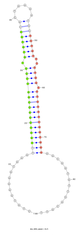
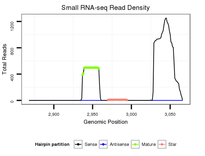
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dse_1841	**scaffold_2529:2918-3016 +**	**candidate-rescued**	**Canonical miRNA**	**intergenic**

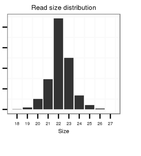
[View on UCSC Genome Browser (Cramd Mmm1)]

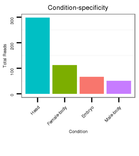
Legend: mature star mismatch in the mature mismatch in the star

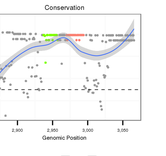
Predicted structure











Show Alternate Folds

Flybase annotation

dRNA:[Dsec]:FAMN:AAGGV000:RA]

No flyanotble element found

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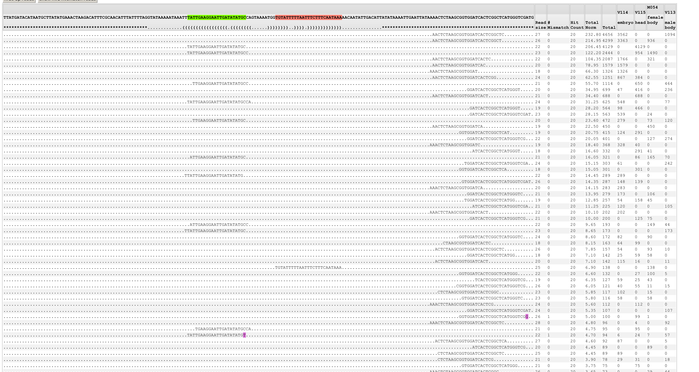
Sense Strand Reads

hide 3p reads | show mid mismatch reads



Anti-sense strand reads

No more available in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	SS	Alignment
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Generated 09/08/2015 at 07:56 PM

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
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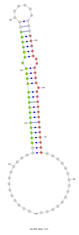
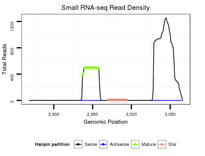
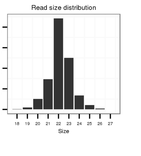
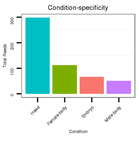
Legend: mature star mismatch in the mature mismatch in the star

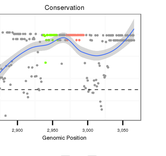
Predicted structure











Show Alternate Folds

Flybase annotation

dRNA:[Dsec]:FAMN:AAGGV000:RA]

No flyanotble element found

names	star
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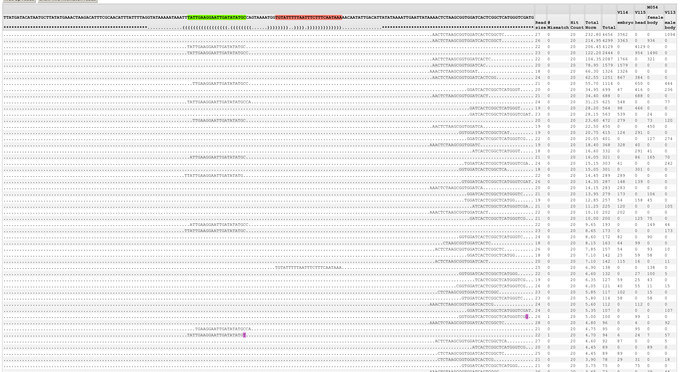
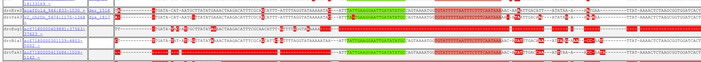
Sense Strand Reads

hide 3p reads | show mid mismatch reads



Anti-sense strand reads



No meta annotation in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment

Generated 09/08/2015 at 07:56 PM

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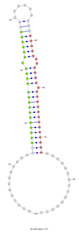

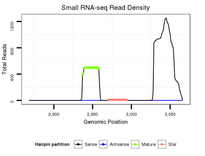

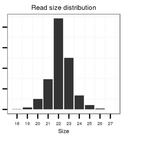

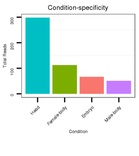

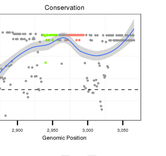

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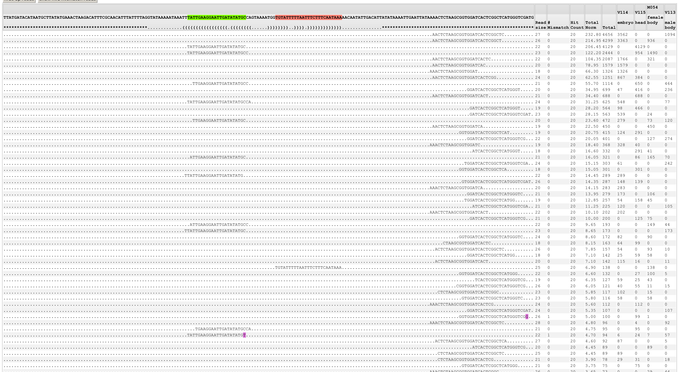
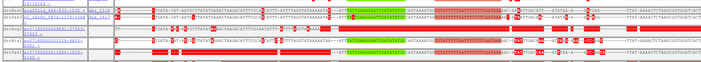
Sense Strand Reads

hide 3p reads | show mid mismatch reads



Anti-sense strand reads



No meta annotation in table

Show Alignment With Reads

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[View on UCSC Genome Browser (Cramd Mmm1)]

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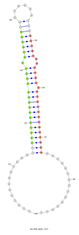
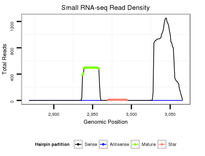
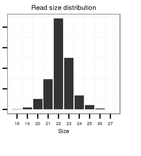
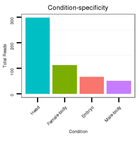
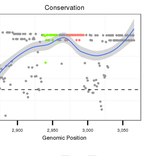
Predicted structure











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No flyanotble element found

names	star
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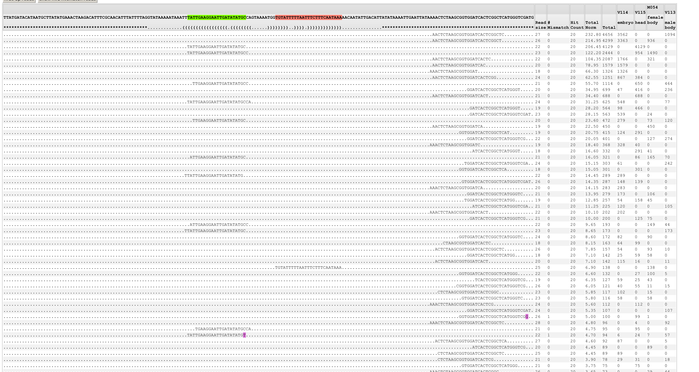
Sense Strand Reads

hide 3p reads | show mid mismatch reads



Anti-sense strand reads

No more available in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	SS	Alignment
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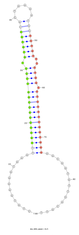
Generated 09/08/2015 at 07:56 PM

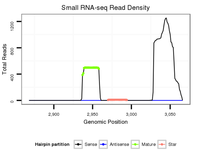
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dse_1841	**scaffold_2529:2918-3016 +**	**candidate-rescued**	**Canonical miRNA**	**intergenic**

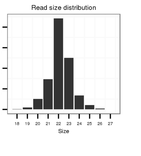
[View on UCSC Genome Browser (Cramd Mmm1)]

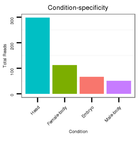
Legend: mature star mismatch in the mature mismatch in the star

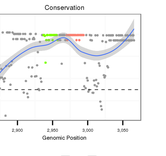
Predicted structure











Show Alternate Folds

Flybase annotation

dRNA:[Dsec]:FAMN:AAGGV000:RA]

No flyanotble element found

names	star
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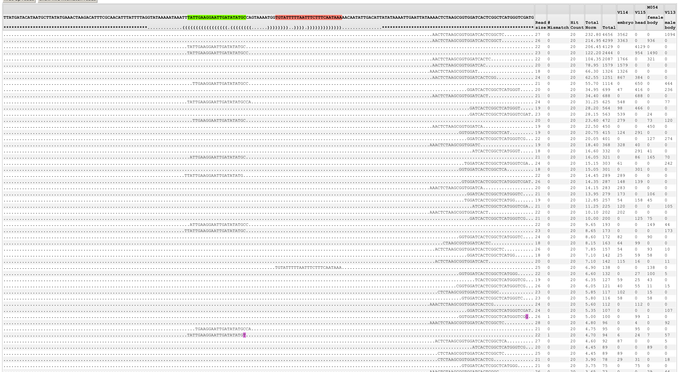
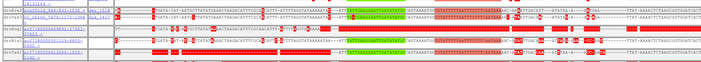
Sense Strand Reads

hide 3p reads | show mid mismatch reads



Anti-sense strand reads



No meta annotation in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment

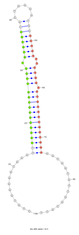
Generated 09/08/2015 at 07:56 PM

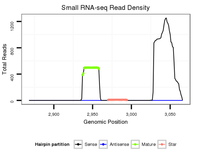
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dse_1841	**scaffold_2529:2918-3016 +**	**candidate-rescued**	**Canonical miRNA**	**intergenic**

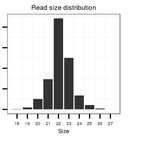
[View on UCSC Genome Browser (Cramd Mmm1)]

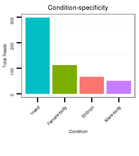
Legend: mature star mismatch in the mature mismatch in the star

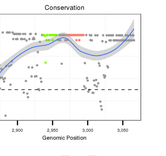
Predicted structure











Show Alternate Folds

Flybase annotation

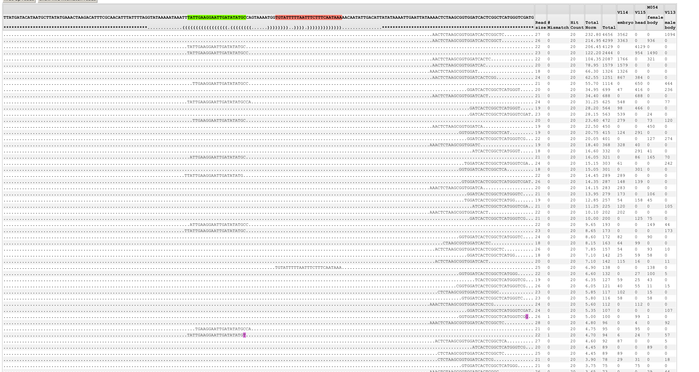
dRNA:[Dsec]:FAMN:AAGGV000:RA]

No flyanotble element found

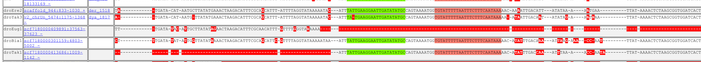
names	star
1. scaffold_39997301-3355 - 2. scaffold_39997301-3355 + 3. scaffold_9669324-3285 - 4. scaffold_13091218-3339 - 5. scaffold_13091218-3339 + 6. scaffold_71958324-3343 - 7. scaffold_4881988-3929 - 8. scaffold_28261328-3467 - 9. scaffold_8107747-3492 - 10. scaffold_8107747-3492 + 11. scaffold_8495488-916 - 12. scaffold_8404413-3456 - 13. scaffold_8404413-3456 + 14. scaffold_8627184-1285 - 15. scaffold_13039128-3412 - 16. scaffold_13039128-3412 + 17. scaffold_2861879-3382 - 18. scaffold_12857484-882 - 19. scaffold_12857484-882 + 20. scaffold_13084-3443 - 21. scaffold_3066158-3761 - 22. scaffold_4364298-3352 - 23. scaffold_7389184-3384 - 24. scaffold_7389184-3384 + 25. scaffold_31631881-3398 - 26. scaffold_30320160-381 - 27. scaffold_30320160-381 + 28. scaffold_7555651-3421 - 29. scaffold_3655128-139 - 30. scaffold_3655128-139 + 31. scaffold_8695392-4454 - 32. scaffold_6354-8932-3873 - 33. scaffold_8457282-3286 - 34. scaffold_18086-388-387 - 35. scaffold_18086-388-387 + 36. scaffold_31299728-3781 - 37. scaffold_1557171-94 - 38. scaffold_1557171-94 + 39. scaffold_12638-928-329 - 40. scaffold_13379326-3477 - 41. scaffold_13379326-3477 + 42. scaffold_4778799-820 - 43. scaffold_7865-8845-3866 - 44. scaffold_33331482-3383 - 45. scaffold_7864-843-3866 - 46. scaffold_7864-843-3866 + 47. scaffold_8273-8825-3946 - 48. scaffold_6447-452-473 - 49. scaffold_6447-452-473 + 50. scaffold_8638185-3228 - 51. scaffold_7027-2295-3280 - 52. scaffold_7027-2295-3280 + 53. scaffold_31892307-838 - 54. scaffold_33354-684-422 - 55. dse_1841 scaffold_2529:2951-3908 - 56. scaffold_8602-1668-3387 - 57. scaffold_8602-1668-3387 + 58. scaffold_7140-763-786 - 59. scaffold_7795-8128-3449 - 60. scaffold_7795-8128-3449 + 61. scaffold_6266-574-1997 - 62. scaffold_18073446-647 - 63. scaffold_18073446-647 +	1. dse_1841 scaffold_2529:2938-2986 + 2. scaffold_39997301-3355 - 3. scaffold_39997301-3355 + 4. scaffold_13047440-364 + 5. scaffold_71958324-3343 - 6. scaffold_71958324-3343 + 7. scaffold_30364-5256 -3280 + 8. scaffold_28261328-3467 - 9. scaffold_28261328-3467 + 10. scaffold_8107747-3492 - 11. scaffold_8107747-3492 + 12. scaffold_8457282-3286 - 13. scaffold_8457282-3286 + 14. scaffold_8627184-1285 - 15. scaffold_13039128-3412 - 16. scaffold_13039128-3412 + 17. scaffold_2861879-3382 - 18. scaffold_12857484-882 - 19. scaffold_12857484-882 + 20. scaffold_13084-3443 - 21. scaffold_3066158-3761 - 22. scaffold_4364298-3352 - 23. scaffold_7389184-3384 - 24. scaffold_7389184-3384 + 25. scaffold_31631881-3398 - 26. scaffold_30320160-381 - 27. scaffold_30320160-381 + 28. scaffold_7555651-3421 - 29. scaffold_3655128-139 - 30. scaffold_3655128-139 + 31. scaffold_8695392-4454 - 32. scaffold_6354-8932-3873 - 33. scaffold_8457282-3286 - 34. scaffold_18086-388-387 - 35. scaffold_18086-388-387 + 36. scaffold_31299728-3781 - 37. scaffold_1557171-94 - 38. scaffold_1557171-94 + 39. scaffold_12638-928-329 - 40. scaffold_13379326-3477 - 41. scaffold_13379326-3477 + 42. scaffold_4778799-820 - 43. scaffold_7865-8845-3866 - 44. scaffold_33331482-3383 - 45. scaffold_7864-843-3866 - 46. scaffold_7864-843-3866 + 47. scaffold_8273-8825-3946 - 48. scaffold_6447-452-473 - 49. scaffold_6447-452-473 + 50. scaffold_8638185-3228 - 51. scaffold_7027-2295-3280 - 52. scaffold_7027-2295-3280 + 53. scaffold_31892307-838 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads



Anti-sense strand reads



No meta annotation in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

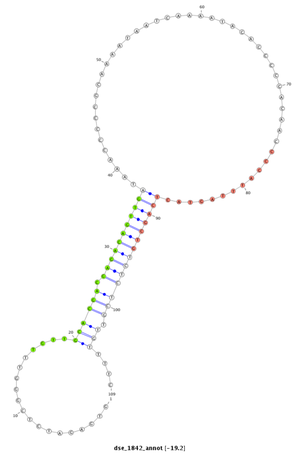
Species	Coordinate	ID	Alignment

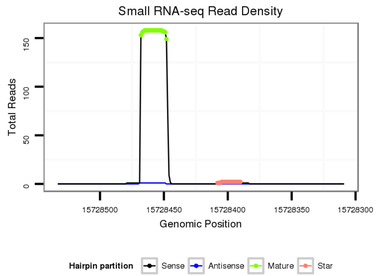
Generated 09/08/2015 at 07:56 PM

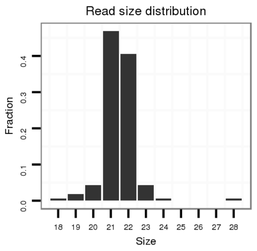
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1842	**scaffold_0:15728359-15728483 -**	**candidate-rescued**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser: [Cornell Mirror1]]

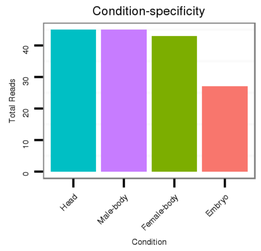
Legend: mature star mismatch in alignment mismatch in read

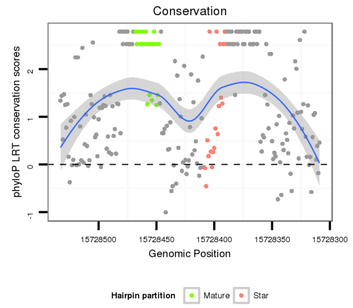
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dsec/GM23880-in]; utr5 [utr5_plus_10181]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATGTGTATCTATATATGTATCTATAAAGTGTCCAGAGTTGTCAAGCGTCAGTGAGATCTCGGGTTTGTTGCACGACGAGACAGTTGATAAACCCCCGCAAAATAATCAAAATACACCCCCACAACCCCATTTAGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGCCATCGAATTGAAGACATTGACCCAGTGATTAGTTATATTAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V113 male head	V115 female body	M054 female body	V114 embryo
**********.....((((((.((((((((((.....)))))))))).)))....**********										
.....TGTTGCACGACGAGACAGTTG.....	21	0	1	74.00	74	29	23	15	7	
.....TGTTGCACGACGAGACAGTTGA.....	22	0	1	63.00	63	8	14	22	19	
.....TGTTGCACGACGAGACAGTT.....	20	0	1	7.00	7	3	3	1	0	
.....TGTTGCACGACGAGACAGTTGAT.....	23	0	1	6.00	6	3	2	1	0	
.....TGTTGCACGACGAGACAGTTGC.....	22	1	1	4.00	4	2	2	0	0	
.....GTTGCACGACGAGACAGTTGAT.....	23	1	1	2.00	2	1	1	0	0	
.....GTTGCACGACGAGACAGTTGA.....	22	0	1	1.00	1	0	1	0	0	
.....TGTTGCACGACGAGACAGTTGG.....	22	0	1	1.00	1	0	1	0	0	
.....TGTTGCACGACGAGACAGT.....	19	0	1	1.00	1	0	1	0	0	
.....TGTTGCACGACGAGACAGTTGATA.....	24	0	1	1.00	1	1	0	0	0	
.....TTGCACGACGAGACAGTTG.....	19	0	1	1.00	1	0	1	0	0	
.....CCCATTTAGTACTCAGCTG.....	19	0	1	1.00	1	0	0	0	1	
.....GTTGCACGACGAGACAGTTGATA.....	23	0	1	1.00	1	0	0	1	0	
.....TGCACGACGAGACAGTTG.....	18	0	1	1.00	1	0	0	1	0	
.....ATTTAGTACTCAGCTGTCTCTC.....	22	0	1	1.00	1	0	0	1	0	

Anti-sense strand reads

TACACATAGATATACATAGATATTTCACAGGTCTCAACAGTTCGCAGTCACTCTAGAGCCCAACACAACGTGCTGCTCTGTCAACTATTTGGGGGCGTTTTATTAGTTTTATGTGGGGGTGTTGGGGTAAATCATGAGTCGACAGAGACAACAAAGCTAAAGCCCTAGAACTGTTGCTGCGGTAGCTTAACTTCTGTAACTGGGTCACTAATCAATATAATT	Read size	# Mismatch	Hit Count	Total Norm	Total	V115 head	M054 female body	V114 embryo
**********.....((((((.((((((((((.....)))))))))).)))....**********									
.....AACAACGTGCTGCTCTGTCAA.....	21	0	1	1.00	1	1	0	0	

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_0:15728309-15728533 -	dse_1842	ATGTGTA---------TCTAT-ATA------TGTAT---------CTATA---------AA-----GTGTCCAG------AGTT--GT---------CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGTAAAC-CCCC---------GCAAAA--TAATCAA---------AA--TACACCCCACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC----CATCGA------ATTGAAGACATTG------ACCCAG---------T--GATTA----GTTAT----ATTAA
droSim2	3r:14862265-14862489 -	dsi_32452	ATGTGTA---------TCTAT-ATA------TGTAT---------CTATA---------AA-----GTGTCCAG------AGTT--GT---------CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAAC-CCCC---------GCAAAA--TAATCAA---------AA--TACACCCCACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC----CATCGA------ATTGAAGACATTG------ACCCAG---------T--GATTA----GTTAT----ATTAA
dm3	chr3R:6216920-6217149 +	dme_373	ATGTGTA---------TCTAT-ATA------TGTAT---------CTATA---------AA-----GTGTCCAG------AGTT--GT---------CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAAC-CCCC---------GCAAAA--TAATCAA---------AA--TACACCCCACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC----CATCGA------ATTGAAGACATTG------ACCCAG---------T--GATTA----GTGAT----ATTAA
droEre2	scaffold_4770:15403301-15403535 -	der_1519	ATGTGTA---------TCTAT-ATATGTATCTGTAT---------CTATA---------AA-----GTGTCCAG------AGTT--GT---------CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAAC-CCCC---------GCAAAA--TAATAA---------AA--TACACCCCACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC----CATCGA------ATTGAAGACATTG------ACCCAG---------T--GATTA----GTGAT----ATTAA
droYak3	3R:10242680-10242915 +	dya_1794	ATGTGTACCATGTACAAGTAT-ATA------TGTAT---------CTATA---------AA-----GTGTCCAG------AGTT--GT---------CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAAC-CCCC---A---------GCAAAA--TAATCAA---------AA--TACACCCCACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC----CATCGA------ATTGAAGACATTG------ACCCAG---------T--GATTA----GTGAT----ATTAA
droEug1	scf7180000409692:687963-688195 +		ATGTGTA---------TCTAT-ATA------TGTAT---------CTATA---------AA-----GTGTCCAG------AGTT--GT---------CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAAC-CCCC---TTT--G---------TATA---------AAAA---AGATAA---------TC--TACACC--CACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACG----TGATCA---TTTGAAGACCGTG------ACCCAG---------T--GATTA----GTGAT----ATTGA
droBia1	scf7180000302402:8304620-8304856 +		ATGTGTA---------TCTAT-ATA------TGTAT---------CTATA---------AA-----GTGTCCAG------AGTT--GT---------CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAAC-CCCC---GCTCCGAG---------T--GCA---GAAAAAAAC----AA---------AA--TAC-AACCACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC----CTCGA---TTCGATCCGAAGAGCCGTG------ACCCAG---------T--GATTA----GTGAT----ATTGA
droTak1	scf7180000415380:1425635-1425858 -		ATGTGTA---------TCTAT-ATA------TGTAT---------CTATA---------AA-----GTGTCCAG------AGTT--GT---------CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAAC-CCCC---C---------A-CAAGTAAAAC----AA---------AAGCACACC--CACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC----CATCGA---TTTGATCTGAAGACCGTG------ACCCAG---------T--GATTA----GTGAT----ATTGA
droEle1	scf7180000490995:524589-524803 -		ATGTGTA---------TCTAT-ATA------TGTAT---------CTATA---------AA-----GTGTCCAG------AGTT--GT---------CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAAC-CCCC---C---------A-CAAGTAAAAC----AA---------AA--TACACCCCACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC----CATCGA---TTGAAGACCGTG------ACCCAG---------T--GATTA----ATGGA----ATTGA
droRho1	scf7180000777158:35501-35710 -		ATGTGTA---------TCTAT-ATA------TGTAT---------CTATA---------AA-----GTGTCCAG------AGTT--GT---------CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAAC-CCCC---C---------A-CAAGTAAAAC----AA---------AA--TACACCCCACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC----CATCGA---TTGAAGACCGTG------ACCCAG---------T--GATTA----GTGAT----ATTGA
droFic1	scf7180000453809:2293368-2293586 +		ATGTGTA---------TCTAT-ATA------TGTAT---------CTATA---------AA-----GTGTCCAG------AGTT--GT---------CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAAC-CCCC---C---------A-CAAGTAAAAC----AA---------AA--TACACCCCACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC----CATCGA---TTTGAAGACCGTG------ACCCAG---------T--GATTA----GTGAT----ATTGA
droKik1	scf7180000302475:1404666-1404904 +		ATGCGCA---------CCAT-ATA------TGTAT---------CGTCG---------AA-----GTGTCCAG------AGTT--GT---------CAAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAAC-CCCC---C---------GC-ACATG---------G---------GAAAC----AAAATAATAAA-ATATA---AA--TACGCCCCACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC----CTAGGA---CGATCGAAAGACCGTG------ACCCAG---------T--GATTA----GTGTT----ATTGA
droAna3	scaffold_13340:938685-938923 +	dan_4037	ATGTGTA---------TCTCA-ATA------TGTAT---CCACAAGAT---------AAAA----ACAGATA---CA----GTGCTAT---------GT--GT---------CAGCGCC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAAC-CCGC---GT----C---------GGGGAGCCC---------GTC--AAC----AAAGACAAACAG---CC--CAGT---CCCA-AATA-CAA--AATAGCGAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGCGCAT---CATCGA---------TAA---------------AG---------T--GATTA----TTTC----GTTCGC
dp5	2:7251726-7252027 +	dps_3825	ATGTGTA---------TCTAT-ATA------TGTGTGTGTGCGAGAGAGTGTACGAGAGTATACT---------CA----ATCTATAG---------AGTT--GT---------CAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAAC-CCCC---C---------A-CAAGCC---------G---------GAGGAGGAGC---CC--G---------CCTTCCCAGCAGACGCCATTGTGATGATGTTGTTGATGATGATGAGGAGGAGC---AGAGAA---------GGAGGAGGAC---CC--G---------CTTCCACTTGCCAACGCGAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGCAACGACGC----CATCAA---------CATTGAACCA---------CAATAATATA
droPer2	scaffold_0:1112328-1112621 -	dpe_2419	ATGTGTA---------TCTAT-ATA------TGTGTGT--GTGCGAGAGAGTGTACGAGAGTATACT---------CA----ATCTATAG---------AGTT--GT---------CAGCGTC-AGTGAGATCTCGGGTTGTTGCACGACGAGACAGTTGCTAAAC-CCCC---C---------A-CAAGCC---------G---------GAGGAGGAGC---CC--G---------CCTTCCCAGCAGACGCCATTGTGAT---GTTGATGATGATGATGAGGAGGAGC---AGAGAA---------GGAGGAGGAC---CC--G---------CTTCCACTTGCCAACGCGAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGCAACGACGC----CATCAA---------CATTGAACCA---------CAATAATATA
droWil2	scf2_1100000004902:91563-91759 -	dwi_5414	ATGTGTA---------TCTCA-TA------TCGT---------TT---GCCC---GT---------CA----ATCTATAG---------AGTT--GT---------CAAGCGTC-GTAGAGATCTCGGGTTGTTGCACGAGCAGCCGCTAAAC-CCCC---CCTT---GCC---------A---------ACACCCT---------CTT---TGC----ATGGTAAATAC---CT--CCT---TT-GAAATTG-TAATATTAGCGCGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTATTAAGA----C---------CCCAG---------T--GATTA----GTGAT----ATTGA
droVir3	scaffold_13047:936843-937029 -	dvi_125	ATGTGTA---------TCTAC-ATA------TGTAT---------CA----ATCTATAG---------AGTT--GT---------CAAGCGTC-GTAGAGATCTCGGGTTGTTGCACGACGAGCCAGCTGCTAAAC-CCCC---CCTT---GCC---------A---------ACACCCT---------CTT---TGC----ATGGTAAATAC---CT--CCT---TT-GAAATTG-TAATATTAGCGCGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGCTAGAGAACGGATCCGAA---CCA---------TCC--GCGCGG---------C---------GATAA----GTGAT----ATTGA
droMoj3	scaffold_6540:4939653-4939874 -	dmo_129	GTATGTA---------TCTCT-ATA------TGTAT---------CATGTATATTCCTGAACAAGGA---------GTGT---------GTTT---GT---------CAAAAAATATTGTGAGATCTCGGGTTGTTGCACGACGAGCCAGCTGCTCGCTAAAC-CCCC---A---------A-CAAGTAAAAC----AA---------AA--TACACCCCACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGACAACGACGC----CATCGA---TTGAAGACCGTG------ACCCAG---------T--GATTA----GTGAT----ATTGA
droGri2	scaffold_14906:5355374-5355618 +	dgr_461	ATGTGTA---------TCTAT-ATA------TGTAT---------CATATATGTTT---------AGGA-----GTGT---CATGTAATTGGCT-GGTTTAGATATATATATATATATATGTATTATATTGTGAGATCTCGGGTTGTTGCACGACGTGCAGCTGCTCGCTAAAC-CCCC---A---------A-CAAGTAAAAC----AA---------AA--TACACCCCACAACCCCATTT--AGTACTCAGCTGTCTCTCGTTGTTTTCGATTTCGGGATCTTGATTGTGCGCTGACCTTATA-TA---------ACCAATATATCA---------ACTATT---------G---TACCA----A-TA---------ACCAA

