCAAGTAGTTAAGTAGTGAGTCGT-CGTTTAGTTTAGTTGTTAC----------
droAna3	scaffold_13340:15787936-15788061 -		TAGTAC---TGATATGA----------CAAACGAT--------GCAA-C-----AAC----AGCAGT-AACGTTAATGAACAACAAAT--ATACTTAAA-GTAATGTTAAACATGTA------CATATGCAACAAGTTAAGTGAGTCTTTGTTTAGTTTAGTTGTTGC----------
droBip1	scf7180000396708:4248372-4248512 +		AAGTAC---TGAAATGAAT----------TGAAAACCAT--------GCAA-C-----AGC----AGCTGCAAACGTTAATGAACAACAAAT--ATACTTAAA-GTAATGTTAAACATGTATGCAAACATATGCAACAAGTTAAGTGAGTCTTTGTTTAGTTTAGTTGTTGC----------
dp5	2:29111728-29111910 -		CAGCAG---AGCAGGGAAGCAAGCCCCCTCCCCACCCAGAAAGGGAACGAACAG--------GCACAGAGAAACCCAGCCGGGAGT-AATGATAAAAAGAG----------------------------AGAAACAAAAGCAAAA--ATACTTAAA-GTAATGTTAAA---A---------TATGCAACAAGTCTAGCAAGTCTTCTGTTTAGTTCACACTCTACTCTCTACCCCTCG
droPer2	scaffold_6:4436022-4436207 -		CAGCAGCAGAGCAGGGAAGCAAGCCCCCTCCCCACCCAGAAAGGGAACGAACAG--------GCACAGAGAAACCCAGCCGGGAGT-AATGATAAAAAGAG----------------------------AGAAACAAAAGCAAAA--ATACTTAAA-GTAATGTTAAA---A---------TATGCAACAAGTCTAGCAAGTCTTCTGTTTAGTTCACACTCTACTCTCTACCCCTCG
droVir3	scaffold_13049:14439782-14439829 +		CAGAAA---AGAAAACA----------AAAACAA--------GAAA-C-----AAA----ATCAAC-AAAC------AACAAACAA--ATACTTAAA-GTAATGTTAAACATCTATGCAAACATATGCAACAAGTTAAGTGAGTCTTTGTTTAGTTTAGTTGTTGC----------
droMoj3	scaffold_6540:2479607-2479680 +		TATACT---TAAA---TT-GTAATGTTAAATCCA-A-----GAAGTACAATGTATTTAGCAAGTCTTCTGTATTAGTTTAGTTGCAAC----------
droGri2	scaffold_14906:6002726-6002776 +		AAGCAA---GCAAAACA----------AAACAAA--------ACAA-A-----ACA----AAAACA-AAACATAAAGCATAAA--ATACTTAAA-GTAATGTTAAACATGTATGCAAACATATGCAACAAGTTAAGTGAGTCTTTGTTTAGTTTAGTTGTTGC----------

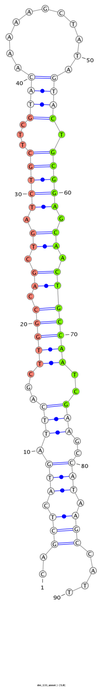
Generated: 09/08/2015 at 07:49 PM

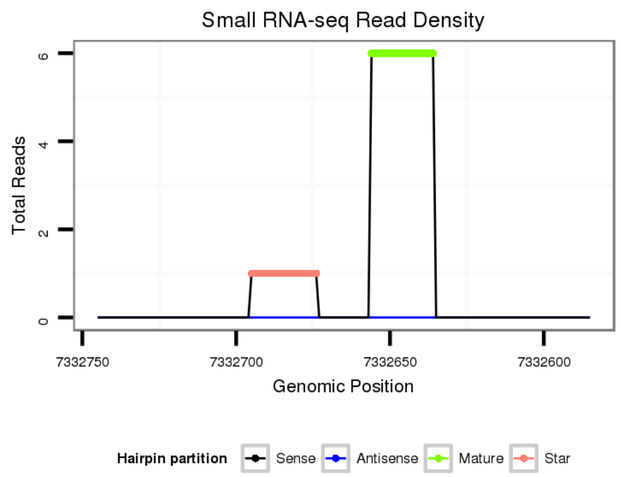
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	0
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	4

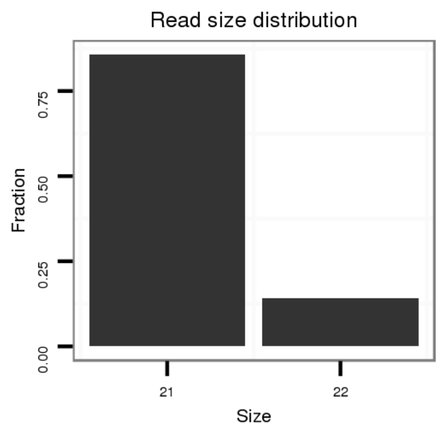
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_133	**scaffold_4784:7332635-7332695 -**	**candidate**	**Canonical miRNA**	**antisense_to_CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

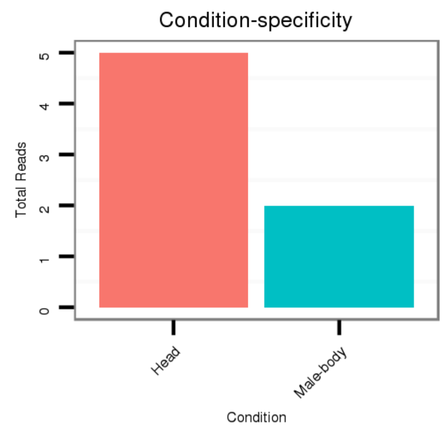
Legend: mature star mismatch in alignment mismatch in read

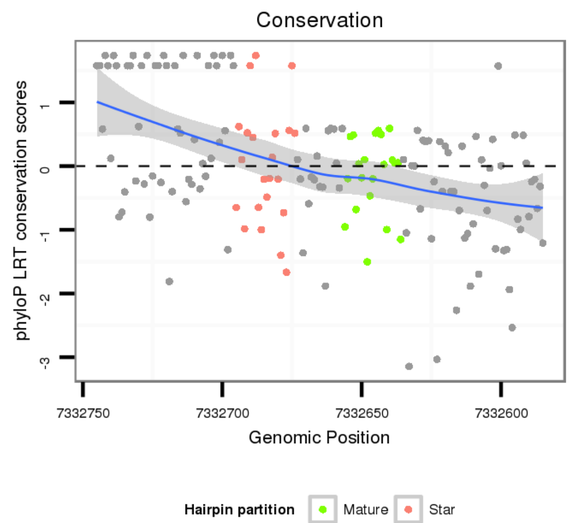
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to CDS [Dere\GG15240-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CCTTGAAGGATCCAAACTAGTGGTTCCCCACACCGCAGCTCATGATTCAGCTTGGCCAGCTGATCTGCTTCGTACAAAAAGCTATAGTACTGCGGAGCAACTGCCAATCGAAGCCATAAGCCATTCCAGGTGCTATGGATCCTATCATGGAGGTATTTGCT	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V107 male body	V060 head
**********..(((.(((.(((...((((((.((.((.((((((...(((((..........))))).))))))..)).)))))))..)))..)))..)))....**********								
.....CTGCGGAGCAACTGCCAATCG.....	21	0	1	6.00	6	3	2	1
.....CTTGGCCAGCTGATCTGCTTCG.....	22	0	1	1.00	1	1	0	0

Anti-sense strand reads

GGAACTTCCTAGGTTTGATCACCAAGGGGTGTGGCGTCGAGTACTAAGTCGAACCGGTCGACTAGACGAAGCATGTTTTTCGATATCATGACGCCTCGTTGACGGTTAGCTTCGGTATTCGGTAAGGTCCACGATACCTAGGATAGTACCTCCATAAACGA	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	V040 embryo	V107 male body
**********..(((.(((.(((...((((((.((.((.((((((...((((..........))))).))))))..)).)))))))..)))..)))..)))....**********								

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4784:7332585-7332745 -	der_133	CCTTGAAGGATCCAAACTAGTGGTTCCCCACACCGCAGCTCATGATTCAGCTTGGCCAGCTGATCTGCTTCGTACAAAAAGCTATAGTACTGCGGAGCAACTGCCA----------ATCGAAGCCATAAGCCATTCCAGGTGCTATGGATCCTATCATGGAGGTATTTGCT
droYak3	3L:5197731-5197891 -		CCTTGAAGGATCCAAACTAGAGGTTCTCCACACCGCAGCTCATGATTGAGATTGGCCAGAGGATCTAGTTCGTACAGAAAGCTATAGTACTGCGGAACAACTGCCA----------ATATATCCCATAAAGCATTCCGGCAGCTGTGGATCCTATCATAGAGGTATATCCT
droSec2	scaffold_2:4604109-4604247 -		CCTTGAAGGATCCAAACCAGAGGTTCCCCACACAGCAGCACATGATTTAGATTGACCAAAGGATCTAGGTCGTACAAGTGGCTATAGTACCGCGAAACAATTGCCA----------ATCGAAACCATGAACCCTTCCATGTGCTGCGGA----------
droSim2	3l:4567641-4567779 -		CCTTGAAGGATCCAAACCAGAGGTTCCCCAGCAGCAGCACATGATTTAGATTGGCCAAAGGATCTAGGTCGTACAAGTAGCTATAGTACCGCGAAACAATTGCCA----------ATCGAAACCATAAACCCTTCCATGTGCTGCGGA----------
dm3	chr3L:4622538-4622676 -		CCTTGAAGGATCCAAACAAGAGGTTCCCCACACAGCAGCACATGATTTAGATTGGCCAGAGGATCTAGGTCGTACAAGTAGCTATAGTACTGCGATACAATTGCCA----------ATCGAAACCATAAACCTTTCCGTATGCTGTGGA----------
droEug1	scf7180000409466:2397866-2398026 -		CCTTGAAGAATCCATACCAAAGGCTCTGCACATCGCAGCTCATGATTAAGTTGGGCCATTGGTCTGGTCATTCCAAAAGTGATAGTACCGCGGAATCACTGGTA----------ATGTAGCCCATAAAAATTTCCAAGGCGTTGCTCCTATCGCTTAGATAATTTTG
droBia1	scf7180000302428:9843267-9843427 +		CCTTGAAGAGCCCAACGCAGAGGCTCTGCACATCGCAACTCGTGGTTGAGCCTAGCCAGGGATCTGTTGTCGTACAAAACGCTATAGTATCGCGGAACCACTGGCA----------ATGTAAGCCATAAACACTGCCAGTGAGCAAGTATCCTGTCGTGAAGGTATCTTCT
droTak1	scf7180000415941:553415-553575 -		CCTTGCAGGACCCAAACCAGTGGTTCCGCACAACGGCAACTCATGGTTGAGTTTAGCCAGAGGATCGGATCGTAAAGAAGCTATAGTAACGCGGAATTACTGGCA----------ATGTGGACCATAAAAAGTTCCAATGGCTGAGAAACCTATCGCTGAGGTATTTTCG
droEle1	scf7180000491249:5536517-5536677 -		CCTTGAAGGCCCAAACCAAAGGTTCTCCACATCGCAATTCATGGTTGAGTTTGCCATAGGATTGGTCGTAAAAATAAGCATACCACTGCAGATCCCTGGTA----------ATGTAAGCATCAAACAATTCCAAAGCTAAGTGTTCTTCGTATATATGCTTTCC
droRho1	scf7180000779636:98284-98444 -		CCTTGAAGCGCCAAACCAAAGGTTCTCCACATCTCAATTCATGGTTAAGTTTGGCCAGAGTGTCTAGGTCGTAAAAATAAGATACCACTGCGGGATCACTGGTA----------ATGTAAGCCAAAACAGTCCCATAGATTAGTATCTATCATATAGATATTTTCC
droFic1	scf7180000454065:961400-961560 +		CCTTGAAGGGACCAAACTAGAGGCTCTGCACATTTCAACACATGGTTAAGTTTGGCCAAAGGAACTGGATCGTGGACAAAACATACCACTGAAGAACTACTGGCA----------TTCGAGACCAAATACGATTCCATAGTAAAACACTCTCTTGAGAAAATATTGTTG
droKik1	scf7180000302486:258145-258305 +		CCTTGAAGGATCCACACCAAAGGCTCACCACATTGCAGTACATGGTTGAGTTTAGCCAGTTTATCGATTGCCAAGACAAAGCAAACTGATTCGGAAATACTAGGT----------AGTCGGAAAGAAAAGTCCCGAATAGAAATGGACGAGTTCTCTCAAGTAACCTAC
droAna3	scaffold_13337:2708582-2708742 -		CCCTGCAGCCGTCCACACCAGCGGCTCCCCGCACACACAACTCGTGGTGGAGCTCCGCCAGGACATCCACTTCCAGCAATGTAGCACTGCCAGTGCCGACGTCCAGCCAGATGTCCTTTGACCCGCCGACCAAACT----------CACGGATTCTCTTCCGCAGAGACTGGCC
droBip1	scf7180000396741:37167-37316 +		CCCTGCAGCATCCAAACCATGGCCTCGCCGCACCGCAGCTCGTGGTTGAGTTCGGCCAGGATGTCCTCCTCGTACAAGTACCGCATGTAAATGCTCGCTTCGTGGAAGCTGTCCTAGCAGGTGGCGCTTCAATCCA----------ATGAGTTTGTTGACCC

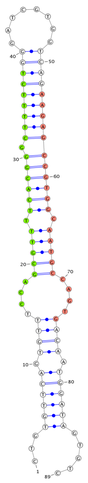
Generated: 09/08/2015 at 07:44 PM

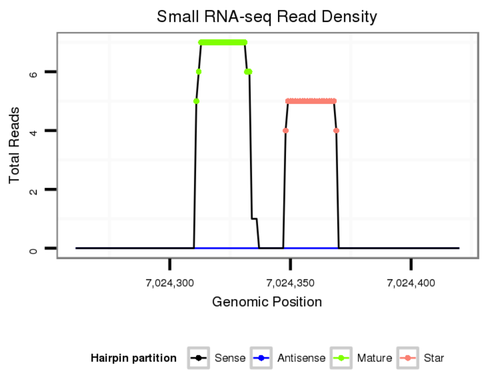
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

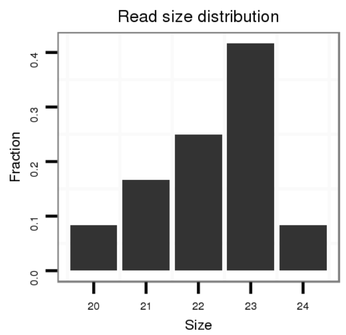
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_200	**scaffold_4770:7024311-7024370 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

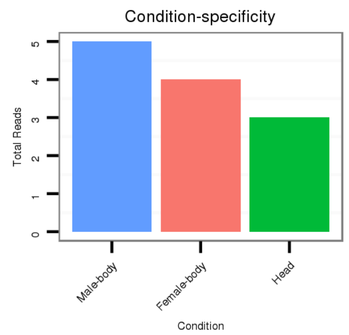
Legend: mature star mismatch in alignment mismatch in read

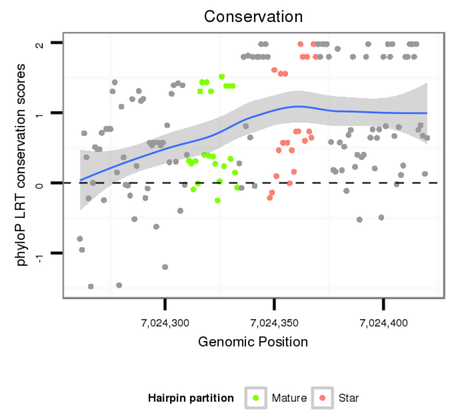
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTTTAGCAGGGGTTTCACTGTATGCGCTGTATTCACTGTGTTCAGTGTTTCCAGCGTTTTCACGGGCTTTTCTGGGATCGTGGTCAGAAGAGCCGTGGCAATGCCAGTGACAATGGATAGTGTCTGCTCCAGAGTGCTCCAAGTGGTTTGCTTGTTTGAA	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	V107 male body	V108 head
.....	23	0	1	5.00	5	2	3	0
.....	22	0	1	3.00	3	0	1	2
.....	21	0	1	1.00	1	0	1	0
.....	20	0	1	1.00	1	1	0	0
.....	21	0	1	1.00	1	0	0	1
.....	24	0	1	1.00	1	1	0	0

Anti-sense strand reads

CAAATCGTCCCCAAAGTGACATACGCGACATAAGTGACACAAGTCACAAAGGTCGCAAAAGTGCCCGAAAAGACCCTAGCACCAGTCTTCTCGGCACCGTTACGGTCACTGTTACCTATCACAGACGAGGTCTCACGAGGTTCACCAAACGAACAAACTT	Read size	# Mismatch	Hit Count	Total Norm	Total
No data available in table					

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4770:7024261-7024420 +	der_200	GTTTAGCAGGGGTTT---------CACTGTAT----------G-----CGCTGT--ATTCACTGTGTT---------CAGTG----TTTC-CAGC----------G---TTTTCACGGGCTTTTCTG----------GGA-------TCGTGGTCAGAAG----------AGC--CGTGGCAATGCCAGTGACAATGGATA----------GTGTCTGCTCCAGAGTGCTCCAAGTGGTTTG----------CTTGTTTGAA
droYak3	3R:3267524-3267677 -		ATTTGC---------CAGGGTTC----------T----CACTGT--ACTCACTGTGTT---------CAGTGTTTCC--AC-CAGT----------G---TATTCACGGGCTTTTCTG----------GGA-------TCGTGGTCAGAAG----------GGC--CGTGGCAATGCCAGTGACAATGGATA----------GTGTCTGCTCCAGAGTACTCCAAGTGGTTTG----------CTTGTTTGAA
droSec2	scaffold_5:5290768-5290905 +		GTTTTC---------CA------CAAGTTTCAT----CACTGT----------A----TATA-CAGT----------G---TTTTCACGGGCTTTCTG----------TGA-------TCGCGGTCAGCGG----------AGC--CGTGGCAATGCCAGTGACAATGGATA----------GCGCTGCTCAGAGTGCTCCAAGTGGTTTG----------CTTGTTTAAC
droSim2	3r:6647797-6647953 +		GTTTTC---------CA------CAAGTTTCAT----CACTGTATAT---------CAGTGTTTTCCAGTG----TTTT-CAGT----------G---TTTTCACGGGCTTTTCTG----------GGA-------TCGCGGTCAGCGG----------AGC--CGTGGCAATGCCAGTGACAATGGATA----------GCGCTGCTCCAGAGTGCTCCAAGTGGTTTG----------CTTGTTTGAC
dm3	chr3R:14609872-14610019 -		GGGTTT---------CAGGGTTTCCACAAGTTTCAT----CGTT----------GTA-TATT-CAGT----------G---TTTTCACGGGCTTTTCTG----------GGA-------TCGCGGTCAGCAG----------AGC--CGTGGCAATGCCAGTGACAATGGATA----------GCGCTGCTCCAGAGTGCTCCAAGTGGTTTG----------CTTGTTTGAC
droEug1	scf7180000409804:840451-840645 -		TTT-GC---------GTTTTCAGAGTAT----------T----CACTGT--GC---------TCACTGTT-TCCAGTG----TTTTCCCGT----------G---TTTTCAGGGCGTTTTCTGCGTT----TTCAAC----TC-TGGGATC----TGCTGGTCAGAAGAGCGGCGAACCCAGA----------GATGCCGAGAGCTGTGTGGCAATGCCAGTGACAATGGCCAC----------T-GTGTCTGT----GAGTGCTCCAAGTGGTTTG----------CTTGTTTGCC
droBia1	scf7180000302402:340629-340806 -		GTTCAG---------TGTTTTCAGGGTTTCGGGG--T----GAGAGCCTG----------A-TCCAGTG----TTTTT-CGGT----------G---TTTCCAGTGGCGTTTCAGG-GCTATGTTCCT----------GGGTTC----TCGTGGTCAGAAGAGCTGCG----------AGCTGTGTGGCCATGCCAGTGACAATGGAA----------GTGTCTGT----GAGTGCTGCGCAGTGGTCCG----------CTTGTTTGCC
droTak1	scf7180000415256:76273-76463 -		GCTTTC---------GTTTTCAGGGTTTCAACGATTT----T----CACTGT--TT---------TCAGTGTT-TCCAGTG----TTTTT-CCGTGTT---------G---TTTTCGGGGCTTTTCTGCGTT----TTCTGCG--TTTC-TGGGA----TCGTGGTCAGAAG----------CCGGGAGCTGTGTGGCAATGCCAGTGACAATGGCCAA----------TGGTGTCTGT----GAGTAGTCCAAGTGCTTTG----------CTTGTTTGCC
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droRho1	scf7180000779900:237451-237627 -		GCTTTT---------CAGGGTTC----------T----CACTGT--TT---------TCAGTGTT-TTCAGTG----TTTTT-TCGT----------G---TTTTCAGCGCGTTTTCTG----------GG-TATTC--GGGATCG----TGTGGTCAGAAGAGCGGCGAACCCA----------GCTGCCGAGAGC--TGTAGAAATGCCAGTGACAATGGCCA----------GTGTCTGT----GAGTGCTCCAAGTGGTTTG----------CTTGTTTGCC
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droKik1	scf7180000302256:407602-407789 +		GA--------GGTTT---------CA---TTC----------G-----CACTGTGTTT---------TC----------CAGTA----TTTTT-CCAAG-GGTTTTCCATGGGTTTTTCAGCGC--------GCT---TTCAGGC--TTTC--GAGA--------TCGCGGTCAGGG----------TGGCAAGTAC--TGTTAAAATGGAATGACAATGGCCAC----------T-GTGTCTGT----GAATGCTCCAAGTGGCTGCTGGTTGGTTGGTTGCCTGCGTTTTGCC
droAna3	scaffold_12911:2965217-2965307 -		AG--GCTTCTGTA----------GGCGTTTC--GGGA--------TCGCGGTCAGC--AACTGCCCATGACAATGCCGA----------AGCC-GGC----GAAGGCCCAAGTACTC-TG----------CTTGTTTGGC
droBip1	scf7180000396714:139414-139479 +		C---GGA-------TCGCGGTCAGCAG--CTGCCCATGACAATGCCC--------------------GCTGC----GAAGGCCACAAGTACTC-TG----------CTTGTTGTGCC
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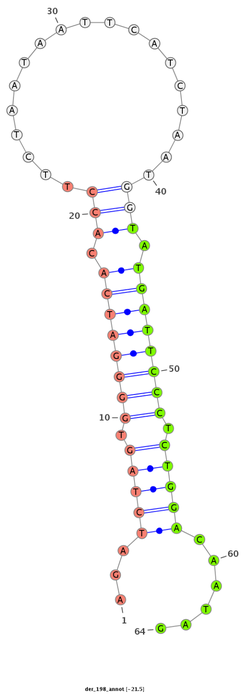
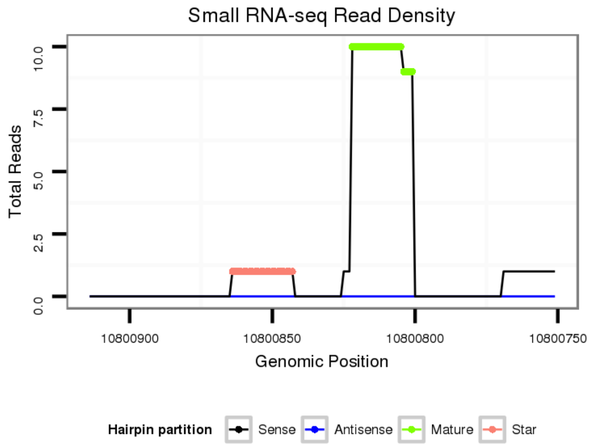
droPer2	scaffold_0:5673400-5673547 +		GTTT--C-GGGATCTCGTGGTCGTGGTCAGCGC----TGGACCGGGAAAGAGCGAGAGAGAGCCAGA--ACTTGAGC--TGCGGCAATGCCAATGACAATGGCCATGGCAATGGCAGCGCTGGTGCTGT----GAATGCTCCAAGTGCTCTG----------CTTGTTTGCC
droWil2	scf2_11000000004921:2840653-2840655 -		CTT--

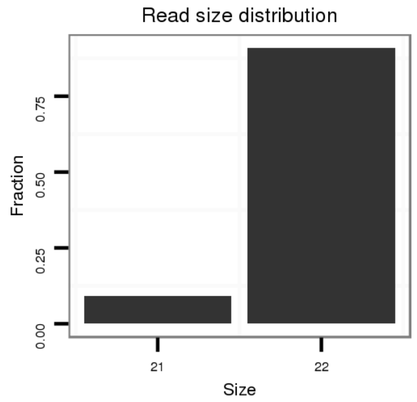
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_198	**scaffold_4770:10800801-10800864 -**	**candidate**	**5p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

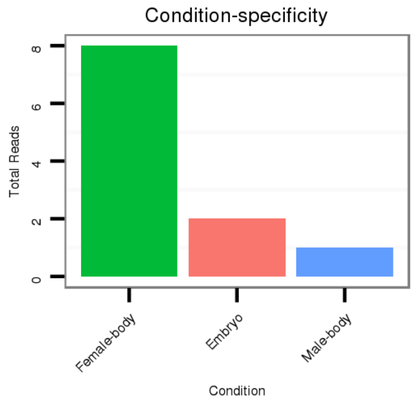
Legend: mature star mismatch in alignment mismatch in read

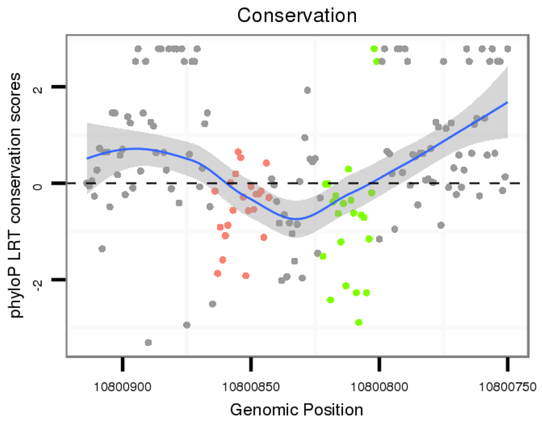
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG20508-in]; CDS [Dere\GG20508-cds]; CDS [Dere\GG20508-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads

CCAGTCCGGATACGAAAGGGACACAGCCATGCTGATCACACGGTGAGTGGAGATCTAGTGGGGATCACACCTTCTAATAATTCATCTAATGGTATGATTCCCTCTGGACAATAGCGAACCCATCTGCGGCAGCGTGCCGGGCAAGATTTGCCACATGCTGGGCT	Read size	# Mismatch	Hit Count	Total Norm	Total		M055 female body	M057 embryo	V040 embryo	V107 male	V108 head	M055 female body	V060 head
...(((((.(((((((((.(((.....................))))..)))))))))..)))))......													
....TATGATTCCCTCTGGACAATAG..	22	0	1	9.00	9	7	1	1	0	0			
....TATGATTCCCTCTGGACAATAGT...	23	1	1	2.00	2	1	0	0	0	1			
....TGGTATGATTCCCTCTGGACA..	21	0	1	1.00	1	1	0	0	0	0			
....ATTTGCCACATGCTGGGCT	19	0	1	1.00	1	1	0	0	0	0			
....AGATCTAGTGGGGATCACACCT..	22	0	1	1.00	1	0	0	0	1	0			