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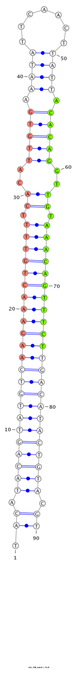
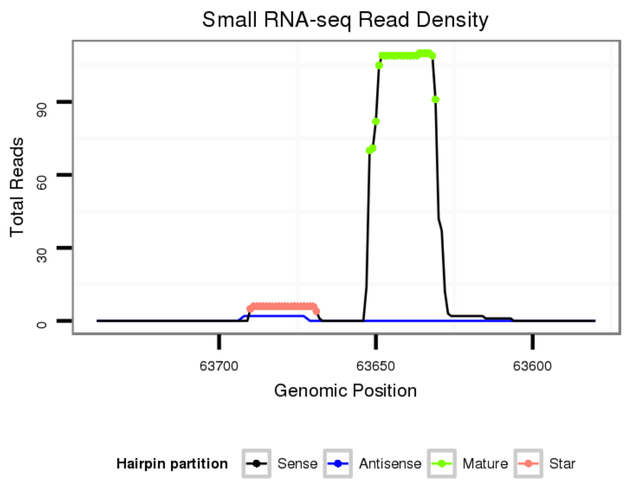
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.mid3	1
crit.top3	1
crit.tptop3	1
crit.uni	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	3
rescue.candidate	9

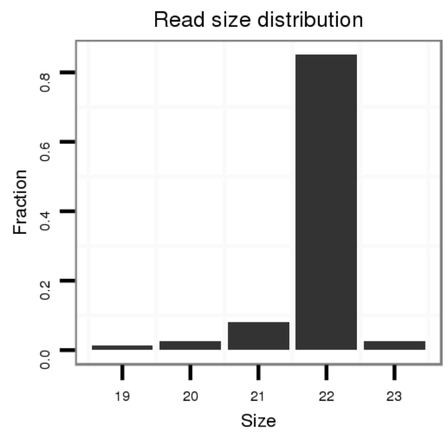
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_208	**scaffold_61:63630-63689 -**	**candidate-rescued**	**Canonical miRNA**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

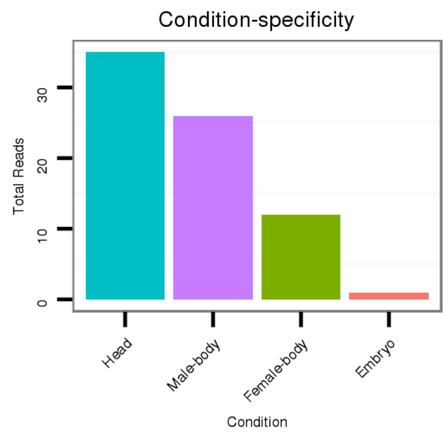
Legend: mature star mismatch in alignment mismatch in read

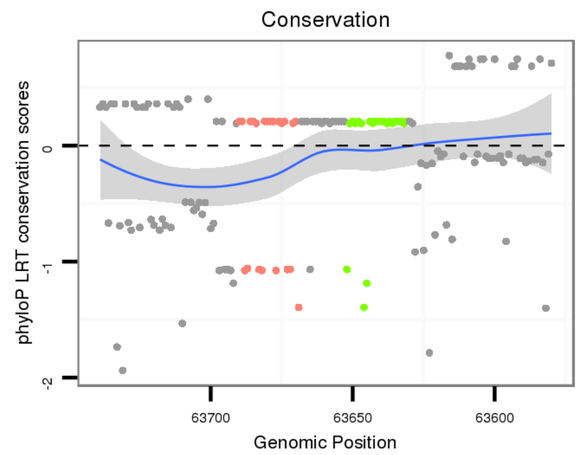
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

Repeatable elements

Name	Class	Family	Strand
S_DM	DNA	TcMar-Tc1	-

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTGCTTGTTAAGACTGCATAACTGTTGACATATTTACATACAGTATGTCAAGAAACTGTTTTCACATTGTGAAATATTCAACTTATTACACAGGTTGTAAACAGTTTCTTGACATACTGTACGTAGGGCCACGTAACCCTGTCTAGCTCCAAGGGATCAG **********.((.((((((((((((((((((((((((.((..(((((.((((.......)))).)))))..)).)))))))))))))))))))))).))**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V115 head	V113 male body	M054 female body	V114 embryo
..........ACACAGGTTGTAAACAGTTTCT..........	22	0	1	49.00	49	24	20	5	0
..........TACACAGGTTGTAAACAGTTTC..........	22	0	1	14.00	14	7	4	2	1
..........CAGGTTGTAAACAGTTTCTTG..........	21	0	1	12.00	12	6	2	4	0
..........ACAGGTTGTAAACAGTTTCTTG..........	22	0	1	10.00	10	5	3	2	0
..........CAGGTTGTAAACAGTTTCTTGA..........	22	0	1	9.00	9	4	0	5	0
..........ACACAGGTTGTAAACAGTTTC..........	21	0	1	4.00	4	3	1	0	0
..........AGGTTGTAAACAGTTTCTTG..........	20	0	1	3.00	3	1	1	1	0
.....AAGAAACTGTTTTCACATTGT..........	21	0	1	2.00	2	0	1	1	0
.....AAGAAACTGTTTTCACATTGTG..........	22	0	1	2.00	2	0	0	2	0
..........ACACAGGTTGTAAACAGTTTCTT..........	23	0	1	2.00	2	0	1	1	0
..........CAGGTTGTAAACAGTTTCTT..........	20	0	1	2.00	2	1	0	1	0
.....AGAAACTGTTTTCACATTGTG..........	21	0	1	1.00	1	0	0	1	0
.....AAGAAACTGTTTTCACATTGTGA..........	23	0	1	1.00	1	1	0	0	0
..........ACATACTGTACGTAGGGCCACG..........	22	0	1	1.00	1	1	0	0	0
..........ACACAGGTTGTAAACAGTTTCC..........	22	1	1	1.00	1	1	0	0	0
..........AGGTTGTAAACAGTTTCTTGAC..........	22	0	1	1.00	1	0	0	1	0
..........CACAGGTTGTAAACAGTTT..........	19	0	1	1.00	1	0	0	1	0
..........CAGGTTGTAAACAGTTTCTTGT..........	22	1	1	1.00	1	0	1	0	0
.....AGAAACTGTTTTCACATTGTGT..........	22	1	1	1.00	1	1	0	0	0
..........ACAGGTTGTAAACAGTTTCTT..........	21	0	1	1.00	1	0	0	1	0
..........ACACAGGTTGTAAACAGTTTCTTG..........	24	0	1	1.00	1	1	0	0	0
..........GTTTCTTGACATACTGTACGT..........	21	0	1	1.00	1	0	1	0	0
..........ACAGGTTGTAAACAGTTTCTTGT..........	23	1	1	1.00	1	0	1	0	0
..........TACACAGGTTGTAAACAGTTTCCA..........	24	2	1	1.00	1	1	0	0	0
.....CATACAGTATGTCAAGAAACT..........	21	0	9	0.33	3	2	1	0	0
.....ATACAGTATGTCAAGAAACT..........	20	0	16	0.06	1	1	0	0	0

Anti-sense strand reads

CACGAACAATTCTGACGTATTGACAACTGTATAAATGTATGTCATACAGTTCTTTGACAAAAGTGTAACACTTTATAAGTTGAATAATGTGTCCAACATTTGTCAAAGAACTGTATGACATGCATCCCGGTGCATTGGGACAGATCGAGGTTCCCTAGTC **********.((.((((((((((((((((((((((((.((..(((((.((((.......)))).)))))..)).)))))))))))))))))))))).))**********	Read size	# Mismatch	Hit Count	Total Norm	Total	M054 female body	V114 embryo	V115 head
.....CAGTTCTTTGACAAAAGTGTAA..........	22	0	1	1.00	1	1	0	0
.....AGTTCTTTGACAAAAGTGTA..........	20	0	1	1.00	1	0	1	0
.....ATGTATGTCATACAGTTCTTT..........	21	0	9	0.11	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_61:63580-63739 -	dse_208	----------GTGCTTGTTAAGACTGCATAACTGTTGACATATTTACATACAGTATGTCAAGAAAC----TGTTTTCAC----ATTGTGAAATATTCAACTTATTACACAGGTTGTAAACAGTTTCTTGACATACTGTACGTAGGGCCACGTAACCCTGTCTAGCTCCAAGGGATCAG
droSim2	31:23802685-23802844 -	dsi_32294	----------GTGCTTGTTAAGACTGCATAACTGTTGACGTATTTACATACAGTATGTCAAGAAAC----TGTTTTCAC----ATTGTGAAATATTCAACTTATTACACAGGTTGTAAACAGTTTCTTGCCATACTGTACGTAGGGCCACGTAACCCTGTCTAGCTCCAAGGGATCAG
dm3	chr2R:1308629-1308737 -	dme_450	TGAA----------AAAATTGGGTTCAATTAAGCAAAGAACCCTTAATTTTACCTTTAAAGTCAAAAATTCAACTTATTTCACAGCGTGTAAACAGTTTCTTGACAAACTGTATATA----------G
droEre2	scaffold_4784:24170629-24170717 +		----------GTGCTTTCGAAGACGGCACTACAATGGACGTATTAACATAT----------T----------T----------TATAATATGTATAGGGTCACCTAATCTTGAGAAGCTCTAAGGGATGAG
droYak3	v2_chr2L_random_028:1161793-1161926 +		AAGGTCAAAACTTTAATTATTGAAAGCCTGGGGGAGTTGTAAGACAATTTGCGGTGTTTATCAGTACGGCACAAAAGTGGAGCGTATGTAAATT----------T----------T----------ACGTGTCGGGTCACCCAATTCTAAGAGGCTTCAAGTTATATG
droTak1	scf7180000414548:4789-4841 -		ACAC----------T----------T----------AGTATTCGTGTGTCGGGTCACCTAATCCTGAGGAGCTCCTGGGAAAAG
droRho1	scf7180000780139:388-438 -		ACAC----------T----------T----------AATGTATGTGTCGGGTCACCTAATCCTGAGGAGCTCCTAGGGAAAAG

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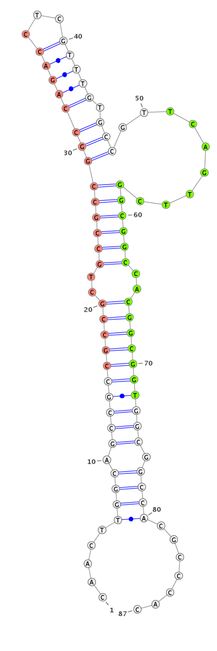
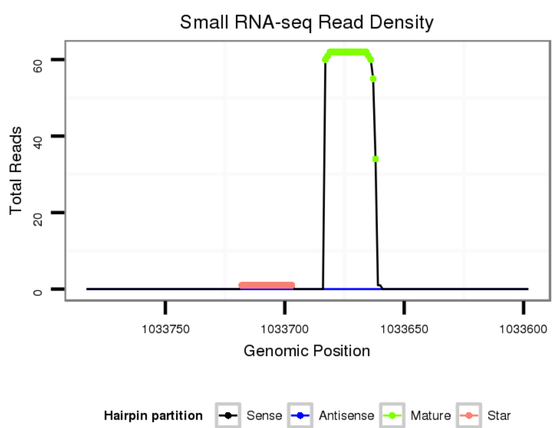
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	0
crit.tptop3	0
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	1

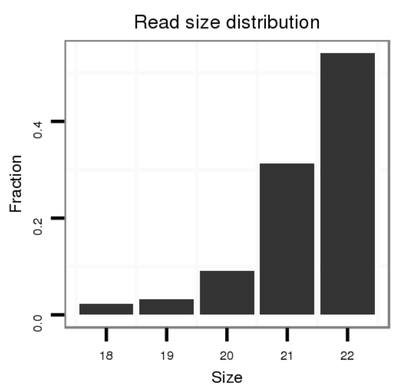
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1834	**scaffold_6:1033648-1033733 -**	**candidate-rescued**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser {Cornell Mirror}]

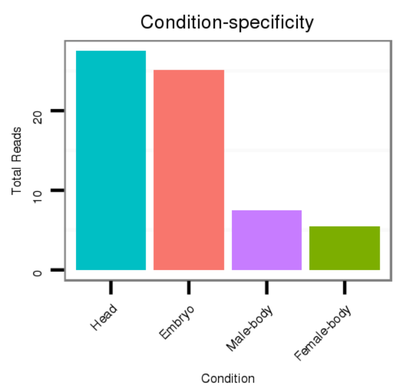
Legend: mature star mismatch in alignment mismatch in read

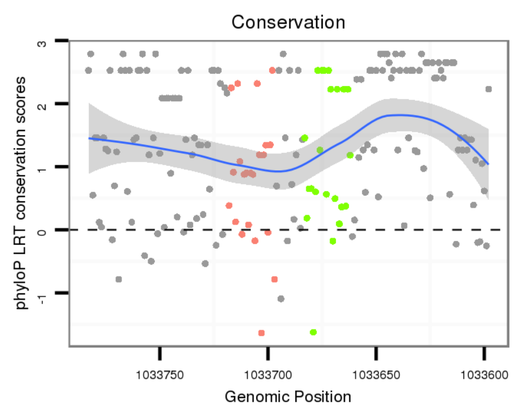
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dsec\GM10664-cds]; intron [Dsec\GM10664-in]; utr3 [utr3_minus_6709]; CDS [Dsec\GM10664-cds]

Repeatable elements

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

mature	star
1. dse_1834 scaffold_6:1033662-1033683 - 2. scaffold_6:1034600-1034621 -	1. dse_1834 scaffold_6:1033697-1033718 - 2. scaffold_6:1034635-1034656 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CAGTACTTGCGGTCTCAGCGGATGCACCCGTACGCGGCGGCCGCCTCGCTCAACTTGGCAGCCGCCGCCGCTGCCGCCGGCCAGACCTCGTTTGTGCCGTTCAGTTCGGCGGCCACGGCGGTGGCGGCCACGCCCACATTCCAGCACCTGCCGCAGATCTCCTGCTACAACGTGTGATGCAGCACC		Read size	# Mismatch	Hit Count	Total Norm	Total	V115 head	V114 embryo	V113 male body	M054 female body
**********.....((((.((((((((((..((((((((((((((...))))))..)))).........))))))..))))))))))).))))).....**********										
.....TCAGTTCGGCGGCCACGGCGGT.....	22	0	2	33.00	66	23	34	7	2
.....TCAGTTCGGCGGCCACGGCGG.....	21	0	2	20.00	40	20	10	8	2
.....TCAGTTCGGCGGCCACGGCGGTT.....	23	1	2	10.00	20	17	0	3	0
.....TCAGTTCGGCGGCCACGGCG.....	20	0	2	5.00	10	4	3	0	3
.....TCAGTTCGGCGGCCACGGCGT.....	21	1	2	3.00	6	6	0	0	0
.....TCAGTTCGGCGGCCACGGCGA.....	21	1	2	2.50	5	3	0	1	1
.....AGTTCGGCGGCCACGGCGGTGG.....	22	0	2	1.50	3	1	1	0	1
.....TCAGTTCGGCGGCCACGGC.....	19	0	2	1.50	3	1	1	0	1
.....TCAGTTCGGCGGCCACGGT.....	19	1	2	1.00	2	1	0	0	1
.....CGCCGCTGCCGCCGGCCAGACC.....	22	0	2	1.00	2	1	1	0	0
.....TCAGTTCGGCGGCCACGG.....	18	0	2	1.00	2	2	0	0	0
.....CAGTTCGGCGGCCACGGCGG.....	20	0	2	1.00	2	0	0	0	2
.....TCAGTTCGGCGGCCACGGCGGTA.....	23	1	2	1.00	2	2	0	0	0
.....TCAGTTCGGCGGCCACGGAT.....	20	2	2	0.50	1	1	0	0	0
.....CAGTTCGGCGGCCACGGCGGT.....	21	0	2	0.50	1	1	0	0	0
.....TCAGTTCGGCGGCCACGGCGGAA.....	23	2	2	0.50	1	1	0	0	0
.....TCAGTTCGGCGGCCACGGCT.....	20	1	2	0.50	1	0	0	0	1
.....TCAGTTCGGCGGCCACGGCGGC.....	22	1	2	0.50	1	0	0	1	0
.....AGTTCGGCGGCCACGGCGG.....	19	0	2	0.50	1	1	0	0	0
.....TCAGTTCGGCGGCCACGGTT.....	20	2	2	0.50	1	1	0	0	0
.....AGTTCGGCGGCCACGGCG.....	18	0	2	0.50	1	1	0	0	0
.....TCAGTTCGGCGGCCACGGCGGTTA.....	24	2	2	0.50	1	0	0	0	1
.....AGTTCGGCGGCCACGGCGGTGGA.....	23	1	2	0.50	1	0	0	1	0
.....TCAGTTCGGCGGCCACGGCA.....	20	1	2	0.50	1	1	0	0	0
.....ACGCCCACATTCCAGCACC.....	19	0	2	0.50	1	0	1	0	0
.....TCAGTTCGGCGGCCACGGCGGTCTA.....	25	3	2	0.50	1	1	0	0	0
.....TCAGTTCGGCGGCCACGGCGGTTT.....	24	2	2	0.50	1	1	0	0	0
.....TCAGTTCGGCGGCCACGGCGTG.....	22	2	3	0.33	1	1	0	0	0
.....TCAGTTCGGCGGCCACGCTA.....	20	3	7	0.14	1	1	0	0	0
.....GCCGCCGCCGCTGCCGCCG.....	19	0	12	0.08	1	0	1	0	0

Anti-sense strand reads

GTCATGAACGCCAGAGTCGCCTACGTGGGCATGCGCCGCCGGCGGAGCGAGTTGAACCGTCGGCGGCGGCGACGGCGGCCGGTCTGGAGCAAACACGGCAAGTCAAGCCGCCGGTGCCGCCACCGCCGGTGCGGGTGTAAGGTCGTGGACGGCGTCTAGAGGACGATGTTGCACACTACGTCGTGG		Read size	# Mismatch	Hit Count	Total Norm	Total	V114 embryo	M054 female body	V115 head
**********.....((((.((((((((((..((((((((((((...)))))))..)))).........))))))..))))))))))).))))).....**********									
.....ACGGCGTCTAGAGGACGATGTTG.....	23	0	2	0.50	1	1	0	0	

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_6:1033598-1033783 -	dse_1834	CAGTACTTGCGGTCTCAG---CGGATGCACCCGTACGC----------GGCGGCCGCCTCGCTCAACTTGGC---AGCCGCCGCCGCTGCCGCCG---------GCCAGAC----------CTCGTTTGTGCCGTTCAGTTCGGCGGCCACGGCGG----------TGGCGGCCACGCCCACATTCCAGCACCTGCCG---CAGATCTCCTGCTACAACGTGTGATG----------CAGCACC---
droSim2	3r:817583-817768 -	dsi_32437	CAGTACTTGCGGTCTCAG---CGGATGCACCCGTACGC----------GGCGGCCGCCTCGCTCAACTTGGC---AGCCGCCGCCGCTGCNGCCG---------GCCAGAC----------CTCGTTTGTGCCGTTCAGTTCGGCGGCCACGGCGG----------TGGCGGCCACGCCCACATTCCAGCACCTGCCG---CAGATCTCCTGCTACAACGTGTGATG----------CAGCACC---
dm3	chr3R:910087-910271 -	dme_377	CAGTACTTGCGGTCCCAG---CGGATGCACCCGTACGC----------GGCGGCCGCCTCGCTCAACTTGGC---AGCCGCCGCCGCTGCCGCCG---------GCCAGAC----------CTCGTTTGTGCCGTTCAGTTCGGCGGCCACGGCGG----------TGGCGGCCACGCCCACATTCCAGCACCTGCCG---CAGATCTCCTGCTACAACGTGTGATG----------CAGCAG----
droEre2	scaffold_4770:1183272-1183457 -	der_59	CAGTACTTGCGGTCTCAG---CGGATGCACCCGTACGC----------GGCGGCCGCCTCGCTCAACTTGGC---AGCCGCCGCCGCTGCCGCCG---------GACAGAC----------CTCGTTTGTGCCGTTCAGTTCGGCGGCCACGGCGG----------TGGCGGCCACGCCCACATTCCAGCACCTGCCG---CAGATCTCCTGCTACAACGTGTGATG----------CAGCACC---
droYak3	3R:1255628-1255813 -	dya_1786	CAGTACTTACGGTCTCAG---CGGATGCACCCGTACGC----------GGCGGCCGCCTCGCTCAACTTGGC---AGCCGCCGCCGCTGCCGCCG---------GACAGAC----------CTCGTTTGTGCCGTTCAACTCGGCGGCCACGGCGG----------TGGCGGCCACGCCCACATTCCAGCACCTGCCG---CAGATCTCCTGCTACAATGTGTGATG----------CAGCACC---
droEug1	scf7180000409759:861172-861357 -		CAGTACTTGCGTTCCCAG---CGGATGCACCCGTATGC----------GGCGGCCGCTCGCTCAACTTGGC---AGCCGCCGCCGCTGCCGCCG---------GACAGAC----------TTCTTTCGTGCCGTTCAGCTCGGCGGCCACGGCGG----------TGGCGGCCACGCCAACATTCCAGCACCTGCCG---CAGATCTCCTGCTACAACGTGTGATG----------CGCAGCC---
droBia1	scf7180000302411:644876-645050 -		CAGTACTTGCGGTCCCAG---CGGATGCATCCCTATGC----------GGCGGCCGCCTCGCTCAACCTGGC---AGCCGC---CCGCTGCCGCCG---------GACAGAC----------CTCATTCGTGCCGTTCAGCTCGGCGGCCAGTGCGG----------TGGCGGCCACGCCCACATTCCAGCACCTGCCG---CAGATCTCCTGCTACAACGTGTGAT---CGGCA----
droTak1	scf7180000415789:614398-614578 -		CAGTATCTGCGGTCCCAG---CGGATGCATCCCTATGC----------TGCGGCCGCTCGCTCAACATGGC---TGCC---GCCGCTGCCGCTG---------GACAGAC----------CTCTTTTGTGCCGTTCAGTTCGGCGGCCACGGCGG----------TCTGGGCCACGCCCACATTCCAGCACCTGCCC---CAGATCTCCTGCTACAACGTGTGATG----------CGCGCA----
droEle1	scf7180000491104:2702002-2702172 -		CAGTACTTGCGGTCTCAG---CGGATGCACCCGTATGC----------GGCGGCCGCCTCGCTCAACTTGGC---CGCCGCCGGCAGCAGCCGCTG---------GACAGAC----------GTCCTTTGTGCCGTTCAGTTCGGCGG---------------------CCACGCCCACATTCCAGCACCTGCCG---CAGATCTCCTGCTAAAATGTGTGATG----------CAGCAGC---
droRho1	scf7180000779558:37755-37925 -		CAGTACTTGCGGTCTCAG---CGGATGCATCCGTACGC----------GGCGGCCGCCTCGCTCAACTTGGC---AGCCGCCGCCGCTGCCGCTG---------GACAGAC----------GTCGTTCGTGCCGTTCAGCTCGGCGG---------------------CCACGCCCACATTCCAGCACCTGCCG---CAGATCTCCTGCTACAACGTGTGATG----------CAGCAGC---
droFic1	scf7180000453850:254221-254406 -		CAGTACTTGAGGTCCCAG---AGGATGCACCCGTACGC----------GGCGGCCGCCTCGCTCAACTTGGC---CGCCGCCGCCGCTGCCGCTG---------GACAGAC----------GTCGTTCGTGCCGTTCAGCTCGGCGGCTACGGCGG----------TCTGGGCCACGCCCACATTCCAGCACCTGCCG---CAGATCTCCTGCTACAACGTGTGATG----------CAGCAGC---
droKik1	scf7180000302634:592884-593061 -		CAGTACCTGCGGTCCCAG---AGATGCATCCGTATGC----------GGCGGCCGCCTCGCTCAACCTGGC---AGCCGCAGGTGCTGCCGCCG---------GACAGAC----------GTCCTTTGTCCCGTTAGCTCGGCGGCCAGAGCGG----------TGGCGGCCACGCCCACATTCCAGCACCTGCCG---CAGATCTCCTGCTACAACGTGTGAT---CGGCA----
droAna3	scaffold_13340:23109603-23109807 -	dan_4055	CAGTACTTGCGGTCGCAG---CGGATGCATCCCTATGC----------GTCGCTAAATCTGGC---AGCCGCCGCCGCTGCCGCCGGCAACTTGGCGCAGACAAC----------ATCGTTTGTGCCGTTCAGCTCGGCGGCCACGGCGG----------TGGCGGCCACGCCCACATTCCAGCATCTGCCG---CAGATCTCCTGCTACAATGTGTGATCAT----------CCGCAGGACAAAGGCAACAGCAAC---
droBip1	scf7180000396395:117223-117445 -		CAGTACTTGCGGTCGCAG---CGGATGCATCCATATGC----------GTCGCTAAATCTGGC---AGCCGCCGCCGCTGCCGCCGGCAACTTGGCGCAGAC----------ATCGTTTGTGCCGTTCAGTTCGGCGGCCACGGCGG----------TGGCGGCCACGCCCACATTCCAGCATCTGCCG---CAGATCTCCTGCTACAACGTGTGATCATCAGGACAGGAGAGATCCGCAGGACAAAGGCAACAGCAAGATA
dp5	2:21905626-21905814 +	dps_3837	CAGTACCTGCGCTCCCAG---CGGATGCACCCGTATGC----------GGCGGCGCCCTCCGCTCAACCTGGC---CGCAGCCGCCGCTGCCGCCGGAGCCTGGCGCAGAC----------CTCGTTTGTGCCATTCGGTCCGGCCG---------CGGCGGCGACGCCCACATTCCAGCATCTGCAGCAGCAGATATCCTGCTACAATGTGTGATC----------CCGTCC---
droPer2	scaffold_3:4687056-4687244 +		CAGTACCTGCGCTCCCAG---CGGATGCACCCGTATGC----------GGCGGCCGCCTCCGCTCAACCTGGC---CGCTGCCGCCGCTGCCGCCGGAGCCTGGCGCAGAC----------CTCGTTTGTGCCATTCGGTCGGGCCG---------CGGCGGCCACGCCCACATTCCAGCATCTGCAGCAGCAGATATCCTGCTACAATGTGTGATC----------CCGTCC---
droWil2	scf2_1100000004943:13032088-13032290 +	dwi_5421	CAATATTTGCGTTCCAG---CGATGCATCCATATTT----------CCTCATCAATTTGGC---CG----------GCAATTTGGGTGATACGGCAACAACAACTGGAGCATTTGGTCGCATTCGGCTGAGCGGCTGCGGGTTCTGCAGCGGCAGCGGCGGTAACGCCAACATTCCAGCATCTGCAG---CAAATTCCTTCTAATAATGTGTGATCAA----------CC----CAAAG----T-AAACC---
droVir3	scaffold_12855:7979105-7979302 +	dvi_24659	CAATATCTGCGCAGCAGCATCGCATGCATCCCTACGCAG---CAGCGGCAGCGGCCGCCTCCCTCGCAGCGGC---AGCGGCCGCCGCCAATTTGG---------GCCAGC----------TTCGTTTGTGCCGTTGTGCACGGCGGCGACGTCGG----------CGACGGCAGCGCCAACATTCCAGCAATCTGCAG---CAAATCTCCTGCTACAACGTGTGATC----------CAAGAAC---
droMoj3	scaffold_6540:23216845-23217051 +	dmo_3161	CAATATCTGCGCACCAGCATCGCATGCATCCCTACGCAGCAGCAGCGGCGGCCGCCTCCCTCGCAGCAGC---AGCGGCGCGCGCCAATTGG---------GTCCGC----------TTCGTTTGTGCCGTTCGAACGGCGGCGACGTCGG------CGACGGCAGCGGCAGCGCCAACATTCCAGCAATCTGCAG---CAATCTCCTGCTACAACGTGTGATC----------CTCGTCC---
droGri2	scaffold_6846:2274-2451 +		CAGCGGCAGCGGCAGCAG---CGGCAGCAGCGGCAGCA-GCGGC---------AGCAGCGCGGAGCGGCAGCATCAGCAGCAGCAGCAGGAGCAGCGG---------CAGCCGC----------AGCATCAGCAGCAGCAAAGCGGCAGCACCAAGAGCAGGAGCAGCA--------G------CAAAAACG---------CAGCACC---

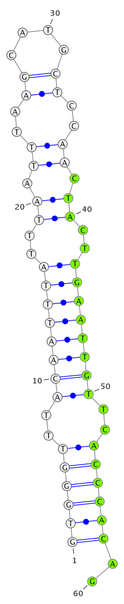
Generated: 09/08/2015 at 07:57 PM

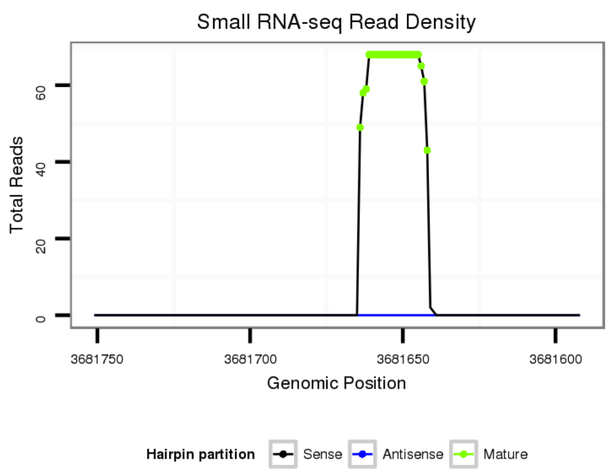
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	3

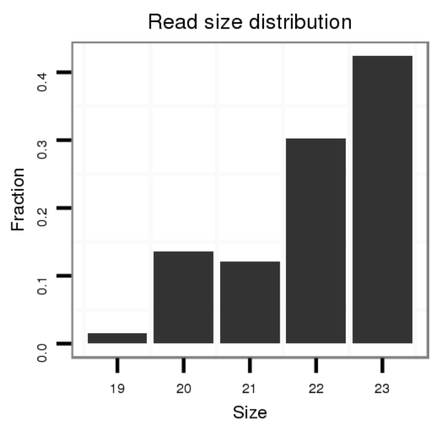
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1293	**scaffold_4:3681642-3681701 -**	**candidate-rescued**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

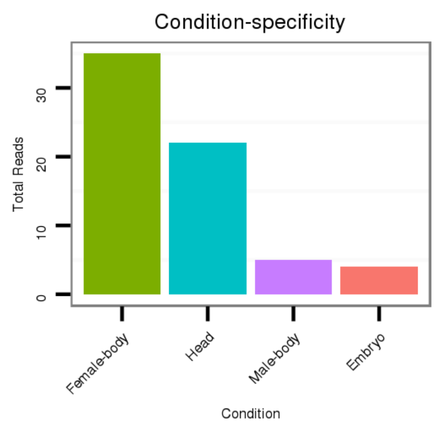
Legend: mature star mismatch in alignment mismatch in read

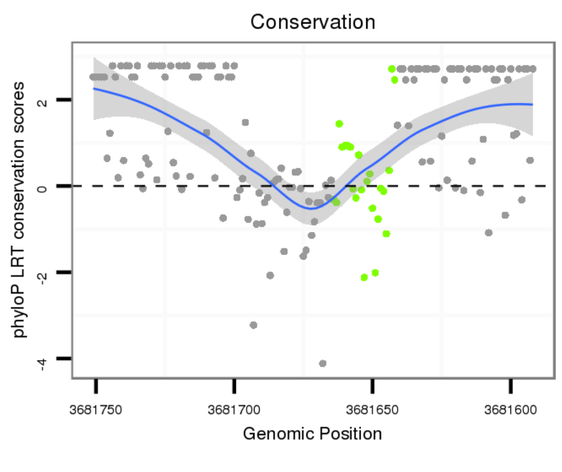
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dsec\GM12273-in]; CDS [Dsec\GM12273-cds]; CDS [Dsec\GM12273-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CCCGCCCTGGTCATGGACGCCATCATGGTGATAATTGGCAAGAAGCCCAGGTGGGTTTACAATTTATTTAATTTAAGCATGCTCCAACTACTTGAATTGTTCACCCACAGAATGATGAAGATCTACCGCAAGATACACAAGCTAAGCAATGTCCTCAAGT	Read size	# Mismatch	Hit Count	Total Norm	Total	M054 female body	V115 head	V113 male body	V114 embryo
**********(((((((..(((((((((..((.((..((....))..)).)).)))))))))..)))))))..**********									
.....CTACTTGAATTGTTCACCCACAG.....	23	0	1	28.00	28	15	7	4	2
.....CTACTTGAATTGTTCACCCACA.....	22	0	1	15.00	15	8	5	1	1
.....CTTGAATTGTTCACCCACAG.....	20	0	1	7.00	7	2	5	0	0
.....TACTTGAATTGTTCACCCACAG.....	22	0	1	5.00	5	3	1	0	1
.....CTACTTGAATTGTTCACCCAC.....	21	0	1	4.00	4	3	1	0	0
.....TACTTGAATTGTTCACCCACA.....	21	0	1	3.00	3	1	2	0	0
.....CTACTTGAATTGTTCACCCA.....	20	0	1	2.00	2	1	1	0	0
.....TACTTGAATTGTTCACCCACAGT.....	23	1	1	2.00	2	0	1	1	0
.....CTTGAATTGTTCACCCACAGT.....	21	1	1	2.00	2	0	1	1	0
.....CTACTTGAATTGTTCACCCACAGT.....	24	1	1	1.00	1	0	0	1	0
.....CTTGAATTGTTCACCCACAGAT.....	22	1	1	1.00	1	1	0	0	0
.....CTTGAATTGTTCACCCACAGA.....	21	0	1	1.00	1	0	1	0	0
.....ACTTGAATTGTTCACCCACAG.....	21	0	1	1.00	1	1	0	0	0
.....TACTTGAATTGTTCACCCA.....	19	0	1	1.00	1	1	0	0	0
.....CTTGAATTGTTCACCCACAGAA.....	22	0	1	1.00	1	0	0	0	1
.....TTGAATTGTTCACCCACAGT.....	20	1	1	1.00	1	0	0	1	0

Anti-sense strand reads

GGGCGGGACCAGTACCTGCGGTAGTACCACTATTAACCGTTCTTCGGGTCCACCCAAATGTTAAATAAATTAAATTCGTACGAGGTTGATGAACTTAACAAGTGGGTGTCTTACTACTTCTAGATGGCGTTCTATGTGTTCGATTCGTTACAGGAGTTCA	Read size	# Mismatch	Hit Count	Total Norm	Total	V114 embryo	M054 female body	V115 head
**********(((((((..(((((((((..((.((..((....))..)).)).)))))))))..)))))))..**********									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_4:3681592-3681751 -	dse_1293	CCCGCCCTGGTCATGGACGCCATCATGGTGATAATTGGCAAGAAGCCCAGGTGGGTTTACAAT-TT--A----------TTTAATTTAAGCATGCTCCAACTACTTGAA----------TTGTTCACCCACAGAATGATGAAGATCTACCGCAAGATACACAAGCTAAGCAATGTCCTCAAGT
droSim2	3r:24180234-24180393 -	dsi_12849	CCCGCCCTGGTCATGGACGCCATCATGGTCGATAATTGGCAAGAAGCCCAGGTGGGTTTACAAT-TT--A----------TTCAATTTAAGCATGCTCCAACTACTTGAA----------TTGTTCACCCACAGAATGATGAAGATCTACCGCAAGATTCACAAGCTAAGCAATGTCCTCAAGT
dm3	chr3R:24819362-24819521 -	dme_160	CCCGCCCTGGTCATGGACGCCATCATGGTGATAATTGGCAAGAAACCCAGGTAGGTTTACAAT-AT--A----------TTTAATTTAAGCGTGCTACAACTACTTGAA----------TTGTTCACCTACAGAATGATGAAGATCTATCGCAAGATCCACAAGCTAAGCAATGTCCTCAAGT
droEre2	scaffold_4820:3217364-3217523 +		CCCGCCCTGGTCATGGACGCCATCATGGTGATAATTGGCAAGAAGCCCAGGTGGGTTTACAAT-TC--A----------ATTCATTTAAGCATGTTACAACTACTTGAT----------TGACTCACCCGCAGAATGATGAAGATCTACCGCAAGATCCACAAGCTGAGCAACGTCCTCAAGT
droYak3	3R:21679775-21679934 +		CCCGCCCTGGTCATGGACGCCATCATGGTGATAATTGGCAAGAAGCCCAGGTGCGTTTACAAT-TT--A----------TTTCATTTAAACATACTCCAACTACTTGAA----------TGGCTCACCCACAGAATGATGAAGATCTATCGCAAAATCCACAAGCTCAGCAATGTCCTCAAGT
droEug1	scf7180000409787:759740-759896 +		CCCGCCCTGGTCATGGATGCCATCATGGTGATAATTGGCAAGAAGCCCAGGTAGGTTTTTTAT-TT--A----------TTTATTTTAATTGCAAAATTAA---------TA--ATTT----------CTGATTTTTCCACAGAATGATGAAGATCTACCGCAAGATCCACAAACTGAGCAATGTCCTCAAGT
droBia1	scf7180000302075:1925603-1925764 +		CCCGCCCTGGTTATGGACGCCATCATGGTGATAATTGGCAAGAAGCCCAGGTGGGTTTTGTTT-ATTGA----------TTATACTGGAGAGAATCTCTA---------AAGTATTT----------TTGCTTGTTCCTCAGAATGATGAAGATCTACCGCAAGATCCACAAACTGAGCAATGTCCTCAAGT
droTak1	scf7180000415700:395450-395530 -		CCCGCCCTGGTTATGGACGCCATCATGGTGATAATTGGCAAGAAGCCCAGGTGGGTTTACTAT-T---------TTACATATTTTATTTAA----------**********----------**********
droEle1	scf7180000491261:1395263-1395423 -		CCCGCCCTGGTCATGGACGCCATCATGGTGATAATTGGCAAGAAGCCGAGGTGGGCCTCTAGT-TC--A----------TTTAATCTATGGGCACTTTA---------TAACATTT----------TTAAATCACCCCCAGAATGATGAAGATCTATCGCAAGATCCACAAACTAAGCAATGTCCTCAAGT
droRho1	scf7180000780007:235822-235981 +		CCCGCCCTGGTCATGGACACCATAATGGTGATAATTGGCAAGAAGCCAAGGTAGGTTTATAAT-CG--A----------TTTAATGTATTGGAACCATTC---------TAACGTTC----------ATAAATGCCCCACAGAATGATGAAGATATACCGCAAGATCCACAAACTGAGCAACGTCCTCAAGT
droFic1	scf7180000454073:3527124-3527283 +		CCCGCTCTGGTCATGGACGCCATCATGGTGATAATTGGCAAGAAGCCCAGGTGGGTCTGCATA-AG--A----------TTTGGTTTAAGGAAACCGTTG---------TAAACTCC----------TTGGTGTTCCCACAGAATGATGAAGATCTACCGCAAGATCCACAAGCTCAGCAACGTCCTCAAGT
droKik1	scf7180000302276:789340-789502 -		CCCGCCCTGGTCATGGACGCCATCATGGTGATCATCGGCAAGAAGCCAAGGTGGGTTTGGAAT-----T---TAG-GGGATTTTCTGGTTTCCA--**********ATCA------**********AACTCAGTATGTTTTTTATTTTTAGGATGATGAAGATATACCGAAAGATCCACAAGCTGAGCAACGTCCTAAAGT
droAna3	scaffold_13340:19749745-19749907 +		CCCGCCCTGGTCATGGATACCATTATGGTTCTTATAGGCAAAAAGCCAAGGTAGGTTTTGTTG-ATTTT----------CTTTGTGAAAGTGTGTTTAA---------ATTTATTT----------TTTATTTTTTCATTAGAATGATGAAAATCTACCGCAAGATTCACAAGCTGAGCAACGTCCTTAAAT
droBip1	scf7180000396413:2642063-2642223 -		CCCGCCCTGGTCATGGATGCCATTATGGTTCTCATAGGCAAGAAGCCAAGGTGGGTCTACTTT-AGTGTA----------CTAAGGATAAATTTTTTAA---------TATTATT----------ATTTTTTGTCCTTAGAATGATGAAAATCTACCGCAAAATTCAATAAACTCAGCAACGTCCTTAAAT
dp5	2:13217451-13217609 +		CCCGCGCTGATCATGGACTTCATTATGGTGATCATTGGCAAGAAACCAAGGTAAGTGCCTACG-AGGATTCTTTAG-AGGGTCTCTTGACTTACGCT----------**********----------CTGTCTTCCCTTAGAATGATGAAGATCTATCGCAAGATCCACAAGCTGAGCAATGTCCTCAAGT
droPer2	scaffold_0:7235646-7235804 -		CCCGCCCTGATCATGGACTTCATTATGGTGATCATTGGCAAGAAACCAAGGTAAGTGCCTAAG-AGGATTCTTTAG-AGGGTCTCTTGACTTACGCT----------**********----------CTGTCTTCCCTTAGAATGATGAAGATCTATCGCAAGATCCACAAGCTGAGCAATGTCCTCAAGT
droWil2	scf2_11000000000048:5347-5510 +		CCCGCCCTGTTTATGGATGCCATTATGATTGTAATTGGCAAGAAACCGCAGGTATATTAAA--CTAT--C----------TATATCTTTGCTGTTCTGTAACTA------**********AATCTAAATCTCTTTTGAATTGCAGAATGATGAAGATCTATAGAAAATACATAAATTGCAGCAATGTCCTTAAGT
droVir3	scaffold_13047:18244391-18244551 -		CCCGCCATGTTCATGGACTTGATAATGGTTCTCATGGGCAAGAAACCCAGGTATTTATTAGAC-ATTCTTCTTTTGCAATGGCATTTGCCTAACATA----------**********T----------TTTCTTTTTGCAGAATGATGAAAATCTATCGCAAAATACACAAGTTCAGCAATGTTCTAAAAT
droMoj3	scaffold_6540:13479886-13480052 +		CCCGCCATCCTCATGGACTTAATTATGGTTCTGATGGGCAAGAAGCCAAGGTAGCGTGTGTGATTAG---C----------TTTTTGCCTTGCATT--TCG----------CATAT---------TG--AAGT----------CTTATT-ATTCCATCCATTCAGAATGATGAAAATCTATCGCAAGATACACAAGTTCAGCAACGTCTTTAAAGT
droGri2	scaffold_15074:6443580-6443756 +		CCCGCCATGTTCATGGACTTGATTATGGTTCTCATGGGCAAGAAACCGCAGGTATGTTTCA---T---T---**********----ATTTAATTGCATGGCAACACTTGCAACATATTTACTCAAACTGAACGAAA-------CTTCTTCATTTGCAGAATGTTGAAATCTATCGCAAGATACACAAGTTCAGCAACGTTCTCAAGT

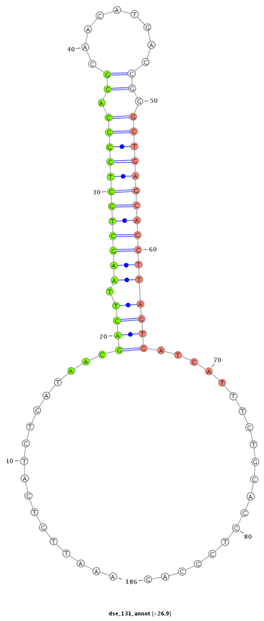
Generated: 09/08/2015 at 10:35 PM

	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	3

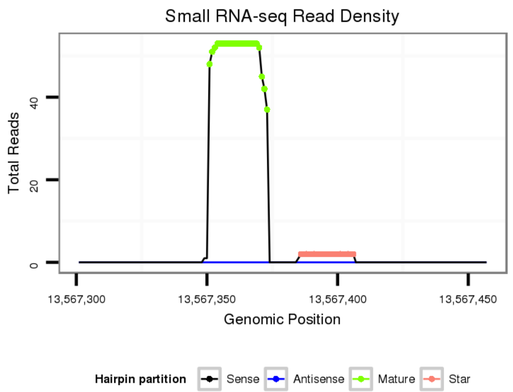
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_131	**scaffold_0:13567351-13567407 +**	**candidate-rescued**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Cornell Mirror)]

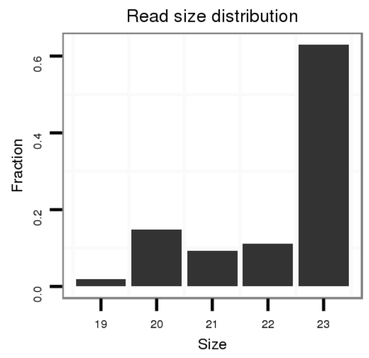
Legend: mature star mismatch in alignment mismatch in read

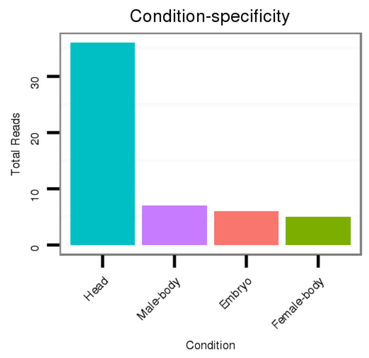
Predicted structure

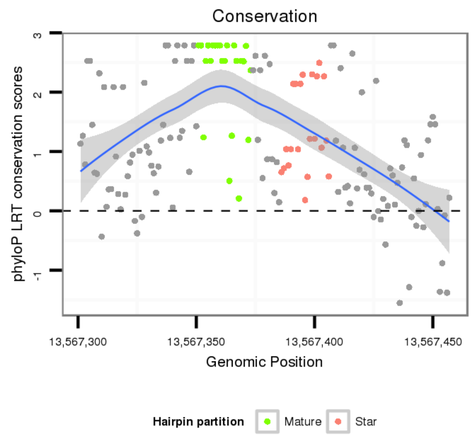


Show Alternate Folds









Flybase annnotation

intron [Dsec\GM25996-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GCAGCTCAGTCGCAGTCGCAGCTCAGTCGGTATAGAAATTGTCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGGCTGAGCAGCTTAGTCATCATTCTCTGCACCTCCCAGAATCCAGCCCATCCTCCTTAGCGAACACACTATTGC	Read size	# Mismatch	Hit Count	Total Norm	Total	V115 head	V113 male body	M054 female body	V114 embryo
**********.....((((.(((((((((((.((.....)).)))))))))))))))).....**********									
.....AACGACTTAAGCTGCTCGGCACG.....	23	0	1	34.00	34	22	4	3	5
.....AACGACTTAAGCTGCTCGGCACGT.....	24	1	1	9.00	9	5	4	0	0
.....AACGACTTAAGCTGCTCGGC.....	20	0	1	6.00	6	5	0	0	1
.....AACGACTTAAGCTGCTCGGCAC.....	22	0	1	3.00	3	2	0	1	0
.....ACGACTTAAGCTGCTCGGCA.....	21	0	1	3.00	3	2	0	1	0
.....ACGACTTAAGCTGCTCGGCACG.....	22	0	1	2.00	2	2	0	0	0
.....ATAACGACTTAAGCTGCTCGGC.....	22	0	1	1.00	1	0	0	0	1
.....CGACTTAAGCTGCTCGGCAC.....	20	0	1	1.00	1	0	1	0	0
.....ACGACTTAAGCTGCTCGGCAC.....	21	0	1	1.00	1	1	0	0	0
.....AACGACTTAAGCTGCTCGG.....	19	0	1	1.00	1	0	1	0	0
.....AACGACTTAAGCTGCTCGGCAT.....	22	1	1	1.00	1	1	0	0	0
.....GACTTAAGCTGCTCGGCACG.....	20	0	1	1.00	1	1	0	0	0
.....GCTGAGCAGCTTAGTCATCAT.....	21	0	1	1.00	1	1	0	0	0
.....GGCTGAGCAGCTTAGTCATCAT.....	22	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

CGTCGAGTCAGCGTCAGCGTCGAGTCAGCCATATCTTTAACAGTAGAGTATTGCTGAATTCGACGAGCCGTGCGTTGTACTGGCCCGACTCGTCGAATCAGTAGTAAAGACGTGGAGGGTCTTAGGTCGGGTAGGAGGAATCGCTTGTGTGATAACG	Read size	# Mismatch	Hit Count	Total Norm	Total	M054 female body	V115 head	V113 male body	V114 embryo
**********.....((((.((((((((((.((.....)).)))))))))))))))).....**********									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_0:13567301-13567457 +	dse_131	GCAGC-TCAGTCGCAGTCG---CA----------GC----------TC----------AGTCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG-----CTGAGCAGCTTAGTCATCATTCTCTGC----ACCT--CCCAG----AATCCAG--------CCCATCC----------TCCTTAG-------CGAACACACT---ATTGC-
droSim2	3r:12738982-12739138 +	dsi_32436	GCAGC-TCAGTCGCAGTCG---CA----------GC----------TC----------AGTCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTCTCTGC----ACCT--CCCAG----AATCCAG--------CCCATCC----------TCCTTAG-------CGAACACACT---ATTGC-
dm3	chr3R:8419613-8419767 -	dme_234	GCAGC-TCAGTCACAGTCC---CA----------GC----------TC----------AGTCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTCTCTGC----ACCT--CCCAG----AATCCAG--------CCCATCC----------TCCTCAG-------CAAA--CACT---ATTGC-
droEre2	scaffold_4770:13232524-13232685 +	der_1512	GCAGC-TCAGTCGCAGTCG---CA-----GTCGCAGC----------TC----------AGTCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTGAGCAGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTCTCTGC----ACCT--CCCAG----AATCCAG--------CCCATCC----------CCC----ATCTTCCAC--CACT---ATTGC-
droYak3	3R:12705470-12705629 -	dya_1782	GCAGC-TCAGTCGCAGTCG---CA----------GC----------TC----------AGTCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTCTCTGC----ACCT--CCCAG----AATCCAG--------CCCATCC----------TC---AGTCGGTCTTCCAC--CACT---GTTGC-
droEug1	scf7180000409615:635456-635601 -		GCTGC-TCAGTCGCAGTCG---CA----------GC----------TC----------AGTCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACTGGG-----CTGAGCAGCATAGTCAGCATTCTCTGC----ACCT--CCCAG----AATCCGT--------TTCAGCC----------TCCTT--------A--------T--TTATAG-
droBia1	scf7180000302402:97575-97735 -		GCTGC-TCAGTCGCAGTCG---CG-----GTCGCAGC----------TCAG-----TCGCAA----------TTCAGCGGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTCTCTGC----ACCT--CCCAG----CATCCAG--------GTCAGCC----------CCGTGGG-------C--------A----G-
droTak1	scf7180000415366:130701-130853 +		GCTGC-TCAGTCGCAGTCG---CA----------GC----------TCAG-----TCGCAA----------TTCAGTCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTCTCTGC----ACCT--CCCAG----AATCCAG--------GTCAGCC----------CCCT---------A--------T--TTG-
droEle1	scf7180000490994:97245-97401 -		GCTGC-TCTGTCGCAG-CT---CA-----GTCGCAGC----------TCAG-----CCGCAA----------GTGAGTCGGTATAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTTCAGC----ACCT--CCCAG----AATGCGCCATATAG--CCCAGC-A----------A-------A--------A------
droRho1	scf7180000777772:6594-6747 -		GCTGC-TCAGCCGCAGTCG---CA----------GC----------TCAG-----TCGCAA----------GTGAGTCGGTATAGAAATC-----GTCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTCTCTGC----ACCT--CCCAG----AATCCAGAAACCAGCACCA---------A-------A--------A---GC-
droFic1	scf7180000453812:694089-694253 +		GCTGC-TCAGTCGCAGTCG---CA----------GC----------TCAG-----TCGCAC----------ATCAGTCGGTATAGAAATC-----GTCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCAG-----CTGAGCAGCATAGTCAGCATTCTCTGC----ACCT--CCCAG----AATCCAG--------CCAGGCA---------A-------A--------A-----CTT-
droKik1	scf7180000302256:649545-649705 +		GCTGC-TCAGCGCGGTGTCG---CAGCTCAGTC---------------------ACTGAGAC---GCCGAGGCGCTGAGTCG---CTCTGTCGGTACAGAAATT-----GTCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG-----CTGAGCAGCATAGTCAGCATTCTCTGC----AGTT--CCCAG----AAGCGAG--------G---------A-------A--------A-----CTT-
droAna3	scaffold_12911:3351170-3351270 -		GCTGC-CTGG---------A---------T-G----------GGGCGGTGTAGCAATT-----GTCATCTCAGAACGACTTAAGCTGCTCGGCACGCAACATGAC----------TGAGCAGCGTAGTCAGCATTCTCTGC----ACCT--CC---A--------A-------A--------A-----CTT-
droBip1	scf7180000396640:216802-216924 -		GCTGC-CTGG---------A---------T-C----------TC----------AGGCGGTGTAGCAATT-----GTCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGAC----------TGAGCAGCGTAGTCAGCATTCTCTGC----ACCT--CCCAGCGCGAAGTCC---------A-------A--------A-----CCTTA-------A--------A---GATGC-
dp5	2:2527942-2528050 -		GCCGC-TCAGTCACAGTCG---CA-----GTCGCAG---------------------AGCCTTTCTCTGT-GGCATAGAAATC-----GTCATCGCATAACGACTTAAGCTGCTCGGCAC----------A--------AGTCAGCATTCTCTGCGAGTACAT--CC---A--------A-------A--------A-----CTT-
droPer2	scaffold_7:2696941-2697049 -		GCCGC-TCAGCGCACAGTCA---CA-----GTAGCAG---------------------AGCCTTTCTCTGT-GGCACAGAAATC-----GTCATCGCATAACGACTTAAGCTGCTCG----------A--------ACAGTCAGCATTCTCTGCGAGTACAT--CC---A--------A-------A--------A-----CTT-
droWil2	scf2_1100000004943:2230161-2230306 -		CTTGC-TC----------A---------A---------A---------A---------A---------A------TATCGAAATCGTCATCGTCATCTCATAACGACTTAAGCTGTCTGAGCAGCGCAGCCTGACTAAGCTCAGCTGAGCAGCATAGTCAGCAATTCTGCAGGAGCAACTCATATT---AACACAT--------CACACAC---------TC-----------CCAC--CAGC-TCAGCA-
droVir3	scaffold_12855:538359-538521 +		GCTGC-TCAGCGC-GCGCAG---CG----------AC----------TTAG-----GCTGCGA----------CTGCGCGCGTGCTGAAACT-----GTTGTCGCATAAAGACTTAAGCTGCTGAGCAGCAGCGACAGCGTCAGCG--C-----A----------TTGCGGT--TGCTT--C----A----GC--------TTTACTGCCCTGGGGCCACACTTGAAGTCACACAC-----AGGC---ACACTCACACTCG-
droMoj3	scaffold_6540:12428190-12428358 -		GCTGCCTCAGCGC-TGCCGG---CG----------AC----------T-GCGACTGCGACTGAGGCA----------GAGCGCCGTTCAAACT-----GTTGTCGCATAACGACTTAAGCTGTTGCAGCACGCAACGTCAACGAT-----TCCGGCTGTTGTCTGC-----TTTGTGC---GCCTT--GG---A--GGGCCA-----A--------A-------A----------CACTTCAAGTCACACAC-----ACGC---ACACT---CTCGCA
droGri2	scaffold_14906:1656740-1656889 +		GCTGC-TTAGTCCTGCCACGCGA-CA-----GTACGCGAGGTGGAGATGGAGACGGAGGTGGAGGCGGAGACGGTGACTGAGACTGAGGCA----------GCCAACACTGTTGAAATTGT---GTTGTCGCATAACGACTTAAGCTGCTGAGCACGCAGCGT-------A-----A----------CAGCGATTCC---A----A-----A---A-------A--------A--------A-----CTT-

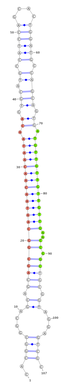
Generated: 09/08/2015 at 07:43 PM

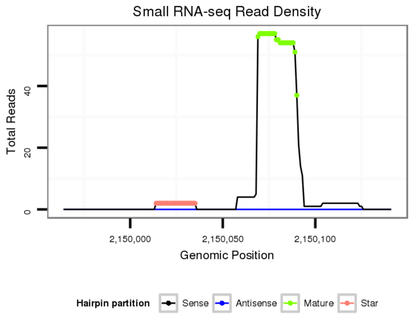
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	4

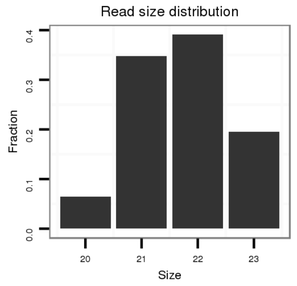
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_197	**scaffold_4:2150014-2150091 +**	**candidate-rescued**	**Canonical miRNA**	**CDS**	[View on UCSC Genome Browser [Cornell Mirror]]

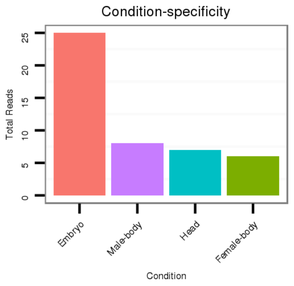
Legend: mature star mismatch in alignment mismatch in read