Anti-sense strand reads

GGTCAGGCCTATGCTTTCCCTGTGTCGGTACGACTAGTGTGCCACTCACCTCTAGATCACCCCTAGTGTGGAAGATTATTAAGTAGATTACCATACTAAGGGAGACCTGTTATCGCTTGGGTAGACGCCGTCGCACGGCCCGTTCTAAACGGTGTACGACCCGA	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	V108 head	M055 female body	V060 head
...(((((.(((((((((.(((.....................))))..)))))))))..)))))......									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4770:10800750-10800914 -	der_198	CCAGTC---CGGATA-CGAAAGGGACACAGCCATGCTGATCACACGGTGAGTGGA-GATCTAG--------TGG----------G-GATCACACCTTCTAATA---ATTCATC------------------TAATGGTATG--ATTC------CCTCTG---GACAATAGCGAACCCATCTGCGGCAGCGTGCCGGGCAAGATTTGCCACATGCTGGGCTT
droYak3	3R:15156541-15156696 +		CCAATC---CGGATA-CGAAAGGGACAGCGGCCATGTTGATCACCGGTAAGTGAA-GAT-----AAG----CC--AC-----A-TCCT---------GG---ATTCACC-----------------TAATGGTATA--TTTC------CCTTTA-AACCCATCAGCGAACCCATCTGTGGCAGCGTGCCGGGCAAGATTTGCCACATGCTGGGCTT
droSec2	scaffold_0:10674750-10674903 +		CCAATC---TGGATA-CGAAAGAGATACAGCCATGTTGATCACACGGTAAGTGGA-GAT-----ATG----GT--TC-----A-CCTT---------GG---GTTCACC-----------------TAATGGCATA--ATTT------CCTTTG---GACAATAGCGAACCCATCTGTGGCAGCGTGCCGGGCAAGATTTGCCATATGCTGGGCTT
droSim2	3r:9954957-9955110 +	dsi_8661	CCAATC---TGGATA-CGAAAGAGATACAGCCATGTTGATCACACGGTAAGTGGA-GAT-----ATG----GT--TC-----A-CCTT---------GG---GTTCACC-----------------TAATTGCATC--ATTT------CTTTTG---GACAATAGCGAACCCATCTGTGGCAGCGTGCCGGGCAAGATTTGCCACATGCTGGGCTT
dm3	chr3R:11273925-11274078 -		CCAATC---TGGATA-CGAAAGAGATACAGCCATGTTGATCACACGGTAAGTGGA-GAT-----ATG----AT--CC-----A-TCTT---------GG---GTTCATC-----------------TAATGGTATA--ATTT------CGTTTG---GACAATAGCGAACCCATCTGTGGCAGCGTGCCGGGCAAGATTTGCCATATGCTGGGCTT
droEug1	scf7180000409281:77403-77557 +		CCCAATC---TGGATA-CGAGAGGGACAGTGCCATGCTAATAACACGGTGAGTAAG-AGG-----TG----A--TCT---C--------TTCCTTTC---AATCTGC-----------------TAATGGAATC--AATT------CCTTTT---ACATCCAGCGAACCAATCTGTGGCAGCGTGCCAGGCAAGATATGCCACATGCTGGGCGT
droBia1	scf7180000302136:868769-868930 -		TACCTA---TGGCTA-CCCAAGGGACACAGCCATGCTGATCACACGGTGAGTGGA-TGAGGAT----C----G----------TGG-TATTTTT-----A--AGGTGAGTCC-----------------TCATCCTACCATTGA------CTTTG---TAACCAGTGAACCCATCTGCGGCAGCGTGCCGGGCAAGATTTGCCACATGCTGGGCGT
droTak1	scf7180000415769:1891995-1892157 +		CAAATC---GAACTA-CGGCAGGGACAGCGGCCATGCTGATAACGCGGTGGGTGAA-AGG-----GTA----TT--CC-----CCC-TATATTT-----T--AGTATCGTCC-----------------TAATATCAAAC-ATTT-T-----TGTCCA--CCCATCCAGAGAACCTATCTGTGGCAAGACGCGTGGCAGTACCTGCCACATGCTGGGCGT
droEle1	scf7180000491080:1040590-1040746 -		CCAGTA---TGGGTA-TCAAAGGGACACGGCAATGCTGATCACACGGTGAGTGGC-GATGGAG--------TGG----------G-G-TATATT-----T--AAGGGTATGC-----------------TAAAGGA---ATGT-----TCTTAA---AACTCCAGCGAACCGATCTGCGGCAGTGTGCCGGGCAAAATCTGCCACATGCTGGGAGT
droRho1	scf7180000779250:57957-58120 +		CCAGTA---CGGCTA-CCAAAGGGACAGTGCCATGCTGATCACCGGTGAGTGGA-TGT-----TTGAAGTGG----------G-GTTATTACT-----C--GAGGGTATCC-----------------TAATGGAATC-----TATGTTCTCAA---AACCCAGCGAAAACATCTGCGGCAGTGTGCCGGGCAAGATCTGCCACATGCTGGGCGT
droFic1	scf7180000452523:627325-627482 -		TCAGTA---TGGATA-TCAAAGGGACAGCGGCCATGCTGATCACGCGGTGAGTTCA-AAG-----AGT----TTATCT-----T---TTT---------GG---GAATTCCTTAATC-----------------TAATTGAGT-------TTATATTTTAT----GACTAGTGAACCCATCTGCGGTAGCGTTCCGGGCAAAATCTGCCACATGCTTGGCGT
droKik1	scf7180000302639:1408982-1409131 +		CCAGAA---GGGCTA-CCACAGGGACACGGCCATGCTGATAACTAGGTGAGTCTG-GAC-----TTAAAGT----------T-----T--------GGTC-GGATGCC---GGTCTAACCGATC-----------CTCTGC-------CTCCCAGGGAACCGATCTGCGGCGGATTCGAGGCAGGAGCTGTCACATGCTGGGCGT
droAna3	scaffold_13340:12859765-12859924 -		TCGGAA---AGGCTA-CCACAGGGACACGGCCATGCTGATAACAAGGTAGGTCCAAGAC-----ATG----G--TCTTTT-AGAA-TCAT----------GAGTTTCCAATACTAAAGTATT-----------GAGTTCCAATACTAAAGTATT-----------CTGGAA-------TCTCACAGAGAACCCATTTGCGGTGGCATTCCGGGCAAGCCTGCCACATGCTGGGTGT
droBip1	scf7180000396691:1741887-1742042 -		CCGGAA---AGGCTA-CCACAGGGACAGCGGCCATGCTGATAACTAGGTAAGTCCA-TAAC----AAG----G--TCT-----T----------TCTGGAA---GACTTTTCAGTGGTAAAGTAAT-----------CTTAAC-------TCTCTCAGAGAACCCATATGCGGTGGCATTCCGGGCAAGCCTGTCACATGCTGGGTGT
dp5	2:6353814-6353970 +		CCAGAA---GGGCTA-CCACTACGACAGCGGCCATGCTGATAACGCGGTAAGACAG-AGG-----ATG----A--GCT---G--T---------GCGCTGAT---CAGCATCTAGAGATAATCGATC-----------TTCCGA-------TCTTCCAGTGAGCCGATCTGCGGGGAATTCCGGAAAGAGCTGCCACATGCTGGGTGT
droPer2	scaffold_0:177949-178105 +		CCAGAA---GGGCTA-CCACTACGACAGCGGCCATGCTGATAACGCGGTAAGACAG-AGG-----ATG----A--GCT---G--T---------GCGCTGAT---CAGCATCTAGAGATAATCGATC-----------TTCCGA-------TCTTCCAGTGAGCCGATCTGCGGGGAATTCCGGAAAGAGCTGCCACATGCTGGGTGT
droWil2	scf2_1100000004902:1559237-1559397 +		TTTGGAAAATAAATT-TCATTACGATGTGCCATATTAATTACTCGGTGAGTTCG-AAG-----AAA----AT--C-----GCAA-AATTTCT-----C--GACATTTTTC---------TTAACTTCTT---------------AACCA---ACCAATAGCGAAGCATCTGCGGAGGATGTGTGATGCACACTGCCATATGCTGGGTTT
droVir3	scaffold_13047:13303664-13303817 +		CAAAGA---GGGCTA-TCATTATGACACAGCCATGCTAATCACTCGGTAGGTGGA-GTG-GC---TTAAAGC----------T----G-T--------GGTCGGGGCGTG-----CCAACTAATC-----------CTTAACTC-------TCCGGCAGCGATGAGATTTGCAGCAATGAACGCGAGGAACGCTGCAGTACTCTAGGCTT
droMoj3	scaffold_6540:10533443-10533603 +		CCAGAA---GGGGCATTCACTACGACACGAGCATTATGTATCACGCGGTAATTGAA-GACCCAACGAGT----CC--C-----GCCG-T--------------AATGGC-----------------TACTAATCCC--TCTC------CCCTTTGTTT-TTTACAGCGATAAGATTTGCAACAATGAGCGGAGGAGCGCTGCAGAACTCTGGGTGT
droGri2	scaffold_14906:4391340-4391499 -		CAAAAA---AGGCTA-TCCCTATGATAGCGGTATGCTATCACACGGTAAGTCCA-ACG-----CTT----TC--C-----GCCC-AAACTGTA----T-GCAAGGCAT---TATATAGCC----------A-ACA------TTTCG---CCGCGCTAGTGATGAGATTTGTTCGAATGAGCGGAGGAGCGCTGCAGAACACTGGGCTT

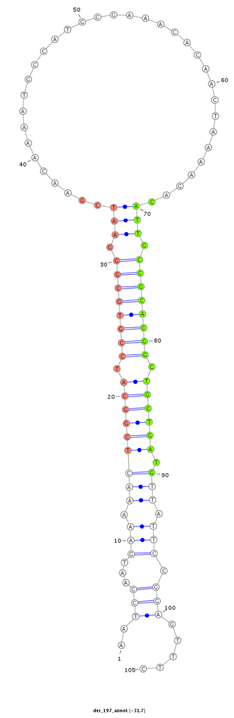
Generated: 09/08/2015 at 10:32 PM

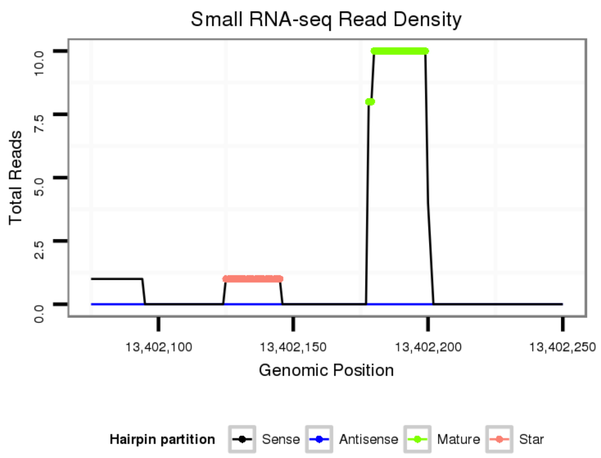
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

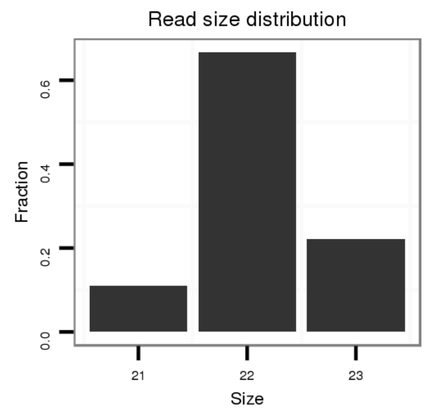
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_197	**scaffold_4845:13402125-13402200 +**	**candidate**	**Canonical miRNA**	**5pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

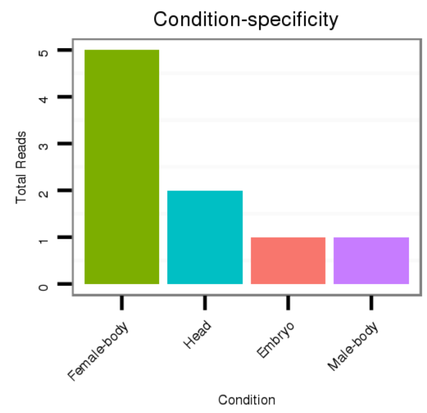
Legend: mature star mismatch in alignment mismatch in read

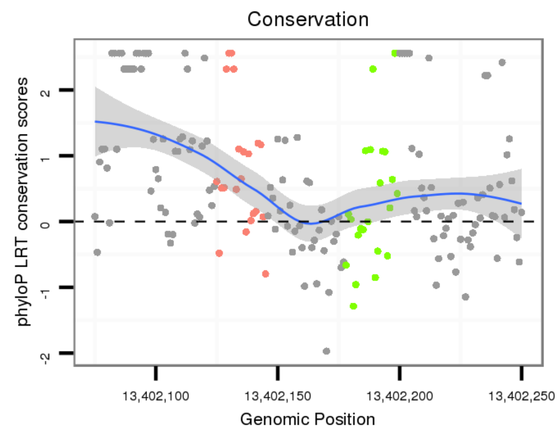
Predicted structure











Show Alternate Folds

Flybase annnotation

utr5 [utr5_minus_3941]; intron [Dere\GG22261-in]; CDS [Dere\GG22261-cds]

No Repeatable elements found

Sense Strand Reads

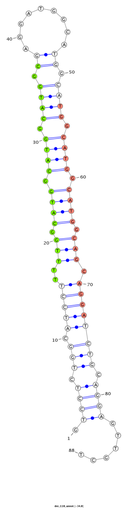
hide 3p reads | show mid mismatch reads

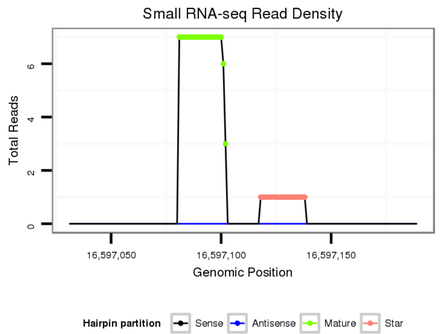
| | | |

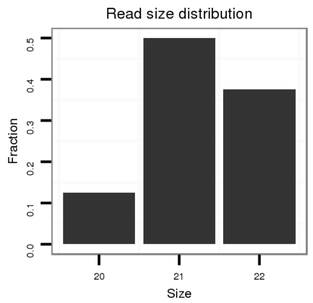
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_118	**scaffold_4845:16597081-16597139 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser [Cornell Mirror]]

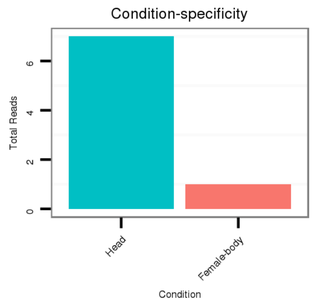
Legend: mature star mismatch in alignment mismatch in read

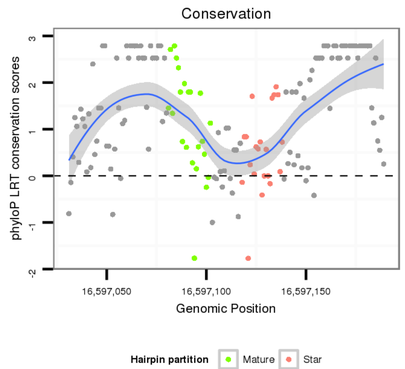
Predicted structure











Show Alternate Folds

Flybase annotation

intergenic

Repeatable elements

Name	Class	Family	Strand
(GCATG)n	Simple_repeat	Simple_repeat	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GCTACATGGCAACGTTTTACGGGGCAGAGAGATAAGTCCTCTGGCATCCTTTTTGGCATGGCATGGCATGGCGAGGATGGCATGGCATGGCATGGCATGGCAGCAGGATCTGTCAGGAGTTGCTCCGCGTTTTGTTGCATAGTTTTGATTTATTGCAGAG **********.((((.(((.(((((..(((.(((((.(((((.(((((.((.........)).)))))..)))))..)))).)))).)))))))))).)))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V060 head	V107 male body	M055 female body	V040 embryo
..........TTTTGGCATGGCATGGCATGGC..........	22	0	1	3.00	3	2	0	0	1	0
..........TTTTGGCATGGCATGGCATGG...........	21	0	1	3.00	3	1	2	0	0	0
..........TGGCATGGCATGGCAGCAGGA...........	21	0	1	1.00	1	1	0	0	0	0
..........TTTTGGCATGGCATGGCATG............	20	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

CGATGTACCGTTGCAAAATGCCCCGTCTCTCTATTCAGGAGACCGTAGGAAAAACCGTACCGTACCGTACCGCTCCTACCGTACCGTACCGTACCGTACCGTACCGTCCTAGACGTCCTCAACGAGGCGCAAAACAACGTATCAAAACTAAATAACGTCTC **********.((((.(((.(((((..(((.(((((.(((((.(((((.((.........)).)))))..)))))..)))).)))).)))))))))).)))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V040 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4845:16597031-16597189 +	der_118	GC-----TACAT----------GGCAACG---------TTT------TACGGGG--CA--GAGAGATAAGTCCTCTGGCATCCTTTTTGGCATGGCAT-GGCATGGCGA------GGATGGCATGG----------CATGGCATGGCATGGCAG----------CAGGATCTGCAG-----GAGTTG----------CT----------CCGCGTTTTGTTGCATAGTTTTGATTTATTGCAGAG
droYak3	2R:7741138-7741291 +		GC-----TACAT----------GGCAACG---------TTT------TACGGGG--CA--GAGAGATAAGTCCTCTGGCATCCTTTTTGGCATGGCAT-GGCGTGGCGA------GGATGGCA---TGGC----------AT-GGCATGGCAG----------CAGGATCTGCAG-----GAGTTG----------CT----------CCGCGTTTTGTTGCATAGTTTTGATTTATTGCAGAG
droSec2	scaffold_1:6741041-6741198 -		GC-----TACAT----------GGCAACG---------TTT------TACGGGG--CA--GAGAGATAAGTCCTCTGGCATCCTTTTTGGCATGGCAT-GGCATGGCTA------GGATGGCGAGGTTGGC----------AT-GGCATGGCAG----------CAGGATCTGCAG-----GAGTTG----------CT----------CCGCGTTTTGTTGCATAGTTTTGATTTATTGCAGAG
droSim2	2r:9886451-9886608 -		GC-----TACAT----------GGCAACG---------TTT------TACGGGG--CA--GAGAGATAAGTCCTCTGGCATCCTTTTTGGCATGGCAT-GGCATGGCTA------GGATGGCGAGGTTGGC----------AT-GGCATGGCAG----------CAGGATCTGCAG-----GAGTTG----------CT----------CCGCGTTTTGTTGCATAGTTTTGATTTATTGCAGAG
dm3	chr2R:9217943-9218090 -		GC-----TACAT----------GGCAACG---------TTT------TACGGGG--CA--GAGAGATAAGTCCTCTGGCATCCTTTTTGGCATGGCTA----------GGAGGGGAGGTTGGC----------AT-GGCATGGCAG----------CAGGATCTGCAG-----GAGTTG----------CT----------CCGCGTTTTGTTGCATAGTTTTGATTTATTGCAGAG
droEug1	scf7180000409663:1026813-1026946 -		--------TACAT----------GGCACGG---------TTT------TACGGGG--CACAGAGAGATAAGTCCTCTGGCATCCTTTTTGGCATCGCAT-GGCA------ ---------- ------TGGCATGGCG----------CAGGATCTGCAG-----GAGTTG----------CT----------TCGCGTTTTGTTGCATAGTTTTGATTTATTGCAGA-
droBia1	scf7180000302291:975490-975622 +		ACA----TACAT----------GGCACGG---------TTT------TACGGAG--CA--GAGATAAGTCCTCTGGCATCCTTTTGGCTTGGCAC-GGCA------ ---------- ------TGGCATGGCG----------CAGGATCTGCAG-----GAGTTG----------CT----------CCGCGTTTTGTTGCATAGTTTTGATTTATTGCAGAG
droTak1	scf7180000415379:384174-384316 -		ACATACATACAT----------GGCACGG---------CTT------TACGGGG--CA--GAGATAAGTCCTCTGGCATCCTTTTTGGCTTGGCCC-GGCATGG---- ---------- ---C---------- ------ATCGCATGGCG----------CAGGATCTGCAG-----GAGTTG----------CT----------CCGCGTTTTGTTGCATAGTTTTGATTTATTGCAGAG
droEle1	scf7180000491282:441651-441817 -		--------ACAT----------GGCACGCTTTT--ACGTTT------TACGGAG--CA--GAGATAAGTCCTCTGGCATCCTTTTGGCATGGCAT-GGCATGGC---- --ATGGGCAAGGC---ATGGCATGGAATAGT-----ATGGCATGGCAG----------CAGGATCTGCAG-----GAGTTG----------CT----------CCGCGTTTTGTTGCATAGTTTTGATTTATTGCGGAG
droRho1	scf7180000779889:45494-45643 -		--------TACAT----------GGCACGCTTTT--ACGTTTTACGTTTACGACGGCA--GAGATAAGTCCTCTGGCATCCTTTTGGCATGGCAT-GGCATA---- ---------- ----T---------- ------ATGGCATGGCAG----------CAGGATCTGCAG-----GAGTTG----------CT----------CCGCGTTTTGTTGCATAGTTTTGATTTATTGCAGAG
droFic1	scf7180000454039:24811-24955 -		--------ACAT----------GGCACGG---------TTT------TACGGGG--CA--GAGATAAGTCCTCTGGCATCCTTTTGGCATGGCAT-GGCATGGC---- -GATGGCA---- ---------- --TGGCAAGCAGCGGCAG----------CAGGATCTGCAG-----GAGTTG----------CT----------CCGCGTTTTGTTGCATAGTTTTGATTTATTGCAGCG
droKik1	scf7180000302277:620934-621080 +		--------ACAT----------GGCACGG---------TTT------TACGGGG--CA--GAGATAAGTCCACTGGCATCCTTTTGGCATGGCACAGGCAC----- ---------- ---------- ------TGGCA------CTGGCAGAGGAGCATCAGGACTGCAGAAGCCAGAGTAG----------CT----------CCGCGTTTTGTTGCATAGTTTTGATTTATTGCAGAG
droAna3	scaffold_13266:16525555-16525702 -		TA-----TACAT----------GGCACGA---------TTT------TACGGGG--CA--GAGATAAGTCCTTTGGCATCCTTTTGGCATGGCACCTTACCTCCCCCTCCGGCCAGC---- ---------- ---------- ---------AAAAGGCAG----------CAGCTTC-CGG-----CAA-GA----------CT----------CCGCGTTTTGTTGCATAGTTTTGATTTATTGCAG--
droBip1	scf7180000396384:635158-635315 -		TA-----TACAT----------GGCACGA---------TTT------TACGGGG--CA--GAGATAAGTCCTCTGGCATCCTTTTGGCATGGCAGCAGGC-------- ---------- ---------- ----------CAGCAGCAGGAGCAG-------CAGCAGCAG-----CAGTAGCACCAGCAACATCAGTTTCCCGGCAAGATGT----------CT----------CCGCGTTTTGTTGCATAGTTTTGATTTATTGCAG--
dp5	3:695435-695591 +		CG-----TACAT----------GGCAACG---------TTT------TACGGGG--CA---CAGATAAGTCCTCTGGCATCCTCTTGGCATGGCAGCGGCACCAGA----C---------- ----AGGG----GAAGAAGAGGCTCTGGCTGCAGG----------CAGAAAGTCCAG-----CAA-GA----------CT----------CCGCGTTTTGTTGCATAGTTTTGATTTATTAGCAAG
droPer2	scaffold_2:861882-862036 +		CG-----TACAT----------GGCAACG---------TTT------TACGCGG--CA---CAGATAAGTCCTCTGGCATCCTCTTGGCATGGCAGCGGCACCAGA----C---------- ----AGGG----GAAGAAGAGGCGCTGGCTGCAGG----------CAGAAAGTCCAG-----CAA-GA----------CT----------CCGCGTTTTGTTGCATAGTTTTGATTTATTAGCAA-
droWil2	scf2_1100000004822:2074459-2074607 -		GC-----CA---------GGCTGACTGGTTGGTTGCCTGTAT----------GGCTGCCTTGG--TTGGAAAACGTTTAGAGA-CA--GACAGATAAGTCCTCTGGCATCCTTTTG--------- ---------- ---------- ---------- ---------- ----------CTGGGAAACGATGCTGGGCGCGCGCGGCTTTTGTTGCATAGTTTTGATTTATTACAGAG
droVir3	scaffold_12875:241406-241505 +		GC-----TGCA---------GGGGCAACGTTTTAACG---------TTT------TATGCGGCA-CA--GACAGATAAGTCCTGTGGCATGCCTTGTGGC-------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------CGGCGTTTGTTGCATAGTTTTGATTTATTACAGAG
droMoj3	scaffold_6496:5258012-5258191 -		GC-----AAAGGGCAGGCAGTCGGGCAGCTCGTT----GTTGGTCGGTTTTGTGGCTAGGTGTACCAGCTGGGCTGGCCAGAGCTTTTGGCTTGGCCAACGTT------ -TTTAACGTTTTA---TATACGGTGC-CA--GC-AGATAAGTCCTTGTGGCATGCCTTGTGGC-------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------CGGCGTTTTGTTGCATAGTTTTGATTTATTACAGAG
droGri2	scaffold_15245:10721298-10721388 -		GC-----AACGA---------TTGAACG---------TTT------TATACGGCA-CA--GACAGATAAGTCCTTGTGGCATGCCTTGTGGC-------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------CGGCGTTTTGTTGCATAGTTTTGATTTATTACAGAG

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

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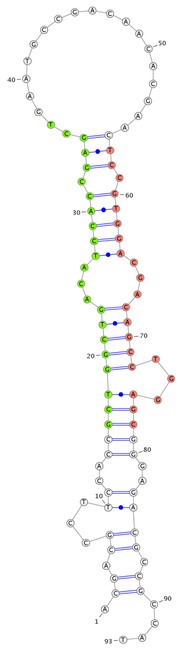
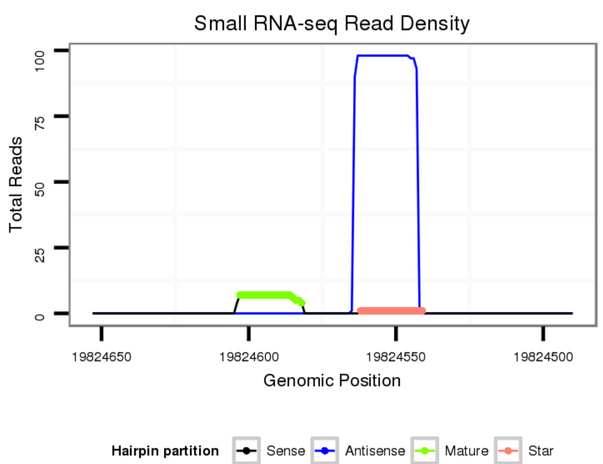
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

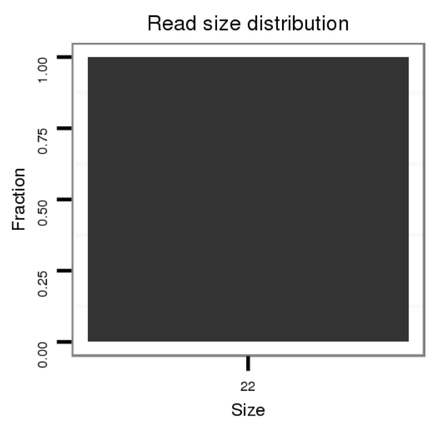
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_231	**scaffold_4929:19824540-19824603 -**	**candidate**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

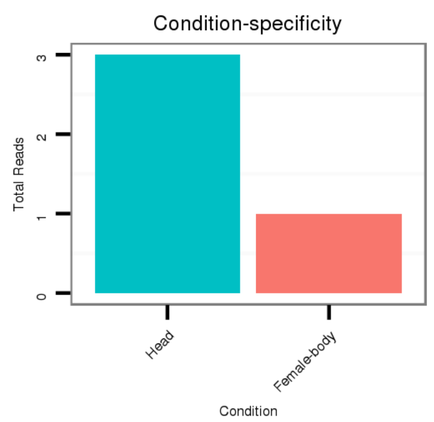
Legend: mature star **mismatch in alignment** mismatch in read

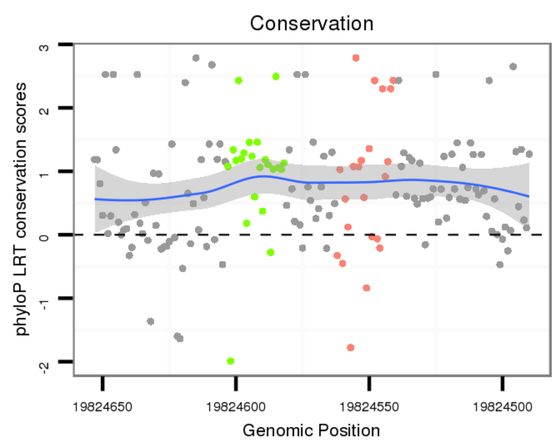
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dere\GG23227-cds]; Antisense to utr3 [utr3_minus_2262]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GCAGCCCGATCGCCGTGGACCGGACGCGGAGCGCGACGACGCCTTCCACCGCTGGCTGACATCCACCGAGCTGAATGCCGACAACACGAACTCCGTGGACGACAGCCTGGAGCGGGAGACGCCGCCATCGACCATAATCGATGATGTTGGCGCGGCCAACAAGA	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V060 head	M055 female body
**********.((.((...((..((((((((((...(((((.(((.....)))).)))))...)))))...)))))..))))....**********								
.....GCTGGCTGACATCCACCGAGCT.....	22	0	1	3.00	3	2	1	0
.....CGCTGGCTGACATCCACCG.....	19	0	1	1.00	1	1	0	0
.....CGCTGGCTGACATCCACCGAGC.....	22	0	1	1.00	1	1	0	0
.....CGCTGGCTGACATCCACCGAGCT.....	23	0	1	1.00	1	1	0	0
.....CGCTGGCTGACATCCACCGA.....	20	0	1	1.00	1	1	0	0
.....TCCGTGGACGACAGCCTGGAGC.....	22	0	1	1.00	1	0	0	1