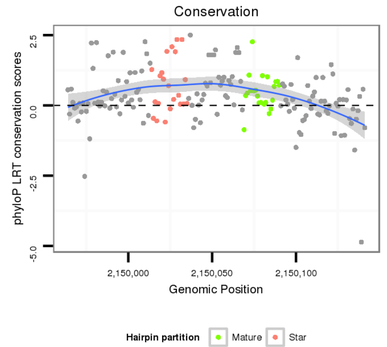
Predicted structure











Show Alternate Folds

Flybase annnotation

CDS [Dsec\GM12670-cds]; utr5 [utr5_minus_11564]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CCGTTACTCCTCGACAGCAGTTCTCCTCTTCTCGCCACGGCGGCAGCAGCAGCGGCAATAACAACAATAACAGTGCATGCCATCCAGCACTGGATGCCAGCAGTGATGTTGTTGTTGTTGAACCGGCTGCGGTAGGAGTCGCACAGGAGAAAGAGCCGGAGCAGAAGCCAGAGAGGAG	Read size	# Mismatch	Hit Count	Total Norm	Total	V114 embryo	M054 female body	V113 male body	V115 head
**********..((((....((.(((((((((((((((((((((((.((.(((.((.(((((((....)))))).)))))..)).)))))))))))))))..))..))))))..)).....))))..**********									
.....ATGTTGTTGTTGTTGAACCGGC.....	22	0	1	15.00	15	9	2	1	3
.....ATGTTGTTGTTGTTGAACCGG.....	21	0	1	14.00	14	3	3	4	4
.....ATGTTGTTGTTGTTGAACCGGCTGC.....	25	0	1	10.00	10	7	1	2	0
.....ATGTTGTTGTTGTTGAACCGGCTG.....	23	0	1	7.00	7	7	0	0	0
.....ATGTTGTTGTTGTTGAACCGGC.....	20	0	1	3.00	3	2	1	0	0
.....ATGTTGTTGTTGTTGAACCGGCTG.....	24	0	1	2.00	2	2	0	0	0
.....TGCCAGCAGTGATGTTGTTGT.....	21	0	1	2.00	2	0	0	2	0
.....AGCGGCAATAACAACAATAACA.....	22	0	1	2.00	2	2	0	0	0
.....CACAGGAGAAAGAGCCGGAGC.....	21	0	1	1.00	1	1	0	0	0
.....ATGTTGTTGTTGTTGAACCGC.....	21	1	1	1.00	1	0	1	0	0
.....ATGTTGTTGTTGTTGAACCGGCA.....	23	1	1	1.00	1	1	0	0	0
.....GTTGAACCGGCTGCGGTAGGAGTCG.....	25	0	1	1.00	1	1	0	0	0
.....TGCCAGCAGTGATGTTGTTGTTG.....	23	0	1	1.00	1	1	0	0	0
.....TGTTGTTGTTGTTGAACCGGCTG.....	23	0	1	1.00	1	1	0	0	0
.....TGCCAGCAGTGATGTTGTTGTT.....	22	0	1	1.00	1	1	0	0	0
.....GATGTTGTTGTTGTTGAACCGGC.....	23	0	1	1.00	1	0	0	1	0
.....GCACAGGAGAAAGAGCCGGA.....	20	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

GGCAATGAGGAGCTGTCGTCAAGAGGAGAAGAGCGGTGCCGCCGTCGTCGTCGCCGTTATTGTTGTTATTGTCACGTACGGTAGGTCGTGACCTACGGTCGTCACTACAACAACAACAACTTGGCCGACGCCATCCTCAGCGTGTCCTCTTTCTCGGCCTCGTCTTCGGTCTCTCCTC	Read size	# Mismatch	Hit Count	Total Norm	Total	M054 female body
**********..((((....((.(((((((((((((((((((((((.((.(((.((.(((((((....)))))).)))))..)).)))))))))))))))..))..))))))..)).....))))..**********							

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_4:2149964-2150141 +	dse_197	CCGTT--ACTCCTCGAC----------AGCAG-T--------TCTC---CTCTTC-----TCGCC----------ACGGCGGCAGCAGCAGCGGCAATAAC----------AACAATAA---CAGTGCATGCCATCCAGCACTGGATG---CCAGCAG----------TGATGTTGTT---GTTGTTGAACCGGCTGCGGTAGGAGTCGCACAG---GA-----GA---AAGAGC--------CGGAGCAGAAGCC----------AGAGAGGAG
droSim2	x14270595-4270778 -	dsi_108	CCGTT--ACTCCTCGAC----------AGCAG-T--------TCTC---CTCTTC-----TCGCC----------ACGGCGGCAGCAGCAGCGGCAATAAC----------AACAATAA---CAGTGCATGCCATCCAGCACTGGATG---CCAGCAG----------TGATGTTGTT---GTTGTTGAACCGGCTGCGGTAGGAGTCGCACAG---GACGAAAGA---AAGAGC--------CGGCGCAGAAGCC----------AGAGAGGAG
dm3	chrX:4579774-4579933 -	dme_464	CCGTT--ACTC------------------------------------GCC----------ACGGCGGCAGCAGCAGCGGCAATAAC----------AACAATAA---CAGTGCATGCCATCCAGCACTGGATG---CCAGCAG----------TGATGTTGTT---GTTGTTGAACCGGCAGCGGTAGGAGTCGCACAG---GACGAAAGA-C---AAGAGC--------CGGAGCAAAGGC----------AGAGAGGAG
droEre2	scaffold_4690:1957109-1957271 -	der_1531	CGTTT--ACTCCTCGAC----------AACAG-T--------TGTC---CTCTTC-----TCGCC----------ACGGCGGCAGCAAGTAT---AACAAC----------AACAATAA---CAGTGCTGCCATCCAGCATTGGATG---TCAGCAG----------TGATGTTGTT---GTTGTTGCACCGGCAGCGATAGGAGGACACAG---GA---AGACGC--------AAGAGC--------CGGAGC-------------------AGA
droYak3	X:13860422-13860602 +		CCGTT--ACTTGTCGAC----------AGCAG-T--------TGTC---CTCTTC-----CCGCC----------ACGGCGGTAGCAAGTATAACAATAATAACAGCAAC----------AGGAACACAGC---GAGTGCGTGCCATTCAGCAATGGATG---CCACAG----------TGTGTTTGTT---GTTGTTGCACCGGCAGCGGTAGGAGGAGCACAG---GA---AGACGC--------AAGAGC--------CC----------AGAGAGGAG
droEug1	scf7180000409548:355290-355458 -		CCGTT--AATCCGAGAC----------AGCAG-G--------TGTC---CTCTTC-----TCGCC----------CAACGGCAA----------AACAATAA---CAGTGATGTCATCCAGCACTGGATG---CCACAG----------TACTGTTGTT---GTTGTTGCACCGGCAGCGGAAGTAGC-TCGAG---G-----AGC---AAGACC--------CG---------GCTGAAGAAGATGAAAAGAGAGGAG
droBia1	scf7180000301703:117349-117559 +		CCGTT--AGTCCGCGAC----------AGCAG-T--------TGTC---CTCTTC-----TCGCC----------ACGGCGGCAGCAA----------AATG----------AACAATAA---CAGTGCGTCCATCCAGCACTGGATG---CCAGCAGTA----------GTGTTGTTGT---GTTGTTGCACCGGCAGCGGCAAGCAGCAACTGCA---AGAGCCGTGCAGCTGGAAGTGGTGGTG-------AAGAGGAGTAGCAGCAGCGCAG
droTak1	scf7180000414746:63447-63601 -		CGA---------GC----------AGCAG-T--------TGTC---CTCTTC-----TCGCC----------ACGGCGGCGGCAGCTAG------AATG----------AACAATAA---CAGTGCGCTCCATCCAGCACTGGATG---CCAGCAGCAGTA----------GTGTTGTTGT---GTTGTTGCACCGGCAGCGGCAAGAGC---ACAG---GA---AGTGCG-------AAGCGC--------C----------AGAGCGCAG
droEle1	scf7180000491011:1727310-1727468 +		CCGTT--ACTCCGCGAC----------AGCAG-T--------TGTC---CTCTTC-----TCGCC----------ACGGCGGCAGCAA----------AATG----------AACAATAA---CGGTGCAGTGCCATCCAGCATTGGATG---CCAGCAG----------TGTGTTGTTGT---GTTGTTGCACCGGCAGCGGCGAAGC---AGCAG---GA---AGAGA---GAGAAC--------C----------C----------CCGAGGAG
droRho1	scf7180000778083:144957-145113 -		CCGCG--ACAA------AGG---AACG-----AGCAG-T--------TGTC---CTCTTC-----TCGCC----------ACGGCGGCAGCAA----------AATG----------AACAATAA---CAGTGCAGTGCATCCAGCATTGGATG---CCAGCAG----------TGTGTTGTTGT---GTTGTTGCACCGGCAGCGGCGAAGC---AACAG---GA---AGGCGC--GAGAAC--------C----------C----------CCGCGAGGAG
droFic1	scf7180000453775:107965-108123 +		CCGTT--ACTCCGCGGAACAGCAGAAAC------AGCAG-T--------TGTC---CTCTTC-----TCGCC----------ACGGCGAGCAA----------AATG----------AACAATAA---CAGTGCAGTGCCATCCAGCACTGGATG---CCAGCAG----------T---GTTGTT---GTTGTTCACCGGCAGCGGCGAGAG---GTC---A---AAC---A----TGT---------CGGAT---------C----------CAGGATGAA
droKik1	scf7180000302469:89829-89979 -		CCGTT--AGTCCGCAGC----------AGCAG-T--------GATGAGC------AGCA----------AATG----------GCCATTGTCATCGTCCTCCACTTCCCATAGCAGCAGCAA---CGGTGCAATGCCATCCAGCACTGGATG---CCAGCAG----------T---GTTGTT---GTTGTTCGCCGGC----------C----------C----------C----------C----------C----------CAGAAA
droAna3	scaffold_13117:4322628-4322779 -	dan_4061	TCGTT--AATCCGCGC----------AGCAA-T--------GACCGTTTCT--CCAGCCCGCC----------AATG----------CGGGCAGCAC----------AATG----------AACAGCAG---CATAGCCTAGTCCAGCAATGGATG---CCAGCAGCAGCA----------GCAGCAGCGTGTCCGC---TGTCCGACCCGGCAAGCAGAACGC----------C----------C----------C----------C----------C----------TTATGGAG
droBip1	scf7180000396383:83283-83431 +		TTGTT--AATCCGCGC----------AGCAA-T--TAT---GGCGGTATCTGC----AGCC----------AATG----------CCGGGACGCAT----------AATG----------AGCAGCAGTGAGTGCTCCAGCCAATGGATG---CCAGCAG----------TGTGTTTGTTGTGCGTCGTCCCAGAGCAGAA----------CGG---C---C---T---C---GA----------CC----------C----------C----------GAACAG
dp5	XL_group1e:7670682-7670813 +	dps_3841	CGCC--C-GAGTGAC----------A----A----------C----------C----------CAGGGCTCTGGGTCGGCCCGTCGCTGCTCTCGCCTGATCGGCAA----------AATG----------AACAATAA---CGAA----------C----------C----------C----------C----------CATCAACCAGCACTGGAA---CGAA---C----------C----------C----------C----------C----------GACGCCACCGCCAACGCATCTGCG
droPer2	scaffold_13:885477-885641 -	dpe_2526	CGGTGTCGTCCGCAGCAGCAGC-G-----AGCAATG----------GCC---CGCAGC----GAG----------ACAGGGCTCTGGGTCGGCCCGGCGCTGCTCTCGCCTGATCGGCAA----------AATG----------AACAATAA---CGAA----------C----------C----------C----------C----------CATCAACCAGCACTGGAA---CGAA---C----------C----------C----------C----------C----------GACGCCACCGCCAACGCATCTGCG
droWil2	scf2_1100000004909:7418254-7418456 -	dwi_5065	CGTTT--ACTAGTATAC----------CTCGAATAGCGG-T--------T----A---AC-TCACCAGCTCTCGCCAACGCAGCAAACAGAATTCATCAACACAATCCCAATGTCAAGCTGTGGGTG----AACGCTGTTCTCGCCTAAGAATACAGC----------AGCAGC---GAT----------C----------C----------C----------C----------CACTGTGGC---CTGTTGGGTGGAGCAAGTTC-GTCCACACG---CCCAAAT---C----AT----------TGCTTC-----A----------TGAGAGGAA
droMoj3	scaffold_6473:8732297-8732365 +		CCGCG--T--AGTGGC----------T----A----------C----------C----------TCAGTCTCTGAG----CAGCGCTGCTCCCGAGTGAGTAAT----------AAC----------AACAATAA---GAATCAT----------C----------C----------C----------C----------C----------C----------C----------C----------C----------C----------C----------C----------C----------
droGri2	scaffold_14853:1619163-1619328 -		CCGCG--G-GGAGAA----------AAC-----AGCAT-GCTTGTCGGTG---AGTAC----------A-TAGCAGCAGCAGCGGCAGCAACAACAATGTGC----------AGT---------C---TGCACAGT------TCCAGTG---CCAGCAGCAACAGTTGCAACACC-----CACAACACA---CATCATCGG----------C----------C----------C----------C----------GCAGCAGCTGTTGCAGCATCAAG

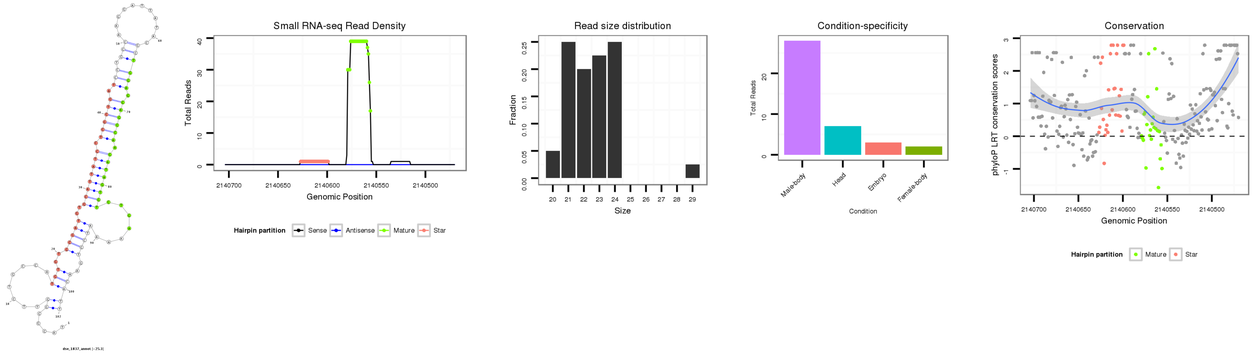
Generated: 09/08/2015 at 07:53 PM

PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	1
crit.top3	1
crit.tpop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	1

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1837	**scaffold_2:2140520-2140654 -**	**candidate-rescued**	**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

	Read size	# Mismatch	Hit Count	Total Norm	Total	M054 V113 male body	M054 V115 female head	V114 embryo
GCAAACAGATATCAAGCCATCTATATATATAGTCGAACCTGCACAAATCAAAAGATCACGTATACGCGGTTCTGCCATGTGTGCGATGTGCATTATCCTGGCTGATCCTGGCAAGGATTATACGCTGGAGCAGCCAAGATAGTGTCTGAAAAATCGTGAACATTCTCAAGCGGAGATCACTGGGCCAATGCAAGTTTTCCTATAGGGGAAACCAGAAAAAAGTTTATTAATAGC								
.....	24	0	1	10.00	10	9	0	1
.....	22	0	1	8.00	8	4	2	2	0
.....	23	0	1	7.00	7	4	0	2	1
.....	21	0	1	6.00	6	5	0	1	0
.....	21	0	1	2.00	2	2	0	0	0
.....	20	0	1	2.00	2	1	0	1	0
.....	21	0	1	2.00	2	2	0	0	0
.....	23	0	1	1.00	1	0	0	0	1
.....	23	0	1	1.00	1	0	0	1	0
.....	20	0	1	1.00	1	0	0	1	0
.....	29	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M054 female body
CGTTTGTCTATAGTTCGGTAGATATATATATCAGCTTGGACGTGTTTAGTTTTCTAGTGCATATGCGCCAAGACGGTACACACGCTACACGTAATAGGACCGACTAGGACCGTTCCTAATATGCGCCTCGTCGGTTCTATCACAGACTTTTTAGCACTTGTAAGAGTTCGCCTCTAGTGACCCGGTTACGTTCCAAAAGGATATCCCCTTTGGTCTTTTTCAAATAATTATCG						
.....	22	0	1	8.00	8	8
.....	23	0	1	7.00	7	7
.....	21	0	1	6.00	6	6
.....	21	0	1	2.00	2	2
.....	20	0	1	2.00	2	2
.....	21	0	1	2.00	2	2
.....	23	0	1	1.00	1	1
.....	23	0	1	1.00	1	1
.....	20	0	1	1.00	1	1
.....	29	0	1	1.00	1	1

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_2:2140470-2140704	dse_1837	GCAAAC---AGATAT----AAGCCATCTAT----------A----------T----ATAT----------AG---TCGAA--CCTGCACAAATCAAA----AGATC----------ACGTATACG------CGGTT-----CTG-CCA[TGTGTGCG-ATGTGCATTATCCTGGC------T=GA]CCTGGCAAGGATTATACGC[TGGAGCAGCCAAGA---------TAGTGTCT-GA]AA----------AATCGTGAA----CATTCTC----------AAGCGGAGATCACTGGGC----------CAATGCA--AGGT----------TTTCC-TATAGGGG-AAACCAGAA----------AAA-AGTTTATTAATAGC-
droSim2	3L:2012794-2013028 -	dsi_32442	GCAAAC---AGATAT----AAGCCATCTAT----------A----------T----ATAT----------AG---TCGAA--CCTGCACAAATCAAA----AGATC----------ACGTATACG------CGGTT-----CTG-CCA[TGTGTGCG-ATGTGCATTATCCTGGC------T=GA]CCTGGCAAGGATTATACGC[TGGAGCAGCCAAGA---------TAGTGTCT-GA]AA----------AATCGTGAA----CATTCTC----------AAGCGGAGATCACTGGGC----------CAATGCA--AGGT----------TTTCC-TATAGGG-AAACCAGAA----------AAA-AGTTTATTAATAGC-
dm3	chr3L:2114883-2115119 -	dme_114	GCAAAC---AGATAT----AAGCATCTAT----------A----------TA---ATAT----------AG---TCGAA--CCTGCACAAATCAAA----AGATC----------ACGTATACG------CGGT----TG-CCA[TGTGTGCG-ATGTGCATTATCCTGGC------T=GA]CCTGCAAGGATTATACGC[TGGAGCAGCCAAGA---------TAGTGTCT-GA]AA----------AATGTGAA----CATTCTG----------AAGGAGATCACTGGGC----------CAATGCA--AGGT----------TTTCC-TATAGGG-AAACCAGAA----------AAA-GTTTATTAATAGC-
droRer2	scaffold_4784|2108748-2108882 -	der_94	GCAAAC---AGATAT----AAGCATCTAT----------A----------T----ATAT----------AG---TCGAA--CCTGCACAAATCAAA----AGATC----------ACGTATACG------CGGT----TG-CCA[TGTGTGCG-ATGTGCATTATCCTGGC------T=GA]CCTGCAAGGATTATACGC[TGGAGCAGCCAAGA---------TAGTGTCT-GA]AA----------AATGTGAA----CATTCTC----------AAGGAGATCACTGGGC----------CAATGCA--AGGT----------TTTCC-TATAGGG-AAACCAGAA----------AAA-GTTTATTAATAGC-
droYak3	2L:2067724-2067957 -	dya_1787	GCAAAC---AGATAT----AAGCATCTAT----------A----------T----ATAT----------AG---TCGAA--CCTGCACAAATCAAA----AGATC----------ACGTATACG------CAGT----TG-CCA[TGTGTGCG-AATGTGCATTATCCTGGC------T=GA]CCTGCAAGGATTATACGC[TGGAGCAGCCAAGA---------TAGTGTCT-GA]AA----------AATGTGAA----CATTCTC----------AAGGAGATCACTGGGC----------CAATGCA--AGGT----------TTTCC-TATAGGG-AAACCAGAA----------AAA-GTTTATTAATAGC-
droEug1	scaffold_4690931:158083-158318 +		GCAAAC---AGATAT----AAGCATCTAT----------A----------T----ATAT----------AG---TCGAA--CCTGCACAATCAAA----AGATC----------ACGTATACG------CAGT----TG-CCA[TGTGTGCG-ATGTGCATTATCCTGGC------T=GA]CCTGCAAGGATTATACGC[TGGAGCAGCCAAGA---------TAGTGTCT-GA]AA----------AATGTGAA----CATTCTG----------AAGGAGATCACTGGGC----------CAATGCA--AGGT----------TTTCC-TATAGGG-AAACCAGAA----------AAA-GTTTATTAATAGC-
droBia1	scaffold_4690932:2281-2837454-2837691 +		GCAAAC---AGATAT----AAGCATCTAT----------A----------T----ATAT----------A---TCGAA--CCTGCACAATCAAA----AGATC----------ACGTATACG------CAGT----TG-CCA[TGTGTGCG-ATGTGCATTATCCTGGC------T=GA]CCTGCAAGGATTATACGC[TGGAGCAGCCAAGA---------TAGTGTCT-GA]AA----------AATGTGAA----CATTCTG----------AAGGAGATCACTGGGC----------CAATGCA--AGGT----------TTCC-TATAGGG-AAACCAGAA----------AAA-GTTTATTAATAGC-
droTak1	scaffold_4690904:144001-142633-142893 -		GCAAAC---AGATAT----AAGCATCTAT----------A----------T----ATAT----------AG---TCGAA--CCTGCACAATCAAA----AGATC----------ACGTATACG------CACA----TG-CCA[TGTGTGCG-ATGTGCATTATCCTGGC------T=GA]CCTGCAAGGATTATACGC[TGGAGCAG-CCAAGA---------TAGTGTCT-GA]AA----------AATGTGAA----CATTCTG----------AAGGAGATCACTGGGC----------CAATGCA--AGGT----------TTTCC-TATAGGG-AAACCAGAA----------AAA-AGTTTATTAATAGC-
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droFic1	scaffold_4690906:453052-945687-945920 +		GCAAAC---AGATAT----AAGCATCTAT----------A----------T----ATAT----------AG---TCGAA--CCTGCACAATCAAA----AGATC----------ACGTATACG------CAGT----TG-CCA[TGTGTGCG-ATGTGCATTATCCTGGC------T=GA]CCTGCAAGGATTATACGC[TGGAGCAGCCAA---------TAGTGTCT-GA]AA----------AATGTGAA----CATTCTG----------AAGAAAGTCTGGGC----------CAATGCA--AGGT----------TTTCC-TATAGGG-AAACCAGAA----------AAA-GTTTATTAATAGC-
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droAna3	scaffold_13337:715292-715597 -	ana_4047	GCAAAC---AGATATC----AGTTTCTAT----------A----------TA---ATAT----------A---TCGAA--AAA-CCAAATCAAA----AGATC----------ACGTATACG------CAGT----TG-CCA[TGTGTGCG-ATGTGCATTATCCTGGC-TCCAGC=GA]CCTGCAAGGATTATACGC[TGGAGCAGCCA---------TAGTGTCT-GA]AA----------AATGTGAA----CATTCTG----------AAGGAGAG-GAATCG----------TTTCC-TATAGGG-AAACCAGAA----------AAA-TATTTATTAATAGC-
droBip1	scaffold_18000039515|42369-42600 -		GCAAAC-GAGATATC----AAGCATCTAT----------A----------T----ATAT----------A---TCAGAGAAA-GA-CAGCAATCAAA----AGATC----------ACGTATACG------CAGT----TG-CCA[TGTGTGCG-ATGTGCATTATCCTGGC------T=GA]CCTGCAAGGATTATACGC[TGGAGCAGCCAA---------TAGTGTCT-GA]AA----------AATGTGAA----CATTCTG----------AAGGAGAG-GAACCAGAA----------AAA-GTTTATTAATAGC-
dp5	XR_group81202010|202202527 -		GCAAAC-GAGATATC----AAGCATCTAT----------A----------TA---ATAT----------GC---TCGAA--CCTGCACAAATCAAA----AGATC----------ATACATATAT-------CG-----AGGGAGGTTGATAAA--GGAGCATGCGA-ATTATCCTGGC------T=GA]CCTGCAAGGATTATACGC[TGGAGCAGCCAAGA---------TAGTGTCT-GA]AA----------AATGTGAA----CATTCTG----------AAGGAGAG-GAACCAGAA----------AAA-GTTTATTAATAGC-
droPer2	scaffold_33|40884-41155 -		GCAAAC-GAGATATC----AAGCATCTATATATATATA----------A----------TA---ATAT----------GC---TCGAA--CCTGCACAAATCAAA----AGATC----------ATACATATAT-------CG-----AGGGAGGTTGATAAA--GGAGCATGCGA-ATTATCCTGGC------T=GA]CCTGCAAGGATTATACGC[TGGAGCAGCCAAGA---------TAGTGTCT-GA]AA----------AATGTGAA----CATTCTG----------AAGGAGAG-GAACCAGAA----------AAA-GTTTATTAATAGC-
droWil2	scaf_11000000047291|1284530-1284754 +		GCAAAC-GAGATATC----AAGCATCTAT----------A----------TA---ATAT----------GC---TCGAA--CCTGCACAAATCAAA----AGATC----------ATACATATAT-------CG-----AGGGAGGTTGATAAA--GGAGCATGCGA-ATTATCCTGGC------T=GA]CCTGCAAGGATTATACGC[TGGAGCAGCCAAGA---------TAGTGTCT-GA]AA----------AATGTGAA----CATTCTG----------AAGGAGAG-GAACCAGAA----------AAA-GTTTATTAATAGC-
droVir3	scaffold_13049|1199061-11993336 +		GCAAAC-GAGATATC----AAGCATCTATAGATATGAATATGCGATCCAATTTAAAGATATCCAATATAGC---AGAT----GA-TCGAA--CCTGCACAAATCAAA----AGATC----------ATAAATATAT-------CG-----AGGGAGGTTGATAAA--GGAGCATGCGA-ATTATCCTGGC------T=GA]CCTGCAAGGATTATACGC[TGGAGCAGCCAAGA---------TAGTGTCT-GA]AA----------AATGTGAA----CATTCTG----------AAGGAGAG-GAACCAGAA----------AAA-GTTTATTAATAGC-
droMoj3	scaffold_6680|8821328-8821449 -		AT-GAC-AGAGAT-CAAGAGTATCTAT----------A----------TAGATATGAATATGCGATCCGCTACAAAGATATCCTAAATAC---AGAT----GA-TCGAA--CCTGCACAAATCAAA----AGATC----------ATACATTATTT-------CG-----AGGGAGGTTGATAAA--GGAGCATGCGA-ATTATCCTGGC------T=GA]CCTGCAAGGATTATACGC[TGGAGCAGCCAAGA---------TAGTGTCT-GA]AA----------AATGTGAA----CATTCTG----------AAGGAGAG-GAACCAGAA----------AAA-GTTTATTAATAGC-
droGri2	scaffold_15110|1143917-1143914 -		GCAAAC-GAGATAT----AAGCATCTAT----------A----------TAAGCGGTCTGATTGAAAGATATCTTACATAC---AGAT----GA-TCGAA--CCTGCACAAATCAAA----AGATC----------ACGTATACG------CCTAGATT---CG-----AGGGAGGTTGATAAA--GGAGCATGCGA-ATTATCCTGGC------T=GA]CCTGCAAGGATTATACGC[TGGAGCAGCCAAGA---------TAGTGTCT-GA]AA----------AATGTGAA----CATTCTG----------AAGGAGAG-GAACCAGAA----------AAA-GTTTATTAATAGC-

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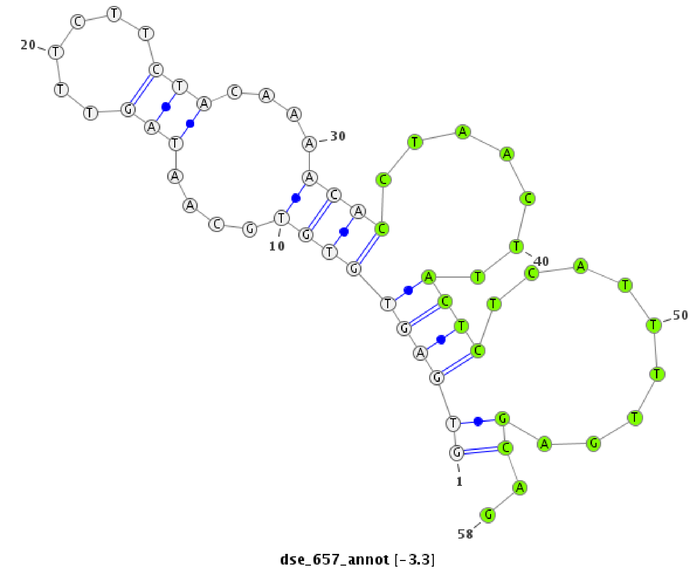
crit.arm	0
crit.half	0
crit.total	1
crit.bias1	1
crit.bias3	1
crit.bias5	1
crit.bias3	1
crit.ori	0
rescue	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.miRNA	1
rescue.candidate	4

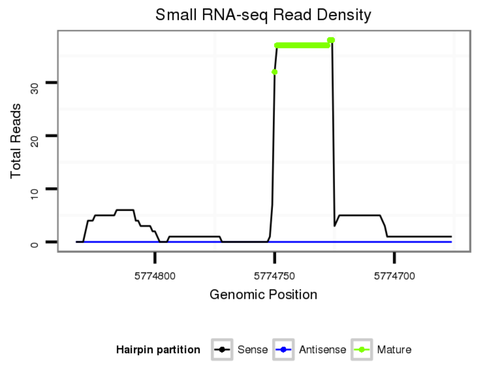
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_657	**scaffold_1:5774726-5774783 -**	**candidate-rescued**	**Mirtron**	**antisense_to_3pUTR**	[View on UCSC Genome Browser (Cornell Mirror)]

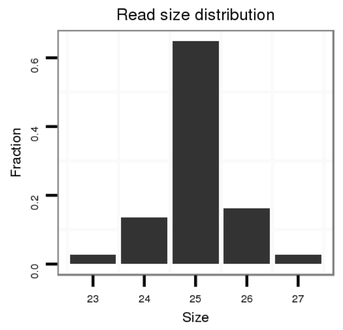
Legend: mature star mismatch in alignment mismatch in read

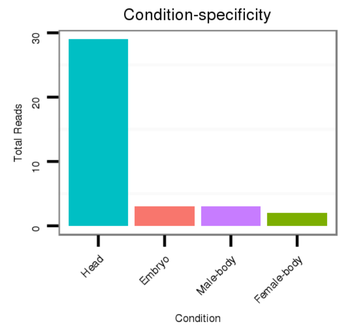
Predicted structure

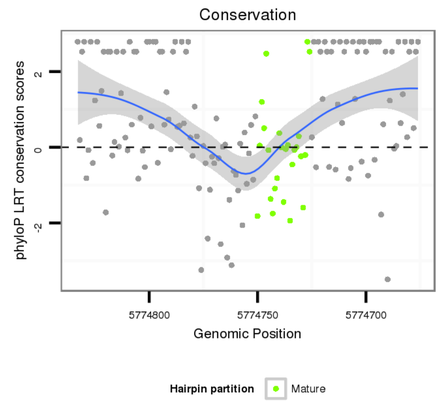


Show Alternate Folds









Flybase annnotation

Antisense to utr3 [utr3_plus_2240]; intron [Dsec\GM20367-in]; CDS [Dsec\GM20367-cds]; CDS [Dsec\GM20367-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTCTTTTGGAGTCGGCCACATCGTTGGCACGGAAAATCCGCAACCAGGAGGTGAGTGTGTGCAATAGTTTCTTCTACAAAACACCTAACTTACTCTCATTTTGAGCAGCTAAGCAGTGTCCAGGTCCTGGAGTCTTTTATCCGACGCATCAAGGAGGT	Read size	# Mismatch	Hit Count	Total Norm	Total	V115 head	V114 embryo	V113 male body	M054 female body
**********(((((((((....(((.....)))....))))).....))))..........))..**********									
.....CCTAACTTACTCTCATTTTGAGCAG.....	25	0	1	24.00	24	21	2	1	0
.....ACCTAACTTACTCTCATTTTGAGCAG.....	26	0	1	6.00	6	5	0	1	0
.....CTAACTTACTCTCATTTTGAGCAG.....	24	0	1	4.00	4	2	1	0	1
....TTTGGAGTCGGCCACATCGTT.....	21	0	1	2.00	2	0	1	0	1
.....CCTAACTTACTCTCATTTTGAGCAGA.....	26	1	1	1.00	1	1	0	0	0
..............ACATCGTTGGCACGGAAA.....	18	0	1	1.00	1	0	1	0	0
.....GCAACCAGGAGGTGAGTGTGTG.....	22	0	1	1.00	1	0	0	1	0
.....CCTAACTTACTCTCATTTTGAGCA.....	24	0	1	1.00	1	0	0	1	0
.....TAAGCAGTGTCCAGGTCCTGG.....	21	0	1	1.00	1	0	0	1	0
.....CTTTTATCCGACGCATCAAGGAGGT	25	0	1	1.00	1	0	1	0	0
.....AAGCAGTGTCCAGGTCCTGGAGT.....	23	0	1	1.00	1	0	1	0	0
.....AGCTAAGCAGTGTCCAGGTCCT.....	22	0	1	1.00	1	0	1	0	0
.....TTGGAGTCGGCCACATCGTTGGCACGG.....	27	0	1	1.00	1	0	1	0	0
.....GAGTCGGCCACATCGTTGGCACGGAA.....	26	0	1	1.00	1	0	1	0	0
.....CACCTAACTTACTCTCATTTTGAGCAG.....	27	0	1	1.00	1	0	0	0	1
.....CTAACTTACTCTCATTTTGAGCA.....	23	0	1	1.00	1	1	0	0	0
.....TTGGAGTCGGCCACATCGTTGG.....	22	0	1	1.00	1	0	1	0	0
.....GCTAAGCAGTGTCCAGGTCCTGG.....	23	0	1	1.00	1	1	0	0	0
.....GCTAAGCAGTGTCCAGGTCCTG.....	22	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

AAGAAAACCTCAGCCGGTGTAGCAACCGTGCCTTTTAGGCGTTGGTCCTCCACTCACACACGTTATCAAAGAAGATGTTTTGTGGATTGAATGAGAGTAAAACTCGTCGATTCGTCACAGGTCCAGGACCTCAGAAAATAGGCTGCGTAGTTCCTCCA	Read size	# Mismatch	Hit Count	Total Norm	Total	M054 female body	V113 male body
**********(((((((((....(((.....)))....))))).....))))..........))..**********								

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_1:5774676-5774833 -	dse_657	TTCTTTTGGAGTCGGCCACATCGTTGGCACGGAAAATCCGCAACCAGGAGGTGAGTGTGTGCAA--------TAG----TTTCT--TCTAC----------------AAAA-CACCTA----AC---------TTACTCTCAT---TTGAGCAGCTAAGCAGTGTCCAGGTCCTGGAGTCTTTTATCCGACGCATCAAGGAGGT
droSim2	2r:8934062-8934219 -	dsi_5234	TTCTTTTGGAGTCGGCCACATCGTTGGCACGGAAAATCCGCAACCAGGAGGTGAGTGTGTGCAA--------TAG----TTTCT--TCTAC----------------AAAA-CACCTA----AC---------TTACTCTCAC---TTGAGCAGCTAAGCAGTGTCCAGGTCCTGGAGTCTTTTATCCGCGCATCAAGGAGGT
dm3	chr2R:8228885-8229042 -	dme_375	TTCTCTTGGAGTCGCCACATCGTTGGCACGGAAAATCCGCAACAGGAGGTGAGTGTGTGCAA--------TCG----TTTCA--TCTAC----------------AAAA-CACCTA----AC---------TTTCATCTAT---CTTGAGCACCTGAGCAGCGTCCAGGTCTTGGAATGCTTTATCCGCGCATCAAAGAGGT
droEre2	scaffold_4845:17563219-17563380 +		TTCTTGTTGGAGTCAGCCACATCGTTGGCGAGGAAAATCCGCAGCCAGGAGGTGAGTGCATGCAG--------TAGAACATACGT--TCTAT----------------AAAA-CACCTA----AC---------ACACTCTCAT---TTTGAGTAGCTAAGCAGCGTCCAGGTCCTGGAGTCTTTTATCCGACGCATCAAGGAGGT
droYak3	2R:8721073-8721230 +		TTCTGCTGGAGCCGGCCACATCGTTGGCGAGGAAAATCCGCAGCCAGGAGGTGAGTGCATGTAG-----TTAGT---TTGGT--TCTAT----------------AAAA-CACCTA----AC---------ACATCTCAT---TGTGAGCAGCTAAGCAGCGTTCAGGTCCTGGAGTCTTCATTCGACGCATCAAGGAGGT
droEug1	scf7180000409462:1887205-1887360 +		TTCTGTTGGAATCGGCCACATCGTTGGCCAGAAGCATCCGCAACCAGGAGGTGAGTGTGTGATG-------TAA----ATCCG--TAGTT----------------AATAATAACTA-----T---------TGTTAT-C-C---TTTTTTCAGTTGAGCAGCGTTCAGGTTTGGAATCGTTCATACGCGCATCAAGGAGGT
droBia1	scf7180000301754:1686756-1686912 +		TTCTACTGGAGTCAGCTACATCGTGGGCAGGAAGCATCCGCAACCAGGAGGTGAGTGCATCAAG-------TAG----TTTATT--TTAAT----------------AAAA-TATCTA-----A---------AATT-TTGA-A---TTCTTTCAGCTGAGTAGTGTCCAGGTTCTGGAGTCTTCATTCGACGCATCAAGAGGT
droTak1	scf7180000415398:78730-78886 -		TTCTCCTTGAGTCAGCCACATCGTGGGCAGGAAGATTCGCAACCAGGAGGTGAGTTTACAAAG-------TAA----TTCTA--TCTAA----------------AGTA-AAGCTA-----T---------ATAT-TAC-T---CTCTTCCAGCTAAGCAGTCCAGGTTTGGAATCGTTCATTCGTCGCATCAAGGAGGT
droEle1	scf7180000491027:123459-123614 -		TACTGTTGCAGTCGGCCACATCGTGGGCAGGAAGATCCGCAACCAGGAGGTGAGTGCATAGAG-------TAA----TCGTT--CTTAT----------------ACTGTTACCTA-----A---------GATTCCG-G---TATTTCAGCTAAGCAGTCCAGGTCCTGGAATGTTCATCCGACGCATCAAGGAGGT
droRho1	scf7180000779469:134491-134646 -		TTCTGTTGGAGTCGGCCACATCGTGGGCAGGAAGATCCGCAATCAAGAGGTGAGTGCAATTAAG-------TAA----TTATA--TACAA----------------AATAATACCTA-----A---------TATTCCC-A---TTATTTCAGCTAAGCAGTGTCCAGGTTCTGGAATCGTTTATCCGCGCATTAAGGAGGT
droFic1	scf7180000453778:303990-304146 +		TTCTGCTGGAGTCAGCCACGTCGTTGGTAGGAAGCATCCGCAACCAGGAGGTAGGTTAATAGC-------TAG----ATCTG-TATCAA----------------GCCA-GAAATA-----T---------GGTTTTC-C---TTTTTCCAGCTAAGCAGCGTTCAGGTCCTGAATCGTTCATAACGCGTATCAAGGAGGT
droKik1	scf7180000302682:2161706-2161863 +		TTCTGCTGGAGTCGCCTCTCGCTGGGCAGAAGATTCGCACCAGGAGGTGAGTTGAGGTAG-------TTA----TTTTT--GTTAT----------------ATTTTTATTAC-----T---------TTTTCAATT---CCTTTCTAGTTGAGCAGCGTCCAGGTCGTCGAATCTTTCATAAGACGCGTCAAGGATGT
droAna3	scaffold_13266:5520914-5521074 -		TTCTGCTAGAATCTGGATCGTGTTGGCAAGAAGCATCCGCAACCAGGAGGTGCGTAGTTGAAAA-AA----GTG----TTGT--GCTTC----------------AAA-TTATGTC-----G---A---ATGATTTA-TTAA-T---TTTCAGTTAAGCAGTGTTCAAGTGCTGGAATCGTTTATTCGACGGTCAAGGAGGT
droBip1	scf7180000395404:57206-57363 +		TCCTGCTAGAATCAGGAACATCAGTGGCCAAAAAGCATCCGCAACCAGGAGGTGCGTTCACGAAA-------CTA----TTTTG-TATCAT----------------A--A-ATACTAATTAT---------TTGGTTCAA-T---TTCCCAGTTAAGCAGTGTCCAAGTGCTGGAATCGTTCATTCGAAGGGTCAAGGAGGT
dp5	3:2793338-2793505 +		TTCTGGTTGAATCGGCATCGTCGTTGGCAGAAAGATACGCAACCAGGAAGTGAGTAGATCTTGATATATGTAG-ATAC-----------ACTAGCCATCAGTA-TAAT------AAC----------TTCTCTCATGTCATCGAATAGCTTAGCAGCGTTCAGGTAATGGAGTCGTTCATACGCGCATCAAGGAGGT
droPer2	scaffold_2:2983317-2983480 +		TTCTGGTTGAATCGGCATCGTCGTTGGCAGAAAGATACGCAACCAGGAAGTGAGTAGATCTTGATA----TAG-ATAC-----------ACTAGCCATCAGTA-TAAT------AAC----------TTCTCTCATGTCATCGAATAGCTTAGCAGCGTTCAGGTAATGGAGTCGTTCATACGCGCATCAAGGAGGT
droWil2	scf2_1100000004558:467069-467236 -		TTCTGTTAGAATCGGGATCATCGTTGGCTAAAAAAATACGAGAGCAAAAGGTGAGCAAAATAGAGG-----TTGAACAT-----TTAA-----AGTCGTCTGG-GTAA-AAGCTA-----T---------TATCTTTA----TCCGTTTAGCTAAGCAGTGTCGAAGTGTTGGAGTCTTTATTGGTCGTATCGAAGAAGT
droVir3	scaffold_12875:6603637-6603795 +		TACTCCTCGAATCGGCCACATCGTGGGCAACCAAAATTCGCAACCAAGAGGTGGACACTTACTT-------TCC----TGTTC--CTGC--ACTGGCCA------TTT---TTA----T---------GCGGTCGTTC---TTTCTCAGCTAAGCAGCGTTCAGGTTCTGGAATCGTTTATAGGTCGCGTTAAGGAAGT
droMoj3	scaffold_6496:23406104-23406269 -		TACTCCTCGAATCGGCCACATCGTGGGCAGAAAAATACGAACCAAGAGGTATAGCGAACTAA--------TCT----TCCAGATGTCAAAGTCTAG---------AAA-TTTA----TA----TTTAT-----TGATCTTTC---TGTTATAGCTAAGCAGTGTTCAGGTTCTGGAATCGTTTATAGCGCATCAAGGAAGT
droGri2	scaffold_15112:1486644-1486803 +		TTCTGGTTGAATCTGGTACAGGATTGGGACCCAAAATTCGCAATCAGAGTAAGTGAAAAAAA--------AAA---AC----TTTTATTTCCTACTC-TAAT------TTC-T---------TTCTTATTTTATTTACAGCTCAGCAGCGTTCAGGTTTGGAGTCGTTTATCCGCGTGTCAAGGAAGT

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	PASS/FAIL
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crit.loop	0
crit.mor	0
crit.half	0
crit.total	1
crit.pairing	0
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crit.tptop3	1
crit.uri	0
crit.back	1
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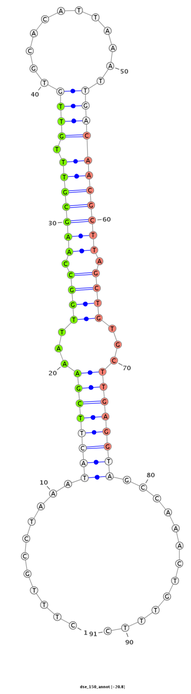
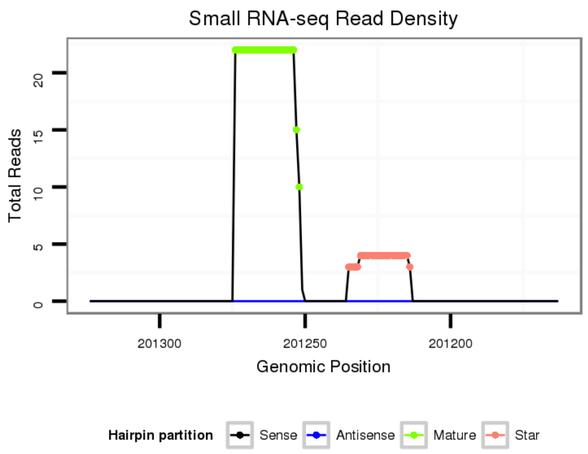
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	3

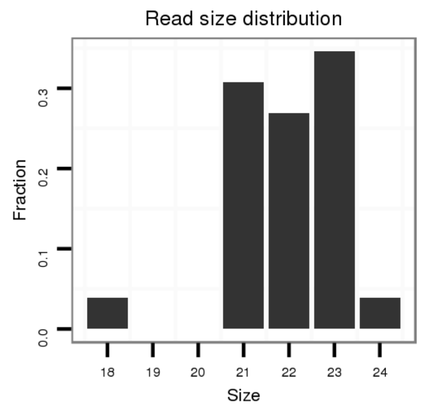
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_150	**scaffold_13:201213-201274 -**	**candidate-rescued**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

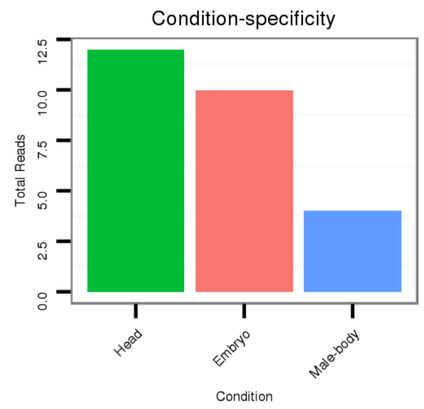
Legend: mature star mismatch in alignment mismatch in read

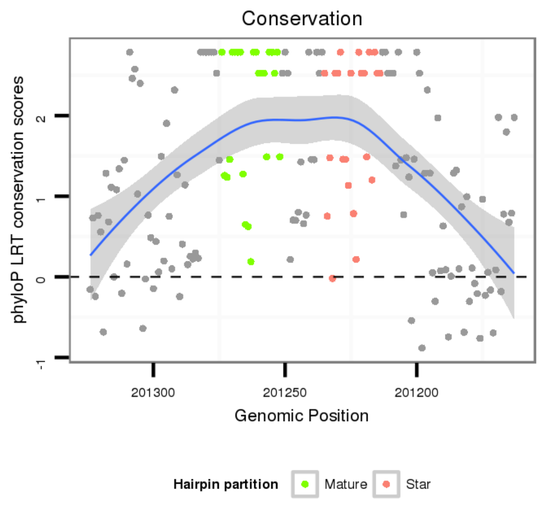
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dsec\GM10251-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GTATGCGTGTGTATCTGTGTCCTGTGCCCTGTGTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCACATTAAATTGACAACGCTTAGCTGTGCTTGAGGTAGCCAAACTGTTTCTACATGCGAAAAGGGTTCGCAAATCATTCTGTGCAT	Read size	# Mismatch	Hit Count	Total Norm	Total	V115 head	V114 embryo	V113 male
************************************.....(((((((((...((((.(((((((.((((...........)))))))))).))))...)))))))).....**********......	size	Mismatch	Count	Norm	Total			body
.....TCGAAATTGGCCAAGCGTTTGTT.....	23	0	1	9.00	9	2	7	0
.....TCGAAATTGGCCAAGCGTTTG.....	21	0	1	7.00	7	4	1	2
.....TCGAAATTGGCCAAGCGTTTGT.....	22	0	1	5.00	5	4	0	1
.....CAACGCTTAGCTGTGCTTGAGG.....	22	0	1	2.00	2	1	1	0
.....CAACGCTTAGCTGTGCTTGAG.....	21	0	1	1.00	1	1	0	0
.....GCTTAGCTGTGCTTGAGG.....	18	0	1	1.00	1	0	1	0
.....TCGAAATTGGCCAAGCGTTTGTTG.....	24	0	1	1.00	1	0	0	1

Anti-sense strand reads

CATACGCACACATAGACACAGGACACGGGACACAGGAAACGGATTTATGAAGCTTTAACCGGTTCGCAAACAACACGTGTAATTTAACTGTTGCGAATCGACACGAACTCCATCGGTTTGACAAAGATGTACGCTTTTCCCAAGCGTTTAGTAAGACACGTA	Read size	# Mismatch	Hit Count	Total Norm	Total	V115 head
************************************.....(((((((((...((((.(((((((.(((((.....)))))))))).))))...)))))))).....**********	size	Mismatch	Count	Norm	Total	

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_13:201163-201324 -	dse_150	GTATGCGT----GT----------GTATCTGTGTCC---TGTGCCCT--GT------GTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCA---CATTA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAACTGTTTCTACATGCGAAAAGGGTT----------CGCAAATCATT-----CT--GTGCAT
droSim2	3r:20925613-20925774 -	dsi_32434	GTATGCAT----GT----------GTATCTGTGTCC---TGTGCCCT--GT------GTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCA---CATTA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAACTGTTTCTACATGCGAAAAGGGTT----------CTCAAATCATC-----CT--GTGCAT
dm3	chr3R:21413218-21413379 -	dme_166	GTATGCGT----GT----------GTATCTGTGTCC---TGTGCCCT--GT------GTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCA---CATTA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAACTGTTTCTACATGCGAAAAGGGTT----------CTCAAATCATC-----CT--GTGCAT
droEre2	scaffold_4820:6629162-6629333 +	der_1511	GTATGCGT----GTGTGTGCTG----------TGTATCTGTGTCC---TGTGCCCT--GT------GTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGCTTGTCGTGCA---CATTA-AATTGACAACGCTTAGCTGTGCCTGAGGTAGCC--AAACTGTTTCAACATGCGAAAAGGGTT----------CTGCAGTCATC-----CT--GTGCAT
droYak3	3R:25065958-25066128 +	dya_69	GTATGCGT----GT----------GTATCTGTGTCC---TGTGCCCT--GT------GTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCA---AATTC-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAACTGTTTCAACATGCGAAAAGGGTT-CATCTG--GCCATCATCCTGTTCGT--GTGCAT
droEug1	scf7180000409798:1138182-1138352 +		GTGTGTGTATCTGT----------GTACTGTGTCC---TGTGTGTCT--GT------GTACTTTGCCTAAATACTTCGAAATTGGTTAAGCGTTTGTTGTGCG---CATCA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAAATGTTTCATCAT----------CATTATCTGCATCTGCATCTGC-ATCACGC-----CT--CGGCAT
droBia1	scf7180000302136:2259458-2259621 -		GTATGCGT----GT----------GTATCTGTGTCC---TACGTCCTGTGTGTACTTTGTACTTTGCCTAAATACTTCGAAATTAACCAAGCGTTTGTTGTGCG---CATCA-AATTGACAACGCTTAGCTTGCTTGAGGTAGCC--AAATCGTTTCCACATGCGAACAGGGTG----------------------------CTG--------GT-GGTGCAT
droTak1	scf7180000415257:293331-293501 -		GTGTGTGT----GTGTATGCGTC----------TGTATCT-----C---TGTGTCCTGTGA------GTACTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCG---CATCA-AATTGACAACGCTTAGCTTGCTTGAGGTAGCC--AAATTGTTTCAACATTCGAACAGGATG----------TG----------------------CTGCATTATC-----CT--CTGCAT
droEle1	scf7180000491280:3121543-3121695 -		GTGTGTGT----GT----------GTATCTGTGTCATGTGTGT-GT--GT------GTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGTC---CATCA-AATTGACATCGCTTAGCTGTGCTTGAGGTAGCC--AAATTGTATTCTACATGCAAAGGGGTA--CT--CTGCAT
droRho1	scf7180000779501:512629-512766 +		GTGTGTGT----GT----------TATCTGTG---T-----CCT--GC------GTCCTTTGCCTAAATACTTCGAAATTGGCTAAGCGTTTGTTGTGTC---CATCA-AATTGACAATGCTTAGCTGTGCTTGAGGTAGCC--AAATTGTTTCTACATTCAAACGG-GG--TC-----CT--CTGCAT
droFic1	scf7180000454055:1329847-1330007 -		GTGCGTGT----GC----------GTGTATGTGTG---TGTGCC---T------GTCCTTTGCCTAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCG---CATCA-AATTGACAACGCTTAGCCGTGCTTGAGGTAGCC--AAATTGATTCTACGAGCAAAGG-GG-T----------GACAACGAGG----------AATGCA-----CT--CTGCAT
droKik1	scf7180000302639:1624824-1624976 +		GTGTGGCG---GC----------CTGTG-----G---GGTCCTGTGT------GT-GTTTGCATAAATACTTCGAAATTGGCCAAGCGTTTGTTGTGCT---TATCA-AATTGACAACGCTTAGCTGTGCTTGAGGTAGCC--AAATTGTTTCAACAGACGCGGAAG----------AG-------A------GGGTG-------CGG--G---TG-----CT-GGTGCAT
droAna3	scaffold_13340:3669026-3669164 -		ATCCGTGT----GT----------TTGTGTGTGTGA---TGA-----G---GTCTGCCTAAATACTTCGAAATTGGCTAAGCGTTTGTTGTGAT---TACCA-AATTGACAATGCTAAGCTGTGCTTGAGGTAGCC--AAGATAAATCTACAA-----CAGG--AC-----CTCGTTGCAT
droBip1	scf7180000396712:683547-683685 +		CCATCCGT----GT----------GTCTGTGTGT---G---------GT------GACG-CTGCCTAAATACTTCGAAATTGGCTAAGCGTTTGTTGTGAT---TATCG-AATTGACAATGCTAAGCTGTGCTTGAGGTAGCC--AAGATGTAATCTACAC--GAACAGG--AC-----CTCGTTGCAT
dp5	2:21156523-21156738 -	dps_3835	ATGTGTGA----GTGTATCTGCATGTGTCACCGTATCTGTATCTGTATCC---TGTATC-T--CC------GTCTTCG-TTAAATACTTCGAAATTGGTTAAGCGTTTGTTGTGCT---TATTA-AACTGACAAAGCTTTGCCGTGCTTGAGGTAGCC-CTAATTGATTCCACAAACGACA------TCACCTGAAGAGGATGAGTGACACACATGACTGTGTGTGTGTGTGT---------TT-----GT--GTGTGT
droPer2	scaffold_3:3931022-3931219 -	dpe_2496	GCATGTGT----CA----------CCGTATCTGTATCTGTATCC---TGTATC-T--CC------GTCTTCG-TTAAATACTTCGAAATTGGTTAAGCGTTTGTTGTGCT---TATTA-AACTGACAAAGCTTTGCCGTGCTTGAGGTAGCC-CTAATTGATTCCACAAACGACA------TCACCTGAAGAGGATGAGTGACACACATGACTGTGTGTGTGTGTGT----------GT--GTGTGT
droWil2	scf2_1100000004943:14640096-14640209 +		GTGTGTTGT----GT----------GTGTGTGTGTG---------GT------GGACTTAAATACTTCGAAATTGCATTAAGCGTTTGTTGTGTTCCATTTCA-ATTTGACTATGCTTAACTAATGCTTGAGGTAGCCTCTAATTGCTTC----------CT--CT--GTGCAT
droVir3	scaffold_12855:6808868-6808987 -	dvi_24643	TTGTGCGT----GC----------GTGTGTGT----G---------GT------GTGCTTTTCTAAATACTTGAAATTGGTTAAGCGTTTGTTGTGCT---TATCA-AATTGAGCACGCTTAACTGTGCTTCAGGTAGCC--TAATTGCTTCACAACGC----------CT--CT--GTGCAT
droMoj3	scaffold_6540:25792877-25793004 +	dmo_3123	ATGTGTGAGT----GT----------GTGTGTGTGTA---G-------TGTGT------GTACGCTTGCTAAATACTTCGAAATTGGTTAAGCGTTTGTTGTGCT---TATCA-AATTGACAACGCTTAACTGTGCTTGAGGTAGCC--TAATTGTTTCAACAGC----------CT--CT--GTGCAT
droGri2	scaffold_14906:2963137-2963259 -	dgr_468	TTGTGTGT----GT----------GAGTGTGTGTCG---A-------G---GTACCGGCGCTAAATACTTCTCAATTGGTTAAGCGTTTGTTGTGCT---TATCA-AATTGACAACGCTTAACTATGCTTGAGGTAGCC--TAATTGTTTCAACAGC----------CT--CT--GTGCAT

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

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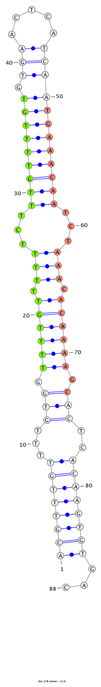
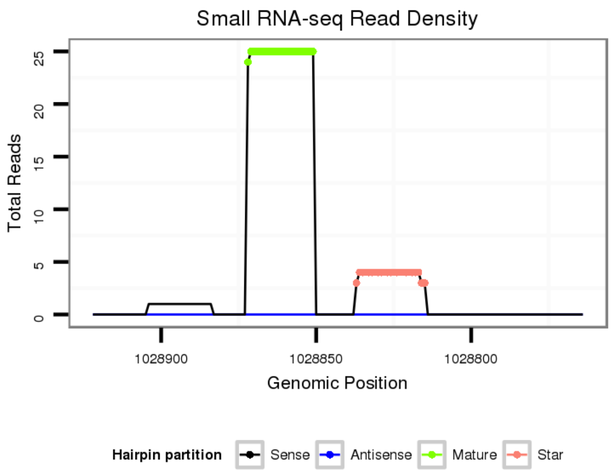
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	8

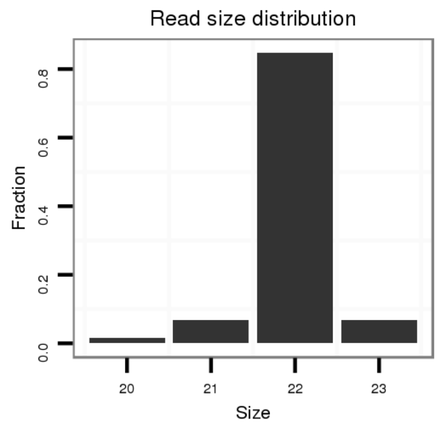
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_158	**scaffold_19:1028814-1028872 -**	**candidate-rescued**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

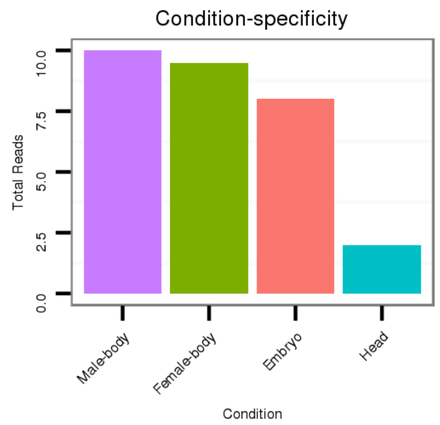
Legend: mature star mismatch in alignment mismatch in read