Anti-sense strand reads

CGTCGGGCTAGCGGCACCTGGCCTGCGCCTCGCGCTGCTGCGGAAGGTGGCGACCGACTGTAGGTGGCTCGACTTACGGCTGTTGTGCTTGAGGCACCTGCTGTCGGACCTCGCCCTCTGCGGCGGTAGCTGGTATTAGCTACTACAACCGCGCCGGTTGTTCT	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	V108 head	M055 female body	V060 head	V040 embryo
**********.((.((...((..((((((((((...(((((.(((.....)))).)))))...)))))...)))))..))))....**********										
.....TGAGGCACCTGCTGTCGGACCT.....	22	0	1	86.00	86	48	18	17	3	0
.....GAGGCACCTGCTGTCGGACCT.....	21	0	1	7.00	7	3	2	2	0	0
.....TGAGGCACCTGCTGTCGGACC.....	21	0	1	3.00	3	1	1	0	1	0
.....CGAGGCACCTGCTGTCGGACCT.....	22	1	1	1.00	1	0	0	1	0	0
.....TTTGAGGCACCTGCTGTCGGACCT.....	24	1	1	1.00	1	0	0	1	0	0
.....TTGAGGCACCTGCTGTCGGACC.....	22	0	1	1.00	1	0	0	0	1	0
.....GAGGCACCTGCTGTCGGA.....	18	0	1	1.00	1	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4929:19824490-19824653 -	der_231	GCAGC-CCGATCGCCGTGGACCGGA----------CGC------GGAGCGCGACGACGCCTTCCACCGCTGGCTGAC---------ATCCACCGAGCTGAATGCCGACAACACGAACTCCGTGGACGACAGCCTGGAGCGGGA---GACGCCGCCATCGACCATAATCGATGATGT----------TGGCGCG---GC-----CAACAAGA
droSec2	scaffold_1:401429-401592 +		GCTAGCCCGATCGCCGTGGACCAGA----------CGC------GAGCGACGACGC-TTCCACCGCTGGCTGAC---------ATCCACCGAGCTGAATGCTGACAACACAAACTCCATGGACGACAGCCTGGAGCGGGA---AACGCCGGCATCGACAATAATCGATGATGT----------TGGCATG---GC-----CAACAAGA
droSim2	2r:3588499-3588662 +		GCAAC-CCGATCGCCGTGGACCAGA----------CGC------GGAGCAAGACGACGCCTTCCACCGCTGGCTGAC---------ATCCACCGAGCTGAATGCTGACAACACAAACTCCATGGACGACAGCCTGGAGCGGGA---AACGCCGGCATCGACAATAATCGATGATGT----------TGGCACG---GC-----CAACAAGA
dm3	chr2R:2723009-2723172 +		GCAAC-CCGATCGCCGTGGACCAGA----------CGC------GGAGCGAGACGACGCCTTCCACCGCTGGCTGAC---------ATCCACCGAGCTGAATGCTGACAACACAAACTCCATGGACGACAGCCTGGAGCGGGA---AACGCCGGCATCGACAATAATCGATGATGT----------TGGCACG---GC-----CAACAAGA
droEug1	scf7180000409672:4743203-4743366 +		GCAAC-ATGATCGCAATGGACCTGA----------CGC------GGAACCGACGACGCCTTCCATCGATGGCTGAC---------ATCCACCGAGCTGAATGCTGACAACACAAACTCGCTTGACGATAACGTGGAGCAGGA---AACGCCGGCATCGACAATAATCGATGATGT----------TGGCATG---GC-----CAACAAGA
droBia1	scf7180000302292:3421511-3421674 -		GCAAC-ATGATCGCAGTGGACCGCG----------CGC------GGAGACCGACGACGCCTTCCACCGCTGGCTGAC---------ATCCACCGAGCTGAATGCTGACAACACGCACTCGCTCGACGACAACTGGAGCAGGA---AACGCCGGCATCGACAATAATCGATGATGT----------TGGCACG---GC-----CAACCAGA
droTak1	scf7180000415420:352497-352666 -		GCAAC-GTGATCGCAGTGGACCCAA----------GAGGGAGCCGGAGCCGCGATGACGCCTTCCACCGCATGGTTGAC---------ATCCACCGAACTGAAGGGTGACAACACAAACTCGACTCGACGATAACCTGGAGCAGGA---AACGCCGGCATCGACAATAATCGATGATGT----------TGGCAGG---AC-----GAACAAGA
droEle1	scf7180000491217:257986-258158 -		GCAAC-ATGATCGCAGTGGACCTGA----------GAACGCCCCTGAGCCTGACGACGCCTTTCACCGCTGGCTGAC---------ATCCACCGAGCTGAATGGTGACAACACAAACTCGCTCGACGATAACCTGGAGCAGGA---AACGCCGGCATCGACAATAATCGATGATGT----------TGGCAGGCGCGC-----CAACAAGA
droRho1	scf7180000779196:89874-90043 +		GCAAC-ATGATCGCAGTGGACCTGACGA----------CGC------GCAGCCTGACGACGCCTTCTCATCGATGGCTGAC---------ATCCACCGAGCTGAATGGTGCCAACACAAACGCGCTCGACGATAACCTGGAGCAGGA---AACGCCGGCATCGACAATAATCGATGATGT----------TGGCACGACGC-----CAACAAGA
droFic1	scf7180000453955:564784-564947 -		GCAAC-ATGACGCCGCAGGACCATGA----------CGC------GGAGCCGAATGACGCCTTCCACCGATGGCTGAC---------ATCCACCGAGCTGAATGGTGACAACACAAACTGCCTGGACGACAACTCGGAGCAGGA---AACGCCGCCATCGACAATAATCGATGATGT----------TGGCCTG---GC-----CAACAAGA
droKik1	scf7180000302630:16315-16481 +		GCAAC-ATGATCGCCGTGGACCATGA----------CGCGGA---GGAGCTCGACGACGCGTTCCACCGATGGCTGAC---------GTCCACAGAGCTGAACGGTGACAACACAAACTCGCCCGACGACAACTCGGAGCAGGA---AACGCCAGCGCTCGACAATAATCGATGATGT----------TGGCACG---GC-----CAACAGGA
droAna3	scaffold_13266:9050231-9050397 +		GCAAC-ATGATCGCAGTGGACCATGA----------GCCGGA---GGAGCTCGATGACGCCTTCCACCGCTGGCTGAC---------ATGTACGGAGCTAAATGCGACAACACAAACCGCTTGACGATAACTTGGAGCAGGA---AACGCCGAACATCGACAATAATCGATGATGT----------GGGCATC---AT-----CAACAAAA
droBip1	scf7180000396427:194050-194216 +		GCAAC-ATGATCGCAGTGGACCACGA----------GCGGGA---GGAGTCCGATGACGCCTTCCATCGATGGCTGAC---------ATCCACCGAGCTGAATGGCGACAACACGAACCGCCTCGACGACAACTTGGAGCAGGA---AACGCCAGCATCGACAATAATCGATGATGT----------GGGCATC---AC-----CAACAAAA
dp5	3:994553-994713 +		GCAAC-CGGATAGGAGCGGTG---G----------CAA------GGACCTCGATGATGCGTTCCATCGTGGCTGAC---------ATCGACGAGCTGAATGGTGACAGCACAAACAGCGCCGGACGATGCCTCGGAGCAGGA---AACAGCAGCATCGACAATAATCGATGATGT----------TGCCATC---AG-----AAACAAGA
droPer2	scaffold_2:1175569-1175729 +		GCAAC-CGGATAGGAGCGGTG---G----------CAA------GGACCTCGATGATGCGTTCCATCGTGGCTGAC---------ATCGACGAGCTGAATGGTGACAGCACAAACAGCGCCGGACGATGCCTCGGAGCAGGA---AACAGCAGCATCGACAATAATCGATGATGT----------TGCCATC---AG-----AAACAAGA
droWil2	scf2_11000000004558:52357-52535 -		GCAAC-ATGAGAAGA-TGATG----------CGC---GA---AGAAGATGATGATGCATTTCATCGTTGGCTAC---------ATTCAGAGAGCTGAATGTTGAAAATACAAATAGACTGGACGTTAGCTTGGAGCAGGAAAAACATCAGCATCAACGATAATCGATGATGT---TGCTGCTGCGTCTGCTGC---TGCTGTTT---GT-----CAATAGAA
droVir3	scaffold_13047:10695900-10696051 -		GCAAC-ATGTTGGCCGTGCAGGAGC----------CGG------TGAGCGCGGCGCAGGAATA-ACAC--------CAACTCACCGAACCGACGTAGCG--------GCGGCGAGAACAAAAATGCCGCAA--GGTGTAGGGCATGGAGCGACGCGATCAATGGTGCACTCAGTGCCGAT-------GG-----GAAGAAGG
droMoj3	scaffold_6473:2959511-2959678 -		CGGGC-ATGG---CGATGGCGATGGCAGCCTGGCGCCCGCCTCCATCGT------AGAGAC--GG-ATCACTTGCACCAGCAGCTGAC----------GC----------AGCCGGTGACGCTGCGG--------AAGAACAGCCGCGCCGGAGGA---GCTGGCAGCTGCCGCAGCTGAC-CATGCAGT----------CGATGCAGCAGCTCACACAGCAGCCA
droGri2	scaffold_14853:216225-216368 +		GCAGC-GCGACGCAGCCGAGGCGA----------CC---------CGCAGAGGCCAACGTCGTGGCTTAATGGCGAGC----------ATA--AAAAGTGAAATGCCGCCACTGCACGGGGCGAGACGCTAACGG----CCGCC---GCGGCCAGCAGCAGCAGCAG-CAGCAGTAGCAG----------CGGCATT----------------									

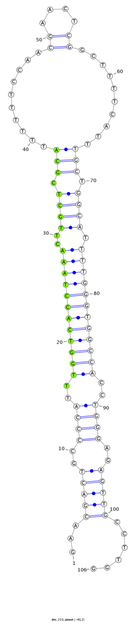
Generated: 09/08/2015 at 07:50 PM

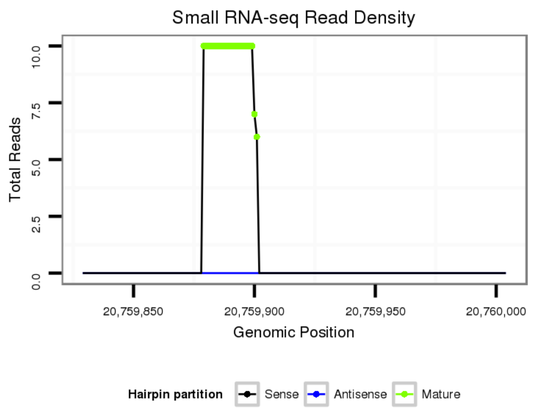
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

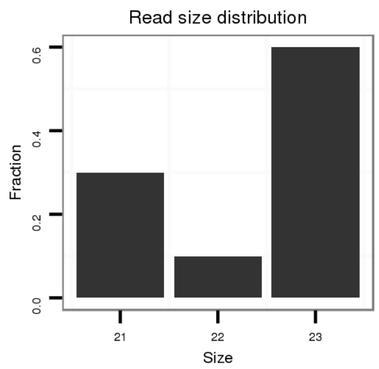
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_223	**scaffold_4784:20759879-20759954 +**	**candidate**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

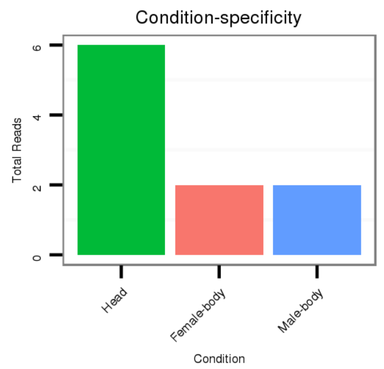
Legend: mature star mismatch in alignment mismatch in read

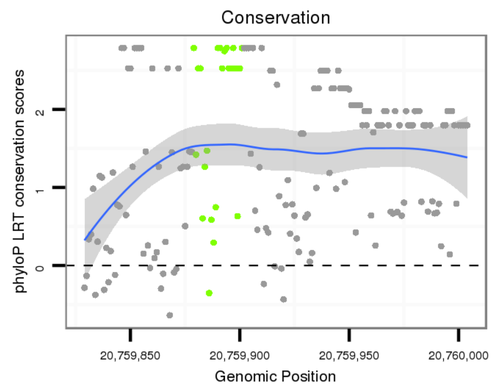
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dere\GG13263-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TGCAACTGGCCTGCTTATATGGCTAATCACCGGACGAACGACTGCCCCATTTGGTCACCTAAACTTGCTCGCATTTTTTCCAACGAACTCGGCTTTTCATTTGCTGGCATTTTGGGTGGCCACCTGGGAGAGTTGCCTTGGCTCGCTTGGCATTTGGCCACGTTCGATTGACGGGG									
..(((((..((((..(((((((((((((..((((.(((..........((....)).........)))).)))).)))))))))))))..)))))..))))).....	Read size	# Mismatch	Hit Count	Total Norm	Total	head	female body	male body	
...TTGGTCACCTAAACTTGCTCGCA...	23	0	1	6.00	6	4	1	1	
...TTGGTCACCTAAACTTGCTCG...	21	0	1	3.00	3	1	1	1	
...TTGGTCACCTAAACTTGCTCGC...	22	0	1	1.00	1	1	0	0	

Anti-sense strand reads

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

Show Alignment With Reads

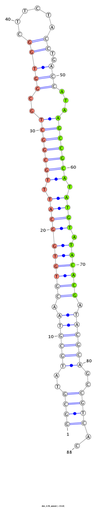
Re-alignment of all predicted orthologs

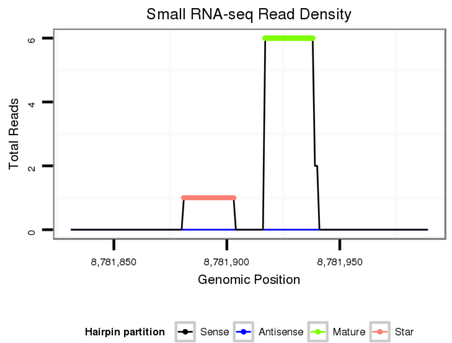
Species	Coordinate	ID	Alignment
droEre2	scaffold_4784:20759829-20760004 +	der_223	TG----CAAC---------TGGCC----TGCTTA------TATGGCTAATCA----------CCGG------ACGAACGACT---------GCCCC--A--TTTGGTCACCTA--AACTTGCTCGCATTTTTTCCA--ACGAACTCG----GC-TTTTCATTT----------G----CTGGC-----ATTTTGGGTGGCCACCTGG-----GAGAGT----------TGCCTTGGCTCGCTTGGCATT-TGGC-CACGTT-CGATTGA-CGGGG
droYak3	3L:19452308-19452482 -		TG----CAAC---------TGGCC----TGCTTA------TATGGCTAATCA----------CCGG------ACGAACGACT---------GCCCC--A--TTGGTCACCTA--AAC-TGCTCGCATTTTTTCCA--ACGAATCG----GC-TTTTCATTT----------G----CTGGC-----ATTTTGGGTGGCCACCTGG-----GAGAGT----------TGCCTTGAGTCGCTTGGCATT-TGGC-CACGTT-CGATTGA-CGGGG
droSec2	scaffold_11:960907-961082 +		TG----CAAC---------TGGCC----TGCTTA------TATGGCTAATCA----------CTGG------ACGAACGAAT---------GCCCC--A--TTTGGTCACCTA--AACTTGCTCGCATTTTTTCCA--ACGAACTCG----GC-ATTTCATTT----------G----CTGGC-----ATTTTGGGTGGCCACCTGG-----GAGAGT----------TGCCTTGGCTTGCTTGGCATT-TGGC-CACGTT-CGATTGA-CGGGG
droSim2	3L:20625402-20625577 +		TG----CAAC---------TGGCC----TGCTTA------TATGGCTAATCA----------CTGG------ACGAACGAGT---------GCCCC--A--TTTGGTCACCTA--AACTTGCTCGCATTTTTTCCA--ACGAACTCG----GC-TTTTCATTT----------G----CTGGC-----ATTTTGGGTGGCCACCTGG-----GAGAGT----------TGCCTTGGCTCGCTTGGCATT-TGGC-CACGTT-CGATTGA-CGGGG
dm3	chr3L:21072460-21072637 +		TG----CAAC---------TGGCC----GCGTTA------TATGGCTAATCA----------TTGG------ACGAACGACT---------GCCCC--A--TTTGGACACCTA--AACTTGCTCACATTTTTTCCA--ACGAACTCG----GC-TTTTCATTT----------G----CTGGC-----ATTTTGGGTGGTCACCTGG-----GAGAGT----------TGCCTTGGCTCGCTTGGCATTTGGGTACGCGTT-CGATTGA-CGGGG
droEug1	scf7180000409711:4924439-4924614 -		TG----CAATG---GTGGCC----GCGTTA------TATGGCTAATCA----------CTGG------ACGAACACT---------GCCCC--A--TTTGGTCACCTA--AACTTGCTCGCATTTTTTCCA--ACGAACTCC--AACTTTT--TTC----------G----CTGGC-----ATTTTGGGTGGCCACCTGG-----GAGACT----------TGCCTTGGCTCGCTTGGCATTTGGC-CACGTT-CGACTGA-CGGGG
droBia1	scf7180000302193:4967442-4967614 -		TG----CAAC---------TGGCC----GCGTTA------TATGGCTAATCA----------CTGG------CGGACGACT---------GCCCC--A--TTTGGTCACCTA--AACTTGCTCGCATTTTTTCCA--ACGAACTCG----AC-TTTTC----------G----CTGGC-----ATTTTGGGTGGCCACCTGG-----GAGACT----------TGCCTTGGCTCGCTTGGCATTTGGC-CACGTT-CGACTGA-CGGGG
droTak1	scf7180000415319:152135-152308 +		TG----CAAC---------TGGAC----GCGTTA------TATGGCTAATCA----------CCGG------ACGCACGACT---------GCCCC--A--TTTGGTCACCTA--AACTTGCTCGCATTTTTTCCA--ACGAACTCG----AC-TTTTCG---------------------G----CTGGC-----ATTTTGGGTGGCCACCTGG-----GAGACT----------TGCCTTGGCTCGCTTGGCATTTGGC-CACGTT-CGACTGA-CGGGG
droEle1	scf7180000491193:2284398-2284570 -		TG----CAAC---------TGGCC----GCGTTA------TATGGCTAATCA----------CTGG------ACGAACCACT---------GCCCC--A--TTTGGTCACCTA--AACTTGCTCGCATTTTTTCCA---GCGAACTCG----AC-TTTT----T----------G----CTGGC-----ATTTTGGGTGGCCACCTGG-----GAGACT----------TGCCTTGGCTCGCTTGGCATTTGGC-CACGTT-CGACTGA-CGGGG
droRho1	scf7180000779687:7057-7231 +		TG----CAATG---------TGGCC----GCGTTA------TATGGCTAATCA----------CTGG------ACAGACGACT---------GCCCC--A--TTTGGTCACCTA--AACTTGCTCGCATTTTTTCCA--ACAAACTCG----AC-TGTT--TTT----------G----CTGGC-----ATTTTGGGTGGCCACCTGG-----GAGACT----------TGCCTTGGCTCGCGTGGCATTTGGC-CACGTT-CGACTGA-CGGGG
droFic1	scf7180000453929:225538-225720 +		TG----CAAC---------TGGCT----AGCTTA------TATGGCTAATCA----------CTGG------ACAGACGACG-A------GCCCC--A--TTTGGTCACCTA--AACTTGCTCGCATTTTTTCCA--ACGAACTCGCCGCGC-TTTGC----------G----ATGCCATTTTATTTTGGGTGGCCACCTGG-----GAGACT----------CGCCTTGGCTCGCTTGGCATTTGGC-CACGTT-CGACTGA-CGGGG
droKik1	scf7180000302260:260229-260432 -		TA----CAAC---TG---GGCCCGCTTAGGCCTGGCTTATATGGCTAATCA----------CTGG------ACGAACGAGTGT---------GCCCC--A--TTTGGTCTGCCT--AACTTGCTCGCATTTTTTCCA--GCGAACTCACTCGC-TTTTCATTT----TTCATTTTA----------G----CTGGC-----ATTTTGGGTGGCCACCTGG-----GAGACT----------CGCCTTGGCTCGCTTGGCATTTGGC-CACGTG-CGACTGA-CGGGG
droAna3	scaffold_13337:8624178-8624368 -		---------C---TG---GGCCCGCTTAGATA------TATGGCTAATGT--GGCTTAATCACCGG------ACGACGGT---------GCCCCCCT-TTTGGTCAACTA--AACTTGCTCGCATTTTTTCCA--GCGAACTCGCGAGAC-TGT-----G----------G----CTGGC-----ATTTTGGGTGGCCACCTGGCATGGGAGAC-C----------TGCCTTGGCTCGATTGGCATTTGGC-CATGTT-CGACTGA-CGGGG
droBip1	scf7180000396541:764709-764907 -		GT----CAC---TG---GGCCCGCTTAGATA------TATGGCTAATAT--GGCTTAATCACCGGCCCCGGTCGCGACGGT---------GCCCCCCT-TTTGGTCAACTA--AACTTGCTCGCATTTTTTCCA--GCGAACTCG-GAGAC-TGT-----G----------G----CTGGC-----ATTTTGGGTGGCCACCTGGCATGGGAGAC-C----------TGCCTTGGCTCGATTGGCATTTGGC-CATGTT-CGACTGA-CGGGG
dp5	XR_group8:3858360-3858549 +		TA----TGAT---------GGTCATGC--TACGAA---------TAAGGCTAATCATCG---------CTGC-C-----ACAAACAGC---CTA--AGACCC--ATTTTGGGCGTTGCC--AACTTGCTCGCATTTTTG-CA--ACGAAA----------CTCG----CGGC-----ATTTTGGGTGGCCACCAGG-----GAGACTGCCGCTCCGTTTGCCTTGGCTCGCTTGGCATTTGGC-CACAAACCGAGTGCCGGGG
droPer2	scaffold_29:86401-86594 +		AGTTTTTGAT----G---GTCATGC--TACGAA---------TAAGGCTAATCATCG---------CTGC-C-----ACAAACCAG---CTA--CGCCCC--ATTTTGGGCGTTGCC--AACTTGCTCGCATTTTTG-CA--ACGAAA----------CTCG----CGGC-----ATTTTGGGTGGCCACCAGG-----GAGACTGCCGCTCCGTTTGCCTTGGCTCGCTTGGCATTTGGC-CAGAAACCGAGTGCCGGGG
droWil2	scf2_1100000004830:39946-40098 +		GG----CGGTGGGTTGCGTGGGTT----TACATA------TAAGGTAATCA----------CTGC-------CTTAACAGCTAGCTCTCAGGTTCCCAA-ATTGG-TATGAACGCAACTTGCTCGCATTTTTTCCA--ATGAATTTG---GT-TTGTTATTTATTTTTTCGTT----------G----TCGGC-----ATTTTGGGTGGCC--
droVir3	scaffold_13049:15269310-15269465 -		--------C---------TGGAC----TGCTTA------TAAGGCTAATGA----------TAGG------CGGGCGAACG-A------GCCCC--A--TTTGGTCAGATA--AACTTGCTGTCATTTGTTATAATATATAAATCT---TTTTT----TTTGTTTTGATTTTCTGCTCGCAACCAAACAAGCAGCGAGGC-----ATTTCGGTTGGCCACCCGG---

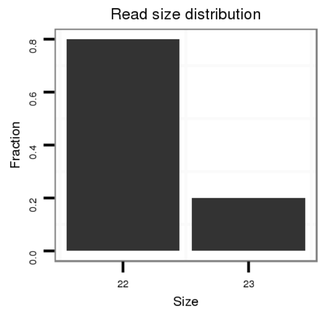
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_120	**scaffold_4820:8781881-8781939 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

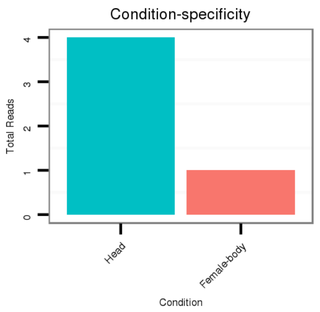
Legend: mature star mismatch in alignment mismatch in read

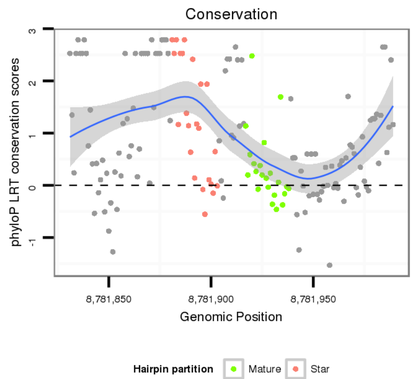
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

							V108	M055 female		
GAACACGACGCAGGCGAATCAAGCCGGGCCTACCTGGCGTATGCGTAACGTGTGGCATTTGCGGCTGCGGTGGCTTCTACCTGACCATAAGCCGCATATGTATACACGATACGCAGCCGTCACACAAGCGGCCACCGAGGGCAGCAGAAATGTTTAACC	Read size	# Mismatch	Hit Count	Total Norm	Total	head	body	embryo body	male body
********************************(((..(((((((.(((((((((.(((((((..(((((.....)).)))...)))))))).)))))).)))))))..)))))..********************************										
.....ATAAGCCGCATATGTATACACG.....	22	0	1	4.00	4	3	1	0	0	
.....ATAAGCCGCATATGTATACACGAT.....	24	0	1	2.00	2	2	0	0	0	
.....TGTGGCATTTGCGGCTGCGGTGG.....	23	0	1	1.00	1	1	0	0	0	

Anti-sense strand reads

							V108	M055 female		
CTTGTGCTGCGTCCGCTTAGTTCGGCCCGGATGGACCGCATACGCATTGCACACCGTAAACGCCGACGCCACCGAAGATGGACTGGTATTCGGCGTATACATATGTGCTATGCGTCGGCAGTGTGTTCGCCGGTGGCTCCCGTCGTCTTTACAAATTGG	Read size	# Mismatch	Hit Count	Total Norm	Total	head	body		
**********************************(((..(((((((.(((((((((.(((((((.....)).)))...)))))))).)))))).)))))..**********************************										

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4820:8781831-8781989 +	der_120	GA-ACACGACGC----------AG--------GC-----------------------------GAATCAA-----GCCGGGCCTACCTGGCGTATGCGTAACGTGTGGCATTT-GCG-----------------GCTGCGG--TGGCTTCTACCTGACCATAAGCC----------------G----------------------C--ATATGTATA----------------------------CACGA---TA---CGCAGCCGTCACACAAGC-GGCCA----------------C--CGAGGG-CAGCAGAAATGTTTAACC
droYak3	3R:20150090-20150258 -		GA-ACACGACGC----------AG--------GC-----------------------------GAATCAA-----GCCGGGCCTACCTGGCGTATGCGTAACGTGTGGCATTT-GCG-----------------------G--TGGCTTCTACCTGACCAAAGCC----------------A----------------------C--ATATAGCTACATACATACATA----------------------CACGA---TAATACACGCCGTCACACA-CC-AACA----------------CCCGAGGG-CACAGAAATGTTTAACC
droSec2	scaffold_0:19630600-19630753 -		GA-ACACGACAC----------AG--------GC-----------------------------GAATCAA-----GCCGGGCCTACCTGGCGTATGCGTAACGTGTGGCATTT-GCG-----------------GCTACGG--TGGCTTCTACCTGACCATAAGCC----------------A----------------------C--ATATA----------------------------CACGA---TA---CACGACGTCACACA-CC-AACA----------------C--CGAGGG-CAGCAGAAATGTTTAACC
droSim2	3r:18809152-18809305 -		GA-ACACGACAC----------AG--------GC-----------------------------GAATCAA-----GCCGGGCCTACCTGGCGTATGCGTAACGTGTGGCATTT-GCG-----------------GCTACGG--TGGCTTCTACCTGACCATAAGCC----------------A----------------------C--ATATA----------------------------CACGA---TA---CACGACGTCACACA-CC-AACA----------------C--CGAGGG-CAGCTGAAATGTTTAACC
dm3	chr3R:19267740-19267893 -		GA-ACACGACAC----------AG--------GC-----------------------------GAATCAA-----GCCGGGCCTACCTGGCGTAGCGTAACGTGTGGCATTT-GCG-----------------GCTACGG--TGGCTTCTACCTGACCATAAGCC----------------A----------------------T--ATATA----------------------------CACGA---TA---CACGACGTCACACA-CC-AACA----------------C--CGAGGG-CAGCAGAAATGTTTAACC
droEug1	scf7180000409473:61458-61591 +		GAGCCACGACGCAAATGTAAGC--CG-----GCCGGGCCTACCTGGCGATGCGTAACGTGTGGCAT----------------GA--TGGCTTCTACCTGACCATAAGC----------------A----------------------C--CTATGT----------------------------ACGAATATA---AAC-C----------A-CA----------------G--CGAGGG-CACTTGAAATGTTTAACC
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droTak1	scf7180000414295:358094-358224 -		GAGCCACGACAAAATGTAAC----------GC-----------------------------GAATGGA-----GCCGGGCTACCTGGCGTATGCGTAACGTGTGGCATTT-GCG-----------------GGCACGG--AGGCTGCTACCTGACCATA----------------TA--AA-CC-AACA----------------C--CGAGGG-CAGCAGAAATGTTTAACC
droEle1	scf7180000491261:312133-312307 +		GA-ACACGACAAAATGTAAGCACACAGA----------GC-----------------------------GATTCGC-----GCCGGGTCTACCTGGCGTATGCGTAACGTGTGGCATTT-GCG-----------------GGTTCGG--TGGCTTCTACCTGACCATAAGCC----------AAAAGCTATG--GC---CATGA---GC---CACGACTTCCGACG-A-CC-AACA----------------C--CGAGGG-CAGCAGAAATGTTTAACC
droRho1	scf7180000780099:243973-244136 -		GA-GCACGAGAAAATGTAAGCACAAAGCA--CAA---GT--GATTCGGGCCGGGCCGGGCCTACCTGGCGTATGCGTAACGTGTGGCATTT-GTG-----------------GGTTCAG--TGGCTTCTACCTGACCATAAGCC----------ATA--AGCCA---TA---CCGC-----------A-CC-AACA----------------C--CGAGGG-CAGCAGAAATGTTTAACC
droFic1	scf7180000453906:580628-580813 +		GA-ACACGACAAAATGTAAC----------C-----------------------------GACTTAG-----ACCGGGCCTACCTGGCGTATGCGTAACGTGTGGCATTT-GCG-----GTCGCTTCGGTGGCAACGG--TGGCTTCTACCTGACCATAAGCA----------ATAAGCCAACAGGCAACAGAGCTAACAGG-GGCCACACCA--ACA-GC-AACA----------------C--CGAGGG-CAGCAGAAATGTTTAACC
droKik1	scf7180000302639:3344190-3344278 +		GA-GCACGACAAAATGTAAACACACAGTCGCAC---AT--GAGA-----GCCGGGCCTACCTGGCGTATGCGTAACGTGTGGCATTTGCG-----------------GCTGCGG---
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dp5	2:2750831-2751039 -		GA-GCACGACAAAATACACACAG----A----------AC-----------------------------AGATAAT-----GCGGGGCCTACCTGGCGTATGCGTAACGTGTGGCATTTGAAGCTGCGGCTACGCGGTGGCAGGAA--CTAGGCTACCTGACCATAAGTG----------T--CGACAAACGCGTAAATATTGGCTCTTTGGGGCCAGTGTGTATG---------------C-----GGTTTGGGGCGTGACATG----CC-CGCAAAAATGTTTAACC
droPer2	scaffold_7:1600863-1601077 +		GA-GCACGACAAAATACACACACAGCA--C----------AC-----------------------------ACCTAAT-----GCGGGGCCTACATGGCGTATGCGTAACGTGTGGCATTTGAAGCTGCGGCTACGCGGTGGCAGGAA--CTAGGCTACCTGACCATAACC----------A--CGACAGACGGAGCGTAAATATTGGCTCTTTGGGGCCAGTGTGTATG---------------C-----GGTTTGGGGCGTGACATG----CC-CGCAAAAATGTTTAACC
droWil2	scf2_1100000004943:9309083-9309251 -		GA-GCACGACAAAATGTAAACACACAGCA--C----------AC-----------------------------AGACAGA---GTCGGGCCTACCTGGCGCATGCGTAACGTGTGGCATGCA-GAG----------A----gg-----------TGCCGCCTAAGCGACAAAGAAGCGAAAAGAAA----------------A----AAAAGCCTCATAAAATATTGTCTATT--GGTT----------------T-TCGGGCGTGTAAAAATGTTTAACC
droVir3	scaffold_13047:8900489-8900693 -		GA-GCACGACAAACTATGGGCACTCGCATA--T----CTCACTCC-----CATA-----CTCGTGA---TCGTATGGGCATTTC-----AGCAGGCGAACACGGCGTATGCGTAACGTGTCGCAACGCGAG----------GGATGAC----AGCTACTCGCCGGAGCGT----------------A----------------------C--AAATTCATCATAAATATTAGCG----------------A---TATGTCATT----------CGC-----AGTGGCGGACATGACAGCG----CCACGTTTAAATCTTTGGCC
droMoj3	scaffold_6540:31767652-31767843 +		GA-GCACGACAAACTATGAGCACCTACCTA--GTCTAGCGT----------GTC-----CCTCGTGA----------TCGTATG-----GCCGGCGGCTACGCGGCGTATGCGTAACGTGTCGCAACGCGAG----------GGATGGCATCGCTCTCTATACTCGCCGTAAGCA----------------A----------------------C--AGATGCAATCATAAATATTAGCG----------------A---TATGGGC----------A-GCACA----------------C--CGAGGGTCTC----CTTTGCGTTCGCG
droGri2	scaffold_15074:732443-732663 +		GA-GCACGACAAACTATGGGCACTCACTCA--C----ATATTCACTCC-----CATT-----CTCGTGATACTCGTATGACATTTC-----AAGGGGCCAACACGGCGCATGCGTAACGTGTCGCAACGCGAG----------GGATGGCGCATTTAACTATAACTGCGCCTAAGCGT----------------A----------------------C--AGATGTCAATCATAAATATTAGCG----------------A---TATGTCGAT----------AGCAGGGATCGGCATCGGACATGACAAAG-----TCTCG-TCAAATCTTTAACC