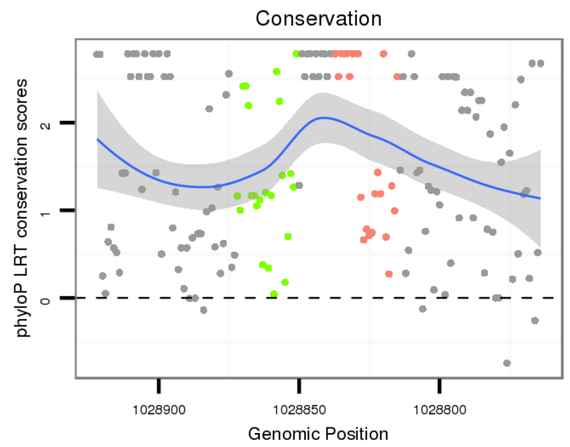
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dsec\GM14895-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTTCAGCGTTTTGAAGGTCGTTTCCACTGTTATTCACGTTTGTTTTGTGGTTTTGTTTTTTCTTTGTTTTGTGTGAACTCATCAATGAAACAATCTAAACACAAAAGCACTCACAAGTGTGACACAGAACGTGACAAAAAAAAATATATAAAAAAACTA	Read	#	Hit	Total		V113 male	M054 female body	V114 embryo	V115 head
((((((((...(((.((((((.(((...((((((((.(((.....)))))))))))...))).)))))).))))..))))))...**********	size	Mismatch	Count	Norm	Total	body				
.....TTTTGTTTTTTCTTTGTTTTGT.....	22	0	1	24.00	24	9	6	7	2
.....TGAAACAATCTAAACACAAAAGC.....	23	0	1	2.00	2	0	2	0	0
.....TGAAACAATCTAAACACAAAA.....	21	0	1	1.00	1	0	1	0	0
.....TTTGTTTTTTCTTTGTTTTGT.....	21	0	1	1.00	1	1	0	0	0
.....GAAACAATCTAAACACAAAAGC.....	22	0	1	1.00	1	0	0	1	0
.....CGTTTCCACTGTTATTCACGT.....	21	0	1	1.00	1	1	0	0	0
.....TTTTGTTTTTTCTTTGTTTT.....	20	0	2	0.50	1	0	1	0	0

Anti-sense strand reads

AAAGTCGCAAAACTTCCAGCAAAGGTGACAATAAGTGCAAACAAAACACCAAAACAAAAAAGAAACAAAACACACTTGAGTAGTTACTTTGTTAGATTTGTGTTTTCGTGAGTGTTCACACTGTGTCTTGCACTGTTTTTTTTTATATATTTTTTTGAT	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
droSec2	scaffold_19:1028764-1028922 -	dse_158	TTTCAGCGT-TTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTGTT-----TTGTGGTTT-TGTTTTT----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACAAAA-GG-ACTCAC-AAGTG----------TGACACAGAA-------CGTGACAAAAAAAAATAT---A----------TAAAAAAACTA
droSim2	3L:18687174-18687331 -	dsi_96	TTTCAGCGT-TTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTGTT-----TTGTGGTTT-TGTTTTT----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACAAAA-GG-ACTCAC-AAGTG----------TGACACAGAA-------CGTGACAAATAAA--TATAA-A----------AAAAAAAACTA
dm3	chr3L:19064540-19064700 -		TTTCAGCGT-TTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTGTT-----TTGTGGTTT-TGTTTTT---------TT------TCTTTG-------TTTTGTATGAACTCATCAATGAAACAATCT----------AAA--CACAAAA-GG-ACTCAC-AAGTG----------TGACACAGAA-------CGTGACAAAAAAA--TATAA-A----------AAAAAAAACTA
droEre2	scaffold_4784:18883315-18883468 -	der_109	TTTCAGCGA-TTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTGTT-----TTGTGGTTT-TGTTTTT----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------GAA--CACAAAA-GG-ACTCAC-AAGTG----------TGACACAGAA-------CGTGACAAAAAAA--TATA---A----------AAAAACTA
droYak3	3L:21530478-21530631 +	dya_1781	TTTCAAGGA-TTTGAAGGTC---GTT-TCCACTGTTATTCTCGTTTGTT-----TTGTGGTTT-TGTTTTT----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACAAAA-GG-ACTCAC-AAGTG----------TGACACAGAA-------CGTGACAAAAAAA--TATAA-A----------AAAAACTA
droEug1	scf7180000409471:411256-411422 +		TTTCAAGGT-TTTGAAGGTC---GTT-TCCACTGTTATTCGCGTTTGTT----TTTGTGATTT-TGCCTTTTC-----TTG------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACAAAA-GG-ACTCAC-AAGTG----------TGACACAGAA-------CGTGACAAAAAAA--TATAAAA----------AAGAAAAACTA
droBia1	scf7180000302529:420860-421014 +		TTCCAAGGT-TTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTGTT----TTCGTGGCTT-TGTTTTC----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACAAAA-GG-ACTCAC-AAGTG----------TGACACAGAA-------CGTGACAAAAA-A--TACA--A----------AAAAAATTA
droTak1	scf7180000414021:74768-74925 -		TTCCAAGGT-TTTGAAGGTC---GTT-TCCACTGTTATTCACGTTTGTT----TTGTGGTTT-TGTTTTT----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACAAAA-GG-ACTCAC-AAGTG----------TGACACAGAA-------CGTGACAAAAAAA--TATAA--A----------AAAACGAACTA
droEle1	scf7180000491249:6350653-6350810 -		TTTCAAGGT-TTTGAAGGTC---GTT-TCCACTGTTATTCACGATTGTT----TTGTGGTTT-TGTTTTC----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACAAAA-GG-ACTCAC-AAGTG----------TGACACAGAA-------CGTGACAAAAAAA--TATA---A----------AAAAAAAACTA
droRho1	scf7180000758657:8-166 +		TTTCAAGGTTTTTGAAGGTC---GTT-TCCACTGTTATTCACGATTGTT----TTGTGGTTT-TGTTTTT----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACAAAA-GG-ACTCAC-AAGTG----------TGACACAGAA-------CGTGACAAAAAAA---ACA---A----------AAAAAAAACTA
droFic1	scf7180000453824:438433-438582 -		TTTCAAGGT-TTTGAAGGTC---GTT-TCCACTGGTGTTCACGATTGTT----TTTGTGGTTT-TGTTTTT----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCC----------AAA--CACAAAA-GG-ACTCAC-AAGTG----------TGACACAGAA-------CGTGACAAAAA-------AAA---A----------AAAACAGTA
droKik1	scf7180000302251:117780-117960 -		TTTCAAGGT-TTTGAAGGTC---GTT-TCCACTGTTATTCACGATTGCT----TTTGTGGTTTTGTTTTT-GTT--TTTCG------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACAAAA-GG-ACTCAC-AAGTG----------TGACACAGAA-------CGTGACAAAAAAG--TATAA-AAAAAAATAA--ACGAAAAAAAACTA
droAna3	scaffold_13337:18377662-18377822 +		TTTTCAAAG-CCTGAAGATC---GTT-TCCACGGA----------GCT----GTTGTGGTTT-TGTTTTT----------TCTTTG-------TTTTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACAAAA-GG-ACTCAC-AAATA----------TGACACAGAA-------CGTGACAAATAAA--TAAAA--AGAAAAAAATGACAAAAAAAACTA
droBip1	scf7180000396741:1561617-1561765 +		TTTCAAGGC-TTTGAAGGTC---GTC-TCCACAGT----------GTT----ATTGTGGTTT-TGTTTT----------------------------GTGTGTGAACTCATCAATGAAACAATCT----------AAA--CACAAAA-GG-ACTCAC-AAATA----------TGACAGAGAA-------CGTGACAAATAAA--TAAAA--AAAAACA---GCAAAAAAAAACTA
dp5	XR_group8:7140825-7140969 -		----AAGGT-TTTGAAGGTC---GTTTTGCACTGT---------GTGTT----TCTGTGGTTT-TGTTTC--GCTCTTTTTGCCCATTTGTGTG-------TGTGATGTGAACTCATCAATGAAACAATCC----------CAAACACACAAAA-GGCACTCAC-AAGTG----------TCACACAAA--------------------------AAAAAAA-CA
droPer2	scaffold_36:165555-165705 +		TTCAAAGGT-TTTGAAGGTC---GTTTTGCACTGT---------GTGTT----TCTGTGGTTT-TGTTTC--GCTCTTTTTGCCCATTTGTGTG-------TGTGATGTGAACTCATCAATGAAACAATCC----------CAAACACACAAAA-GGCACTCAC-AAGTG----------TCACACAAA--------AA---------AAAAACA-CA
droWil2	scf2_1100000004762:3231747-3231876 +		TTGAAAACTTTTTGAAGGTCATTGTT-TCCACTTA----------A--------------TGTGTG-------CTGTGTGTGAACTCATCAATGAAACAATAC----------ACA--CACACGC-AG-ACACAC-AACAG----------CACAGAGAA-------CGTGACAAAACAA---AA---A----------AAAAAAAATCA
droVir3	scaffold_13049:13362168-13362290 -		TTTTCACGT-TTTGAAGGTC---GTT-TCCACTGT---AGGCGATTCTTG---TCAGTGTTAT-TGTTGTT----------GCGAT-------TATTGTGTGAACTCATCAATGAAACAATAC----------AGAGAACCCAACACAG-ACACAC-AAATG----------TG---------------------------------------
droMoj3	scaffold_6680:13991813-13991990 +		TTTTCACGT-TTTGAAGGTC---GTT-TCCACTGTGCGCGAATCTTGTC-ATTGTTGTCG--T-TGTTGTT-GCTCT---TG------TGCTGCTGCGATTATTGTGTGAACTCATCAATGAAACAATACAGAAAGAATCGTGGACAAA--CACACA--C-ACTTACACTCTG----------TGTATATAAAGGCCGATGTGAT----------------AAGCA
droGri2	scaffold_15110:18794186-18794314 -		TTTTCACGT-TTTGAAGGTC---GTT-TGCACTGT---GCACGTT-GTT----ATTGTTGT--------------------------TGTTGTGTGAACTCATCAATGAAACAATAC----------AATGGAGACAACA-AGAGCGCAC-AAGCGAACTGCTTTTGG-------------------------A----------CAGAGATACTA

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

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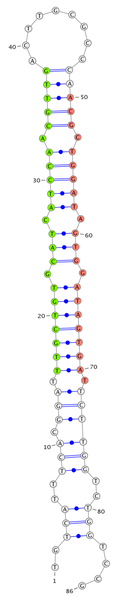
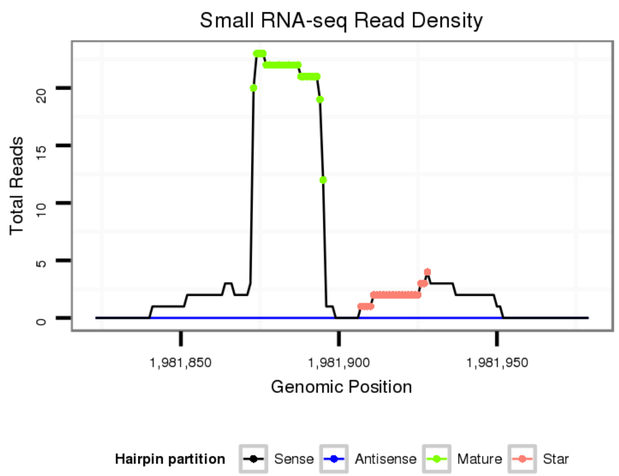
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	2

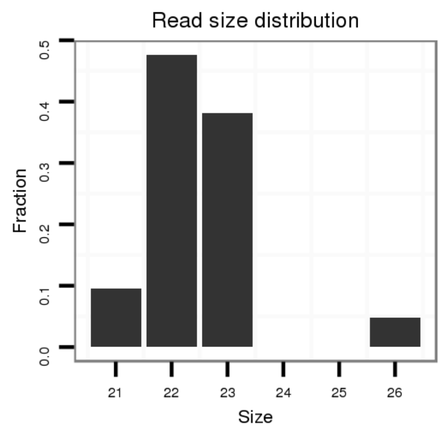
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_153	**scaffold_12:1981873-1981929 +**	**candidate-rescued**	**Canonical miRNA**	**3pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

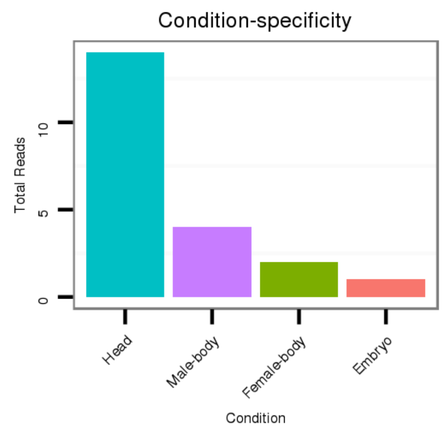
Legend: mature star mismatch in alignment mismatch in read

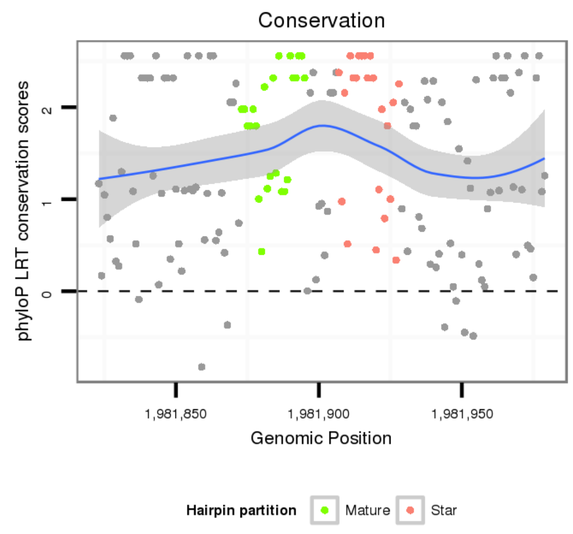
Predicted structure











Show Alternate Folds

Flybase annnotation

utr3 [utr3_minus_7866]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AACCGCGTATTTCTTGGCCTTCGCGCCCCTGTCGTTGTCATTTCACGGATTTGCTGTGCATCATCCAACGTTGACTTGCGCCCAACGCTGGATAGTGGATAGTGATTCTTGGTCTGGTCCGATCCGATACGTTCCGGTCTCCCTCTGTCTCGCCTCT **********..(((..(((.(((.(((((((.(((.((((((.((((((.........)))))).)))))).)))..)))))))..)))))))..)))....**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V115 head	M054 female body	V113 male body	V114 embryo
.....TTGCTGTGCATCATCCAACGTTG.....	23	0	1	8.00	8	4	1	2	1
.....TTGCTGTGCATCATCCAACGTT.....	22	0	1	6.00	6	5	0	1	0
.....TGCTGTGCATCATCCAACGTTG.....	22	0	1	3.00	3	3	0	0	0
.....TTGCTGTGCATCATCCAACGT.....	21	0	1	2.00	2	2	0	0	0
...........TGTCGTTGTCATTTCACGGATTTGC.....	25	0	1	1.00	1	0	1	0	0
.....TTTGCTGTGCATCATCCAACGTT.....	23	0	1	1.00	1	0	0	1	0
..............CTTCGCGCCCCTGTCGTTGTCATTTC.....	26	0	1	1.00	1	0	1	0	0
..........TTCACGGATTTGCTGTGCATCATC.....	24	0	1	1.00	1	0	1	0	0
.....TTCTTGGTCTGGTCCGATCCGATA.....	24	0	1	1.00	1	0	1	0	0
.....TGGATAGTGGATAGTGATTCTTGGTC.....	26	0	1	1.00	1	0	1	0	0
.....GATTCTTGGTCTGGTCCGATCCGA.....	24	0	1	1.00	1	0	1	0	0
.....ACGCTGGATAGTGGATAGTGAT.....	22	0	1	1.00	1	0	0	1	0
.....TTGCTGTGCATCATCCAACGTTGACT.....	26	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

TTGGCGCATAAAGAACCGGAAGCGCGGGGACAGCAACAGTAAAGTGCCTAAACGACACGTAGTAGGTTGCAACTGAACGCGGGTTGCGACCTATCACCTATCACTAAGAACCAGACCAGGCTAGGCTATGCAAGGCCAGAGGGAGACAGAGCGGAGA **********..(((..(((.(((.(((((((.(((.((((((.((((((.........)))))).)))))).)))..)))))))..)))))))..)))....**********	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
droSec2	scaffold_12:1981823-1981979 +	dse_153	AA-CCGCGTATTTCTTGGCC--------TTCGCGCCCC----------TGTCGTTGT-------CATTTCA---CGGATTTGCTGTGCATCATCC-AACGTTGACTTGCGCCCAACGCTGGATAGTGGATA-----GTGATTCTTGGTCTGGT-----CCGATCCGATACGTTCCGGTCTCCCTCTGTCTC---GCCTCT
droSim2	3r:9085278-9085434 +	dsi_32444	AA-CCGCGTATTTCTTGGCC--------TTCGCGCCCC----------TGTCGTTGT-------CATTTCA---CGGATTTGCTGTGCATCATCC-AACGTTGACTTGCGCCCAACGATGGATAGTGGATA-----GTGATTCTTGGTCTGGT-----CCGATCCGATACGTTCCGGTCTCCCTCTGTCTC---GCCTCT
dm3	chr3R:12165038-12165194 -	dme_390	AA-CCGCGTATTTCGTGGCC--------TTCGCGCCCC----------TGTCGTTGT-------CATTTCA---CGGATTTGCTGTGCATCATCC-AACGTTGACTTGCGCCCAACGCTGGATAGTGGATA-----GTGGTCTTGGTCTGGT-----CCGATCCGATGCGTTCCGGTCTCCCTCTGTCTC---GCCTCT
droEre2	scaffold_4770:11691441-11691597 -	der_1538	AA-CCGCGTATTTCGAGGCC--------TTCCGCGCCC----------TGTCGTTAT-------CATTTCA---CGGATTTGCTGTGCATCATCC-TACGTTGACTTGCGCCCAATGCTGGATAGTGGATA-----GTGGTCTTGGTCTGGT-----CCGATCCGATCCGTTCCGGGCTCCCTCTGTCTC---GCCTCT
droYak3	3R:14251362-14251523 +		AA-CCGCGTGTTTCGTGGCC--------TTTGCGCCTC----------TGTTGTTAT-------CATTTCA---CGGATTTGCTGTGCATCATCC-TACGTTGACTTGCGCCCAACGCTGGATAGTGGATA-----GTGGTTCTTGGTCTGGTCTGGTCCGATCCGATCCGTTCCGGTCTCCCTCTGTCTC---GCCTCT
droEug1	scf7180000409557:389434-389590 +		AA-CCGCGTATTTCGAGGCC--------TTTGCGCCCC----------TGTCGTTCA-------CATTTCA---TGGATTTGCTGTACATCATCC-AACGTTGACTTGCGCCCAACGCTGGATAGTGGATA-----GTGGTCTTGGTCTGGT-----CCGCTGCGATCCGTTCCGAGTCTCCCTCTGTTTC---GCCTCT
droBia1	scf7180000299102:89087-89243 -		AA-CCGCGTATTTCGAGGCC--------TTCGCGCCCC----------TGTCGTTAT-------CATTTCA---CGGATTTGCTGTGCATCATCC-AACGTTGACTTGAGCCCAACGCTGGATAGTGGATA-----GTGGTCTTGGTTTGGT-----CCGCTCCGATTCGTTCCTGTCTCCCTCAGTCTC---GCCTCT
droTak1	scf7180000415580:530550-530706 +		AT-CCGCGTATTTCGAGGCC--------TTCGCGCCCC----------TGTCGTTGT-------CATTTCA---CGGATTTGCTGTGCATCATCC-AACGTTGACTCGCGCCCAACGCTGGATAGTGGATA-----GTGGTCCTGGTCTGGT-----CCGCTCCGATTCGATCCGGTCTCCCTCTGTCTC---GCCTCT
droEle1	scf7180000490967:406830-406986 -		AA-CCGCGTATTTCGAGGCC--------TTCGCGCCCC----------TGTCGTTGT-------CATTTCA---TGGATTTGCTGTGCATCATCC-AACGTTGCCTTGCGCCCAACGATGGATAGTGGATA-----GTGGTCTTGGTCTGGT-----CCGCTCCAATCCGGTCCGGTCTCCCTCTGTCTC---GCCTCT
droRho1	scf7180000776828:26653-26809 +		AA-CCGCGTATTTCGAGGCC--------TTCGCGCCCC----------AGTCGTTAT-------CATTTCA---TGGATTTGCTGTGCATCTTCC-AACGTTGACTTGCGCCCAACGCTGGATAGTGGATA-----GTGGTCTTGGTCTGGT-----CCGCTCCGATCCGTTCCGGTCTCCCTCTGTCTC---GCCTCT
droFic1	scf7180000453580:91107-91263 -		AA-CCGCGTATTTCGAGGCC--------TTCGCGCCCC----------TGTCGTTAT-------CATTTCA---CGGATTTGCTGTGCATCATCC-AACGTTGACTCGCGCCCAACGCTGGATAGTGGATA-----GTGGTCTTGGCCTGAT-----CCGCTCAGATCCGATCCAGTCTCCCTCTGTCTC---GACTCT
droKik1	scf7180000302307:375667-375813 -		AA-CCGCGAATTTCAGGGCC--------TTCGCGCCCC----------AGTCGTTAT-------CATTTCA---CGGATTTGCTGTGCATCATCC-AACGTTGCCTTGCGCCCAACGCTGGATAGTGGATA-----GTGATCCCTGGTCTGGT-----GTGG----------TCCGGTCTCCCTCTGTCTC---GTCTCT
droAna3	scaffold_13340:15515709-15515850 -	dan_4044	AA-CCGCGTATTTCGAGGCC--------TTTGCGCCCC----------AGTCGTTGT----GT-CATTGAC---AGGATTTGCTGTGCATCATCC-AACGTTG-CTTGCAGCCAACGCTGGATAGTGGATA-----GTGGTCGTTGGTCTGCT-----CCGC----------CTCCCTCTTTCTT---GCCTCC
droBip1	scf7180000396708:4517217-4517357 +		AATCCGCGTATTTCGAGGCC--------TTGCGCCCC----------AGTCGTTGT-------CATAAAC---AGGATTTGCTGTACATCATCC-AACGTTG-CTAGCAGCCAACGCTGGATAGTGGATA-----GTGGTCTTGGTCTGCT-----CCGC----------CTCCCTCTTTCTT---GCCTCC
dp5	2:22444142-22444303 +	dps_3838	AC-AC--TCATTTCGTGGCC--------TTTGCGCCCTGTGCCCTCCATGTCGATATCGCTATCCATGTCAATCAGGAGTTGCTGTGGCACATTTGAACGTTG----------CTGGATAGTGGCTGGCCGTGTGGTGCTTGGTCTGGT-----TTGATCTCAGCG-CTCTGGTCTCCCT----CTC---GTCTTT
droPer2	scaffold_3:5224950-5225111 +		AC-AC--TCATTTCGTGGCC--------TTTGCGCCCTGTGCCCTCCATGTCGATATCGCTATCCATGTCAATCAGGAGTTGCTGTGGCACATTTGAACGTTG----------CTGGATAGTGGCTGGCCGTGTGGTGCTTGGTCTGGT-----TTGATCTCAGCG-CTCTGGTCTCCCT----CTC---GTCTTT
droVir3	scaffold_13047:1793975-1794089 -	dvi_24648	CA-C-----ATTTCGTGGCC--------TTTTCGACCA----------TATGAATGG-------AATTTCA---CGGA----------TCATCC-AACGTTGTCTTGCGCCCAACGCTGGATAGTGTC--------------------------CGGTCG------TTAAGATCTTCCTCTATCTT---TCCTCT
droMoj3	scaffold_6540:15377815-15377928 +	dmo_3159	CA-C-----ATTTCGTGGCC--------TTTTCGACCA----------TATGAATGG-------AATTTC---------GCATCATCC-AACGTTGTCTTTGACCCAACGCTGGATAGTGTC--------------TGGT-----CG----------TTAAGATCTTCCTCTATCTC---TCCTCT
droGri2	scaffold_14906:12613627-12613756 -		CT-CACCACATTTGTGGCCAAAAAAACCTTTCGCCCA----------TATGAATGG-------AATTTC---------CGCATCATCC-AACGTTGTCTTGCGCCCAACGCTGGATAGTGCC--------CGGTCCT---------------TGTGATCTTCCTCTATCTCTCTACCTCT

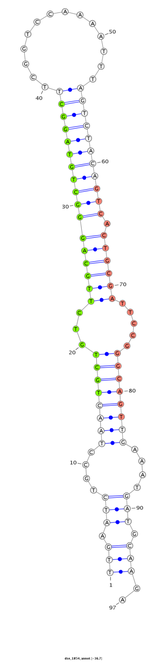
Generated: 09/08/2015 at 07:44 PM

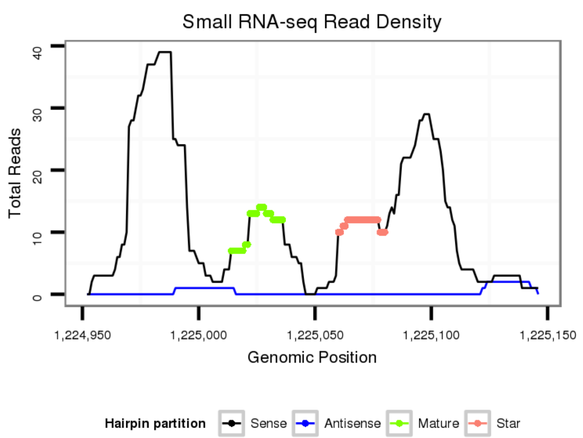
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	2

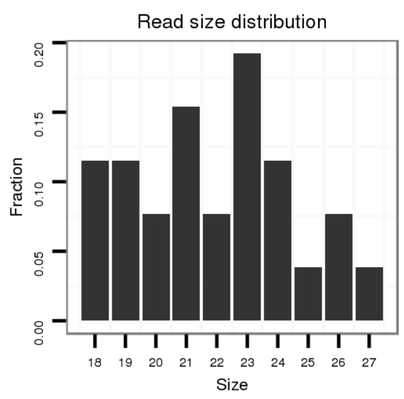
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1854	**scaffold_5:1225002-1225096 +**	**candidate-rescued**	**Canonical miRNA**	**3pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

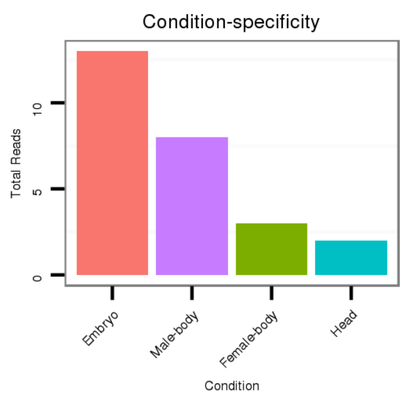
Legend: mature star mismatch in alignment mismatch in read