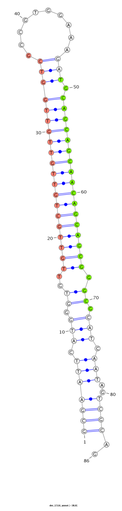
Generated: 09/08/2015 at 07:50 PM

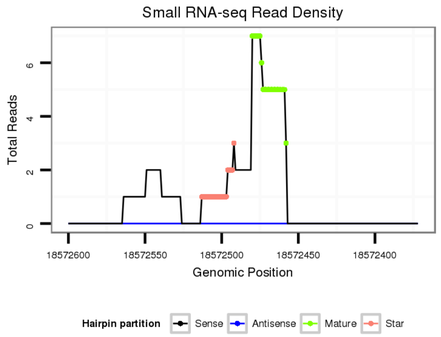
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

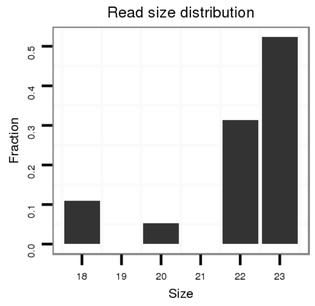
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1516	**scaffold_4929:18572422-18572550 -**	**candidate**	**Canonical miRNA**	**5pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

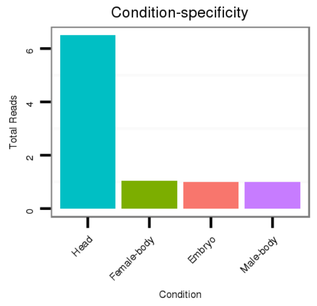
Legend: mature star mismatch in alignment mismatch in read

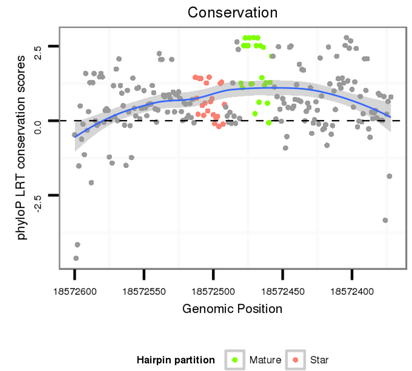
Predicted structure











Show Alternate Folds

Flybase annnotation

utr5 [utr5_plus_3417]

Repeatable elements

Name	Class	Family	Strand
Gypsy8-I_Dpse-int	LTR	Gypsy	-

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ACTCGCGCGCGTTTGTGTGTGCGTGTGTGTGTGTGTGAGAAGAGCGGCCAGCGGCATAATGCCGGCGACAGCGAATTCATGGGTGTTGTTGCTGTTGTTGGTCGCCGTGGAAAGATGCAGCAGCAACAGCAGCGGGCGCATCAATAGTCGCAGCAGCAGCAGCGGCTACAGGAAGTTTCACTGGCAGGAGCAACAGGAGGCCCCCACTTTGCGTCCTCTTCCTG	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V107 male body	M055 female body	V040 embryo	M057 embryo
**********(((((((.(((.((..((.(((((((((((((((((((((.....)))).)))))))))))))))))).)).)))).)))))..)))))..**********										
.....TGCAGCAGCAACAGCAGCGGGCG.....	23	0	1	3.00	3	3	0	0	0	0
.....TGCAGCAGCAACAGCAGCGGGC.....	22	0	1	2.00	2	2	0	0	0	0
.....GTGAGAAGAGCGGCCAGCGGCATAA.....	25	0	1	1.00	1	0	1	0	0	0
.....GGTCGCCGTGGAAAGATGCAGCA.....	23	0	1	1.00	1	1	0	0	0	0
.....TTGTTGCTGTTGTTGTTGGTCG.....	22	0	1	1.00	1	0	0	0	1	0
.....AGCGGCATAATGCCGGCGACAGC.....	23	0	1	1.00	1	0	0	1	0	0
.....GCCGTGGAAAGATGCAGC.....	18	0	1	1.00	1	0	1	0	0	0
.....AGATGCAGCAACAGCAGCGGGCGT.....	27	1	1	1.00	1	1	0	0	0	0
.....TTGTTGCTGTTGTTGTTGGT.....	20	0	2	0.50	1	1	0	0	0	0
.....TGCAGCAGCAACAGCAGCGGCTT.....	23	2	6	0.17	1	1	0	0	0	0
.....TGCAGCAGCAACAGCAGC.....	18	0	20	0.05	1	0	0	1	0	0

Anti-sense strand reads

TGAGCGCGGCGAAACACACACGCACACACACACACACACTCTTCTCGCCGGTCGCCGTATTACGGCCGCTGTCGCTTAAGTACCCACAACAACGACAACAACAACCAGGCGGCACCTTTCTACGTCGTCGTTGTCGTCGCCCGGTAGTTATCAGCGTCGTCGTCGTCGCCGATGTCCTTCAAAGTGACCGTCCTCGTTGTCCTCCGGGGGTGAAACGCAGGAGAAGGAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	V040 embryo
**********(((((((.(((.((..((.(((((((((((((((((((.....)))).)))))))))))))))))).)).)))).)))))..)))))..**********							
.....TGCAGCAACAACAGCAGCGGGCG.....	23	0	1	3.00	3	0	0
.....TGCAGCAACAACAGCAGC.....	18	0	20	0.05	1	0	1

Show Alignment With Reads

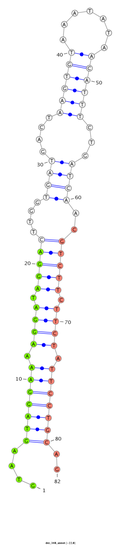
Re-alignment of all predicted orthologs

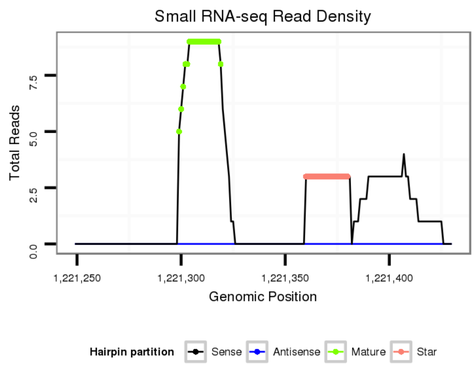
Species	Coordinate	ID	Alignment
droEre2	scaffold_4929:18572372-18572600 -	der_1516	ACT-C--GCGCGCG------TTTGTGTG--------TGCGTGTGTGTGTGTGTGAGAAG----------ACGCGCCAGCGGCATAAT-GCCGGCGACAGCGAA----------TTCATGGGTGT-TGTTGC--TGTTGTT------GTTGGTCGCCGTGGA--AAGATGCAGCAGC---AACAGCAGCGGG---CGCATCAA---TAGTCGC------AGCAGCAGCAGC------GGCTACAGGAAGTT----TCACTGGCAGGAGCAACAGGAGGCCC------CCACTTTGCGTCCTCTTCCTG
droYak3	2L:16712448-16712668 +	dya_1790	AGT-C--GCGCGCG------TGTGTTG--------TGC--------GTGTGTGTGAGAG----------AGCGGCCAGCGGCATAAT-GCCGGCGACAGCGAA----------TTCATGGGTGT-TGTTGC--TGTTGTT------GTTGGTCGCCGTGGA--AAGATGCAGCAGC---AACAGCAGCGGG---CGCATCAA---TAGTCGC------AGCAGCAGCAGC------GGCTACAGGAAGTT----TCAGTGGCAGGAGCAACAGGAGGCCC------CCACTTTGCGTCCTCTTCCTG
droSec2	scaffold_11:1701919-1702144 +	dse_126	AGT-C--GCGCGC----CGGTGTGTGTG--------TGCGTG----GTGTGTGCGAGAG----------AGAGGCCAGCGGCATAAT-GCCGGCGACAGCGAA----------TTCATGGGTGT-TGTTGC--TGATGTT------GTTGGTCGCCGTGGA--AAGATGCAGCAGC---AACAGCAGCGGG---CGCATCAA---TTTTCGC------AGCAGCAGCAGC------AGCTACAGGAAGTT----CCAGTGGCAGGAGCAACAGGAGGCCC------CCACTCTGCGTCCTCTACGCG
droSim2	2r:4879049-4879267 +	dsi_14	GACTT--G------------TGTG--------TGCGTGGTACGTTGTGTGCGAGCAG----------AGCGGCCAGCGGCATAAT-GCCGGCGACAGCGAA----------TTCATGGGTGT-TGTTGC--TGTTGTT------GTTGGTCGCCGTGGA--AAGATGCAGCAGC---AACAGCAGCGGG---CGCATCAA---TTTTCGC------AGCAGCAGCAGC------GGCTACAGGAAGTT----CCAGTGGCAGGAGCAACAGGAGGCCC------CCACTCTGCGTCCTTCCGG
dm3	chr2R:4062109-4062330 +	dme_405	AGT-C--GCGCGC----CGGTGTGTGTG--------TGCGTGGTACGTTGTGTGTGAGCAG----------AGCGGCCAGCGGCATAAT-GCCGGCGACAGCGAA----------TTCATGGATGT-TGTTGC--TGTTGTT------GTTGGTCGCCGTGGA--AAGATGCAGCAGC---AACAGCAGCGGG---CGCATCAA---TAGTCGC------AGCAGCAGCAGC------GGCTACAGGAAGTT----CCAGTGGCAGGAGCAACAGGAGGCCC------CCACTCTGCGTCCTTCCGG
droEug1	scf1800004094474:2883177-2883402 +		AAG-A-GTAGTGTT--------GT----------A-GTGTGCAGCAG----------AGCGGCCAGCGGCAAAT-GCCGGCGACAGCGAAT---------TCGAA--------TTCGTGGGTGT-TGTTGC--TGTTGTT------GTTGGTCGCCGTGGA--AAGATGCAGCAGC---AACAGCAGCGGG---CGCATCAA---TAGTCGC------AGCAGCAGCAGC------GGCAGCGC-----GGCAGCAA--GGCAGCGCGGCATTGGAAACGGAAAAT----CCATCGGCAGGAGCAACAGGAGTCC------CCACTTTGCGTCCTCTAAAG
droBia1	scf1800000302291:1913606-1913811 +		AGC-A--GC-----------------------------GTGTGCGAGCAG----------AGCGGCCAGCGGCAAAT-GCCGGCGACAGCGAA----------TTCGTGGGTGT-TGTTGC--TGTTGTT------GTTGGTCGCGTGGA--AAGATGCAGCAGC---AACAGCAGCGGG---CGCATCAA---TAGTCGC------AGCAGCAGCAGC------GGCGATCGGAAAATC---GCAGTGGCAGGAGCAACAGGAGTCCC------CCAGCGTTGCGCGCGTCGCG
droTak1	scf1800000415088:43520-43719 -		AAC-T--------------------------------AAC----------AGCGGCCAGCGGCAAAT-GCCGGCGACAGTGAA----------TTCGTGGGTGT-TGTTGC--TGTTGTT------GTTGGTCGCGTGGA--AAGATGCAGCAGCAACAACAGCAGCGGT---CGCATCAA---TAGTCGCAGCAGGAGCAG-----AGCAGCGGCTATAGGAAATC---GCAGTGGCAGGAGCAACAGGAGGCCC------CACGCTGCGCGCGTTTCCG
droEle1	scf1800000491240:859161-859360 +		GTGTT--G------------TGTGTGCGAGCAG----------AGCGGCCAGCGGCAAAT-GCCGGCGACAGCGAA----------TTCGTGGGTGT-TGTTGC--TGTTGTT------GTTGGTCGCCGTGGA--AAGATGCAGCAGC---AACAGCAGTGGG---CGCATCAA---TAGTCGC------AGTAGCGAC-----GGCTACAGGAAGTT----TCAGTGGCAGGAGCAACAGGAGTTCC------CCACTTTGCGTCCTTCCAG
droRho1	scf1800000770177:147416-147615 +		AGC-A--G------------TGTGTGTGAGAAG----------AGCGGCCAGCGGCAAAT-GCCGGCGACAGCGAA----------TTCGTGGGTGT-TGTTGC--TGTTGTT------ATTGGTCGCGTGTGGA--AGATGCAGCAGC---AACAGCAGTGGG---CGCATCAA---TAGAAGC------AGCAGCAGC------GGCTATAGGAAAAC---GCAGTGGCAGGAGCAACAGGAGTCG------CCACTTTAGGTCGCTACGAG
droFic1	scf1800000453215:147112-147305 -		AGC-A--G------------TGTGTCGTAAAG----------AGCGGCCAGCGGCAAAT-GCCGGCGACAGCGAA----------TTCGTGGGTGT-TGTTGC--TGTTGTT------GTTGGTCGCCGTGGA--AAGATGCAGCAGC---AACAGCGCGGG---CGCATCAA---TAGTCGC------AGCAGCATC---------------AGGAAAAGC---CACTGGCAGGAGCAACAGGAGTCCC------CCACTTTGCGTCCTCTACGG
droKik1	scf1800000302411:115768-115958 -		GGG-GCAGGAG----------------------GATGTGTGAGAG----------AGCGGCCAGCGGCAAAT-GCCGGCGACAGCGAA----------TTCGTGGGTGT-TGTTGC--TGTTGTT------CGTCGTCGCCGTGGA--AAGATGCAGCAGC---AGCAGCAGTAGC---A-----AA---GAG---------AGTGCGAG---G-----AGCGGAA---GTT---GCAGT---TGCAGCAACAGGAGTCCT------CCACTTTACGTCCTTCCGG
droAna3	scaffold_13266:1925293-1925468 -	dan_4048	GGC-A--GCG----------------------CGGAGAAG----------AGCGGCTTGCGGCAAGAT-GCCGGCGACAGCGAA----------TTCGTGGGTGT-TGTTGC--TGTTGTTCGGCGTCGTCGTCGCCGTGGA--AAGCAGCAGCAT-C---AT-AGCA-----------AA---AAGGGC-----AGCAGCAGC---------------------AGCAACAGGAGTCCTTGACGTCCAGCGCTCGTCCTCTACGG
droBip1	scf1800000396730:2911780-2911960 -		GGA-T--------------------------CGCGGAGAAG----------AGCGGCTTGCGGCAAGAT-GCCGGCGACAGCGAA----------TTCGTGGGTGT-TGTTGC--TGTTGTTCGGCGTCGTCGTCGCCGTGGA--AAGCAGCAGCAGC---ATCAGCAGCAGC---A-------------------GCAGCAGCAAAAGGG---C---------AGCAACAGGAGTCCTCGACGTCCAGCGCTCGTCCTCTACGG
dp5	XL_groupla:2554619-2554766 -		AAA-T--------------------------------AG----------GCGTGCCATCGCATGTGCGCGTCGTCGTC----------GTCGTCGCGTTGCCGTTGCGTGC------GTGCGTCGCAGCAACAGC--AA----CAGCAGC---AACAGCAAGCAAC---AGCAGC------AGCAACAG-------CAGCAACAGCAGCAACAGAT--------------------
droPer2	scaffold_2:2217506-2217644 +	dpe_2519	AAG-C--G------------------------------TGAAG----------AGCAGCT--GCGGCAAGAT-GCCGGCGACAGCGAA----------TGTGCGGGTGT-TGTTGT--TGTTGTGCTGCGT--CCGTGGTTGTGGA--TAGCA------GT---AA----------------A-TTGC-------------------CAGG---AGCAGCAACAGGAGTCCT------CCAGCGAACAAACGCTCGGATG
droWil2	scf2_1100000004729:2691956-2692147 -		AGA-A-ATGTGGCATATGCATCTGCCA-------TGCGTGA----GTGTGTATTAAAA----------------------------------

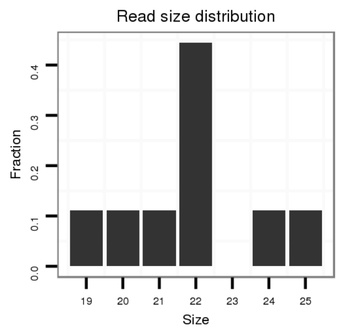
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_348	**scaffold_4690:1221299-1221380 +**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

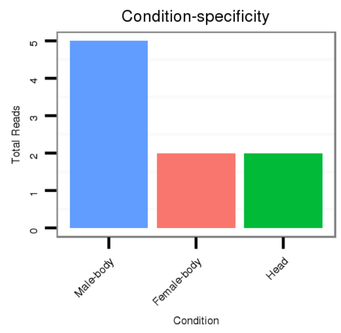
Legend: mature star mismatch in alignment mismatch in read

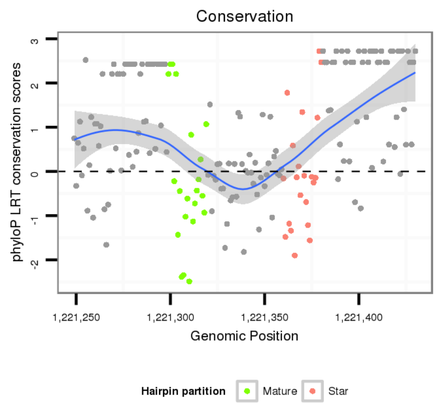
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG18683-in]; CDS [Dere\GG18683-cds]; CDS [Dere\GG18683-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AGAGCGTCCTGGCACCCACGGATGCTGATCTAACCGATTTAAATAAATTAGTAAGTAGGAAAAGGATAGGACTTGGTGATGACTAAGTGTAAATATAACATTTCTGATCAACGTCTTCTTCTATTCCTGCAGTGGAAGGAACTGGAGCCCGAGCAGCTGATGGACGCCAAACTGAAGTGCGT	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	M055 female body	V108 head	M057 embryo	V040 embryo
**********....(((((((.(((((.(((((....((((....((((((.....))))))...))))))..))))).))))))).**********..**********										
.....CGTCTTCTTCTATTCCTGCAGT.....	22	0	1	3.00	3	0	2	1	0	0
.....GTAAGTAGGAAAAGGATAGGA.....	21	0	1	1.00	1	0	0	1	0	0
.....AGTAGGAAAAGGATAGGACTTG.....	22	0	1	1.00	1	1	0	0	0	0
.....TAGGAAAAGGATAGGACTTGGT.....	22	0	1	1.00	1	1	0	0	0	0
.....GTAAGTAGGAAAAGGATAGGACTT.....	24	0	1	1.00	1	1	0	0	0	0
.....GTAAGTAGGAAAAGGATAGGA.....	22	0	1	1.00	1	1	0	0	0	0
.....AAGTAGGAAAAGGATAGGA.....	19	0	1	1.00	1	0	0	1	0	0
.....GGAACTGGAGCCCGAGCAGCTG.....	22	0	1	1.00	1	1	0	0	0	0
.....GATGGACGCCAAACTGAAG.....	19	0	1	1.00	1	0	1	0	0	0
.....GAAGGAACTGGAGCCCGAGCAGCTGAT.....	27	0	1	1.00	1	1	0	0	0	0
.....CTGGAGCCCGAGCAGCTGATGGAC.....	24	0	1	1.00	1	0	0	0	0	1
.....GTAAGTAGGAAAAGGATAGG.....	20	0	1	1.00	1	1	0	0	0	0
.....GTAAGTAGGAAAAGGATAGGACTTG.....	25	0	1	1.00	1	0	1	0	0	0
.....TAAGTAGGAAAAGGATAGGACT.....	22	0	1	1.00	1	0	1	0	0	0

Anti-sense strand reads

TCTCGCAGGACCGTGGGTGCCTACGACTAGATTGGCTAAATTTATTTAATCATTCATCCTTTTCCTATCCTGAACCACTACTGATTCACATTTATATTGTAAAGACTAGTTGCAGAAGAAGATAAGGACGTCACCTTCCTTGACCTCGGGCTCGTCGACTACCTGCGGTTTGACTTCACGCA	Read size	# Mismatch	Hit Count	Total Norm	Total	V060 head	M055 female body	GSM1528801 follicle cells	V040 embryo
**********....(((((((.(((((.(((((....((((....((((((.....))))))...))))))..))))).))))))).**********..**********									

Show Alignment With Reads

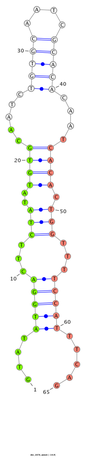
Re-alignment of all predicted orthologs

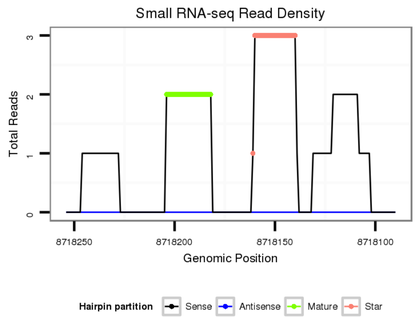
Species	Coordinate	ID	Alignment
droEre2	scaffold_4690:1221249-1221430 +	der_348	AGAGCGTCCTGGCACCCA-CGGATGCTGATCTAACCGATTTAAATAAATTAGTAAGTAGGA-------AAAGGATAG----------GA----------CT--TGGTGATGACTAAGTGTAAATATAACATTTCTGATCAACGT-------CTTCT-TCTATTCCTGCAGTGGAAGGAACTGGAGCCCGAGCAGCTGATGGACGCCAAACTGAAGTGCGT
droYak3	X:4576881-4577043 -		AGAGCGTCATGCACCAT-AGGATGCTGATCTAACCGATTTAAATAAATTCGTAAGTTTTTTTCTTACTGA-ATAA-G----------||----||----------GCTTTCTGATCAACGT-GT-----CTTCT-TATGCTGCGCAGTGGAAGGAACTGGAGCCCGAGCAGCTGATGGACGCCAAACTGAAGTGCGT
droSec2	scaffold_4:2871789-2871972 -		AGAGCGTCCTGGCACCGTTTGGATGCTGATCTAACGATTTAAATAAATTCGTAAGCAGAA-------AC-GGATAG----------AA----------CTCTTAATGATAGCAATAGTGTTATATTAATTTCTAATCAACGT-------CGTAT-TCTACGACGCAGTGGAAGGAGCTGGAGCCCGAGCAGCTGATGGACGCCAAACTGAAGTGCGT
droSim2	X:3541246-3541428 +	dsi_19016	AGAGCGTCCTGGCACCGTTGGATGCTGATCTAACGATTTAAATAAATTCGTAAGCAGAA-------AC-GGATAG----------AA----------CTCTTAATGATAGCAATAGTGTTATATTAATTTCTAATCAACGT-------CGTAT-TCTACGACGCAGTGGAAGGAGCTGGAGCCCGAGCAGCTGATGGACGCCAAACTGAAGTGCGT
dm3	chrX:3845729-3845911 +		AGAGCGTCCTGGCACCCA-TGGATGCTGATCTAACGATTTAAATAAATTCGTAAGGGAA-------AC-AATAG----------GA----------CTCTTAATGATCGCAATAGTGTGTATATTAACATTTCTATCAACGT-------CGTAT-TCTACACGCAGTGGAAGGAGTCTGGAGCCCGAGCAGCTGATGGACGCCAAACTGAAGTGCGT
droEug1	scf7180000409553:93371-93435 +		T----------||----------||----------||

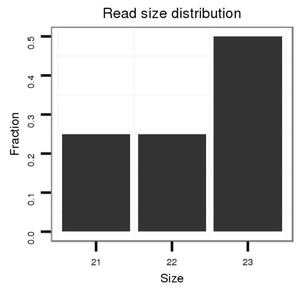
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1076	**scaffold_4845:8718140-8718204 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

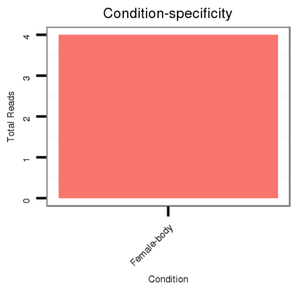
Legend: mature star mismatch in alignment mismatch in read

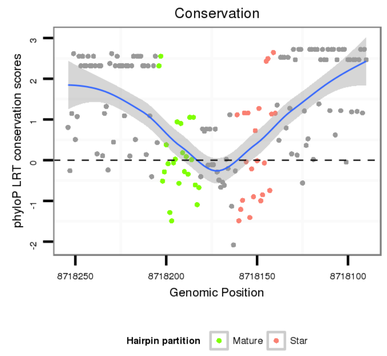
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG20959-in]; CDS [Dere\GG20959-cds]; CDS [Dere\GG20959-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AGCACCTGTCCTCCAGTCCAGACGTGGAGCCGCCTCACTTTGCGCCCCAGGTATATGGACTTCTATATGTGCAATCTGTGCAATCGCACACAATCACACTGGTTTTCCATTTCAGACGCGTGCCACCATTAGGTTTATACAGGAGAATCAGTTCCCCGCCGTCAC	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body	V107 male body	V040 embryo	V108 head	V060 head
..........CACACTGGTTTTCCATTTCAGT..	22	1	1	6.00	6	2	3	0	1	0
..........GTATATGGACTTCTATATGTGCA..	23	0	1	2.00	2	2	0	0	0	0
..........CACACTGGTTTTCCATTTCAGTT..	23	2	1	1.00	1	1	0	0	0	0
..........CACCATTAGGTTTATACAGGAGA..	23	0	1	1.00	1	0	0	1	0	0
..........TCACACTGGTTTTCCATTTCAG..	22	0	1	1.00	1	1	0	0	0	0
..........GTATATGGACTTCTATATGTG.	22	1	1	1.00	1	0	1	0	0	0
..........TTTATACAGGAGAATCAGT..	19	0	1	1.00	1	0	1	0	0	0
..........CACACTGGTTTTCCATTTCAG..	21	0	1	1.00	1	1	0	0	0	0
.......TCCTCCAGTCCAGACGTGG..	19	0	1	1.00	1	1	0	0	0	0
..........CACACTGGTTTTCCATTTCAGA..	22	0	1	1.00	1	1	0	0	0	0