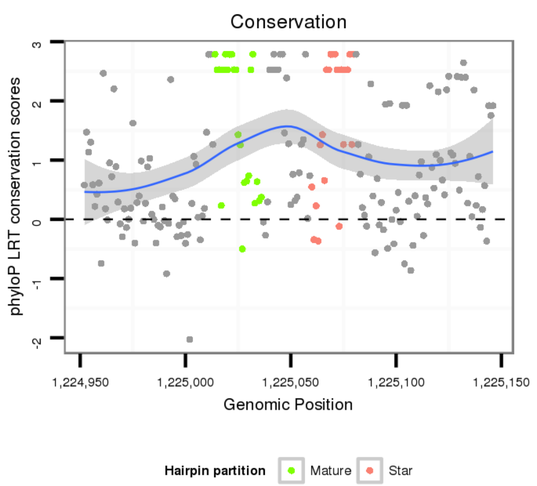
Predicted structure











Show Alternate Folds

Flybase annnotation

utr3 [utr3_plus_232]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CACAGCTAGAAGAGATAAGTCAACAGATTGGATTTGCGTCGATCGGCTTGAATCTGCCTAACTGCTGTCTTGCAGGGCTGTAGGCTTCGGTCCAAAATTTAGTCTACAGTCACTGCGATTCCGGGGCAGTTGAAATGATGCAAGATGAGAGGCCCAGTCCATAACACTTAACGCTTTGTGCACCGTACAATTCAGT	Read size	# Mismatch	Hit Count	Total Norm	Total	V114 embryo	V113 male body	V115 head	M054 female body
**********(((.(((....(((((((...(((((((((((((((((.............)))))))))))).))))))....)))))))....))).)))..**********									
..................GTCAACAGATTGGATTTGC....	19	0	1	9.00	9	7	2	0	0
..................GTCAACAGATTGGATTTGCGTCGAT....	25	0	1	4.00	4	4	0	0	0
..................GTCAACAGATTGGATTTGCGTCGATC....	26	0	1	4.00	4	2	2	0	0
..........TGCTGTCTTGCAGGGCTGTAGGC....	23	0	1	2.00	2	1	1	0	0
..GTCACTGCGATTCCGGGCAGT....	21	0	1	2.00	2	2	0	0	0
..CAGCTAGAAGAGATAAGT....	18	0	1	2.00	2	2	0	0	0
..........TGCAGGGCTGTAGGCTTCGGTCCA....	24	0	1	2.00	2	0	1	1	0
..........GATTGGATTTGCGTCGAT....	18	0	1	2.00	2	0	0	1	1
..........AACTGCTGTCTTGCAGGGCTGTAGGC....	26	0	1	2.00	2	1	1	0	0
..GTCACTGCGATTCCGGGCAGTT....	22	0	1	2.00	2	2	0	0	0
..............GATAAGTCAACAGATTGGATTTGC....	24	0	1	2.00	2	1	1	0	0
..................ACAGATTGGATTTGCGTCGAT....	21	0	1	2.00	2	0	0	2	0
..........TGCAGGGCTGTAGGCTTCGGTCC....	23	0	1	2.00	2	1	1	0	0
..GTCACTGCGATTCCGGGCA....	19	0	1	2.00	2	2	0	0	0
..GATGCAAGATGAGAGGCCCAGTCCA....	25	0	1	2.00	2	1	1	0	0
..TGAAATGATGCAAGATGAGAGGCCC....	25	0	1	2.00	2	2	0	0	0
..TAACGCTTTGTGCACCGTAC....	20	0	1	2.00	2	1	1	0	0
............AGATAAGTCAACAGATTGGATTTGC....	25	0	1	1.00	1	0	1	0	0
..................CAACAGATTGGATTTGCGTCGAT....	23	0	1	1.00	1	0	1	0	0
..AGTCACTGCGATTCCGGGCAGTT....	23	0	1	1.00	1	1	0	0	0
..........TGCAGGGCTGTAGGCTTCGGT....	21	0	1	1.00	1	0	1	0	0
..TGTGCACCGTACAATTCAGT	20	0	1	1.00	1	1	0	0	0
..AAGATGAGAGGCCCAGTCC....	19	0	1	1.00	1	1	0	0	0
..........CTGCCTAACTGCTGTCTTGCAGGG....	24	0	1	1.00	1	0	1	0	0
..GAAATGATGCAAGATGAGAGGCC....	23	0	1	1.00	1	0	0	0	1
..........ATTTGCGTCGATCGGCTTGA....	20	0	1	1.00	1	0	1	0	0
..TGAAATGATGCAAGATGAG....	19	0	1	1.00	1	1	0	0	0
..ATGCAAGATGAGAGGCCCAGTC....	22	0	1	1.00	1	1	0	0	0
..................AGTCAACAGATTGGATTTGCGTCGATC....	27	0	1	1.00	1	1	0	0	0
..GATGAGAGGCCCAGTCCATAACACT....	25	0	1	1.00	1	1	0	0	0
..GATGCAAGATGAGAGGCCCAGT....	22	0	1	1.00	1	1	0	0	0
..AAATGATGCAAGATGAGAGGCCC....	23	0	1	1.00	1	1	0	0	0
..................CAACAGATTGGATTTGCGTCGATC....	24	0	1	1.00	1	1	0	0	0
..GAAATGATGCAAGATGAGA....	19	0	1	1.00	1	0	0	0	1
..TAGTCTACAGTCACTGCGATTCCGGGC....	27	0	1	1.00	1	0	0	0	1
..........ATTGGATTTGCGTCGATCGGCT....	22	0	1	1.00	1	0	1	0	0
..........AGATTGGATTTGCGTCGATCGGC....	23	0	1	1.00	1	0	0	0	1
..GTCACTGCGATTCCGGGCC....	19	1	1	1.00	1	1	0	0	0
..TGAAATGATGCAAGATGAGA....	20	0	1	1.00	1	1	0	0	0
..GATGAGAGGCCCAGTCCAT....	19	0	1	1.00	1	1	0	0	0
..................TAAGTCAACAGATTGGATTTGC....	22	0	1	1.00	1	1	0	0	0
..................TAAGTCAACAGATTGGATTTGCGTCGAT....	28	0	1	1.00	1	0	1	0	0
..TACAGTCACTGCGATTCCGGGCAGT....	25	0	1	1.00	1	0	1	0	0
..........GATTTGCGTCGATCGGCTTGA....	21	0	1	1.00	1	0	1	0	0
..GATGCAAGATGAGAGGCC....	18	0	1	1.00	1	1	0	0	0
..................AGTCAACAGATTGGATTTGC....	20	0	1	1.00	1	1	0	0	0
..GAGAGGCCCAGTCCATAACACT....	22	0	1	1.00	1	0	0	1	0
..........GGGCTGTAGGCTTCGGTCC....	19	0	1	1.00	1	1	0	0	0
..GAAATGATGCAAGATGAGAGGCCC....	24	0	1	1.00	1	1	0	0	0
..........TGCAGGGCTGTAGGCTTC....	18	0	1	1.00	1	0	0	1	0
..CTGCGATTCCGGGCAGTTGA....	20	0	1	1.00	1	0	0	0	1
..................AACAGATTGGATTTGCGTCGAT....	22	0	1	1.00	1	0	0	1	0
..................AACAGATTGGATTTGCGTCGATC....	23	0	1	1.00	1	0	1	0	0
..GATGCAAGATGAGAGGCCC....	19	0	1	1.00	1	1	0	0	0
..........ATTGGATTTGCGTCGATCGGCTTGAATC....	28	0	1	1.00	1	0	1	0	0
..AAATGATGCAAGATGAGAGGCCCAGTCC....	28	0	1	1.00	1	0	1	0	0
..ATGATGCAAGATGAGAGGCCCAGTCC....	26	0	1	1.00	1	0	1	0	0
..........CGGCTTGAATCTGCCTAACTGCTGTCT....	27	0	1	1.00	1	1	0	0	0
..AGATGAGAGGCCCAGTCC....	18	0	1	1.00	1	1	0	0	0
...AGCTAGAAGAGATAAGTCAACAG....	23	0	1	1.00	1	1	0	0	0
..ATGAGAGGCCCAGTCCATAACACTT....	25	0	1	1.00	1	1	0	0	0
..........ATTGGATTTGCGTCGATCGGCTTGAAT....	27	0	1	1.00	1	0	1	0	0
..GAAATGATGCAAGATGAGAGGCCCA....	25	0	1	1.00	1	0	1	0	0
..ATGATGCAAGATGAGAGGCCCAGT....	24	0	1	1.00	1	0	1	0	0
..GTTGAAATGATGCAAGATGAGAGGC....	25	0	1	1.00	1	1	0	0	0
..GAAATGATGCAAGATGAGAGGC....	22	0	1	1.00	1	1	0	0	0
..........TGCTGTCTTGCAGGGCTG....	18	0	1	1.00	1	1	0	0	0
..ATGATGCAAGATGAGAGGCC....	20	0	1	1.00	1	0	0	1	0
..ATGAGAGGCCCAGTCCATAACACT....	24	0	1	1.00	1	1	0	0	0
..................TCAACAGATTGGATTTGCGT....	20	0	1	1.00	1	1	0	0	0
..GTCACTGCGATTCCGGGC....	18	0	1	1.00	1	1	0	0	0
..GTTGAAATGATGCAAGATGAG....	21	0	1	1.00	1	0	1	0	0
..CACTGCGATTCCGGGCAGTTG....	21	0	1	1.00	1	0	1	0	0
..........CTTGCAGGGCTGTAGGCTTC....	20	0	1	1.00	1	0	0	0	1

Anti-sense strand reads

GTGTCGATCTTCTCTATTCAGTTGTCTAACCTAAACGCAGCTAGCCGAACTTAGACGGATTGACGACAGAACGTCCCGACATCCGAAGCCAGGTTTTAAATCAGATGTCAGTGACGCTAAGGCCCGTCAACTTTACTACGTTCTACTCTCCGGGTCAGGTATTGTGAATTGCGAAACACGTGGCATGTTAAGTCA	Read size	# Mismatch	Hit Count	Total Norm	Total	V115 head	V114 embryo	M054 female body
**********(((.(((....(((((((...(((((((((((((((((.............)))))))))))).))))))....)))))))....))).)))..**********								
..........AGCTAGCCGAACTTAGACGGATTGAC....	26	0	1	1.00	1	0	1	0
..GCGAAACACGTGGCATGTTAA....	21	0	1	1.00	1	1	0	0
..GAAACACGTGGCATGTTAAGTC.	22	0	1	1.00	1	1	0	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_5:1224952-1225146 +	dse_1854	CACAGCTAGAA--GAGATAAGTCAACA----------GA--T--TGGATTTGCG----TCGATCGGCTTGAATCT------GCC--TAACTGCTGTCTTGCAGGGC-T--GTAGGC---TTCGGTCCAAA---ATTT-AGTCTACAGTCACTGCGATTCCG-GGCAGTTGAAA-TG---ATGCAA-GATGAGAG---GCCC-A--GTCCATAACACTTAACGCTT--TGTGCACC-GT-----ACAATT-CAGT----------
droSim2	2L:2946894-2947088 +	dsi_32463	CACAGCTAGAA--GAGATAAGTCAACA----------GA--T--TGGATTTGCG----CGATCGGCTTGAATCT------GCC--TAACTGCTGTCTTGCAGGGC-T--GTAGGC---TTCGGTCCAAA---ATTT-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGAAA-TG---ATGCAA-GATGAGAG---GCTC-A--GTCCATAACACTTAACGCTT--TGTGCACC-GT-----ACAATT-TAGT----------
dm3	chr2L:3067709-3067903 +	dme_436	CACAGCTAGAA--GAGATAAGTAACA----------GA--T--TGGATTTGCG----TCGATCGGATTGAATCT------GCC--TAACTGCTGTCTTGCAGGGC-T--GTAGGC---TTCGGTCCAAA---ATTA-AGTCTACAGTCTCTGCGATTCCG-GGCAGTTGAAA-TG---ATGCAA-GATGAGAG---GCTC-A--GTCCATAACACTTAACGCTT--TGTGCACC-GT-----ACAATT-TAGT----------
droEre2	scaffold_4929:3115452-3115635 +	der_1527	CACAGCTAGAA--GAGAT---GCC--TAACTGCTGTCTTGCAGGGC-T--GTAGGC---TTCGGTCCAAA---ATTT-AGTCTACAGTGCTGCGATTCCG-GGCAGTTGAAA-GG---ATGCAA-GATGAGAG---GCCC-A--GTCCATGACACTTAACGCTT--TGTGCACC-GT-----ACATTTCAGT----------
droYak3	2L:3063708-3063893 +	dya_1801	CACAGCTAGAA--GAGAT---GCC--TAACTGCTGTCTTGCAGGGC-T--GTAGGC---TTTGGTCCAAA---ATTT-AGTCTACAGTGCGTGCGATTCCG-GGCAGTTGAAA-TG---ATGCAA-GATGAAAGAGCCC-G--GTCCATAACACTTAACGCTT--TGTGCACC-GT-----ACAATT-CAGT----------
droEug1	scf7180000409554:3024267-3024462 -		CACAGCTAAAA--GAGATAAGTCAACA----------GG--T--TGGATTTGGAG---CGGATCGGATTGAATCT------GAT--TAACTGCTGTCTTGCAGGGC-T--GTAGTAC---TGTGGTCCAAA---ATTT-AGTCTAAGTGCTGCGATTCTG-GGCAGTTGTAA-GG---ATAAAAAGATGAGAG---GCCC-A--AACCATCACACTTAACGCTT--TGTGCACC-AT-----ACAGATTAGT----------
droBia1	scf7180000302188:2122002-2122202 +		CACAGCTAGAG--GAGATAAGTAAACAGAT----------GGGA--T--TGGACTGGAG----TGGATCGGATTGCATGC------GCC--TAACTGCTGTCTTGCAGGGC-C--GTAGTAC---TTTGGTCCAAA---ATTT-AGTCTACGGTGCGTGCGATTCCG-GGCAGTTGAAA-GG---ATGCAA-GACGAGAG---AGTC-A--GTCCACTAGCACTTAACGCTT--TGTGCACC-GT-----ACAGTTCCAGT----------
droTak1	scf7180000415438:753079-753224 -		CACAG--GA--T--G------GAG---TGGATCGGATTGCATCT------GCC--TAACTGCTGTCTTGCAGGGC-C--GTGGAC---TTTGGTCCAAA---ATTT-AGTCTATGGTGCGTGCGATTCCG-GGCAGTTGAAA-GG---ATGCCA-AATGAGAG---ACCC-A--------ACCTAACGCTT--TGTGCACC-GT-----------ACAGT----------
droEle1	scf7180000491046:1758544-1758740 +		CACAGTTAGAA--GAGATAAGTCAACG----------GA--T--GGATTGGAG---TGGATCGGATTGCGTCT------GCC--TAACTGCCGTCTTGCAGCAC-T--GTAGTC---TTGGTCCAAA---ATTT-AGTCTACAGCGGCTGCGATTCTG-GGCAGTTGAAA-GG---ATGCAATGATGACAG---GCCC-A--GACCATCACACTTAACGCTT--TGTGCACC-GT-----ACAGTT-CAGT----------T
droRho1	scf7180000780028:158223-158417 +		CACAGCTAGAG--GAGATAAGTCAACG----------GA--T--GGATTGGAA---TGGATTGGATTGCATCT------GCC--TAACTGCCGTCTTGCAGCGC-T--GTATTAC---TTGGTCCAAA---ATTT-AGTCTAAAGTGCTACGATTCTG-GGCAGTTGAAA-TG---ATCCAA-GACGAGAG---GCCC-A--ATCCATCACACTTAACGCTT--TGTGCACC-GT-----ACAGTT-CAGT----------
droFic1	scf7180000453924:1051725-1051931 +		CACAGCTAGAA--GAGATAG-------------------------GA--T--GGATTGGAGTGGATCGATCGCCTGGGATCT------GCC--TAACTGCCGTCTTGCAGCGC-C--GTAGTAC---TTGGTCCAAA---ATTT-AGCCTACGGCGCCTACGATTCCG-GGCAGTTGAAA-GG---ATCCAG-GATGCGAGAT-CGCCC-A--ACCCTTCACACTTAACGCTT--TGTGCACC-GT-----ACAGTT-CAGTAGTTCAGTACAGT
droKik1	scf7180000302246:274520-274657 +		CGCAGC--GA--T--G----------GAC----------------------C--AAACTGCTGTCTTGCAGCGCT--GTGGAC---TGTGGTCCAAA---TTTA-AGTCTACAGTGCGTGCGATTCCG-GGCAGTTGATT-GCCCCATGCTG---------------ATCCCACTTAACGCTTCGTGTGCACC-GCAGAGAAGAGTT-CAGT----------
droAna3	scaffold_12916:9588076-9588233 -	dan_4042	CACAGCTTTAA--G--GA--T--G----------GAACGCTTT--ATCT-----GCCATTAACTGCTGTCTTGCAGAGTCT--GTGGAC---G-TGGTCCAAA---TTT-TGTCTACAGCCACTGCGATTCCG-GGCAGTTGAAAGTG---AT--AA-TACGGACT---GCCCAAAAACACATCACATCT-GCGCTT--TGTGCACC-GC-----AC-----------
droBip1	scf7180000396580:1442851-1443009 +		CACAGCTTTAA--G--GA--T--G----------GATCAGCAT--TTCT-----CCCATTAACTGCCGTCTTGCAGCGCT--GTGGAC---G-TGGTCCAAA---TTT-TGTCTACAGCGGCTGCGATTCCGGGCAGTTGCAACGTG---AAACCA-TACGGATT---CGTCAA--ATACATCACATCT-GCGCTT--TGTGCACC-GC-----AC-----------
dp5	Unknown_singleton_3046:27-210 +	dps_31	CACAGCAACAA--AAGATAAAACTA--ATCTC----------GGA--T--GGGATGTTCC---------CTTAAA---------CGT--TAACTGCCGTCTTGCAGCGCCT--GTGGACG--ATAGGTCCAAA---ATTTGAGTCTACAGCGCTGCGATTCCG-GGCAGTTGAGT-GG---AT----GGGATT---CCACCT--TTAAATCACACTTAAGCTA--TGTGCACA-GA---GTACACT--AGT----------
droPer2	scaffold_1:8612772-8612955 -	dpe_229	CACAGCAACAA--AAGATAAAACTA--ATCTC----------GGA--T--GGGATGTTCC---------CTTAAA---------CGT--TAACTGCCGTCTTGCAGCGCCT--GTGGACG--ATAGGTCCAAA---ATTTGAGTCTACAGCGCTGCGATTCCG-GGCAGTTGAGT-GG---AT----GGGATT---CCACCT--TTAAATCACACTTAAGCTA--TGTGCACA-GA---GTACACT--AGT----------
droWil2	scf2_1100000004945:407277-407435 +	dwi_5419	CACAGTTAAATACATGATATATGCTCC----------AAATGTGAA--T--TAGATATAAG----TT-ATATCGAGTGATGC-----ATT--TAATGCCGTCTTGCAGGGCTCTTTGTAAGAATCCAGGTCCAAATT-AAAT-TCTTTATAGATCCTGCGATTCTG-GGCAATTGAATT-GA---C----------------------------ACACTT-G----------
droVir3	scaffold_12963:14467456-14467604 -	dvi_24646	CATGTCCA---------------ACA----------GT--T--TAGCAAGTC---------TATGTAT---------ATG--TAACTGCCGTCTTGCACGGCT--GTGATA-CAAAGGTCCAAA---AATT-AATCCACACGAGTTGCGATTCTG-GGCAGTTGA---------------TTTTACTAAAATCTT--TATGCACATGTAAACCATGGGA-GAGT----------
droMoj3	scaffold_6500:15423873-15424035 -	dmo_3155	AA--TCCACAA--CACATTCCCA---CAA---CCAACGATTTTGGA--CGGTAGACAACAG----CACAGCAGCGGCACTC----GTCTT--TAACTGCCGTCTTGCAGCTCT--GTGATG-CCCAGGTCCAATT---AAGT-AATCCACACGTGCTGCGATTCCG-GGCAGTTGAGGGG---AGCAA-CAGGAT--
droGri2	scaffold_15252:2029221-2029382 +	dgr_469	TACAATTCGAA--TAGAGGAATCATCA----------TAATT--TGTATT---A----TCAATCTA-TATAATCTTACAATGAT--TAACTGCCGTCTTGCCGGGCCT--GTGGGCA-CCCAGGTCCAAACAAAAGT-TGCCACAGTGCTGCGATTCTG-AGCAGTTAAA----------------------------

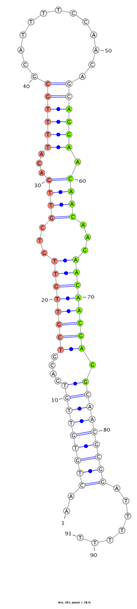
Generated: 09/08/2015 at 07:54 PM

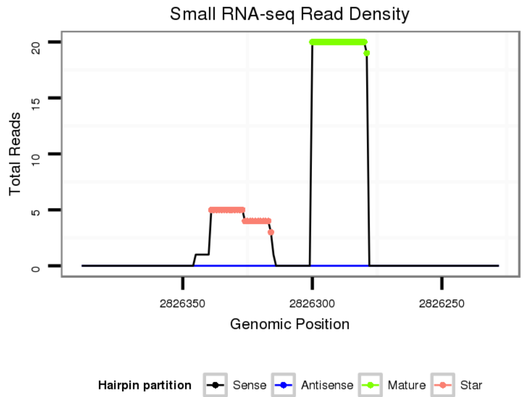
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	0
crit.uri	0
crit.back	0
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	10

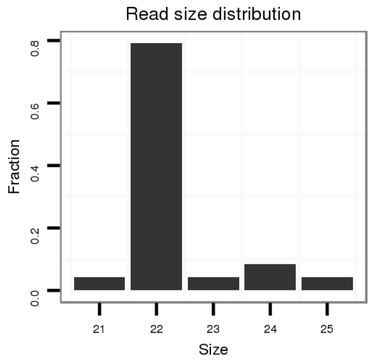
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_303	**scaffold_2:2826278-2826339 -**	**candidate-rescued**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser {Cornell Mirror}]

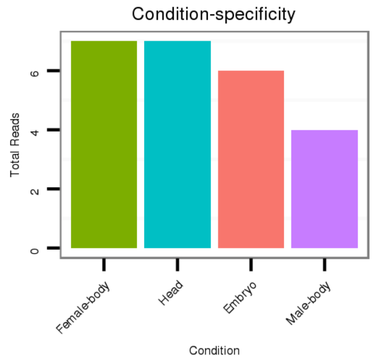
Legend: mature star mismatch in alignment mismatch in read

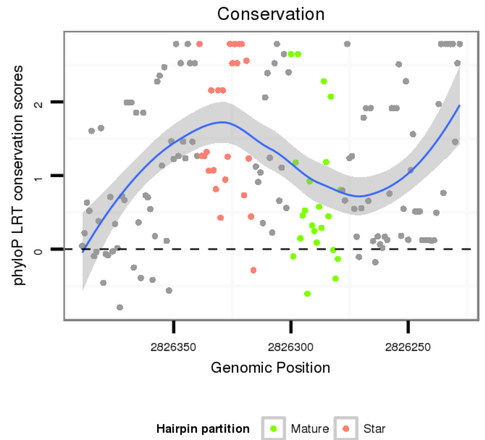
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to intron [Dsec\GM14515-in]; intron [Dsec\GM14102-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAAAAACCAACAAAATGGCAAACAAAAATGAAAAAAACTGTGTTGTGACGTCGTTGTTGTCGTTGACATTTTGCGCATTTTCCAACAGCAGGAACAACAAGAACAACGAGGCAACGCGGATTTTTTACAACTTTTTTGCAATTTTTTTTCTTTTTTTTTACA	Read size	# Mismatch	Hit Count	Total Norm	Total	M054 female body	V114 embryo	V115 head	V113 male body
********************************..(((((((((....(((((((((...((((...((((((.............))))))..))))...))))))))).)))))))))).....********************************										
.....AGGAACAACAAGAACAACGAGG.....	22	0	1	19.00	19	5	4	7	3
.....TCGTTGTTGTCGTTGACATTTTGC.....	24	0	1	2.00	2	0	1	0	1
.....AACAACAAGAACAACGAGGTT.....	21	2	1	1.00	1	0	1	0	0
.....AGGAACAACAAGAACAACGAG.....	21	0	1	1.00	1	1	0	0	0
.....GTGACGTCGTTGTTGTCGT.....	19	0	1	1.00	1	0	1	0	0
.....TCGTTGTTGTCGTTGACATTTTGCG.....	25	0	1	1.00	1	0	1	0	0
.....TCGTTGTTGTCGTTGACATTTTG.....	23	0	1	1.00	1	1	0	0	0
.....AGGAACAACAAGAACAACGAGGTT.....	24	2	1	1.00	1	0	0	1	0

Anti-sense strand reads

TTTTTTGGTTGTTTTACCGTTTGTTTTTACTTTTTTTGACACAACACTGCAGCAACAACAGCAACTGTAAAACGCGTAAAAGGTTGTCGTCCTTGTTGTTCTTGTTGCTCCGTTGCGCCTAAAAAATGTTGAAAAAACGTTAAAAAAAAGAAAAAAAAATGT	Read size	# Mismatch	Hit Count	Total Norm	Total	M054 female body
********************************..((((((((((....(((((((((...((((...((((((.............))))))..))))).))))).....))))))))).))))).....********************************						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_2:2826228-2826389 -	dse_303	AAAAAA---------CCAACAAAATGGCAAACAAAAATGAAA--A---------A-AACTG-----TGTTGTGACGTCG--TTGTTGT----------CGTT--GACATTTTGCGCATTT----------TCCAACAGCAGGAACAA----------C---A---AGAACAAC----GAG----------GCAACGCGG---AT----------TTTTTACAACTTTT---TTGCAATTTTTTTCTTTTTTTTTACA
droSim2	3l:2688642-2688802 -		AAAAAA---------ACAACAAAATGGCAAACAA-AAATGAAA--A---------A-AACTG-----TGTTGTGACGTCG--TTGTTGT----------CGTT--GACATTTTGCGCATTT----------TACAACAGCAGCAACAA----------C---A---AGAACAAC----GAG----------GCAACGCGG---AT----------TTTTTACAACTTTT---TTGCAATTTTTTTCTTTTTTTTTACA
dm3	chr3L:2805652-2805798 -	dme_376	CA----------AACAAAATGGCAAACAA-AAATGCAA--A---------A-AACTG-----TGTTGTGACGTCG--TTGTTGT----------CGTT--GACATTTTGCGCATTT----------TACAACAGCAGCAACAA----------C---A---AGAACAAC----GAG----------GCAACGCGG---AT----------TTTTTACAACGTTT---TTGCAATTTT-------TTTTTTTACA
droEre2	scaffold_4784:2831152-2831305 -		AAAA-T---------ACAACAAAATGGCAAACA-GAATGTAA--A---------A-AACTG-----TGTTGTGACGTCG--TTGTTGT----------CGTT--GACATTTTGTGCATTT----------TACAACAGCAGCACAA----------C-AAC---AGAACAT----GG----------GCAACGCGG---AT----------TTTGTACAATTTTT--TTTGCAT---------TTTTTTTACA
droYak3	3L:9128782-9128940 +	dya_1638	AAAAAT---------ACAACAAAATGGCAAAAAGAATGCAAAAA---------A-AACTG-----TGTTGTGACGTCG--TTGTTGT----------CGTT--GACATTTTGCGCATTT----------TACAACAGCAGCAGCAG----------C-AAC---AGAACAACAAC-GGG----------ACAACGCGG---AT----------TTTTTACAACTTTT---TTGCGAT---------TTTTTTACA
droEug1	scf7180000409466:535794-535941 -		CAAA--------------AATGGCAAAAA-GAATGCAAAAA---------A-AACTG-----TGTTGTGACGTCG--TTGTTGT----------CGTT--GACATTTTGGCAATTT----------TACAACAGCAACAATTGA----------GAAC---ACAACAAC----AAC----------GCAACGCGG---AT----------TTTTTACAACTTTT-TTTTTGCAT---------TTTTTTACA
droBia1	scf7180000302428:9600382-9600508 -		AAAA--------------------A-GAATGCAA--A---------A-ACCTG-----TGTTGTGACGTCG--TTGTTGT----------CGTT--GACATTTTGGCATTT----------TACAACAGCAACAAC--------------C---G---AGAACAAC----AGC----------GCACGCGG---AT----------TTT-TACAACTTTT-T-TTTCA----------TTTTTTTACA
droTak1	scf7180000415857:664162-664286 -		AAAA--------------------ATGCAA--A---------A-ACCTG-----TGTTGTGACGTCG--TTGTTGT----------CGTT--GACATTTTGGCATTT----------TACAACAGCAGCAACAA----------C---C---------------------------AACGCGGTTTTATTT----------T----TTTACACAACTTTT--TTTGCAATTTT-------TTCTTTTACA
droEle1	scf7180000491249:2538650-2538774 +		AA----------------GATTGCAAAAAAGAATGCAA--A---------A-AACTG-----TGTTGTGACGTCG--TTGTTGT----------CGTT--GACATTTTGGCATTT----------TACAACAGCAACA----------C---A---------------------AAGCGG---ATTT----------TTTTAACACTTTTTT-TTTCAT---------TTTTTTTTACA
droRho1	scf7180000770020:1619-1746 -		A----------------------TTGC----------AA--A---------A-AACGG-----TGTTGTGACGTCG--TTGTTGT----------CGTT--GACATTTTGGCATTT----------TACAACAGCAACAAC--------------C---G---AGAACAAC----AAC----------GCAACGGTG---ATTT----------TTTTTACAACTTTTTTTTGCAAT---------TTTTTTTACA
droFic1	scf7180000454105:1140092-1140239 -		AATAA---------------AAACGGCAAAAAAGAATGCAA--A---------A-ACCTG-----TGTTGTGACGTCG--TTGTTGT----------CGTT--GACATTTTGGCATTT----------TACAACAGCAACAACAG----------C-AAC-ACGAGCACAAC----AAC----------GTAACGCGG---AT----------TTT-TAAAACTTTT-TTTCGCAA----------TTTTTTACA
droKik1	scf7180000302441:874828-874915 +		AACAA---------------AGGCAGCAAAAAAAAATGT--A---------A-ACGTG-----TGTTGTGACGTCG--CTGTTGT----------CGTT--GACATTTTCTACAATT----------TACA----------C---C---------------------ACGCGT---AT----------C---------------TTTTTTTACA
droAna3	scaffold_13337:9281788-9281940 +		AAA----------------------------A---------A-ATTTG-----TGTTGTGACGTCG--TTGTTGC----------CGCT--GACATTTTGT----T-GCCAGTAAAGTTACAGCAGCAGCACGAA----------C-AAC---ACAACAACAATG---T---------TGCAACGCGG---A---CGCATACTTTATTTTCTGTTTTTTTTTT-TTTGCAT-T---------TTTTTTTACA
droBip1	scf7180000396544:93099-93231 +		AAAAA---------------------------T----A---------A-AGTGG-----TGTTGTGACGTCG--TTGTTGC----------CGCT--GACATTTTGT----T-GCCAGTAAAGTTACAGCAGCAGCACGAG----------C-AAC---GCAACAACAATG---T---------TGCAACGCGA---A---CGCGAAG----------TTTT----ATTTTT-TTTTGC----------TTTTTTTACA
dp5	XR_group8:3631144-3631284 -		AAAAATTTA----ACACATTCACATTGCAAAAAGAAACGACA-AA---------A-AAATGTGCGGTGTTGTGACGTCG--------------TT--GACATTTTGGCACAGT----------TACAACAACAGCAACAG----------C-AGC---A-GCACATCG---T---------TGCAACGACA----A---T----------TTTTTTTACA
droPer2	scaffold_23:1546069-1546209 +		AAAAATTTA----ACACAATCACATTGCAAAAAGAAACGACA-AA---------A-AAATGTGCGATGTTGTGACGTCG--------------TT--GACATTTTGGCACAGT----------TACAACAACAGCAACAA----------C-AGC---A-GCACATCG---T---------TGCAACGACA----A---T----------TTTTTTTACA
droWil2	scf2_1100000004511:11148347-11148463 +		GTACAT---------ACATTCACGTCGAAAACAAGCAAGA--A---------A-AACTG--TGTTGTTGTGACGTCG--T------------------TT--GACATA---AAAAAT----------TCAAAAACAACAACAG----------C-AGC---A-GCA----------A---AACGCGA---A---C----------TTTTTTTACA
droVir3	scaffold_13049:14927696-14927835 -		AAAA--------------------------A---------A-ATTG-----TGTGTGACGTCG--TTGCCGT----------CGTT--GACATTTTGGCATA-TTACAAACAAGGCAGCAACAGCAGCAACAACAGCGGCAGCAGCAGCAGAACA---ACAACAAC----AGCGTACCACAAACGGCAACGCGT---A---C----------TTTTTTTACA
droMoj3	scaffold_6680:21967608-21967770 +		AGAGAAGTGTGCCTTACATTCACATT--------------A--A---------A-AATTT-----TGTAGTGACGTGG--TTGCCGT----------CGTT--GACATTTTGGCATA-TTACAAACGAGGCAACAGCAGCAGCAACAACAACGG-CA-TAACAA-AAAC---ACAACAAC----TGCG---CAC-AACAGCAACGCGT---A---C----------TTTTTTTACA
droGri2	scaffold_14906:11102272-11102465 +		GAAAAG---------CAAACAGCAACACAAAC------AAAA-AAAAAATGCACGTAA-TT-----TA-TTTGTCATGAATTGGCTGGCAATAAATCAGACAATCACAAAAATGCTGTCAAGATTAAGACATGTGAA----T--ACGAATACATTTGCAACAGCACAGCGA----------C-AGC---GCAGCAC----------A---AAGAGTT--GGTGC----------TGTTTGGCTGGTTTT---TTG----------TTGTTTTGCA