Anti-sense strand reads

TCGTGGACAGGAGGTCAGGTCTGCACCTCGGCGGAGTGAAACGCGGGGTCCATATACCTGAAGATATACACGTTAGACACGTTAGCGTGTGTTAGTGTGACCAAAAGGTAAAGTCTGCGCACGGTGGTAATCCAAATATGTCCTCTTAGTCAAGGGGCGGCAGTG	Read size	# Mismatch	Hit Count	Total Norm	Total	GSM1528801 follicle cells	V040 embryo
..........GTATATGGACTTCTATATGTGA..	23	0	1	2.00	2	2	0
..........CACACTGGTTTTCCATTTCAGTT..	23	2	1	1.00	1	1	0
..........TCACACTGGTTTTCCATTTCAG..	22	0	1	1.00	1	1	0
..........GTATATGGACTTCTATATGTGT..	22	1	1	1.00	1	0	1
..........CACACTGGTTTTCCATTTCAG..	21	0	1	1.00	1	1	0
..........CACACTGGTTTTCCATTTCAGA..	22	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4845:8718090-8718254 -	der_1076	AGCACCTGTCCTCCAGTCCAGACGTGGAGCCGCCTCACTTTGCGCCCCAGGTATATG----------G---A-C---TTCTA--TATGT----------GCA----------ATCTGTGCAATCGCAC-ACAATCACACTGGT----------TTTCCATTTCAGACGCGTGCCACCATTAGGTTTATACAGGAGAATCAGTTCCCCGCCGTCAC
droYak3	2R:14674283-14674449 +		AGCACCTGTCCTCCAGTCCAGACGTGGAGCCGCCTCACTTTGCGCCAGGTATATGC----------G---A-C---TTCTAAG---C----------ATC----------TCTAGCAATGATACATAAGTTACTGT----------TGTTTCATTCAGACGCGTGCCACCATTAGGTTTATACAGGAGAATCAGTTCCCCGCCGTCAC
droSec2	scaffold_1:12036742-12036899 -		AGCACCTGTCCTCCAGTCCAGACGTGGAGCCGCCTCACTTTGCGCCAGGTATGG----------A---A-C---A-T-----TATGTTTCTGTGCAGTCACAATACACTT-----GA----------TAA-CTGCATTGCAGACGCGTGCCACCATTAGGTTTATACAGGAGAATCAGTTCCCCGCCGTCAC
droSim2	2r:15176240-15176397 -		AGCACCTGTCCTCCAGTCCAGACGTGGAGCCGCCTCACTTTGCGCCAGGTATGG----------A---A-C---A-T-----TATGTTTCTGTGCAGTCACAATACACTT-----GA----------TAA-CTGCATTGCAGACGCGTGCCACCATTAGGTTTATACAGGAGAATCAGTTCCCCGCCGTCAC
dm3	chr2R:14529028-14529189 +		AGCACCTGTCCTCCAGTCCAGACGTGGAGCCGCCTCACTTTGCGCCAGGTATGCAT----------A---------T---A-GTATAATATA----------TATGTTTCTGTGCAGACACAATAAGTT-----T----------TTTTTTAATTGCAGACGCGTGCCACCATTAGGTTTATACAGGAGAATCAGTTCCCCGCCGTCAC
droRug1	scf7180000409663:838020-838278 +		AGCACCTGTCCTCCAGTCCGACGTGGAGCCGCCACATTTGCGCCAGGTTAGTTCCATTCAAAGCTTTCTGGTTGAGATCTGCAC----------AGTTTTCCATCTTGATGCTG----------AG---A-C---------T----------AACTT-----TATAATAGGCTTTGTTAAGTTCTTTTCAGCTTAATGAAGACTAAGAATTTATTATTCCCCTGTTAATTCCTCATCATTA-ACCCATTCCAGACGCGTGCCACCATTAGGTTTATACAGGAGAACAGTTCCCCGCCGTCAC
droBia1	scf7180000302291:1183560-1183621 -		T----------TTTCCATTTCAGACGCGTGCCACCATTAGGTTTATACAGGAGAACAGTTCCCCGCCGTCAC
droTak1	scf7180000415910:184324-184400 -		AA----------TTTCCATTTCAGACGCGTGCCACCATTAGGTTTATACAGGAGAACAGTTCCCCGCCGTCAC
droEle1	scf7180000491228:482854-482941 +		TATAA----------ACTGT----------G---A-C---TTCTAAC---C----------ATC----------GTATCAAATTACTTTG----------TTTATTTCAGACGCGTGCCACCATTAGGTTTATACAGGAGAACAGTTCCCCGCCGTCAC
droRho1	scf7180000766409:256897-256967 +		AGCACCTGTCCTCCAGTCCGACGTGGAGCCGCCTCACTTTGCGCCCCAGGTCGCGT----------G---A-C---TTCTAAC---C----------ATC----------TGGTTTGCGTGNG----------
droFic1	scf7180000453811:446906-447078 +		AGCACCTGTCCTCCAGTCCGACGTGGAGCCGCCTCACTTTGCGACCCAGGTCGCGTCC----------G---GA-C---TTCTAAC---C----------AT---A-ATATTAATAATATAAATATTATTTCCTTTTGCCT---TATGCTACT----------GCT----------TCA-ACCATTCAGACGCGTGCCACCATTAGGTTTATACAGGAGAACAGTTCCCCGCCGTCAC
droKik1	scf7180000302682:202001-202161 -		AGCACCTGTCCTCCAGTCCGAGGTGGAGCCGCCACATTTGCGCCCAGGTTAAA----------G---A-C---TTCTAAC---C----------ATGAGTGGAGAATCTTCAGCAAACTGT----------TACTTATTCTGTATAA----------TTTCCATTTCAGACGCGTGCCACCATTAGTTTATCAGGAGAACAGTTCCCCGCCGTCAC
droAna3	scaffold_13266:4842115-4842278 +		AACACCTGTCCTCCAGTCCAGACGTGGAGCCGCCACACTTTGCGCCAGGTTACGTCC----------G---AG-C---TTCTAAG---C----------ATC----------TCCCGCTGGGACATC----------GCTGATCTAATTGCCTC----------CCG----------TTCTTTCGTTTCAGACGCGTGCCACCATTAGTTTATACAGGAGAACAGTTCCCCGCCGTCAC
droBip1	scf7180000395751:647194-647351 +		AACACCTGTCCTCCAGTCCAGACGTGGAGCCGCCACACTTTGCGCCAGGTTACGTCC----------G---A-C---TTCTAAC---C----------GTC----------TCCCGCTGAGACGTC----------GCTGATCTAATTGCCGTC----------TCTCTTCGTTTCAGACGCGTGCCACCATTAGTTTATACAGGAGAACAGTTCCCCGCCGTCAC
dp5	3:3538896-3539065 +		AGCATTTGTCCTCCAGTCCGAGGTGGAGCCGCCACATCTTGCGCCCAGGTGCGTCC----------G---TT-C---TTCTAAC---C----------GCG----------CCCCGCAGGGA-GTC----------AGTGATCTAATTGCTTTA----------C----------TCATTGTCATTTCAGACGCGTGCCACCATTAAATTCATACAGGAGAACAGTTCCCCGCCGTCAC
droPer2	scaffold_2:3727064-3727233 +		AGCATTTGTCCTCCAGTCCGAGGTGGAGCCGCCACATCTTGCGCCCAGGTGCGTCC----------G---TT-C---TTCTAAC---C----------GCG----------CCCCGCAGGGA-GTC----------AGTGATCTAATTGCTTTA----------C----------TCATTGTCATTTCAGACGCGTGCCACCATTAAATTCATACAGGAGAACAGTTCCCCGCCGTCAC
droWil2	scf2_1100000004514:159865-160045 -		AACATTTGTCCTCCAGTCCGAGGTGAGCCGCCACATTTGCGACTGTCCAGTGGCTATGATGTTTTTTAGT----------GTCCTGCC----------A---A-C---TTCTAAC---C----------CTCTAATTGG----------TTCCTATTTTTTTC----------TCATTTGTCTTGCAGACGCGTGCCACCATTAGGTTTATACAGGAGAACAGTTCCCCGCCGTCAC
droVir3	scaffold_12875:14222777-14222949 +		AGCATTTGTCCTCCAGTCCGACGTGGAGCCGCCACATTTGCGCCAGGTGCGTTC----------G---GA-C---TTCTAAC---C----------ACCAAG---A-C---TTCTAAC---C----------ACCT---T---GTC----------GCATGGT----------TGTATTGCTATTGC----------CTGCGGG----------GGCTTTCCATTGCAGAGTGCGTGCCACCATAGCATTTATACAGGAGAACAGTTCCCCGCCGTCAC
droMoj3	scaffold_6496:9676120-9676219 +		AGCATTTGTCCTCCAGTCCAGACGTGGAGCCGCCACATTTGCGCCCAGGTTCCGTCC----------G---AA-C---TTCTAAC---C----------ATC----------TCCCGCTGAGACGTC----------GCTGATCTAATTGCCGTC----------TCTCTTCGTTTCAGACGCGTGCCACCATTAGGTTTATACAGGAGAACAGTTCCCCGCCGTCAC
droGri2	scaffold_15245:14200237-14200404 +		AACATTTGTCCTCCAGTCCGAGGTGGAGCCGCCACATTTGCGCCCAGGTTCGTAT----------G---AAAA---TCC-AAAATATA-TATC----------CCC---CAAGAGAGA----------GCTATAACTAATTGTGTGA----------TTTGTA--TTAGATGCGTGCCACATTAGATTTATACAGGAGAACAGTTCCCCGCCGTCAC

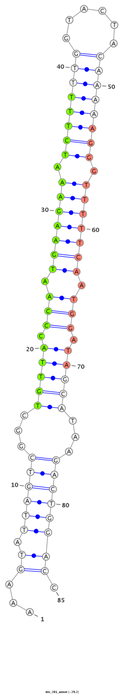
Generated: 09/08/2015 at 11:46 PM

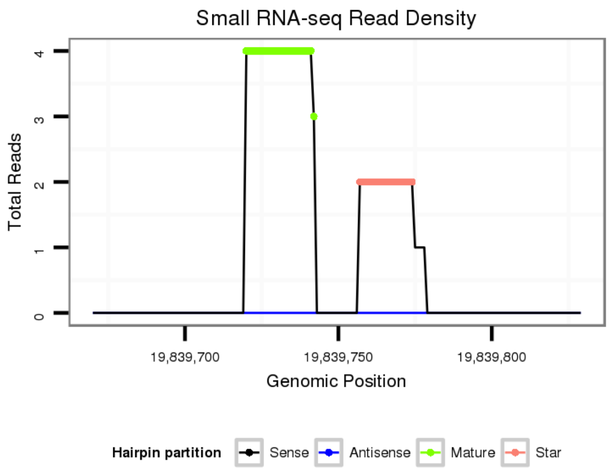
PASS/FAIL	
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

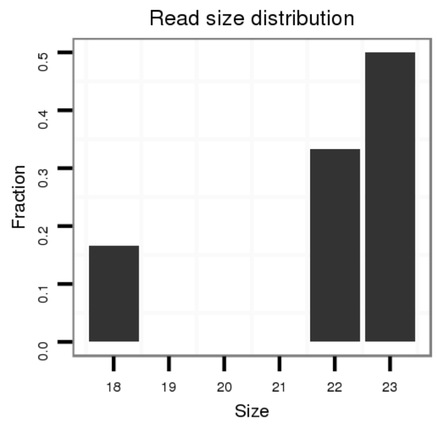
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_201	**scaffold_4845:19839720-19839779 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

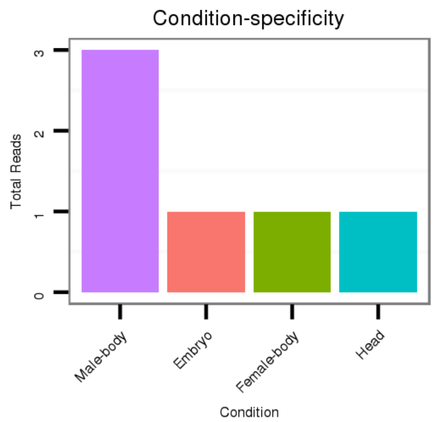
Legend: mature star mismatch in alignment mismatch in read

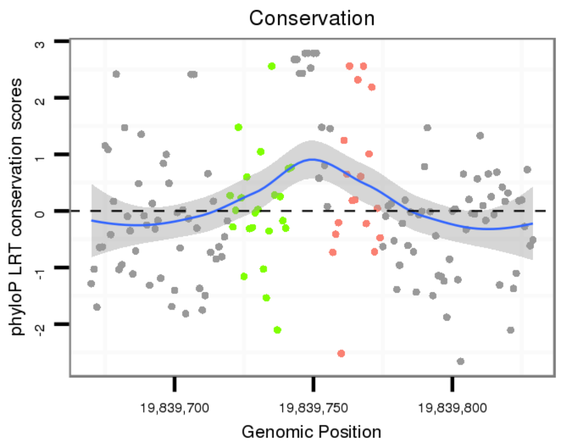
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG22771-in]

No Repeatable elements found

Sense Strand Reads

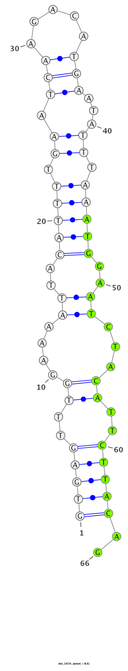
hide 3p reads | show mid mismatch reads

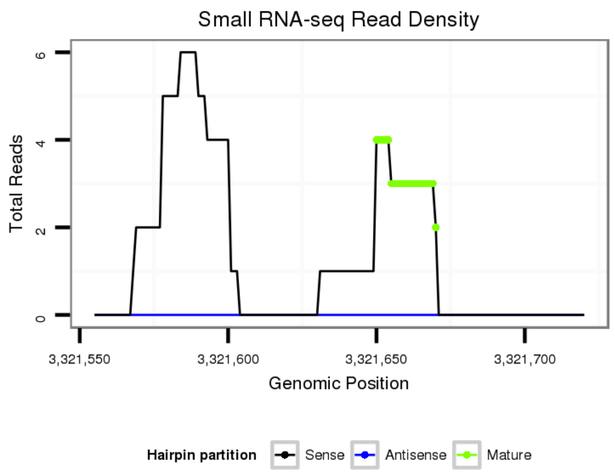
| | | |

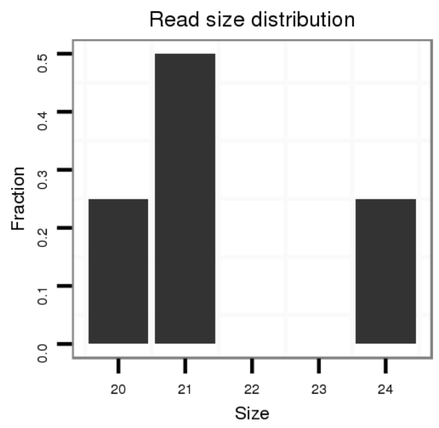
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1034	**scaffold_4845:3321605-3321670 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

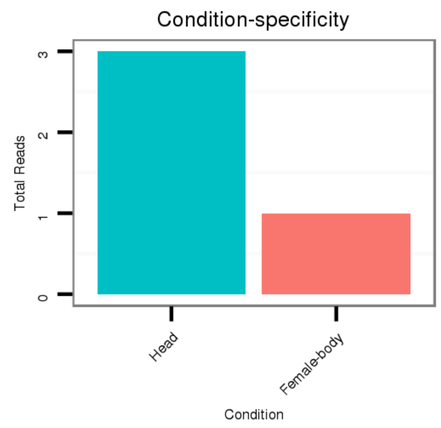
Legend: mature star mismatch in alignment mismatch in read

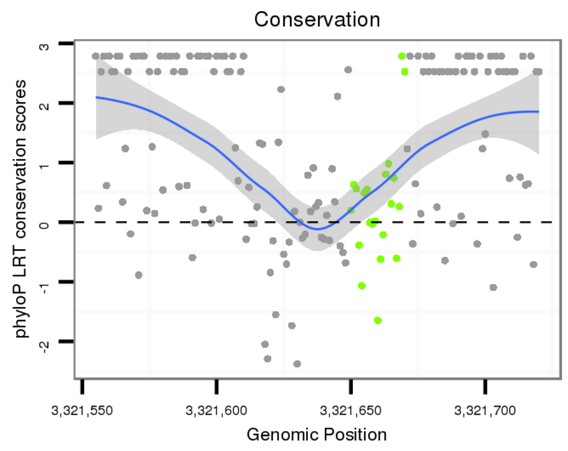
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG21516-in]; CDS [Dere\GG21516-cds]; CDS [Dere\GG21516-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATGAGTGCATACGCTACATCCGCGAGAAAGTTGGCAACAATAAGGTGTTGGTGAGTTTGGAAAATTACATTTTGAATCAAGACATGAATATTTAAATGGAATCTACATTCTTACAGCTGCTGGTCAGCGGCGGCGTGGATTCGAGTGTTTGTGCAGCTTTGCTCCG **********(((((..((....((..(((((.((.(((.....)))...)).)))))..))...))..)))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V107 male body	M055 female body	GSM1528801 follicle cells	V040 embryo	M057 embryo
.....ATGGAATCTACATTCTTACAG.....	22	1	1	10.00	10	8	1	1	0	0	0
.....GAGAAAGTTGGCAACAATAAGGT.....	23	0	1	3.00	3	0	0	0	3	0	0
.....ATGGAATCTACATTCTTACAG.....	21	0	1	2.00	2	2	0	0	0	0	0
.....ATGGAATCTACATTCTTACA.....	20	0	1	1.00	1	1	0	0	0	0	0
.....CTACATCCGCGAGAAAGTTGGC.....	22	0	1	1.00	1	0	1	0	0	0	0
.....TACATCCGCGAGAAAGTTGGCAAC.....	24	0	1	1.00	1	0	0	0	0	0	1
.....TCAAGACATGAATATTTAAATGGA.....	24	0	1	1.00	1	0	0	1	0	0	0
.....GTTGGCAACAATAAGGTGTT.....	20	0	1	1.00	1	0	0	0	0	1	0

Anti-sense strand reads

TACTCACGTATGCGATGTAGGCGCTCTTTCAACCGTTGTTATTCCACAACCACTCAAACCTTTTAATGTAAAACTTAGTTCTGTACTTATAAATTTACCTTAGATGTAAGAATGTCGACGACCAGTCGCCGCCGCACCTAAGCTCACAAACACGTCGAAACGAGGC **********(((((..((....((..(((((.((.(((.....)))...)).)))))..))...))..)))))..**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M055 female body
ATGGAATCTACATTCTTACAGT.....	22	1	1	10.00	10	8

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4845:3321555-3321720 +	der_1034	ATGAGTGCATACGCTACATCCGCGAGAAAGTTGGCAACAATAAGGTGTTGGTGAGTTTGGAAAA--------TT----------------ACATTTTGAAT----------C-AAGACATGAATAT--TTAAATGGAATCTACA----TT-C--TTACAGCTGCTGGTCAGCGGCGGCGTGGATTCGAGTGTTTGTGCAGCTTTGCTCCG
droYak3	2R:1597180-1597339 +		AGGAGTGCATACGCTACATCCGCGAGAAAGTGGGCAGTAATAAGTGTTGGTGAGTTTAGGAAA--------TT----------------TCATTTTGATA----------T-AAGACATGAATAT--TTAAATG-----TACA----TT-A--TTACAGCTACTGGTCAGCGGCGGCGTGGATTCGAGTGTGTGTGCAGCTTTGCTCCG
droSec2	scaffold_18:1097888-1098052 -		AGGAGTGCATACGCTATATTCGCGAGAAAGTGGGCAACAATAAGGTGTTGGTGAGTTTGGGAAA--------TT----------------AAATTTTGAAT----------C-AAGACATGAATAT--GTTAATGCAATCAACA----TT-A--TTCCAGCTGCTGGTCAGCGGCGGCGTGGATTCGAGTGTGTGTGCAGCTTTGCTCCG
droSim2	2l:20612304-20612468 -		AAGAGTGCATACGCTATATCCGCGAGAAAGTGGGCAACAATAAGGTGTTGGTGAGTTTGGCAAA--------TA----------------AAATTTTGAAT----------C-AAGACATGAATAT--CATAATGCAATCTACA----TT-A--TTACAGCTGCTGGTCAGCGGCGGCGTGGATTCGAGTGTGTGTGCAGCTTTGCTCCG
dm3	chr2L:21176556-21176720 -		AGGAGTGCATACGCTATATCCGTGAGAAAGTGGGCAACAATAAGGTGTTGGTGAGTTTGGCAAA--------AT----------------AAATTTTCAAT----------C-AAGACATGAATAT--GTCAATACAATCTACA----TT-A--TTACAGCTCCTGGTCAGCGGCGGCGTGGATTCGAGTGTGTGTGCAGCTTTGCTCCG
droEug1	scf7180000409767:134305-134467 +		AGGAGTGCATGCGCTATATCCGCGAGAAAGTGGGCAACAATAAGGTGTTGGTGAGTTTGGAAAA--------AT----------------TGATAACCATT----------T--AGACTTCCATGT--TTAAATGGCATCTACA----TT-A--TTACAGCTGCTGGTCAGCGGCGGCGTGGATTCGAGTGTGTGTGCAGCTTTGCTCCG
droBia1	scf7180000302422:6928220-6928383 +		AGGAGTGCATACGCTACATTCGCGAGAAAGTGGGCAACAATAAAGTGTTGGTGAGTTTGGAAAC--------TT----------------TTTTGACTG----------GCA-AAGACTAGCGTAT--TCTAATGAAATCTAAC----TC-A--TTACAGCTGCTGGTCAGTGGCGGCGTCGATTCGAGCGTGTGTGCAGCTTTGCTTCG
droTak1	scf7180000415708:269471-269635 +		AGGAGTGCATACGCTACATTCGCGAGAAAGTGGGCAGCAATAAGGTGTTGGTGAGTTTGGAAAT--------GA----------------TT-TTATCCTT----------AAAGGACTGTCTTAT--TTAAATGAATATCTACA----AT-A--TTACAGCTGCTGGTCAGCGGAGGCGTGGATTCGACTGTTTGTGCAGCTTTGCTCCG
droEle1	scf7180000491338:447067-447232 +		AGGAGTGCATACGCTATATCCGCGAGAAAGTGGGCACCAACAAGGTGTTGGTGAGTTTGAAAAC--------CA----------------TAATGCCCACT----------A-GATAGTTGCAGCT--GTAAATGGTATCTATA----TC-A--TTGCAGCTGCTGGTCAGCGGCGGCGTGGATTCGAGTGTCTGTGCAGCTTTGCTTCG
droRho1	scf7180000780102:76285-76449 +		AGGAATGCATACGCTACATCCGCGAAAAAGTGGGAACCAATAAAGTGTTGGTGAGTTTGAAAT--------AT----------------TAATGTCCAGT----------A-AAGAGTTGCATAT--GTAATTGGAATCTATA----CT-A--TTATAGCTGCTGGTCAGCGGAGGCGTGGATTCGAGTGTCTGTGCAGCTTTGCTTCG
droFic1	scf7180000453842:653547-653711 -		AGGAGTGCATCCGCTATATCCGAGAGAAAGTGGGCACCAATAAGGTGTTGGTGAGTTTGCAGAC--------AT----------------TAATTCTCAGT----------A-AAAGGTTGCGTAT--GTTAAACTGAATCTGCA----TT-A--TTATAGCTGCTGGTCAGCGGCGGCGTGGATTCCAGTGTCTGTGCAGCCTTGCTTCG
droKik1	scf7180000302643:214346-214511 -		AGGAGTGCATACGGTATATCCGAGAGAAAGTGGGCACAATAAGGTGTTGGTGAGTAG--AAAA--------TG----------------GCATTTCAACTC----------CACA-TAGAGTTGCATAT--GTAAATT-----GTATACCCTTT-A--TTGTAGCTGCTGGTCAGCGGCGGCGTGGATTCGAGTGTCTGTGCAGCCTTGCTTACG
droAna3	scaffold_12916:4511619-4511777 +		AGGAGTGCATACGATACATCCGAGAGAAAGTGGGAAGCAATAAGGTGTTGGTGAGTGGGAAAATT--------TT----------------CATGCCTTCT----------AAGGATCAGCTAT----------A-A----------TATAAAGT---ATTAT----TT-A--TTACAGCTGCTGGTCAGCGGCGGTGTGGATTCGAGTGTCTGTGCAGCTTTGCTCCG
droBip1	scf7180000396737:274957-275115 -		AGGAGTGCATAAGATACATCCGAGAGAAAGTGGGAAGCAATAAGGTGTTGGTGAGTGGGAAAAGC--------TT----------------AATATCTTCC-TATGATCAGCTAT----------A-A----------TATAAAGT---ATGG----TT-A--TTACAGCTGCTGGTCAGCGGCGGAGTGGATTCAAGTGTCTGTGCAGCTTTGCTCCG
dp5	4_group1:4902249-4902417 +		AGGAGTGCATACGGTACATACGAGAGAAAGTGGGCAGTAATAAAGTGCTTGGTAGGTTG-----TCCATACCTTAAAGAATCATTTAAACCGT-AA--------------TCCCCAAT----------A-A----------TGAAATGTC--TTGCT----AT-A--TTGCAGCTCTTGGTCAGTGGCGGTGTGGATTCGAGTGTATGTGCAGCCTTGTTCCG
droPer2	scaffold_5:314853-315021 -		AGGAGTGCATACGGTACATACGAGAGAAAGTGGGCAGTAATAAAGTGCTTGGTAGGTTG-----TCCATACCTTAAAGAATCATTTAAACCGT-AA--------------TCCCCAAT----------A-A----------TGAAATGTC--TTGCT----AT-A--TTGCAGCTCTTGGTCAGTGGCGGTGTGGATTCGAGTGTATGTGCAGCCTTGTTCCG
droWil2	scf2_1100000004851:490210-490383 +		ATGAGTGCATACGCTATATACAAGAAAAAGTGGGCAGCAACAAGTGCTTGGTATGTAGCATAAA-----ATTTAAAA--ATATTTTATATTAT-TC--------------ATCTTCATTCATATTTCACCTTCC-A--------------G-----GTGT---TT-A--GTACAGCTTTTAGTCAGCGGTGGATGTGGATTCCAGTGTTATGTGCAGCTGTATTCCG
droVir3	scaffold_12963:19645367-19645532 -		AGGAATGCATACGCTATATACGCGAAAAAGTGGGCAATAACAAGTGCTTGGTTATGTCTCTAAAT--------TTCGT----------AAATATTGTAT----------T-AAGAAAACTATAT--CAAATTGTTT--AAACT----CT-A--TTGCAGTTGCTGGTCAGCGGCGGCGTTGATTCGAGTGTGTGTGCGCATTACTACG
droMoj3	scaffold_6500:23553133-23553295 +		AGGAATGCATTCGGTACATACGCGAAAAAGTGGGCAAAATAAAGTGTTTGGTATGTATCTAAGCATA-----AT----------AAA--------A-T-AGAAATCCATAT--GTCATTGTTTCACAAA----TT-GTTAAACAGTTGCTCGTCAGTGGAGGCGTCGATTCAAGTGTCTGTGGTGCATTGCTCCG
droGri2	scaffold_15252:11118517-11118688 -		AGGAATGCATACGCTACATACGCGAAAAAGTGGGCAATAACAAGTGTTGGTATGTCTATAAAT--------CT-GT----------AAATAT-ATAC-AAAGATCA----------A---AAAA--GTATGTTAAACTGAC-TCCCT----CTTGCAACACAGTTACTCGTCAGCGGCGGCGTCGATTCAAGTGTCTGTGCAGCGCTGCTCCG

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

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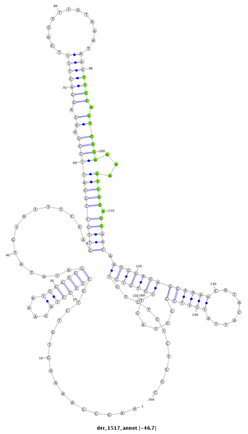
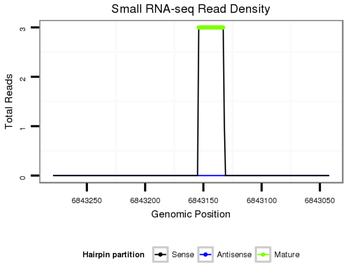
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

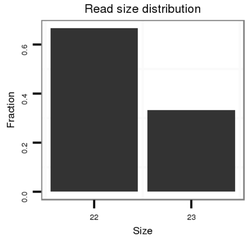
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1517	**scaffold_4784:6843092-6843229 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

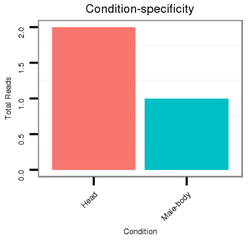
Legend: mature star mismatch in alignment mismatch in read

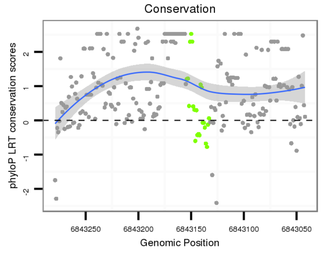
Predicted structure











Hairpin partition Sense Antisense Mature

Hairpin partition Mature

Show Alternate Folds

Flybase annnotation

intron [Dere:GG14220-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

						V107	V060	V108	M055 female		
AGGCGAGAGACAGAAAAAAGAAAAGAAAAGCCGAGAAGCCAAAAGTGTCTGCCCCCTAGAAATGGGGGGATATATGTATTTCGAGTTCCCCGATTCCGAACAGGAGTTTTGAGTTTATAAATAAGTTCCAGTCGGAAAAGTCGGAGGAACAAGGGAGAGGAAAACATACATTATTTTCCCGTACTTCTCTGTCTCTCTCGCTTCGTCATCGCAGCTGCTGCCGTGCGCTTGTGTGC	Read size	# Mismatch	Hit Count	Total Norm	Total	male body	head	head body	body	embryo
**********************************											
22	0	1	2.00	2	1	1	0	0	0
23	0	1	1.00	1	0	0	1	0	0

Anti-sense strand reads

					V040
TCCGCTCTCTGTCTTTTTCTTTTCTTTTCGGCTCTTCGGTTTTCACAGACGGGGGATCTTTACCCCCCTATATACATAAAGCTCAAGGGGCTAAGGCTTGTCCTCAAAACTCAAATATTTATTCAAGGTCAGCCTTTTCAGCCTCCTTGTTCCCTCTCCTTTTGTATGTAATAAAAGGGCATGAAGAGAGACAGAGAGAGCGAAGCAGTAGCGTCGACGACGGCACGCGAACACACG	Read size	# Mismatch	Hit Count	Total Norm	Total	embryo
**********************************						

Show Alignment With Reads

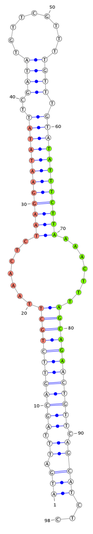
Re-alignment of all predicted orthologs

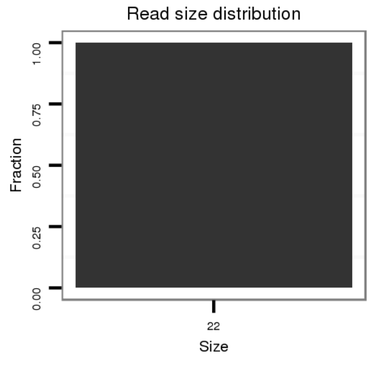
Species	Coordinate	ID	Alignment
droEre2	scaffold_4784:6843042-6843279 -	der_1517	AGGCGAGAGACAGAAAAAAG----AAAAGAAAAGCCGAGAAGCCAAAAGTGTCTGCCCCC-TAGAA-ATGGGGGG--ATATAT----------GTATTT---CG----------AG------TTCCC-CG-----AT----------TCCG--AACAGGAGTTTTGAGTTTATAAATAACTTC----------CAGTCGGA-------AAAGTCGGAGGAAC--AAGGGAGAGGAAAACATACATTATTTTCC----------CGTACTTCTCTCTG-TCTCTCTCGCTTCGTCATCGCAGCTGCTGC----------C----------GTGCGCTTGTG-TGC
droYak3	3L:4705266-4705499 -	dya_1792	AGGCGAGAGACAGAG----------AAAGAAAAGCCGAGAAGCCAAAAGTGTCTGCCCCC-TAGAA-ATGGGGG--ATATAT----------GTATTT---CG----------AG------TTCCC-CG-----AT----------TCCG--AACGGAGTTTTGAGTTTATAAATAACTTC----------CAGTCGGA-------AAAGTCGGAGGAAC--AAGGGAGAGGAAAACATACATTATTTTCC----------CGTACTTCTCTCTG-TCTCTCTCGCTTCGTCATCGCAGCTGCTGC----------C----------GTGCGCTTGTG-TGC
droSec2	scaffold_21412651?-4126758 -	dse_1840	AGGCGAGAGACAGAAAAAGAAAAGAAAAGCCGAGAAGCCAAAAGTGTCTGCCCCC-TAGAA-ATGGGGG--ATATAT----------GTATTT---CG----------AG------TTCCC-CG-----AT----------TCCG--AACGGAGTTTTGAGTTTATAAATAACTTC----------CAGCGGGA-------AAAGTCGGAGGAAC--AAGCAGAGGAAAACATACATTATTTTCC----------CGTACTTCTCTCTG-TCTCTCTCGCTTCGTCATCGCAGCTGCTGC----------C----------GTGCGCTTGTG-TGC
droSim2	3L:4094320-4094559 -	dsi_150	AGGCGAGAGACAGAAAAAGAAAAGAAAAGCCGAGAAGCCAAAAGTGTCTGCCCCC-TAGAA-ATGGGGG--ATATAT----------GTATTT---CG----------AG------TTCCC-CG-----AT----------TCCG--AACGGAGTTTTGAGTTTATAAATAACTTC----------CAGTCGGA-------AAAGTCGGAGGAAC--AAGCAGAGGAAAACATACATTATTTTCC----------CGTACTTCTCTCTG-TCTCTCTCGCTTCGTCATCGCAGCTGCTGC----------C----------GTGCGCTTGTG-TGC
dm3	chr3L:4134010-4134251 -	dme_412	AGGCGAGAGACAGAAAAAGAAAAGAAAAGCCGAGAAGCCAAAAGTGTCTGCCCCC-TAGAA-ATGGGGG--ATATAT----------GTATTT---CG----------AG------TTCCC-CG-----AT----------TCCG--AACGGAGTTTTGAGTTTATAAATAACTTC----------CAGTCGGA-------AAAGTCGTTAAAC--AAGCAGAGGAAAACATACATTATTTTCC----------CGTACTTCTCTCTG-TCTCTCTCGCTTCGTCATCGCAGCTGCTGC----------C----------GTGCGCTTGTG-TGC
droEug1	scf1180000409466:1900969-1901196 -		A----------------AAAGAAAAGCCAGAAGCCAAGTGTCTGCCCCC-TGAA-ATGGGGG--AATATGCGCTGCCTGCCGTGTTTT---CG----------TCCC-CG-----AT----------TCCG--AGGAGTTTTGAGTTTATAAATAACTTC----------CAGTCGA-------AAAGC--AGAAAG--AAGCAGAGAAAACATACATTATTTTCC----------CGTAGTTTCTCTG-TCTCTCTCGCTTCGTCATCGCAGCTGCTGC----------T----------GTGCGTTGTG-TGC
droBia1	scf1180000302428:831690-833922 -		A-GCAAGG----------AGGGGGCAAAAGCCAAGAAGCCAAGTGTCTGCCCCC-TGAA-ATGGGGG--AT----------TATTT---CG----------AG------TTCCC-CG-----AT----------TCCG--AGGAGTTTTGAGTTTATAAATAACTTC----------CAGTCGGATGAACCAGCAAATAAGC--CAGGGAGAGGAGCAGCATAGCAGTTATTTTCC----------CGTAGTTTCTCTG-TCTCTCTCGCTTCGTCATCGCAGCTGCTGC----------T----------GCCC----------C-TGTGTTGTG-TGC
droTak1	scf1180000415778:22373-22566 +		GA----------------------AACCCAGAAGCCAAGTGTCTGCCCCC-TGAA-ATGGGGG--AT----------TATTT---CG----------AG------TTCCC-CG-----AT----------TCCG--AGGAGTTTTGAGTTTATAAATAACTTC----------TCAGTCGCAGCCAGC----------CAGCAGCAGGCAGCAGCATAGCAGTTATTTTCC----------CGTAGTTTCTCTG-TCTCTCTCGCTTCGTCATCGCAGCTGCTGC----------T----------GCTGCT----------C-TGTGTTGTG-TGC
droEle1	scf1180000491249:4987979-4988160 -		GC--GAGAGA-----A---------AA----------------AAAAAGTCTGCCCCC-TGAA-ATGGGGG--AT----------TATTT---CG----------AG------TTCCC-CG-----AT----------TCCG--AGGAGTTTTGAGTTTATAAATAACTTC----------CAGTCGA-CA-----A---------TAAA--AAGCAGAGAAAGCATACAT----TTCCC----------CGTAGTTCTCTGTG-TCTCTCTCGCTTCGTCATCGCAGCTGCTGC----------T----------GCTGTTGTG-TGC
droRho1	scf1180000779198:19068-19236 +		GC--GAGAGA-----A---------AA----------------AAAAAGTCTGCCCCC-TGAA-ATGGGGG--AT----------TATTT---CG----------AG------TTCCC-CG-----AT----------TCCG--AGGAGTTTTGAGTTTATAAATAACTTC----------CAGTCGA-GC-----A---------AAAA--AAGCAGAGAAAGCATACAT----TTCCC----------CGTAGTTCTCTGTG-TCTCTCTCGCTTCGTCATCGCAGCTGCTGC----------T----------GCTGTTGTG-TGC
droFic1	scf1180000454113:1363530-1363736 -		C---GAGAGA-GAGAAA---AAAAAAGAAAAGCCAGAAGCCAAGTGTCTGCCCCC-TGAA-ATGGGGG--AATA----------TATTT---CG----------AG------TTCCC-CG-----AT----------TCCG--AAGGAGTTTTGAGTTTATAAATAACTTC----------CAGTCGAGAGGC----------AAAC--AGCAGAGAAAGCATACAT----TTCCC----------CGTAGTTCTCTGTG-TCTCTCTCGCTTCGTCATCGCAGCTGCTGC----------T----------GTGCTTGTG-TGC
droKik1	scf1180000302383:514810-515030 -		AGAGGAGAG----------------------AAGCCAGAAGCCAAGTGTCTGCCCCC-TGAA-ATGGGGG--AT----------TCCCTCCGT-GGAGTTTTGAGTTTATAAATAACTTC----------TCAGTCGCAGCAGCGAAGCAGCAGAGCAAAGCATACAT----TTCCC----------CGTAGTTCTCTGTG-TCTCTCTCGCTTCGTCATCGCAGCTGCTGC----------T----------TGTTTGT-GTGTATGTGTG-TGC
droAna3	scaffold_13337:16554299-16554491 -		GAA----------------------AA----------------AAAAAGTCTGCCAGTGTCTGCAGTTCGGCATGGGAGAA-ATAATGTGC----ATCCGTTCTTCTTC----TG----------TCCC-CG-----AT----------TCCG--AAGGAGTTTGAGTTTATAAATAACTGC----------ATGTTTCCAGCCCAGC----------CAGCAGCAAAAGCCATACAT----TTTCCCGTCCGACGTCGTCGGTGGCGCTCTG-TG-TGCTCGCTTCGTCATCGCAGCTGCTGC----------T----------GTGCTGCTGG-TGC
droBip1	scf1180000396641:755026-755232 +		AGCAA----------------------AA----------------AAAAAGTCTGCAGTTCGGCATGGGAGAA-ATAATGTGC----ATGCCGTTCTTCTTC----TG----------TCCC-CG-----AT----------TCCG--AAGGAGTTTGAGTTTATAAATAAGTC----------ATGTTTCCAGCCCAGC----------CAGCAGCAAAAGCCATACAT----TTTCCCGTCCGACGTCCCGGTGGCGCTCTG-TG-TGCTCGCTTCGTCATCGCAGCTGCTGC----------T----------GCTGCAGCTGCGGCG----------T-TAT-CGTGTGTGT
dp5	XR_group8:8300041-8300299 -		AG--CCAGAAGCCAAGTGTCGCCCCC-TGAA-ATGGGGG--AT----------TGTGCTTGT----TG----TGCCTTCCCGTAC----AT----------TCCCGAACGGAGTTTGAGTTTATAAATAACTTC----------ATGTTTCCAGCCCAGC----------CAGCAGCAAAAGCCATACAT----TTTCCCGTCCGACGTCGTCGGTGGCGCTCTG-TGCTGCTGATGTCGCTCTGCCTCTGCCATCGTAGTCGTCGCTT--CGTCATCGTCGTGGCCAGCAGCTGCGCTGCAGCTGC----------A----------GTGCTGCTGG-TGC
droPer1	scaffold_4D:4905597-4908879 -		GC--AAGC------TG-GAAAACTATAAGCCAGAAGCCAAGTGTCGCCCCC-TGAA-ATGGGGG--AT----------TGTGCTTGT----TG----TGCCTTCCCGTAC----AT----------TCCCGAACGGAGTTTGAGTTTATAAATAACTTC----------ATGTTTCCAGCCCAGC----------CAGCAGCAAAAGCCATACAT----TTTCCCGTCCGACGTCGTCGGTGGCGCTCTG-TGCTGCTGATGTCGCTCTGCCTCTGCCATCGTAGTCGTCGCTT--CGTCATCGTCGTGGCCAGCAGCTGCGCTGCAGCTGC----------A----------GTGCTGCTGG-TGC
droWil2	scf2_1100000004762:4227391-4227661 -		AG-AA--AA----------------------AA----------------AAAAAGTCTGCCAGTGTCTGCAGTTCGGCATGGGAGAA-ATAATGTGC----ATCCGTTCTTCTTC----TG----------TCCC-CG-----AT----------TCCG--AAGGAGTTTGAGTTTATAAATAACTTC----------ATGTTTCCAGCCCAGC----------CAGCAGCAAAAGCCATACAT----TTTCCCGTCCGACGTCGTCGGTGGCGCTCTG-TGCTGCTGATGTCGCTCTGCCTCTGCCATCGTAGTCGTCGCTT--CGTCATCGTCGTGGCCAGCAGCTGCGCTGCAGCTGC----------A----------GTGCTGCTGG-TGC
droVir3	scaffold_13049:1991446-1991459 +		T--

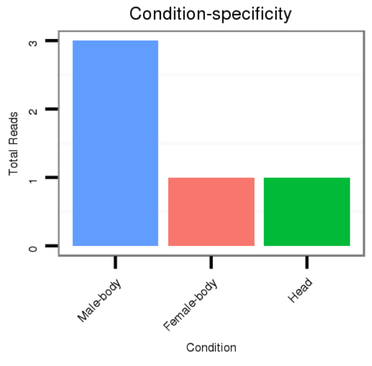
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_135	**scaffold_4929:14394530-14394598 +**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

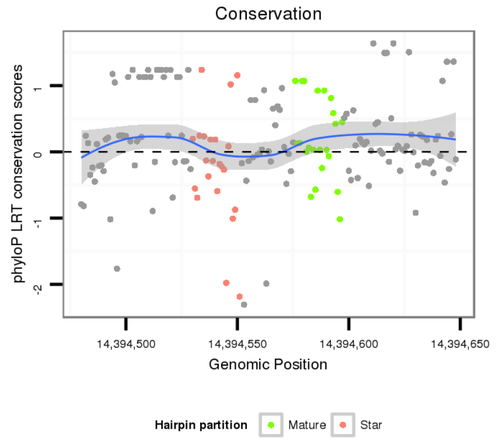
Legend: mature star mismatch in alignment mismatch in read

Predicted structure









Show Alternate Folds

Flybase annnotation

intron [Dere\GG10332-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GGGCTACGTTTATATTGTAAACGTCGGGGGTCCAAATGATTTAGCAGTTCTGCTTAAACTCTAAGGAATATATTCGATATGTTCGTTTTGTTTGTATATTTCTTAAAACTTTAGCAGAACTGTTCAGCATCTCCGCCCCATCAACGTTTCAGTTTCGACCAATCTTAAG	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	M055 female body	V108 head
**********(((.((.(((((((((((((.......((((((((((((..((((.........))))).))))))))))))).....)))))))))).))))))...**********								
.....TATTTCTTAAAACTTTAGCAGA.....	22	0	1	3.00	3	2	0	1
.....TGCTTAAACTCTAAGGAATATA.....	22	0	1	2.00	2	1	1	0
.....TATATTGTAAACGTCGGGGGTCCAAAT.....	27	0	1	1.00	1	1	0	0

Anti-sense strand reads

CCCGATGCAAATATAACATTTGCAGCCCCCAGGTTTACTAAATCGTCAAGACGAATTTGAGATTCCTTATATAAGCTATACAAGCAAAACAAACATATAAAGAATTTTGAAATCGTCTTGACAAGTCGTAGAGGCGGGGTAGTTGCAAAGTCAAAGCTGGTTAGAATTC	Read size	# Mismatch	Hit Count	Total Norm	Total	V040 embryo
**********(((.((.(((((((((((((.......((((((((((((..((((.........))))).))))))))))))).....)))))))))).))))))...**********						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4929:14394480-14394648 +	der_135	GGGCTACGTTTATATTGTAAACGTCGGGGGTCCA--AATGATTTAGCAGTTC----T-GCTTAAACTCTAAGGAATATAT---------TCGATAT--------GT----------TCG----------TTTTGTTTGTATATTTCTTAAAACTTTAGCAGAACTGTTCAGCA--------TCTCCGCCCCATCAACGTTTCA----------GTTTCGACCAATCTTAAG
droYak3	2L:7445047-7445193 -		G-------GTTATATTCTAAACGTCGGGGGTCCAA-AATGATTTAGCAATT----T-GCTTAAGCACTAAGGAACATGT---------TGATAA--------GT----------TCG----------TTTTGTTGTATATTTCT----------ACGGTTCAGCA--------TCTCCGCCCCATCAATGCTTGA----------GTTTCGGCAATCTTAAG
droSec2	scaffold_3:6452301-6452454 -		GGGCTACGTTTATATTCTAAACGTAGGGGGTCCAA-AATGATTAAGCATTC----T-GCTTAAAAACTATGAAATATGTA---CAAGTATGATAA--------GT----------TAA----------TTTTGTTTGCATAATT----------TAGCA--------TCTCCGCCCCATCAATGTTTCG----------GTTTCGACCAATCTTAAG
droSim2	2L:10708731-10708878 -		GGGCTACGTATATATTCTAAACGTAGGGGGTCGAA-AATGATTAAGCATTC----T-GCTTAAAAACTATGAAATATGT---------ATGATAA--------GT----------TAA----------TTTTGTTTGCATAATT----------TAGCA--------TCTCCGCCCCATCAATGTTTCG----------GTTTCGACCAATCTTAAG
dm3	chr2L:11051039-11051186 -		CAGCTACGTTTATATTCTAAACGTAGGGGGTCCAA-AATGATTAAGCATTC----T-GCTTAAAAACTATGGGAATATGT---------CTGATAA--------GT----------TAA----------TTTTGTTTGCCTAATT----------TCAGCA--------TCTCCGCCCCATCTAATGTTTCA----------GTTTGACCAATCTTAAG
droEug1	scf7180000407253:484959-485124 -		AGGTCATGAAATCTTATACACTTGGAGGTCTTC-AATGATTAGCAATTT----TTGCTATACACAATT--GCTTC---------T-----GT----------TCG----------GT---TTCGTATATTTCTTACAACTTAG--------TAAGCGTATTCGCCTTCTCTAACGCACTTGCTGC----------C-CTTA-----AAA--A-----GTTTCAACCAATTTTAAG
droBia1	scf7180000302422:2052949-2053112 +		TTG----------CGAACGTGGGAGGTCTAG-AATGATTTGGCAATTC----T-TGTTAAAGACAGAGAAATTA-ATATTCAACTCAAATAA--------GC----------TAG----------CTCGAAAGCG--------GCTCCGCCCCATCATGGTTTT-CCC---TCT--------AA-TACC---T-TTAATTCGACAACAA-GTTTTTGCCTTTCGACCA---TCGAG
droTak1	scf7180000414023:125498-125665 -		TTG----------TAAACGTGGGAGGTCCAG-AATGAGTTAGCGCATC----T-TGTTAAAGACTG----------------------------CTTTCTATATTTCTATAAATTTAAGCTCAACTCTTAAACG--------AATCCGCCCCATCAACGTTTT-TTTCCCTTT--------AT-TACC---A-CTTATTCCACAACAAAATTGCTGCTTTTCGACCAATTTCGAT
droEle1	scf7180000490644:475768-476014 +		AGATCAATGTAAATGTTGTAAACGTGTGAGGTCTG--AATGATTTAGCAATTC----T-CTTTGAGCTCTAAACAATATT-A----CACTTATAAAAATAGTTTCCTTCACATGGTTGGAGAAGATTGAAAATT-GTTTGTGGTCTTAACATGACTAAAG--------AATGTTCCCAAATTTT----------TAAGC-------TCTCCGCCCCATTATTAATTT-CCC---CTC--------GTTTCTC---C-CTTAGTCCACAGCAA-TTTTTTACTTAACGTCCAATCTCAAG
droFic1	scf7180000449585:852-960 +		ATGTTTGATAGGTTT----------|----------|----|-|----------|---------|---------|---|----------|---TGTTGGTATATTTATTAGAGTTAAA----------GGAG--------ACTACGCCCATCAATTTTT-CTT---ACT---ATCT---T-TTCC---T-CTTATTCCGAAAA---A--GTTGTT---------TTTTAAA
droKik1	scf7180000302677:269117-269273 -		AGGTCGTGTAAATATTATAAGCGTGGGAGGTCTAGCAATGATTGAGCAAATATTTCG-GTTTAGGCATACAAATATGTA-----------|---------|---------|---|----------|---TTCTCGACCGAATCAATGTTCTTCTT---ATATCCAATCTG----CCC---T-CTCTTTCGGAACTAA-A--GTTGATTTGCAAGTGA---TCAAG
dp5	4_group3:6386011-6386065 -		----------|----------|----|-|----------|---------|---------|---|----------|---|----------|--------CTCCGCCGAATCAATGTTCT-CTT---TTCTTCGATCTTT----GCCAAAGG-TTTCTCCACAA----------|----------
droPer2	scaffold_1:7876593-7876647 -		----------|----------|----|-|----------|---------|---------|---|----------|---|----------|--------CTCCGCCGCAATCAATGTTCT-CTT---TTCTTCGATCTTT----GCCAAAGG-TTTCTCCACAA----------|----------

PASS/FAIL

Generated: 05 Jan 2015 at 07:50 PM

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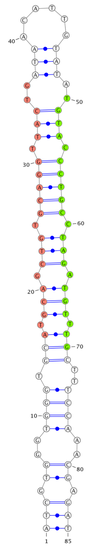
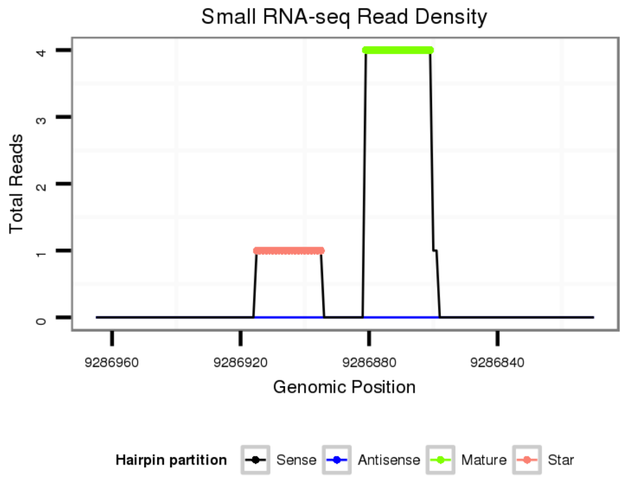
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

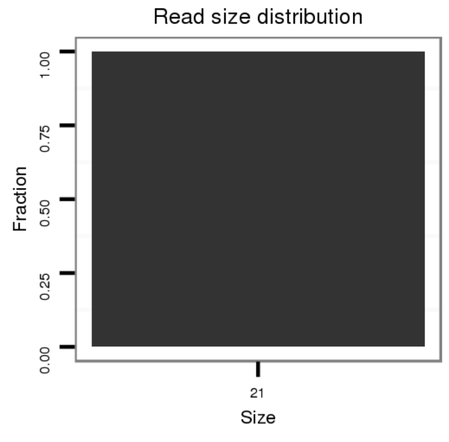
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_199	**scaffold_4929:9286860-9286915 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

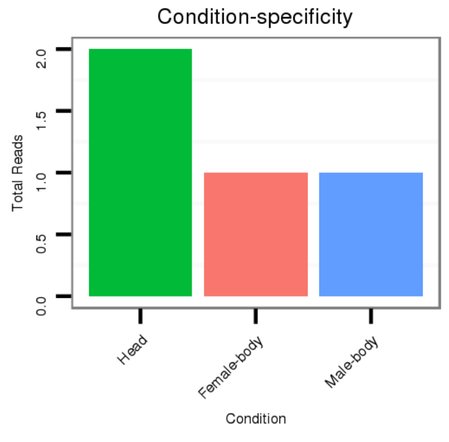
Legend: mature star mismatch in alignment mismatch in read

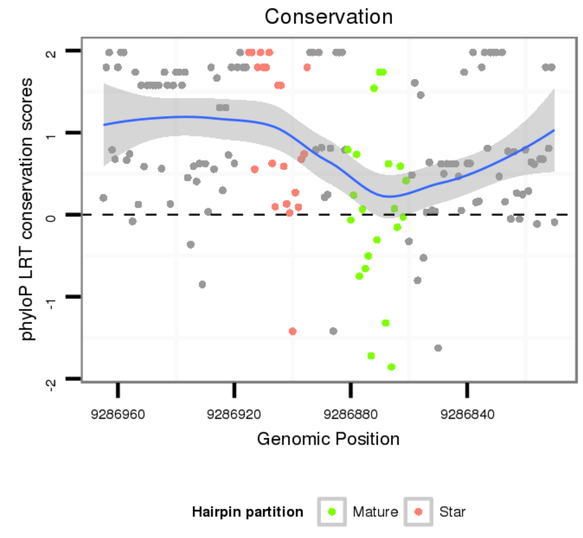
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere\GG24056-in]; utr3 [utr3_minus_879]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AGTTGCATCATTTCGGGGCGTTGCCATGAGCTCCGATCGTGGGTGGGTGCATGCAGCTGTGCAGGTTACTGATAACATTGTATATGTACCCTGCCTAGATGTTTGCTTTCCAAACGAGATTTCTACCTGGCAATTAGACAGTGTTTTGCGGCGTCC **********(((.((..((((.((((.(((.((((.((((((.(((..(((.....))))..))).))))))..))))..))))..))))..))))..))).))**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	M055 female body	V060 head	V107 male body	V040 embryo
.....TGTACCCTGCCTAGATGTTTG.....	21	0	1	3.00	3	2	1	0	0	0
.....TGTACCCTGCCTAGATGTTTGCT.....	23	0	1	1.00	1	1	0	0	0	0
.....ATGCAGCTGTGCAGGTTACTG.....	21	0	1	1.00	1	0	0	0	1	0

Anti-sense strand reads

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

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4929:9286810-9286965 -	der_199	A--GTTGCATCATTTCGGGGCGTTGCCATGAGCTCCGATCGTGGG----TGGGTGCATGCAGCTGTGC-AGGTTACTGATAACA---TTG-----TATATGTA-CCCTGC----------CTA--GATG----TTTGC-TTTCCAAACGAGATTTCTACCTGGCAATTAGAC----------AGTGTTTTGCGGCGTCC
droYak3	2L:11343485-11343649 -		A--GTTGCATCATTTCGGGGCGTTGTCATGAGCTCACATCGTGGG----TGGGTGCATGCAGCTGCGC-AGGTTGCTGATAATA---TTA-----TATATGTA-TGT---------ATGTATGTATGTAGCGAGATTTGC-TTCCCAAGCGAGATTTCTACCTGGCAATTAGAC----------AGTGCTTTGCGGCGTCC
droSec2	scaffold_3:4176589-4176746 -		A--GTTGCATCATTTCGGGGCGTTGTCATGAGCTCAGATCGTGGG----TGGGTGCATGCAGCTGTGC-AGGCTACTGATAATA---TTG-----TATATGTA-CCCTCCCT----------CTA--GATG----TTTGC-TTCCCAGGCGAGATTTCTACCTGGCAATTAGAC----------AGTGCTTTGCGGCGTCC
droSim2	2l:8409537-8409695 -		A--GTTGCATCATTTCGGGGCGTTGTCATGAGCTCAGATCGTGGG----TGGGTGCATGCAGCTGTGCCAGGCTACTGATAATA---TTG-----TATATATA-CCCTCCCT----------CTA--GATG----TTTGC-TTCCCAAGCGAGATTTCTACCTGGCAATTAGAC----------AGTGCTTTGCGGCGTCC
dm3	chr2L:8695048-8695204 -		A--GTTGCATCATTTCGGGGCGTTGTCATGAGCTCAGATCGTGGG----TGGGTGCATGCAGCTGTGC-AGGCTACTGATAATA---TTA-----TATATGTA-CCCTCC----------CTA--GATG----TTTGCTTTCCAAGCGAGATTTCTACCTGGCAATTAGAC----------AGTGCTTTGCGGCGTCT
droEug1	scf7180000409554:819255-819399 +		A--GTTGCATCATTTCTGGGCGTTGTCATGAGCTCAGATCGTGGG----TGGGTGCATGCAGCTGCGC-AAGTCACTGATAATC---TTA-----TATATATA-TCT--C----------CTA--TACA----TT---------AGCTGGAATCTACCTGACAATTAGAC----------AATATTTTGCGGCGTCC
droBia1	scf7180000301518:1080816-1080972 +		A--GTTGCATAATTTCTGGGCGTTGTCATGAGTTCAGATCGTGGG----TGGGTGCATGCAGCTGCGC-ATGGTACTGATAATA---CCG-----TATACGTA-CCCTTC----------CTA--AAGG----TTCCGT-TTTCTGAGACAGGTTTCAACCTGCAGTTAGAA----------AAATTTTTTGCTGCGCCC
droTak1	scf7180000410803:67099-67254 -		A--GTTGCATCATTGCTGGGCGTTGTCATGAGCTCAGTTCGTGTG----TGGGTGCATGCAGCTGCGC-AAGCTACTGATAATA---TTA-----TATATGTA-CCCACC----------CTA--CATG----ATCGT-TTCCCAAGCAATATTTCTACCTGGCAATTAGAC----------AATATTTTGCGGCGTCC
droEle1	scf7180000491186:1529348-1529501 -		A--GTTGCATCACTGCTGGGCGTTGTCATGAGCTCAAATCGTGGG----TGGGTGCATGCAGCTGCGC-AAGTTACTGATAATA---TTA-----TATATATA-CCC--C----------CTA--TATG----TTTGT-TTCCTAAGCGAGATTTCTACCTGGCAATTAGAC----------AGCATATAGCGGCGTCC
droRho1	scf7180000779312:152174-152327 +		A--GTTGCATCACTTCTGGGCGTTGTCATGAGCTCAAATCGTGGG----TGGGTGCATGCAGCTGCGC-AAGTTACTGATAATA---TTA-----TATATGTA-CCC--C----------CTA--TAAG----TTTGC-TTTCTAAGCAAGATTTCTACCTGGCAATTAGAC----------AACATATGGCGGCGTCC
droFic1	scf7180000454102:345443-345598 +		A--GTTGCATCATTTCTGGGCGTTGTCATGAGCTCAAATCGTGGG----TGGGTGCATGCAGCTGCGC-AAGCTACTGATAATAATATTC----TATATGCA-GCC--C----------CTA--TCTG----TTTGT-TTCCAAGC-AGATTCCTACCTGGCAATTAGAC----------AATATATTGCGGCGTCC
droKik1	scf7180000302412:839875-840041 -		A--GTTGCATCATTTCTGGGCGCGTGCCATGAGATCAGATCGTGGGTGGGTGGGTGCATGCAGCTGCGC-GAATCACTGATAATA---TTA-----TATATGTA-AGG--C---TATATATACATA--TATG----ATTGC-TTACGAAGCGTAGATTTCCACCTGGCAATTAGAC----------AGTATTTTGCGACGTCC
droAna3	scaffold_12916:10341612-10341780 -		G--GTTGCATCACTTCTGGGCGTTGTCATGAGGAGACAGCG----GGGTGCATGCAGCTGCGC-AATCTGCTGATAATATTACTTTATACTATATGTCC-CTATCCCG----------CTACATAAG----CAGAT-GTCCCCATAAAGATTTCCAGGTGGCAATTATACTATA------ATATACTTTGCAGCGTCC
droBip1	scf7180000396572:14482-14654 -		G--GTTGCATCACTTCTGGGCGTTGTCATGACCAGAGAACGT---GGGTGCATGCAGCTGCGC-AACCTGCTGATAATA---CTTGATACTATATGGCTCTAAACCGCT--------ATA--AACG----CAGAT-GTCCCCATAAAGATTTCCACCTGGCAATTATAATATACATAATATATATTTTTCAGCGTCT
dp5	4_group5:968161-968245 +		CTGGTAACATGCA----------AGC----GTGTGCATCCAGCTT---AGTGTGGATCATC---TTA-----TATGTGTA-------------------------------------CCTTTCAATTA-AC----------AATATTTCTGTTGTGTCT
droPer2	scaffold_5:5373506-5373590 +		CTGGTAACATGCA----------AGC----GTGTGCATCCAGCTT---AGTGTGGATCATC---TTA-----TATGTGTA-------------------------------------CCTTTCAATTA-AC----------AATATTTCTGCTGTGTCT

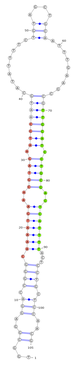
Generated: 09/08/2015 at 07:50 PM

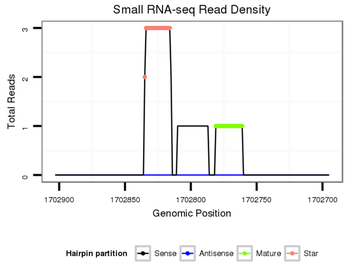
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

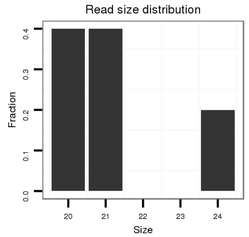
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1510	**scaffold_4784:1702745-1702853 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

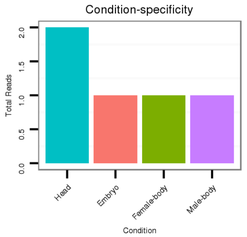
Legend: mature star mismatch in alignment mismatch in read

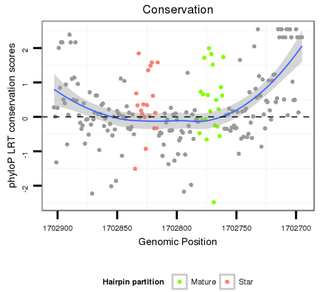
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dere'GG14570-in]; CDS [Dere'GG14570-cds]; CDS [Dere'GG14570-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTCACGGGTCCCCTGTAAGTGGACGAAGGAGCCTCTTTGGCGGCGTTAACTTCTGGCGGAGGACCGGGCAAAATGAAACGTAGAATGCAATGCATATTTTCTGTAGCTGCAATTTGAAGCCGTTGCATCCTGCGACTCATTTTACTCCTGCTCCAACGCAAAACCCATACTAATCCTCCGCTTCCAACTAGATGCGATATGCGCTGTCCG	Read size	# Mismatch	Hit Count	Total Norm	Total	V040 embryo	V108 head	M055 female body	V107 male body
..TTGCATCCTGCGACTCATTTT	21	0	1	1.00	1	0	0	1	0
..CAAAATGAAACGTAGAATGC	20	0	1	1.00	1	0	1	0	0
..AAAATGAAACGTAGAATGCA	20	0	1	1.00	1	1	0	0	0
..CAAAATGAAACGTAGAATGCA	21	0	1	1.00	1	0	1	0	0
..ATATTTTCTGTAGCTGCAATTTGA	24	0	1	1.00	1	0	0	0	1

Anti-sense strand reads

AAGTGCCCAGGGGACATTCACCTGCTTCCTCGGAGAAACCGCCGCAATTGAAGACCGCCTCCTGGCCCGTTTTACTTGCATCTTACGTTACGTATAAAAGACATCGACGTTAAACTTCGGCAACGTAGGACGCTGAGTAAAATGAGGACGAGGTTGCGTTTTGGGTATGATTAGGAGGCGAAGTTGATCTACGCTATACGCGACAGGC	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	V040 embryo
..CAAATTTCCTCATCTTACGTTACGTATAAAAGACATCGACGTTAAACTTCGGCAACGTAGGACGCTGAGTAAAATGAGGACGAGGTTGCGTTTTGGGTATGATTAGGAGGCGAAGTTGATCTACGCTATACGCGACAGGC	84	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4784:1702695-1702903 -	der_1510	TTCACGGGTCCCCTGTAAGTGGACG--AAG---GA-GC---CTCTTT---GGCGGCGTTAACTTCTGGCGGAGGA----------CCG-GC==C====AAAATGAAACGTAGAATGCAATGCAT-A----TTT-TCTGTAGCTGCAA----------TT-TG-----AAGCCGTTGCATCCTGCGACTCATTTTACTCCTGC----------TCCAACGCAAA---------ACCCATACTAATCCT-CCGCTTC-----AACTAGATGCGATATGCGCTGTCCG----
droYak3	3L:1671795-1671966 -	dya_668	TTCACGGGTCCCCTGTAAGTGGA-C---A---G---G-----A----------A----------T-A-GG==C====AAAATGAAACGTAGAATGCAA-CCAT-A----TT-ATGTTCTGCTGC----------TT-TG-----AAGCCGTTGCATCCTGCGCGTCATTTTACTCCTGC----------TCCAACGCAAA---------ACCCATACTAATCCT-CCGCTTC-----AACTAGATGCGATATGCGCTGTCCG----
droSec1	scaffold_211746:169-174637 -	dse_994	TTCACGGGTCCCCTGTAAGTGACG--AG----G---GC---CTCTTT---GGCGGCGCAAGTTCTTCGGCGAAGGA----------T-A-GG==C====AAAATGAACGTAGAATGCAAT-A----TTT-TCTGTCTGCTGC----------TT-TA-----AGCCGTTGCATCCTGCGACTCATTTTACTCCTGC----------TCCAACGCAAA---------ACCCATACTAATCCT-CCGCTTC-----AACTAGATGCGATATGCGCTGTCCG----
droSim2	3L:1629600-1629810 -	dsi_4243	TTCACGGGTCCCCTGTAAGTGGACG--AG----GA-GC---CTCTTT---GGCGGCGCAAGTTCTTCGGCGAAGGA----------TTA-GG==C====AAAATGAACGTAGAATGCAAT-CAT-A----TTT-TCTGTCTGCTGC----------TT-TA-----AGCCGTTGCATCCTGCGACTCATTTTACTCCTGC----------TCCAACGCAAA---------ACCCATACTAATCCT-CCGCTTC-----AACTAGATGCGATATGCGCTGTCCG----
dm3	chr3L:1719327-1719936 +	dme_418	TTCACGGGTCCCCTGTAAGTGGACG--AAG----GC---CTCTTT---GGCGGCGCAAGTTCTTCGGCGAAGGA----------T-A-GG==C====AAAATGAAACGCAGAATGCAAT-CAT-A----TTT-TCTGTCTGCTGC----------TT-TA-----AGCCGTTGCATCCTGCGACTCATTTTACTCCTGC----------TCCAACGCAAA---------ACCCATACTAATCCT-CCGCTTC-----AACTAGATGCGATATGCGCTGTCCG----
droEug1	scf1180000407756:39377-39604 +		TTCACGGTCCCGTGTAAGTGGACGCAAAG-TGAAGGA-GC---CTCTTT---GGCGGCGTAAGTTCTTCGGCGAAGGA----------T-ATACGCC==C====AAAATTAAACGTAGAATGCCTTC-GCG---AG-TGT---AATAATGTT----------TTTAT-G-TT----AAACCAAATGCATCCTGCGACTCATTTTACTCCTGC------GAGTTAGGTTATC----------A-CCAG-CTA----------AAAATACTAATCCT-CCGCTTC-----AACTAGATGCGATATGCGCTTCCCG----
droBia1	scf1180000302428:8410930-8411008 +		----------
droYak1	scf1180000415095:39985-40122 +		ATAT----------
droEle1	scf1180000491249:3840550-3840699 +		TGCACGGCAGTCTGTGT-G-ACAAGAG-TCCCG-TGA-T---GCA---------GCTA-------GACCGGGATGCCTGCAG----------
droRho1	scf1180000776850:217162-217404 +		TTCACGGGTCCTGTAAGTGGACGTAGAGAGA-GT---GTCTTT---C----------G-------TGACAT----------CATCGAATGGCACATGGATACGGG==C====AAAATGAAACGAGATGGTATGCAAT-G----TT---AGCAATTTC---ATTAAGGTTTTTTA-TACTT----AATTTACTGCATCCTGAGTCTGCGATATC----------TCAAG-CAAA---------AGCGTACTAATCCT-CCGGTTC-----AACTAGATGCGATGCGCTGTCCG----
droFic1	scf1180000454113:356509-356697 +		TTCACGGGTCCCTGTAAGTGGACGTAGTCGAAGTAA-GC---GCTTTT---A----------G-------TATTGGGG----------TT-TG-----AAGGC----------TT-TG-----TGCCGCAGTGCATCCTGCGACTCATTTTACTCCTAAC-------TAATTTATGCCC----------AAAGACCCCCTCTAAC-------TAATTTATGCCC----------AAAGATGCGATGCGCTGTCCG----
droKik1	scf1180000302577:200415-200640 -		TTTACGGGTCCCCTGTAAGTGGAG--AGAG---GA-GCTGCCTCTTGCCTCGGAAGTAATCATTCTC-G-T-----TTGAGGTTTAC-A-CC----AAAATGAACGTAGAATGCTTTACAT-GCATGCC-ACA----------TTTTATTA----------AT-TT-T----TTTACCGCTGACATCGTAGTCACTTTGT-TGT-CCCGTGGCGCTTTGCCAAGTCTCCTTGCCACCTACGC----------AGCGTACTAATCCT-CCGTTC-----AATAGATGCGATGCGCTGTCCG----
droAna3	scaffold_13337:1119443-1119685 +		TTCACGGGTCCCTGTAAGTCGGCG--AGGC---AT-GA---TCTTTT---CA-CCAAAAGGG-GATGGGATAGAC----------CCCAG-GG----T-GTTATGGAGAGCGTCGGCCGTAGATGCTTACAT-C----TTTCA----------TTT----------TTACACACCTTTTAGTTTGGCGATGGATGGTGACTTGTTATGACCCCGGGGCTGTATGCTTGATTTCCCTC-AA-G-G-GAA----------T-G-GCCATAATCCT-TCGCTTC-----AACTAGATGCGATGCGATGCGTTCCCG----
droBip1	scf1180000396371:1451541-1451788 +		TTCACGGGTCCCTGTAAGTCGGG--AGAGG---AT-GATTCG-TTTT---CA-CCAAAAGGAACTAGGCATAGAC----------TCCAG-GG----T-TTTATAGAGAGCGTCGGCCGTAGATATGCTTCAT-C----TTTCA----------TTTGA----------TTACATAAAAGTTTTAGTTTAA-AAGAACAGAGACATTTGTATGACCCGGGGGCTGTATGCTTTGTTTACCCCAAAA-G-G-GAA----------T-T-GCCATAATCCT-CCGCTTC-----AACTAGATGCGATGCGATGCGTTCCCG----
dp5	XR_group61315918-13160095 +		GCGG----GGAT-G-CTCGCAGGAGCGATCT-CGAGAGG-T---ACA---------G-TA-------GGCCCGGACTGCAATCAGACGTGC----------GAGCTGGCAGCCCGGAGACGGGACGTCAGTGCAGCATTGGCTGGAGCAGTGCCCAGTGCACGCGCCCCTGCACCTTCCTGGCTA
droPer2	scaffold_88:198690-198867 +		GCGG----GGAT-G-CTCGCAGGAGCGATCT-CGAGAGG-T---ACA---------G-TA-------GGCCCGGACTGCAATCAGACGTGC----------GAGCTGGCAGCCCGGAGACGGGACGTCAGTGCAGCATTGGCTGGAGCAGTGCCCAGTGCACGCGCCCCTGCACCTTCCTGGCTA
droWil2	scf2_1100000004511:937410-937452 -		CCTC----------
droVir3	scaffold_13049:2352013-2352243 -	dvi_18051	TTTACGGGTCCCCTGTAAGTGGAC-AA----GT---GA-AT---TCAA-T----AAAATT----------
droMoj3	scaffold_6654:1516860-1517086 +		TTCACGGGTCCCCTGTAAGTGGA-T-AGT---GT---GA-AT---TCAA-T----AAAATT----------
droGri2	scaffold_15110:3382653-3382886 -		TTCACGGGTCCTGTAAATGGACT-AGT---GA-AT---TCAA-T----AAAATT----------

Generated: 09/08/2015 at 1751PM

Message	
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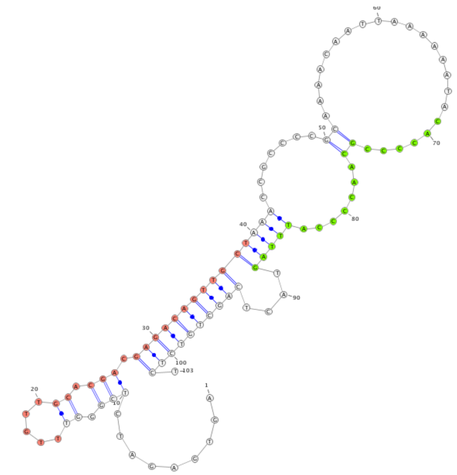
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.gloop	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	3

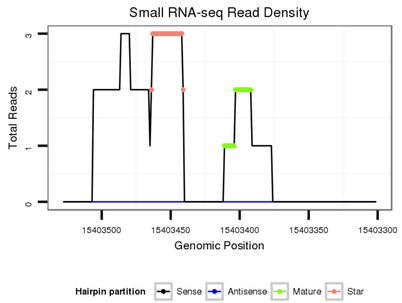
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1519	**scaffold_4770:15403351-15403478 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

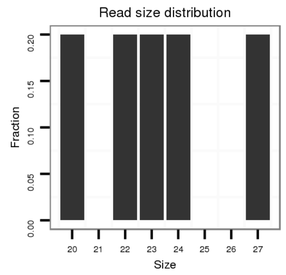
Legend: mature star mismatch in alignment mismatch in read

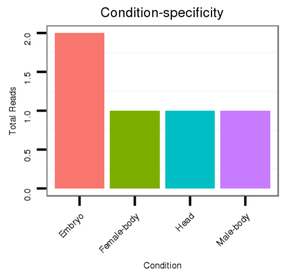
Predicted structure

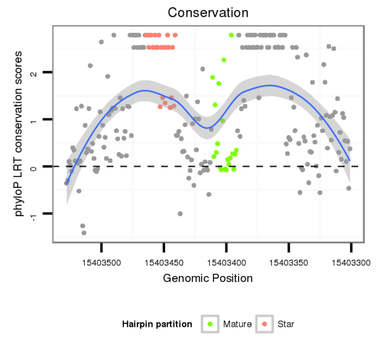


der_1519_annot [-16.6]









Show Alternate Folds

Flybase annnotation

intron [Dere\GG17540-in]; utr5 [utr5_plus_10181]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CCTATATATGTATCTTGTATCTATAAAGTGTCCAGAGTTGTCAAGCGTCAGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGCTAAACCGCCCCGCAAAACAATTAAAAAATACACCCCGCAACCCCATTTAGTACTCAGCTGTCTCTCGTTGTTTCGATTTCGGGATCTTGACAACGACGCCATCGAATTGAAGACATTGACCCAGTGATTAGTGATATTAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V040 embryo	M055 female body	V107 male body	M057 embryo	V108 head	V060 head
**********.....(((.((.....)).))).(((((((((((((((.....((.....)).....)))))))))))))).**********											
.....CACCCCGCAACCCCATTTAG.....	20	0	1	1.00	1	0	0	0	1	0	0
.....AACCCCATTTAGTACTCAGCTGTCTCT.....	27	0	1	1.00	1	0	1	0	0	0	0
.....ATAAAGTGTCCAGAGTTGTCAAGC.....	24	0	1	1.00	1	1	0	0	0	0	0
.....TTGTTGCACGACGAGACAGTTGCT.....	24	0	1	1.00	1	0	0	0	0	1	0
.....TGTTGCACGACGAGACAGTTGC.....	22	0	1	1.00	1	0	0	1	0	0	0
.....TGTTGCACGACGAGACAGTTGCT.....	23	0	1	1.00	1	1	0	0	0	0	0
.....AAGCGTCAGTGAGATCTCGGG.....	21	0	1	1.00	1	0	0	1	0	0	0
.....GTCAGTGAGATCTCGGGTT.....	19	0	1	1.00	1	0	0	0	1	0	0
.....ATAAAGTGTCCAGAGTTGTCAAGCGTC.....	27	0	1	1.00	1	0	0	0	0	1	0

Anti-sense strand reads

GGATATATACATAGAACATAGATATTTCACAGGTCTCAACAGTTCGCAGTCACTCTAGAGCCCAACAACGTGCTGCTCTGTCAACGATTTGGCGGGGCGTTTTGTTAATTTTTTATGTGGGGCGTTGGGGTAAATCATGAGTCGACAGAGAGCAACAAAAGCTAAAGCCCTAGAACTGTTGCTGCGGTAGCTTAACTTCTGTAACTGGGTCACTAATCACTATAATT	Read size	# Mismatch	Hit Count	Total Norm	Total	V040 embryo	V060 head	M055 female body	V108 head
**********.....(((.((.....)).))).(((((((((((((((.....((.....)).....)))))))))))))).**********									

Show Alignment With Reads

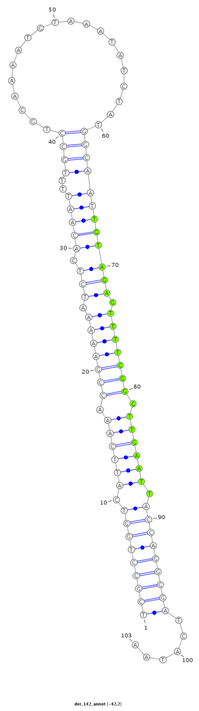
Re-alignment of all predicted orthologs

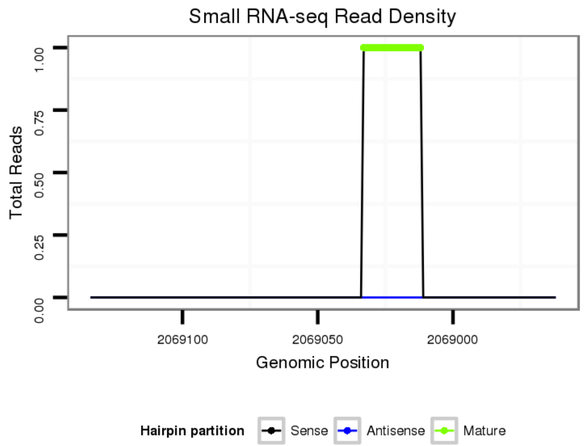
Species	Coordinate	ID	Alignment
droEre2	scaffold_4770:15403301-15403528 -	der_1519	CCTATA------TATG-----TATC-TTGTATC------T----ATAA----AGTGTCCAGAGTTGT-CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAACCGCC-CC----------GCAAAA---CAATTA----------AAA---------AATACACCC-CGCAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTCGATTTCGGGATCTTGACAACGACGCCA----------TCGA----ATTGAAGACATTG--------ACCCAGTG----------ATTA-----GTGAT-----ATTAA
droYak3	3R:10242687-10242915 +	dya_1794	CCCATC------TA---CAAGTATATAGTATC-------T----ATAA----AGTGTCCAGAGTTGT-CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAACCGCC-TA----------GCAAAA---CAATCA----------AAA---------TAACACCCTCAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTCGATTTCGGGATCTTGACAACGACGCCA----------TCGA----ATTGAAGACATTG--------ACCCAGTG----------ATTA-----GTGAT-----ATTAA
droSec2	scaffold_0:15728309-15728526 -	dse_1842	TCTATA------T---------------A-TGTATC-------T----ATAA----AGTGTCCAGAGTTGT-CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAACCGCC-CC----------GCAAAA---TAATCA----------AAA---------TAACACCCTCAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTCGATTTCGGGATCTTGACAACGACGCCA----------TCGA----ATTGAAGACATTG--------ACCCAGTG----------ATTA-----GTGAT-----ATTAA
droSim2	3rr:14862265-14862482 -	dsi_32455	TCTATA------T---------------A-TGTATC-------T----ATAA----AGTGTCCAGAGTTGT-CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAACCGCC-CC----------GCAAAA---TAATCA----------AAA---------TAACACCCTCAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTCGATTTCGGGATCTTGACAACGACGCCA----------TCGA----ATTGAAGACATTG--------ACCCAGTG----------ATTA-----GTGAT-----ATTAA
dm3	chr3R:6216932-6217149 +	dme_373	TCTATA------T---------------A-TGTATC-------T----ATAA----AGTGTCCAGAGTTGT-CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAACCGCC-CC----------GCAAAA---TAATCA----------AAA---------TAACACCCTCAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTCGATTTCGGGATCTTGACAACGACGCCA----------TCGA----ATTGAAGACATTG--------ACCCAGTG----------ATTA-----GTGAT-----ATTAA
droEug1	scf1800000409692:687970-688195 +		TCTATC------T---------------A-TGTATC-------T----ATGA----AGTGTCCAGAGTTGT-CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAATGCCCTTT-C----------A----------ATAAAAAAACAAACA----------AAC---------TAACACCCTCAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTCGATTTCGGGATCTTGACAACGACGCATTT--------S-AAA-TTTGATCTGAAGACCTG--------ACCCAGTG----------ATTA-----GTGAT-----ATTTA
droBia1	scf1800000302402:8304625-8304856 +		TGTATC------T---------------A-TGTATC-------T----ATGA----AGTGTCCAGAGTTGT-CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAAGCCCTCC----------GAGGACAGA----------AAAAAAAC----A----------AAA---------TGCAACCCTCAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTCGATTTCGGGATCTTGACAACGACGCCA----------TCGATTCGATCCGAAGACCTG--------ACCCAGTG----------ATTA-----GTGAT-----ATTGA
droTak1	scf1800000415380:1425635-1425851 -		TCTATC------T---------------A-TGTATC-------T----ATGA----AGTGTCCAGAGTTGT-CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAACCGCC-CC----------GCAAGAAAC----A----------AAA---------ATAACACCCTCAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTCGATTTCGGGATCTTGACAACGACGCGCA----------TCGATTGATGTGAAGACCTG--------ACCCAGTG----------ATTA-----GTGAT-----ATTA
droEle1	scf1800000490995:524589-524800 -		TC-----------------------------A-TGTATC-------T----ATGA----AGTGTCCAGAGTTGT-CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAACCGCC-CC----------GCAGGAAAC----A----------AAA---------TAACACCCTCAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTCGATTTCGGGATCTTGACAACGACGCAG----------TCGA----TCTGAAGACCATG--------ACCCAGTG----------ATTA-----GTGAT-----AATGA
droRho1	scf1800000777158:35501-35707 -		TC-----------------------------A-TGTATC-------T----ATGA----AGTGTCCAGAGTTGT-CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAACCGCC-CC----------GCAGGAAAC----A----------AAA---------TAACACCCTCAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTCGATTTCGGGATCTTGACAACGACGCCA----------TCGA----TCTGAAGACCATG--------ACCCAGTG----------ATTA-----GTGAT-----AATGA
droFic1	scf1800000453800:2293375-2293580 +		TCTATC------T---------------A-TGTATC-------T----ATGA----AGTGTCCAGAGTTGT-CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAACCGTC-CC----------GCAAAGAAAC----A----------GAA---------TAACACCCTCAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTCGATTTCGGGATCTTGACAACGACGCGCA----------TCGA----TTTGAAGACCATG--------ACCCAGTG----------ATTA-----GTGAT-----ATTGA
droKik1	scf1800000302475:1404661-1404904 +		TCTATAGCCGCCA---------------A-TGTATC-------C----AGGA----AGTGTCCAGAGTTGT-CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAACCGCA-CCACATC----------------GAAAA----AAAATAATAAAATATGA----------TAACACCCTCAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTCGATTTCGGGATCTTGTAACGACGCGT---------ACAGACGA----TCTAAGACCATG--------ACCCAGTG----------ATTA-----GTGAT-----ATTGA
droAna3	scaffold_13340:938692-939815 +	dan_4037	CCTTCA------A---------------A-TGTATCACAAGAAGAGATA----AGTGTCA---TGT-CAGCGC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAACCGT-C-C----------GGGGGA----------GCCCGTA---AAAA----A----------AAAACACAAACAGCCGATT--CCAGAAATAC-AC-TA---AATACCAGCTGTCTCTCGTTGTTTCGATTTCGGGATCTTGTAACGACGCAT---------C-A-TCGA----T----------------------ATAA----GTGAT-----TCTT
droBip1	scf1800000394085:58809-59009 -		TCTATA------A---------------A-TGTATC-------G----AGA----AATA----G---TGCC---C-GTGTCCAGAGTTGT-CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAACCGCC-C----------GGGGGAGGG----------GCC---AAAA----A----------AAA---------GCC---CAATTA----CCAACCCTCAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTCGATTTCGGGATCTTGTAACGACGCAT---------CAA-C----------CATT-----A-TAGG----------ATTA-----GTGAT-----ATTA
dp5	2:7251724-7252000 +	dps_3825	CGAGAG------AGTATACAGAAGTATATTATAA----TCT----AT---------AGAGTTGTTCAGTGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTCCGAGCCACCTCG-TTCCCAGCAGACGCCATTGTGATGATGTTGTTGATGATGATGATGAGGAGGAGGAGAGGAGGAGGAGGCC------TA---------------TA---------TA---------TA---

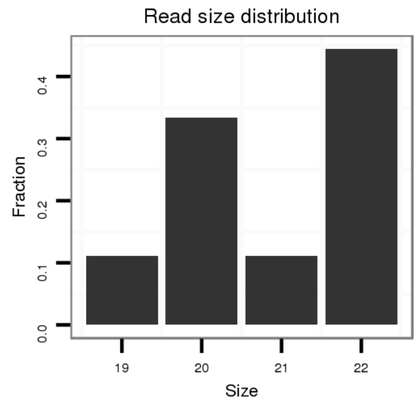
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_142	**scaffold_4644:2069012-2069084 -**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

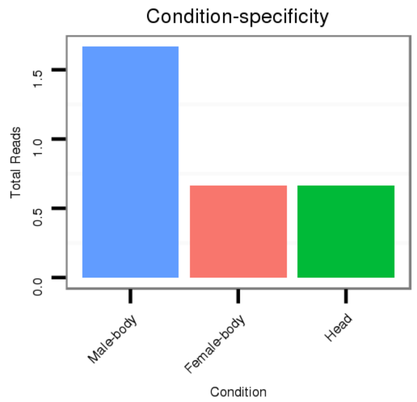
Legend: mature star mismatch in alignment mismatch in read

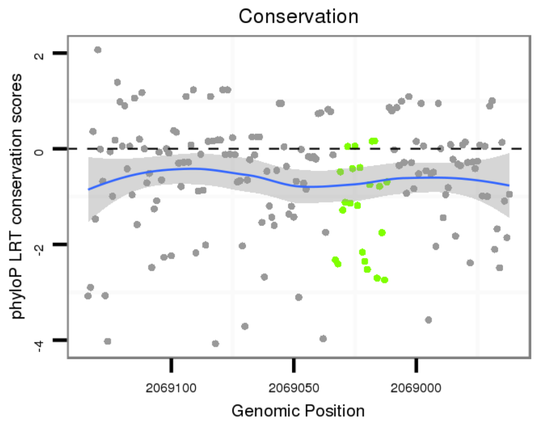
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. der_1437 scaffold_4644:2068541-2068562 - 2. der_142 scaffold_4644:2069012-2069033 - 3. scaffold_4644:2069884-2069905 -	

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CATTTTTCCATCTTCGATCCATCGCCTGATTATGATCGCCTGGTCATTCAAACCGAAAAATCTCACAATTTTGCCTGCAAAATGTAAATATCTATGGCAATTGTAGAGTTTTCGGCTTGAATTACCAGGCGATCATAATCAGAAGCAGGCTGCTACAGAAAACCAAACGATCG **********(((((((((.(((((((.(((((((.(((.(((((..((((.....)))))))))))).)))))).)))))).)))))))))).....**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**M055 female body**	**V107 male body**	**V108 head**	**M057 embryo**	**V040 embryo**
.....TGTAGAGTTTTCGGCTTGAATT.....	22	0	3	1.00	3	0	2	1	0	0
.....AGAGTTTTCGGCTTGAATTACC.....	22	0	3	0.67	2	2	0	0	0	0
.....TGTAGAGTTTTCGGCTTGAA.....	20	0	3	0.67	2	0	2	0	0	0
.....ATCGCCTGGTCATTCAAACCG.....	21	0	2	0.50	1	1	0	0	0	0
.....CTGATTATGATCGCCTGGTCA.....	21	0	2	0.50	1	1	0	0	0	0
.....TTGTAGAGTTTTCGGCTTGA.....	20	0	3	0.33	1	1	0	0	0	0
.....TGTAGAGTTTTCGGCTTGAAT.....	21	0	3	0.33	1	0	1	0	0	0
.....TTGTAGAGTTTTCGGCTTGAAT.....	22	0	3	0.33	1	0	0	1	0	0
.....TAGAGTTTTCGGCTTGAAT.....	19	0	3	0.33	1	1	0	0	0	0

Anti-sense strand reads

GTAAAAAGGTAGAAGCTAGGTAGCGGACTAATACTAGCGGACCAGTAAGTTTGGCTTTTTAGAGTGTTAAAACGGACGTTTTACATTTATAGATACCGTTAACATCTCAAAAGCCGAACTTAATGGTCCGCTAGTATTAGTCTTCGTCCGACGATGTCTTTTGGTTTGCTAGC **********(((((((((.(((((((.(((((((.(((.(((((..((((.....)))))))))))).)))))).)))))).)))))))))).....**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V107 male body**	**V108 head**	**M055 female body**	**M057 embryo**	**V040 embryo**	**V060 head**
.....GTAAGTTTGGCTTTTTAGAGTG.....	22	0	3	0.33	1	0	1	0	0	0	0
.....AGTGTTAAAACGGACGTT.....	18	0	20	0.05	1	0	0	0	0	1	0
.....AGAGTGTTAAAACGGACGTTTT.....	22	0	20	0.05	1	0	0	1	0	0	0
.....AACTTAATGGTCCGCTAGTA.....	20	0	20	0.05	1	0	1	0	0	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4644:2068962-2069134 -	der_142	CATTTTTCCATCTTCGA--T----------CCATCGCCTG-ATTATGATCGCCTGGTCAT-------TCAAACCGAAAAATCTCACAATTTTGCCTGCAAAA-TGT----------AAA-TATCTATGGCAA----------T--TGTAGAGTTTTCGGCTTGA--------ATTACCAGGCGATCATAA-TCAGAAGCAGGCTGCTACAG------AAAACCAA----------ACGATCG
droYak3	X:2729633-2729785 +		CACCTCCTGA-------A----------AATTTCTGTTCGCCTGGTATC------TGAAATTCGAAATATC--TGCATTTTTCGAACAAAA-CA----------AATGTCCGGTTTT-TGCGCATATTCGTTCTTTA--------TGCACCAGGCAATCATAA-TTAGCAGAAGGTGCTACTA------AAATCGAA----------ATGATCG
droSec2	scaffold_2513:1637-1812 -		ATCTTTCGACT-TTCGAATT----------CCTTC-TGGAATTCTTGTTCGCCTGGTAAT-------TAAACCGAAAAATATCTCAATTTGCCAACAAAA-TGC----------GCA-TTTTTGTGCAAAA----------TTTTTGGATCTTTCGACTTTA--------GATACCAGGCGATGATAA-TCAGTAGCGGGTGTCTACAG------AAAACCAA----------CTTTATTG
droSim2	node_28291:150-292 +		TGT----------A----------AATTTCTGTTCGCCTGGTAAT-------TAAACCGAAAAATCTCGCAATTTGCCTACAAAA-TGC----------GCA-TTTTTGTGCAAAA----------TTTTTGGATCTTTCGATTTA--------GATACCAGGCGATGATAA-TCAGTAGCGGGTGTCTACAG------AAAACCAA----------CTTTATCG
dm3	chrUextra:8418576-8418720 +		TGT----------A----------AATTTCTGTTCGCCTGGTAAT-------TAAAATCGAAAAATCAAACAATTTGCCCTAAAAAA-TAT----------GGT-TTTTTGTGGCAAA----------TTTTATAGATTTTTGGTTGCTT--------GTTACAAGGCGATCATAATTGAGTAGCAGGTGTATACTG------AAACCAA----------CAGATCG
droEug1	scf7180000404989:1053-1154 -		TTTCTC---ATTTTTGA--T----------A------AGG-GGTAACA--------TCATTCAAATTT-----GCGAAAAATCGCAAAATTTTA--------A---------A---A----------AC----A----------ATTTCA------AACA------TGTGAATG---A--------CAGTTTTTAAAG------AAA-TTAA----------AAAA--T
droBia1	scf7180000300910:1775406-1775595 +		CTTCTCTATAC------A----------A-GTAG-TAAGATTTCTGTTCGCCTGGTGGT--------TAAATCGAAAAATATCTTGGCTTGGCAGCCAAAA-GG-ACTGCCGAAAACACGAAAAACCCATGCCA-A----------TTCCTCGATTTCTAGATTGA--------AGTACCAGGCGAACAGAA-GACTTAGCAAGCGGCGATCAGCTGTT-A-A-----CTTCCAGGCAACATATAT
droTak1	scf7180000415909:89068-89229 +		AATTTTCCGATTTTGA--T----------A------ATG-ATCATGATTTTTGGTAAA-------AATAAATAAACCCATAATAATAAAATT--AAAAA-TGTTACTATC--------A---A-------GGTAA----------T--AGTTAATCCTTTTGTTAGCCTTCTAGT-------TGTAATTATAC-TTAAAATCCGTTTGCTCCCG------TAA-GT-A----------GTAACTT
droEle1	scf7180000491212:535721-535885 +		TT----------A----------AATGTCGCCTGGTGTT-------TCAAACCGACAAATCTTTCAAATTGACTGACAAAA-TCG----------ACA-C-------A-AATTGAACGTTTC-GAAGCAGGTTTTTCGATTTT--------GACACCAGGCCAACACAA-ATCCCAAGAAGGTGCTACTGGGCTCTAAGAACCAATTTCGCGGAGCCTCCCA
droRho1	scf7180000779334:60041-60253 +		TTTGTTGTAGC-TTTGCTGGTTAACGCAGAAAACTGATATTACGTATCCAG-TAATTTTTATGCTCGTCTAGTGTT-------GCAAAGCGATAAATCTA--AATTTGGTGTCAACTTGG-ACCGGCAAAACCAAATATTTCCCATGCAA-A---------C-TGCGCAACTTCCTATTTTGA--------AGCACCAGGCGAACATAAATGATCAGCAAGTAG--ACAG-------CGCCCCAA----------ACGAGTG
droFic1	scf7180000454055:921952-922017 -		AGTATTCCTTGTTTTGC--T----------A----------AG-GATTTTACCATAACATTTATTTT-------TAAATCGAAAAAATA---ATTTT----------A---A----------A---A----------A--A----------A--------A----------A----------A----------A----------A----------A----------A
droAna3	scaffold_13334:788715-788724 +		TTTTTTCCCA------A----------A----------A----------A----------A----------A---A----------A---A----------A----------A--A----------A--------A----------A----------A----------A----------A----------A
droBip1	scf7180000396423:583669-583674 +		CATTTT----------A----------A----------A----------A----------A---A----------A---A----------A----------A--A----------A--------A----------A----------A----------A----------A----------A
droWil2	scf2_1100000006624:509-521 -		CATTTTTCATTT-----A----------A----------A----------A----------A---A----------A---A----------A----------A--A----------A--------A----------A----------A----------A----------A----------A
droVir3	scaffold_10714:1177-1204 -		CATTTTCGAAC------A----------A-CAG-CCG-ATTTGATC---------A----------A---A----------A---A----------A----------A--A----------A--------A----------A----------A----------A----------A----------A

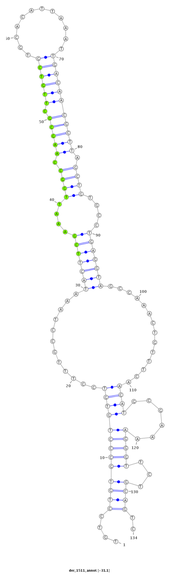
Generated: 09/08/2015 at 07:53 PM

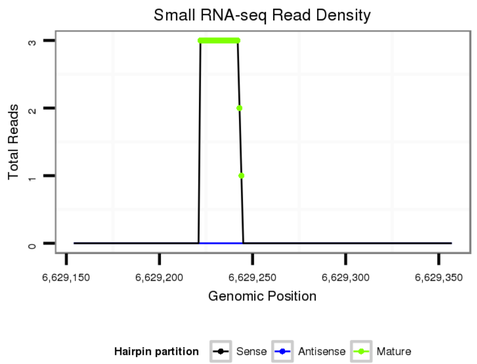
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	1

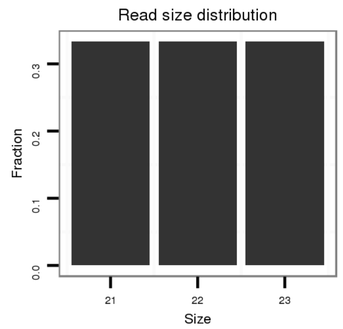
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_1511	**scaffold_4820:6629204-6629307 +**	**candidate**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser [Cornell Mirror]]

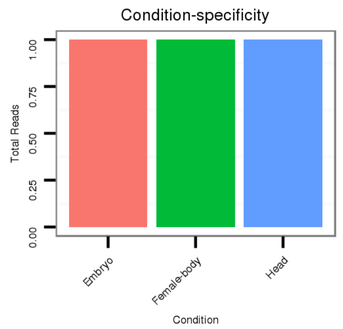
Legend: mature star mismatch in alignment mismatch in read

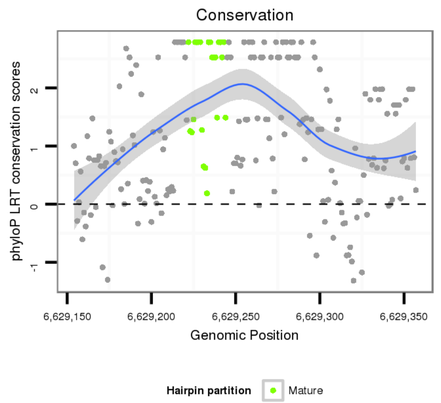
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dere\GG11413-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTGTGCCTGTATGCGTGTGTGCGTGTATCTGTGTCCTGTGCCCTGTGTCCTTGCCTAAATACTTCGAAATTGGCCAAGCGCTTGTCGTGCACATTAAATTGACAACGCTTAGCTGTGCCTGAGGTAGCCAAACTGTTTCAACATGCGAAAAGGGTTCTCGAGTCATCCTGTGCATCCTTGTGCCATGATTAAGGATTAA	Read size	# Mismatch	Hit Count	Total Norm	Total	female body	head	embryo	male body
**********....(((((((((((.....(((((((....(((((.(((((.(((((((.....)))))))))).)))))....)))))))..............))))))...)))))..**********									
.....TCGAAATTGGCCAAGCGCTTGTC.....	23	0	1	1.00	1	0	0	1	0
.....TCGAAATTGGCCAAGCGCTTG.....	21	0	1	1.00	1	1	0	0	0
.....TCGAAATTGGCCAAGCGCTTGT.....	22	0	1	1.00	1	0	1	0	0
.....GTGTGTGCGTGTGTATCTGTGT.....	22	0	9	0.11	1	0	1	0	0

Anti-sense strand reads

CACACGGACATACGCACACACACGCACACATAGACACAGGACACGGGACACAGGAAACGGATTTATGAAGCTTTAACCGGTTCGCGAACAGCACGTGTAATTTAACTGTTGCGAATCGACACGGACTCCATCGGTTTGACAAAGTTGTACGCTTTTCCCAAGACGTCAGTAGGACACGTAGGAACACGGTACTAATTCCTAATT	Read size	# Mismatch	Hit Count	Total Norm	Total	V107 male body	V108 head	M057 embryo
**********....(((((((((((.....(((((((....(((.(((((.(((((((.....)))))))))).)))))....)))))))..............))))))...)))))..**********									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_4820:6629154-6629357 +	der_1511	GTG----------T----------GCCTGT----ATGCGTGTGT-------GTGC-----GT----GTGTAT-------CTGTGTCC---TGTGCCCT---------GTGTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGCTTGTCGTGCA---CATTA-AATTGACAACGCTTAGCTGTGCCTGAGGTAGCC--AAACTGTTTCAACATGCG--AAAA--GGGTT----------CTGCC--A----------GTCATC-----CT--GTGCATCCTTG---TGCCAT---GATTAAGGATTAA
droYak3	3R:25065940-25066155 +	dya_69	GTG----------T----------GCGTGT----ATGCGTGCGT-------AGC-----GT----GTGTAT-------CTGTGTCC---TGTGCCCT---------GTGTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTGTTGTGTGCA---AATTG-AATTGACAACGCTTAGCTGTGCTGAGGTAGCC--AAACTGTTTCAACATGCG--AAAA--GGGTTCATCTG----------GC--G----------ATCATC-CTGTTGT--GTGCATCCTTGCCGTGCCAT---GATTAAGGATTAA
droSec2	scaffold_13:201139-201332 -	dse_150	GTG----------C----------GTCTGT----AGCGTGT-------AGC-----GT----GTGTAT-------CTGTGTCC---TGTGCCCT---------GTGTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTGTTGTGTGCA---CATTA-AATTGACAACGCTTAGCTGTGCTGAGGTAGCC--AAACTGTTTCAACATGCG--AAAA--GGGTT----------CCAA-A----------ATCATT-----CT--GTGCATCCTTG---TGCCAT---GATTAAGGATTAA
droSim2	3r:20925589-20925782 -	dsi_32434	GTG----------C----------GTCTGT----AGCGTGT-------AGC-----AT----GTGTAT-------CTGTGTCC---TGTGCCCT---------GTGTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTGTTGTGTGCA---CTTA-AATTGACAACGCTTAGCTGTGCTGAGGTAGCC--AAACTGTTTCAACATGCG--AAAA--GGGTT----------CTCA--A----------ATCATC-----CT--GTGCATCCTTG---TGCCAT---GATTAAGGATTAA
dm3	chr3R:21413194-21413387 -	dme_166	GTG----------C----------GTCTGT----AGCGTGT-------AGC-----GT----GTGTAT-------CTGTGTCC---TGTGCCCT---------GTGTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTGTTGTGTGCA---CATTA-AATTGACAACGCTTAGCTGTGCTGAGGTAGCC--AAACTGTTTCAACATGCG--AAAA--GGGTT----------CTCA--A----------ATCATC-----CT--GTGCATCCTTG---TGCCAT---GATTAAGGATTAA
droEug1	scf7180000409798:1138174-1138376 +		GTA----------T----------GTATGT----AGCGTGT-------AGC-----GT----GTGTAT-------CTGTGTCC---TGTGCCCT---------GTGTCCTTTGCCTAAATACTTCGAAATTGGCTTAAGCGTTGTTGTGTGCC---CATCA-AATTGACAACGCTTAGCTGTGCTGAGGTAGCC--AAATGTTTCAATCAT----C----C-----CATTATCTGCATCTGCATCTGCATCAGC----CT--CGGCATCCTTG---TGCCAT---GATTAAGGATTAA
droBia1	scf7180000302136:2259434-2259627 -		GCG----------A----------GCGTGT----AGCGTGT-------AGC-----GT----GTGTAT-------CTGTGTCC---TAGCTGCTGTGTGTACTTTGTTCCTTTGCCTAAATACTTCGAAATTAACCAAGCGTTGTTGTGTGCC---CATCA-AATTGACAACGCTTAGCTTTGCTTGAGGTAGCC--AAATGTTTCAACATGCG--AAGA--GGGTG----------CTG--A----------G---T-----GCTGCATCCTTG---TGCCAT---GATTAAGGATTAA
droTak1	scf7180000415257:293307-293509 -		GCG----------G----------GTG--TGT--GTGTGT-----GTGTATGC-----GT----GTGTATCT-----CTGTGTCC---TGT-----------AGTACTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGTGCC---CATCA-AATTGACAACGCTTAGCTTTGCTTGAGGTAGCC--AAAATGTTTCAACATTCG--AAGA--GGATT----------GTG-CTGCC--A----------TTATC-----CT--CTGCATCCTTG---TGCCAT---GATTAAGGATTAA
droEle1	scf7180000491280:3121519-3121725 -		GTA----------TGCGTTAGTGTGT-----TGTGTGTGTGGTGTGT--------GTGT-----GT----GTGTAT-------CTGTGTGCATGTGTGT-GT---------GTGTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGTGC---CATCA-AATTGACATCGCTTAGCTGTGCTGAGGTAGCC--AAAATGTATTCATCATGCA--AAAC--GGGTT----------CCAA-A----------ATCATC-----CT--CTGCATCCTTG---TGACAT---GATTAAGGATTGC
droRho1	scf7180000779501:512619-512790 +		GTA----------T-GC----------GTCATGT----AGCGTGT-------AGC-----GT----GTGTAT-------CTGTG---------GCCT---------GCGTCCTTTGCCTAAATACTTCGAAATTGGCTAAGCGTTTGTTGTGTGC---CATCA-AATTGACAACGCTTAGCTGTGCTGAGGTAGCC--AAAATGTTTCAACATTCA--AAGC--GGCG----------CCAA-A----------ATCTC-----CT--CTGCATCCTTG---TGCCAT---GATTAAGGATTAA
droFic1	scf7180000454055:1329823-1330026 -		GTAGATGA-----T----------GTCGCC---ATGTGTGCGTGTGCGTGTATG-------A-----AT----CCCCT-------GTGTGT---T---CCC-C---C---------CTGTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGTGC---CATCA-AATTGACAACGCTTAGCGTGCTGAGGTAGCC--AAAATGTATTCAACGAGCA--AAGC--GGGT----------GACAACGAGG----------ATTGCA-----CT--CTGCATCCTTC---TGCCAT---GATTAAGGATTAA
droKik1	scf7180000302639:1624816-1625000 +		GTG----------T----------GTGCGT----AGCGTGT-------GTGC-----G---C--CGC---------GTCGTT---T-----CCTGT---------GTGTG-TTTGCATAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGTGC---TATCA-AATTGACAACGCTTAGCTGTGCTGAGGTAGCC--AAAATGTTTCAACAGACGGAAGAGAGGGTG----------CGA-T-----------G---TG----CT--GCTGCATCCTTG---TGCACT---GATAAAGGATTAA
droAna3	scaffold_13340:3669011-3669172 -		GTG----------G----------GCCTAT----AGCGTGT-------CCGT-----GT----GTGTGT-------GTGTGTGA---TGA-----------A-GCGTGCCTAAATACTTCGAAATTGGCTAAGCGTTTGTTGTGTGAT---TATCA-AATTGACAAAGCTAAGCTGTGCTGAGGTAGCC--AAGATAAATCTACAA---C--CA--GGA----------CCAA-A----------ATCGT-----CT--CGTTGCATCCTTG---C-----C---CAGGATTAC
droBip1	scf7180000396712:683541-683700 +		GCG----------A----------GCCCAT----AGCGTGT-------GGC-----GT----GTGTGT-------GT-----C-----GTGTG---TGTGAGCGCTGCCTAAATACTTCGAAATTGGCTAAGCGTTTGTTGTGTGAT---TATCC-AATTGACAAAGCTAAGCTGTGCTGAGGTAGCC--AAGATGAATCTACAA---G--AA--GGA----------CCAA-A----------ATCGT-----CT--CGTTGCATCCTTG---T-----C---CAGGATTAC
dp5	2:21156495-21156751 -	dps_3835	CTGCTCTCTGTCTAGT-------GTGAGTGT----ATG-------CTGCATGTGTCACC--GTATCTGTAT-------CTGTATCC---TGTATCT---------CCGTGCTTGCGTTAAATACTTCGAAATTGGCTTAAGCGTTTGTTGTGCT---TATTA-AAGTGACAAAGCTTGCGCTGCTGAGGTAGCC-CTAATTGTATTCACAAAGG--ACA---CA----TCACCTGAAGAGGATGAGTGACACACATGACTGTGTGTGTGTGTGT----CA----TT----GT--GTGTGTACTTG---TGGGTGGGAGATCATGTACTAA
droPer2	scaffold_3:3930994-3931233 -	dpe_2496	GTG----------T----------GAGTGT----ATG-------CTGCATGTGTCACC--GTATCTGTAT-------CTGTATCC---TGTATCT---------CCGTGCTTGCGTTAAATACTTCGAAATTGGCTTAAGCGTTTGTTGTGCT---TATTA-AAGTGACAAAGCTTGCGCTGCTGAGGTAGCC-CTAATTGTATTCACAAAGG--ACA---CA----TCACCTGAAGAGGATGAGTGACACACATGACTGTGTGTGTGTGTGT----CA----TT----GT--GTGTGTACTTG---TGGGTGGGAGATCATGTACTAA
droWil2	scf2_1100000004943:14640085-14640209 +		TTA----------T----------GTGTGT----ATG-------GTGTTGTG---A---C----AAA---------GTGTGT---A---C----AGTGT---------GTGCAAAGTTCGAAATTGCATTAAGCGTTTGTTGTGTTCCATTTCA-ATTGACTATGCTTAGCTGTGCTGAGGTAGCCTCTAATTGTGTTC---------CA----CA----------CA----CA----------CA----CA----------CA----CA----------
droVir3	scaffold_12855:6808868-6808987 -	dvi_24643	TTG----------T----------GTGGT----GTGGTGT-------GTGT-----G---C--AAA---------GTGTGT---T-----GTGTG-CTTTCTAAATACTTCGAAATTGGCTTAAGCGTTTGTTGTGGCT---TATCA-AATTGACGACGCTTAGCTGTGCTGAGGTAGCC--TAATTGTTTCAACAAGCA--CA----CA----------CA----CA----------CA----CA----------CA----CA----------
droMoj3	scaffold_6540:25792867-25793004 +	dmo_3123	GTG----------T----------ACGTGT----AGCGTGT-------ATGT-----GA---GTGTGT-------GTGTGTGT---T---CGTGT---------GTGTACGTTGCTAAATACTTCGAAATTGGCTTAAGCGTTTGTTGTGTGC---TATCAAAATTGACAACGCTTAGCTGTGCTGAGGTAGCC--TAATTGTTTCAACAAGCA--CA----CA----------CA----CA----------CA----CA----------CA----CA----------
droGri2	scaffold_14906:2963137-2963258 -	dgr_468	GTG----------T----------GTGTGA----AGCGTGT-------GTGT-----GT---G----T-------GTGTG---T-------GTGTG---------GAGTACGGCGCTAAATACTTCTCAATTGGCTTAAGCGTTTGTTGTGCT---TATCA-AATTGACAACGCTTAGCTATGCTGAGGTAGCC--TAATTGTTTCAACAAGCA--CA----CA----------CA----CA----------CA----CA----------CA----CA----------

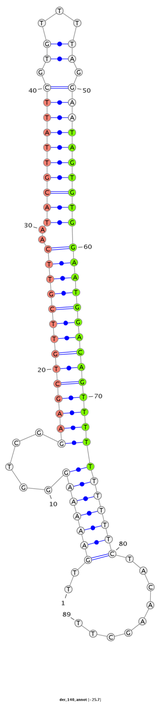
Generated: 09/08/2015 at 07:51 PM

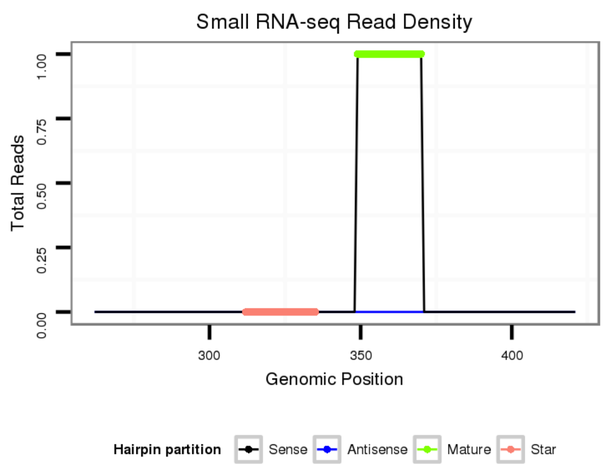
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	0
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	8

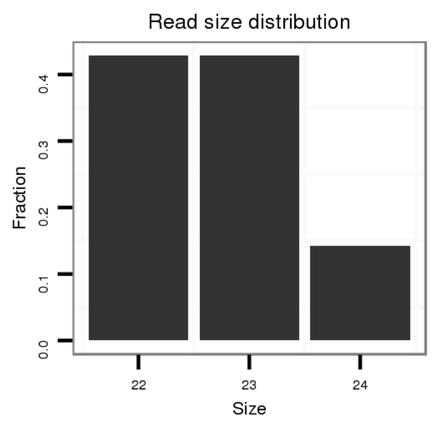
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
der_140	**scaffold_2603:312-371 +**	**candidate**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

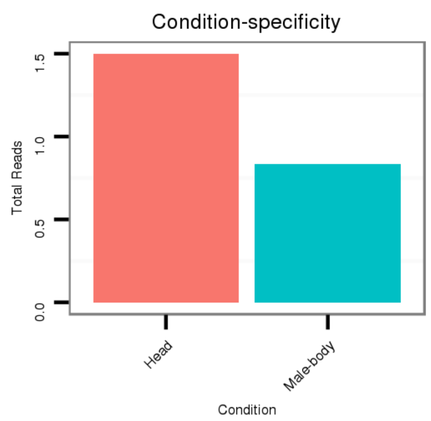
Legend: mature star **mismatch in alignment** mismatch in read

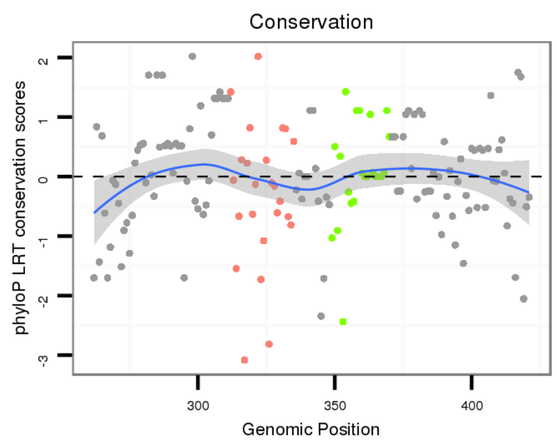
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

mature	star
1. der_140 scaffold_2603:349-370 + 2. scaffold_2603:550-571 +	1. der_140 scaffold_2603:312-335 + 2. scaffold_2603:513-536 + 3. scaffold_2603:714-737 +

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CTCGACTAGTGATCCGGAGTAGAAATAGATTTAGTTTGAAAAAGGGTCGGAAGCTGTTCGTTCAATACGTTATTCGTGTTTTAGGAATAGTGTGGAATGGACAGTTTTTTTTTTCTACAAGCTTAGCGCAAACTTTCTAGCTGATATTATACATTTTCCC **********..(((((((.....((((((((((((((..((((((((((.((...)).)))))))))))))))))))))))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V108 head	V107 male body	V040 embryo	M055 female body
.....TAGTGTGGAATGGACAGTTTTT.....	22	0	2	1.00	2	2	0	0	0
.....ATAGTGTGGAATGGACAGTTTTT.....	23	0	2	0.50	1	1	0	0	0
.....TAGTGTGGAATGGACAGTTTTTA.....	23	1	2	0.50	1	0	0	1	0
.....TAGTGTGGAATGGACAGTTTTTT.....	23	0	2	0.50	1	0	1	0	0
.....GCAAACTTTCTAGCTGAT.....	18	0	3	0.33	1	1	0	0	0
.....GAAGCTGTTCGTTCAATACGTT.....	22	0	3	0.33	1	0	0	0	1
.....AAGCTGTTCGTTCAATACGTTATT.....	24	0	3	0.33	1	0	1	0	0

Anti-sense strand reads

GAGCTGATCACTAGGCCTCATCTTTATCTAAATCAAACTTTTTCCCAGCCTTCGACAAGCAAGTTATGCAATAAGCACAAAATCCTTATCACACCTTACCTGTCAAAAAAAAAAGATGTTCGAATCGCGTTTGAAAGATCGACTATAATATGTAAAAGGG **********..(((((((.....((((((((((((((..((((((((((.((...)).)))))))))))))))))))))))))))))).....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M057 embryo	V040 embryo

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droEre2	scaffold_2603:262-421 +	der_140	CTCGACTAGTGATCCG----------GAGTAGAAATAGATTTAGTTT----------GAAAAAGGGTCGGAAGCTGTTCGTTCAATACGTTATTCGTGTTTTAGGAATAG----------TGTGGAATGGACAGTTTTTTTTTTCTACAAGCTTAGCGCAAACTTTC----------TAGCTGAT--ATTATACATTTTCCC
droYak3	2R:1041212-1041359 +		CTCGGCTATTGATCCT----------GATCAAGAATATATATACTTT----------AATATGGTCGGAAAGCTTCCTTCTGTCTGTTACATAC--TTTTCAACGAA----------TCTAGTATA--CC---CTTTTACTCTACGAGTAACGCGTATAATGAC-AAAATATCAAA-------AAAAAAAA-----ACATTTTTCA
droEug1	scf7180000408984:862906-863062 -		GAGGAGGCAGTTGTCGTTCTA---ATTTCG----------TGTTGGGCAACAACGTCTGTGGTAACGG-------GCT-ATTTCTGTTTTCTATGCTAG--------TTGCAAGTCTAATATTATCCGTTTCCAATCTGTTTTTTTCTATA----------CAGTTGCTGTTGGTTAAGTTTGGAG-------AAAAAAAA--ATT-----GGTTGGA
droBia1	scf7180000301549:3866-3933 +		CTCGACTAGTGACGCT----------GATCAAAAATATACATATTT----------AATGGGGTCGGAAAGTTCGTTTACTCGGTT----------TCTAGTATA--CC---CTTTTACTCTACGAGTAACGCGTATAAATAC------TCAAAA-------AAAAAAAA--ATTATTATTTTTGCC
droTak1	scf7180000415385:136103-136250 +		CTCGCCTAGTGATCCT----------GATCAAGAATATATATAGTTT----------AATAGGGTCGGAAAGCTTCCTTCTACCTGTTACATAC--TTTTGCACGAA----------TCTAGTATA--CC---CTTTTACTCTACGAGTAACGCGTATAAATAC------TCAAAA-------AAAAAAAA--ATTATTATTTTTGCC
droEle1	scf7180000491238:1099690-1099849 -		GTTGAGGCAGATGCACTTCCTGCTATTTCG----------TGTTGTGGCACAACTTCAGTTTCAACAGG-------ACT-ATGGCTGTTGTCTAGTGTAT--------TTGTAAGTCTTATATTATCCGTTTCCAGGCTATTTTTCGTAATA----------CAGTTGTTGTTGCTTATGTTTGGAA-------AAAAAAAA--ATT-----GGTTTGC
droRho1	scf7180000761866:4887-5042 +		CTCGCCTAGTGACCCT----------GATCAAGAATATATATACTTT----------AATAGGGTCGGAAAGCTTCCTTCTAGCTGTTACATAC--TTTTGCACGAA----------TATAATATA--CC---CTTTTACTCTACGAGTAACGCGTATAA----------AAATAATTAAAGTTGGTATAAC-TATATTTTCGC
droFic1	scf7180000454086:37460-37619 -		GTTGAGGCAGATGCGTTTTCTGGTATGTCG----------TGTTGAGCACCCACATCTGTGTTCACAGG-------ACT-ATTGCTGTTGTCGATTGTAT--------TTGCAAGTCTAATATTATCCGTTTCCAAGCTATTTTTGGACAGA----------CAGTTATTGTTGCTCACGTTCGGAG-------AAAAAAAA--ATT-----GGTTTGT
droAna3	scaffold_13045:745515-745691 -		GTCGAGGGGACGAGCACCTATTAATTCGTTTTCAGAACTGTGAACGTTTTGTTGAATAGTATCCGAAGTTATTGG-------TCT-AGTATTGGTCTCTATTGTAT--------CTAGAGATCTATTGTTTTCCGAATCCGAGTTACTTTTAGCTACGTCTC----------ATATGTTGGTCGTCACGTTGGGGG-------AAAAAAAA--AAC-----TAT----
droBip1	scf7180000395890:5107-5287 -		GTGAAGGGGACGTGGCACCTACTAATTCGTTTTCAGAACTGTGAACGTTTTGTGAAACAGTTTCTGTATTAATTGTGG-------TCT-ATTATTAGTCTCTATTGTAT--------CTAGAGATCTGTTGTTTTCCGAATCCGAGATACTTTTAGCTAAGTTTG----------ATATGTTGGTCGTCACGTTGGGAG-------AAAAAAAA--AAC-----TGTTTGC
dp5	Unknown_group_723:38-52 -		GTTGGGGTGAAGTAG----------|||||||||||||||||||||----------|||||||||||||||||||||----------|																			