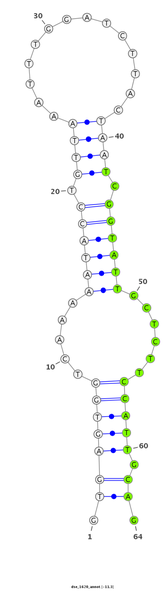
Generated: 09/08/2015 at 07:54 PM

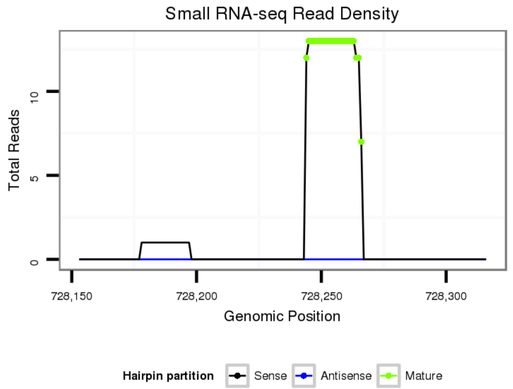
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	1

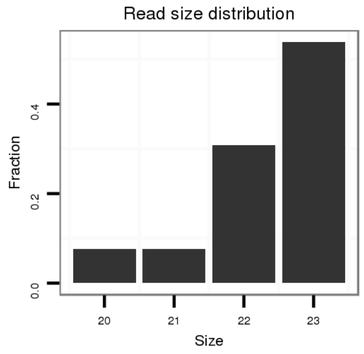
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1620	**scaffold_9:728203-728266 +**	**candidate**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

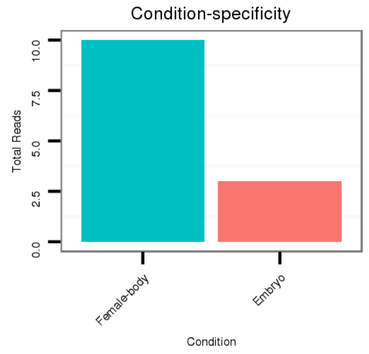
Legend: mature star mismatch in alignment mismatch in read

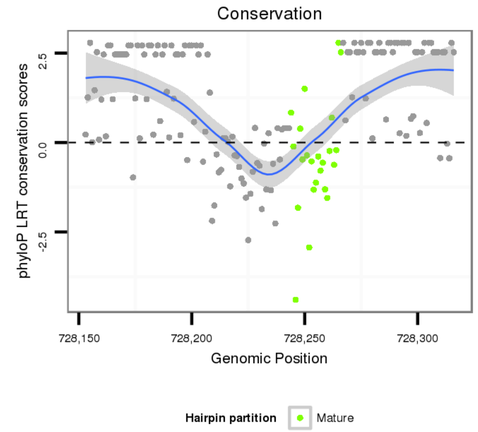
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dsec\GM15838-in]; CDS [Dsec\GM15838-cds]; CDS [Dsec\GM15838-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

CGATACGGCCAAGCCGGCCATCATCACCTACCACGATTTGGGCCTCAACTGTGAGTGGTCAAAAATACCTGTTAAATTTGGATCTTACTAATCGGTATTGCTCTTCCATTGCAGACGCCACCAGCTTTGCTGGCTTCTTCAATTTTCCAGTGATGCGAGGTCTG	Read size	# Mismatch	Hit Count	Total Norm		Total		M054 female body	V114 embryo	V113 male	V115 head body
.(((((((.....((((((.((((.............)))))..))))))......)))))).)).												
..........TCGGTATTGCTCTTCCATTGCAG..........	23	0	1	7.00	7	6	1	0	0			
..........TCGGTATTGCTCTTCCATTGCA..........	22	0	1	4.00	4	2	2	0	0			
..........ACCTACCACGATTTGGGCCT..........	20	0	1	1.00	1	0	0	1	0			
..........TCGGTATTGCTCTTCCATTG..........	20	0	1	1.00	1	1	0	0	0			
..........CGGTATTGCTCTTCCATTGCA..........	21	0	1	1.00	1	1	0	0	0			

Anti-sense strand reads

GCTATGCCGGTTCGGCCGGTAGTAGTGGATGGTGCTAAACCCGGAGTTGACACTCACCAGTTTTATGGACAATTTAAACCTAGAATGATTAGCCATAACGAGAAGGTAACGTCTGCGGTGGTCGAAACGACCGAAGAAGTTAAAAGGTCACTACGCTCCAGAC	Read size	# Mismatch	Hit Count	Total Norm	Total	V113 male body	M054 female body	V115 head
.(((((((.....((((((.((((.............)))))..))))))......)))))).)).								

Show Alignment With Reads

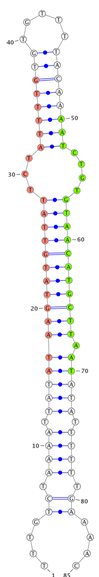
Re-alignment of all predicted orthologs

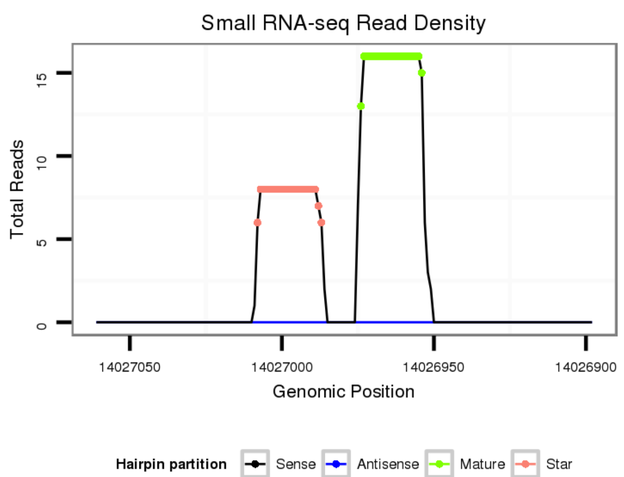
Species	Coordinate	ID	Alignment
droSec2	scaffold_9:728153-728316 +	dse_1620	CGATACGGCCAAGCCGGCCATCATCACCTACCACGATTTGGGCCTCAACTGTGAGTGG------TCA---AAAATACCTG----------TTAAAT----------TTGGA-T-----CTTACTAATC---CGG----------TATTGCTCTTCCATTGCAGACGCCACCAGCTTTGCTGGCTTCTTCAATTTTCCAGTGATGCGAGGTCTG
droSim2	2r:17952545-17952708 +		CGATACGGCCAAGCCGGCCATCATCACCTACCACGATTTGGGCCTCAACTGTGAGTGG------TCC---AAAATACCTG----------TTCAAT----------TCGGA-T-----CATGCTAATC---CAG----------TATTTTCCTCCCATTGTAGACGCCACCAGCTTTGCTGGCTTCTTCAATTTTCCAGTGATGCGAGGTCTG
dm3	chr2R:17398516-17398677 +		CGATACGGCCAAGCCGGCCATTATCACCTACCACGATTTGGGCCTCAACTGTGAAGTGT------TCA---AATACCTG----------GTCAAA----------TCGGA-T-----CGTACTAATC---CGG----------TATTGTTCTCACCATTGTAGACGCCACCAGCTTTGCTGGCTTCTTCAATTTTCCAGTGATGCGAGGTCTG
droEre2	scaffold_4845:11543597-11543762 +		CGATACGGCCAAGCCGGCCATCATCACCTACCACGATTTAGGCCTAAACTGTGAGTGA------TCA---AAGTACTG----------TGCA-----G----------GTACCCGCCCT-----CTTACTAATC---CCG----------TATATTTATCCAATTACAGACGCCACCAGCTTTGCTGGCTTCTTCAACTTTCCAGTGATGCGAGGTCTG
droYak3	2R:11781101-11781263 -		CGATACGGCCAAGCCGGCCATCATCACCTACCACGATTTGGGCCTCAACTGTGAGTAA------TTA---ATACTAG----------TACT---AGTT----------TTGCCA------ATTACTAATC---CCG----------TATAACTCTTCAATTACAGACGCCACCAGCTTTGCTGGCTTCTTCAACTTTCCAGTGATGCGAGGTCTG
droEug1	scf7180000409474:534046-534205 -		CGACACGGCCAAGCCGGCCATCGTCACCTACCACGATTTGGGCCTCAACTGTGAGTGG------TCC---AAATATTCT----------AGTCAAAC----------ATATATCTTAATC---------AACTGA----------------------

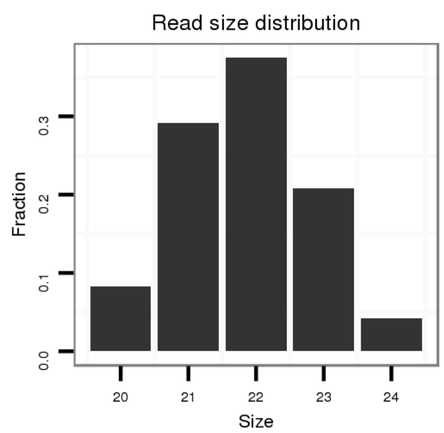
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_234	**scaffold_1:14026948-14027011 -**	**candidate-rescued**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

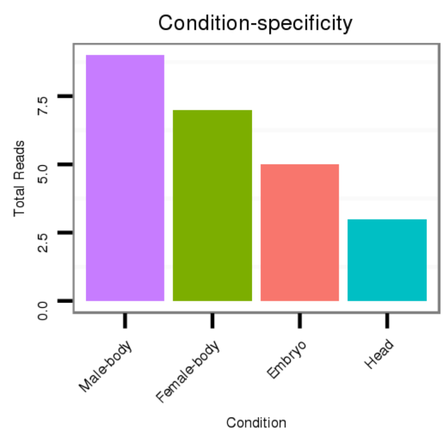
Legend: mature star mismatch in alignment mismatch in read

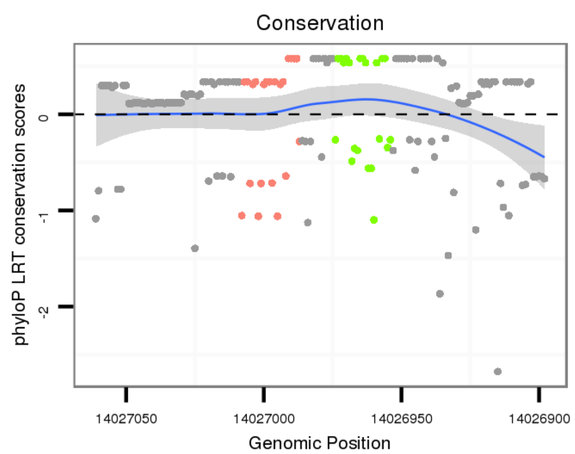
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GCTATTCTATAAGCTAACGAGCATTCATTAAAACTTCGTTTGTCTAAAATTATATAAGTATGTTATTCTATTTTGTGTGTTTTACAAAATCTGTGTAACATGCTTAATATATTTTTTGAAAACTATCAACCTACCACCGAAGTGTAGAAATTAAAAAAAAAAAG	Read size	# Mismatch	Hit Count	Total Norm	Total	V113 male body	M054 female body	V114 embryo	V115 head
************************************....((.((((.((((((((((((((((((...(((((((((.....)))))))))....))))))))))))).)))))).))))....************************************									
.....AATCTGTGTAACATGCTTAAT.....	21	0	1	4.00	4	1	1	0	2
.....AAATCTGTGTAACATGCTTAAT.....	22	0	1	4.00	4	0	2	1	1
.....ATAAGTATGTTATTCTATTTTG.....	22	0	1	3.00	3	1	2	0	0
.....ATCTGTGTAACATGCTTAATATA.....	23	0	1	2.00	2	1	1	0	0
.....AAATCTGTGTAACATGCTTAATA.....	23	0	1	2.00	2	0	0	2	0
.....ATCTGTGTAACATGCTTAATATT.....	23	1	1	1.00	1	1	0	0	0
.....TAAGTATGTTATTCTATTTTGT.....	22	0	1	1.00	1	1	0	0	0
.....AATCTGTGTAACATGCTTAATA.....	22	0	1	1.00	1	1	0	0	0
.....AATCTGTGTAACATGCTTAA.....	20	0	1	1.00	1	1	0	0	0
.....ATCTGTGTAACATGCTTAAT.....	20	0	1	1.00	1	1	0	0	0
.....TATAAGTATGTTATTCTATTT.....	21	0	1	1.00	1	0	1	0	0
.....TAAGTATGTTATTCTATTTTG.....	21	0	1	1.00	1	0	0	1	0
.....ATAAGTATGTTATTCTATTTT.....	21	0	1	1.00	1	1	0	0	0
.....ATAAGTATGTTATTCTATTTTGT.....	23	0	1	1.00	1	1	0	0	0
.....AAATCTGTGTAACATGCTTAATAT.....	24	0	1	1.00	1	0	0	1	0
.....AATCTGTGTAACATGCTTAATATT.....	24	1	1	1.00	1	1	0	0	0

Anti-sense strand reads

CGATAAGATATTCGATTGCTCGTAAGTAATTTTGAAGCAAACAGATTTTAATATATTCATACAATAAGATAAAACACACAAAATGTTTTAGACACATTGTACGAATTATATAAAAAACTTTTGATAGTTGGATGGTGGCTTCACATCTTTAATTTTTTTTTTTC	Read size	# Mismatch	Hit Count	Total Norm	Total	V113 male body	M054 female body	V115 head
....((.((((.((((((((((((((((((...(((((((((.....)))))))))....))))))))))))).)))))).))))....**********************************									

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_1:14026898-14027061 -	dse_234	GCTATTCTATAAGCTAACGAGCATTCATTAAAACTTCGT-TTGTCTAAAATTATATAAGTATGTTATTC-T-ATTTTGTGTGTTTTACAAAATCTGTGTAACATGCTTAATATATTTTTTGAAAACTATCAACCTACCACCGAAG-TGTAGAAATT-AAAAAAAAAAAG
droSim2	2r:17042163-17042325 -	dsi_81	GCTATTCTATAAGCTAACGAGCATTCATTAAAACTTCGTTTTTTCTAAAATTATATAAGTATGTTATTC-T-ATTTTGTGTGTTTTACAAAATCTGTGTAACATGCTTAATATATTTTTTGAAAACTATCCCCCTACCACCGAAG-TGTACAAATT-AAAA--AAAAAG
dm3	chr2R:16472563-16472690 -		A----------ACTTGGTTTTTCTAAAATTATTAGGTCCGTTTTGCAT-ATTTTAGGTGTTTTACAAAATCTGTGTAACATACTTAATATATTTTTAGAAAACTAACA--------CCTAAG-TGTACGGAATCAAAAAAAAAAG
droEre2	scaffold_4845:10618905-10619024 -	der_62	----------TTTTCCAGAAATATTAAGTCTGTTATGCATAGTTTTGTGAGTTTGACAAAATCTGCACAACGCGCTTAATGTATTTTTAGAAAACGAGCACACTT--------AGTTGTAAAGAAT-AAACTTAATTGTA
droYak3	2R:12724097-12724108 +		GTTATTCTGCAA----------|----------|--|----------|----------|----------
droTak1	scf7180000415401:101002-101060 -		A----------|----------|--|--TTTTGTAGATTTTACAATATCTGCGTAACGAGCCTACAATATTTATAAAAAATTATCA----------|----------|----------

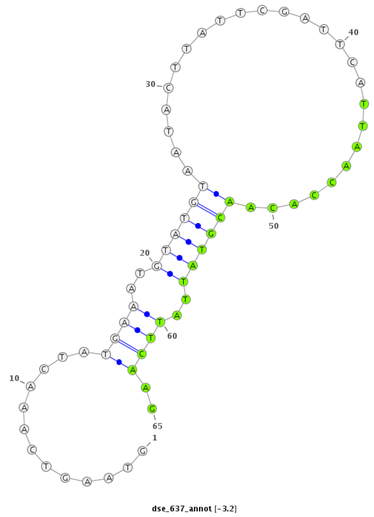
Generated: 09/08/2015 at 05:04 PM

PASSFAIL	
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	4
rescue.candidate	1

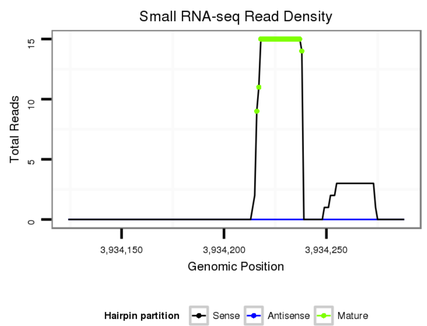
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_637	**scaffold_1:3934174-3934238 +**	**candidate-rescued**	**Mirtron**	**intron**	[View on UCSC Genome Browser (Comell Mirror)]

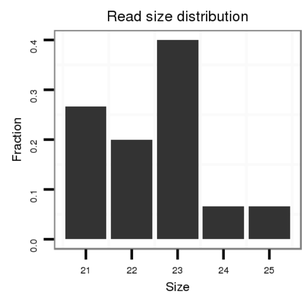
Legend: mature star mismatch in alignment mismatch in read

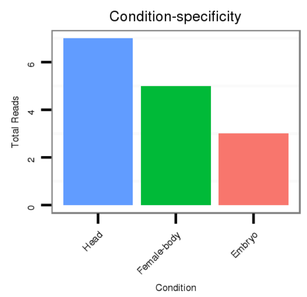
Predicted structure

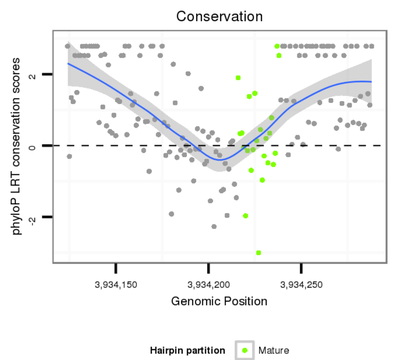


dse_637_annot [-3.2]









Show Alternate Folds

Flybase annotation

intron [Dsec\GM21217-in]; CDS [Dsec\GM21217-cds]; CDS [Dsec\GM21217-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

ATTCCAGCTGTGATAAAGCCACAAAGCGGCGATAGGCCAGATATAAAAAAGTAAGTCAAACTATGAAATGTATGTAATACTTATTCGATTCATTAACCACAACGTATTATTCAAGCATGTTGGTTGACGACAACTCCAACAAGTGCGTGGAGCACGACAGCAACA	Read size	# Mismatch	Hit Count	Total Norm	Total	V115 head	M054 female body	V114 embryo	V113 male body
**********.....(((((..(((((((.....))))))..))))..)))))..**********									
.....TTAACCACAACGTATTATTCAAG.....	23	0	1	6.00	6	1	3	2	0
.....AACCACAACGTATTATTCAAG.....	21	0	1	4.00	4	3	1	0	0
.....TTAACCACAACGTATTATTCAAGA.....	24	1	1	2.00	2	0	0	1	1
.....TAACCACAACGTATTATTCAAG.....	22	0	1	1.00	1	1	0	0	0
.....GACAACTCCAACAAGTGCGTGG.....	22	0	1	1.00	1	0	0	0	1
.....ATTAACCACAACGTATTATTCAAGA.....	25	1	1	1.00	1	1	0	0	0
.....CATTAACCACAACGTATTATTCAAG.....	25	0	1	1.00	1	0	0	1	0
.....ATTAACCACAACGTATTATTCAAG.....	24	0	1	1.00	1	1	0	0	0
.....TTAACCACAACGTATTATTCAA.....	22	0	1	1.00	1	1	0	0	0
.....GACGACAACTCCAACAAGTGCGTGG.....	25	0	1	1.00	1	0	1	0	0
.....TAACCACAACGTATTATTCAAGA.....	23	1	1	1.00	1	1	0	0	0
.....AACTCCAACAAGTGCGTGGA.....	20	0	1	1.00	1	0	0	0	1
.....TTAACCACAACGTATTATTCAAGG.....	24	1	1	1.00	1	1	0	0	0

Anti-sense strand reads

TAAGGTCGACACTATTTCGGTGTTTCGCCGCTATCCGGTCTATATTTTTTCATTCAGTTTGATACTTTACATACATTATGAATAAGCTAAGTAATTGGTGTTGCATAATAAGTTCGTACAACCAACTGCTGTTGAGGTTGTTCACGCACCTCGTGCTGTCGTTGT	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
droSec2	scaffold_1:3934124-3934288 +	dse_637	ATTCCAGCTGTGATAAAGCCACAAAGC---GGCGATAGGCCAGATATAAAAAAGTAAGTC--------AAAC----------TATGAAATGTATGTA----------ATA----------CTTATT-C----------GATTCAT----------TAACCACA--ACGTA-TTATTCAAGCATGTTGGTTGACGACAACTCCAACAAGTGCGTGGAGCA---------CGACAGCAA----------CA
droSim2	2r:7089819-7089981 +		ATTCCAGCTGTGATAAAGCCACAAGC---GGCGATAGGCCAGATATAAAAAAGTAAGTC--------AAAC----------TAA--GGGGTATGTA----------ATA----------TTTAGT-C----------GGATGT----------TAACACA--ACGTA-TTATTCAAGCATGTTGGTTGACGATAACTCCAACAAGTGCGTGGAGCA---------CGACAGCAA----------CA
dm3	chr2R:6321829-6321981 +	dme_399	ATTCCAGCTGTGATAAAGCCACAAGC---GGCGATAGGCCAGATATAAAAAAGTAAGTC--------AA----A----------TGTA----------ATA----------CTTAGT-C----------CGATGT----------TAACACA--ACGTA-CTTTCAAGCATGTTGGTTGACGACAACTCCAACAAGTGCGTGGAGCA---------CGACAGCAA----------CA
droEre2	scaffold_4929:8059006-8059165 -		ACTCGTGCTGTGATAAAGCCACAAGC---GGCGATAGGCCAGATATAAAAAAGTAAGTC--------AGAA----------TGA--GGATATGTA----------ATA----------CTTGT-A----------AGATGT----------TAACCAA--AGATA-CTATTCAAGCATGTTGGTTGACGACAACTCCAACAAGTGTGTGGAGCA---------CGACAGCAA----------CA
droYak3	2L:18958195-18958357 +		ATTCCAGCTGTGATAAAGCCACAAGC---GGCGATAGGCCAGAATATAAAAAAGTAAGC--------AAAC----------TAA--GGATATGTC----------ATA----------AATATT-C----------GGATGT----------TAACCAA--AGATA-TTATTTAGCATGTTGGTTGACGACAACTCCAACAAGTGTGTGGAGCA---------CGACAGCAA----------CA
droEug1	scf7180000409672:4696538-4696707 -		ATTCCAGCTGTGATAAAGCCACAAGCGCCGGCGATAGCCAGAAATCAAAAAGTAAGTA--------AA----A----T----------TA-------TATC----------GTTTTAGAGTTCATA----------CTTATG-A----------TGATGT----------TAACCACA--ACATA-TTATTCAGCATGTTGGTTGACAACTCCAACAAGTGCGTGGAGCA---------CGATAGCAA----------CA
droBia1	scf7180000301506:11720-11830 +		ATTCCAGCTGTGATAAAGCCAGAGGC---GGCGATAGCCAGATATGAAGAAGTAAGC--------AAA----------------------GA-AGTGA----------AGA--TGAATGGTT----------G-----A----------TTTTAGCTA-------------------CAGAGCTA-ATCAA-TAT-GCCTC-ATTTCGAGCATGTTGGTTGACGACAACTCCAACAAGTGCGTGGAGCA---------CGACAGCAA----------CA
droTak1	scf7180000415683:134642-134800 -		ATTCCAGCTGTGATAAAGCCACAAGC---GGCGATAGCCAGACAATCAAGAAGTAGCGA--------AAA----------------A----------A--TTCTAATA----------TTTAGT-T----------AGATGCT----------TAACCAGTGCACTC-TT-TTTCGAGCATGTTGGTTGAATGACAACTCCAACAAGTGCGTGGAGCA---------CGACAGCAA----------CA
droEle1	scf7180000491349:1137791-1137959 -		ATTCCAGCTGTGATAAAGCCACAAGC---AGCGATAGCCAGATATAAAAAAGTATCAAAT--------CT-T----------TAT----------ATA----------TGTATATATATAAA----------G-----T----------GTAATGT-------TAAACCTAA-------------ATTC-TTCCTTAGCATGATGGTTGATGACAACTCCAACAAGTGCGTGGAGCA---------CGACAGCAA----------CA
droRho1	scf7180000779999:449094-449262 -		ATTCCAGCTGTGATAAAGCCACAAGC---GGCGATAGCCAGATATAAACAAGTAAGTGC--------AA----------A--A----------AGAGCTCAAATATTTC----------GTTGTAATGATCATA----------C-----A----------TAA-TA--------------TTC----------TTA--ATGTA-TTATTCAGCATGATGGTTGATGACAACTCCAACAAGTGCGTGGAGCA---------CGACAGCAA----------CA
droFic1	scf7180000454066:1364456-1364715 -		ATCTCAGCTGTGATAAAGCCACAAGC---GGCGATAGCCAGATATAAAAAAGTAAGTTTA--------AAA----------TA--GAATATGTACTCAA----------GAGTTCATACTTTTGAAGTAGATAAACTTTAATTCTTTCTTATCTCATACATACAATATAAACATAAAGTGTATTATCAAAATCAAGCTAGTTTTTATA-A----------AGACAT----------TAAATA-TA--AGTTC-TTCTTTAGTATGATGGTTGATGACAACTCCAACAAGTGCGTGGAGCA---------CGACAGCAA----------CA
droKik1	scf7180000302385:964461-964621 -		ATCTCAGCTGTGATAAAGCCACAAGTGC---GGCGATAGCCAGATACGAAAAGGTAACCTC------AAGGT---T----------CA--T----------CCTGCTTAA-TACC----------CAC---A----------AATTA--------T-ATTAAACGATTCCGA-------------------T-TCCTTAGCATGTTGGTTGACGACAACTCCAACAAGTGCGTTGGAGCA---------TGACAGCAA----------CA
droAna3	scaffold_13266:17791386-17791549 +		ATTCCAGCTGTGATAAAGCCACAAGC---GGCGATAGCCAGATATGAAAAAGTAATCCT------AAG-GAAGTATAAACAAGAGG-A--GG---------------------A-----A----------AGG-TC---------TTCTAATAGTTTC-TCT-----------C-GCTTGCAGCATGATAGTTGATGACAATTCCAACAAGTGCGTTGAGCA---------CGACAGCAA----------CA
droBip1	scf7180000396735:1056419-1056576 +		ATCTCAGCTGTGATAAAGCCACAAGC---GGCGATAGCCAGATATGAAAAAGTAATCTTC----AA---A----GATAATAGGGA--GG---------------------A-----A----------TAA-TC---------TTCTAACAGTTTG-TCT----------C-GCTTGCAGCATGATAGTTGATGACAACTCCAACAAGTGCGTTGAGCA---------CGACAGCAA----------CA
dp5	3:16280630-16280792 -		ATTCCAGCTGTGATAAAATCTATCGGGC---GGCGATAGCCAGATATGAAAAAGTTCGTA--------AA----A----T----------TA--AAGTGTTGGC----------GGA----------G-----A----------TTTTTATTG-------------AAGAGCTT-TTCTCAC--ACC---A-TTTTGCAGCATGATCATAGTGACGACAACTCCAACAAGTGCGTGGAGCA---------CGACACAA----------CA
droPer2	scaffold_4:484207-484369 +		ATTCCAGCTGTGATAAAATCTATCGGGC---GGCGATAAAGCCAGATATGAAAAAGTTCGTA--------AA----A----T----------TA--AAGTGTTGGC----------GGA----------G-----A----------TTTTTATTG-------------AAGAGCTT-TTCTCAG--ACC---A-TTTTGCAGCATGATCATAGTGACGACAACTCCAACAAGTGCAGGAGCA---------CGACACAA----------CA
droWil2	scf2_1100000004822:2474325-2474508 -		ANTCCAGCTGTGATAAAGCCAAAAGT---GGCGATAAAAGCAGATGTAAAACGGTTACCT------AATATT--T----------TA--T----------TA-C----------TCGATC-T----------TAA--T-TAACTAATTCTAAATTTA---------T-TTTTT-AATTGCAGCATAAATAATTGATGATAATCAACAAATAGTGTGGATGCGGATGAAGATCACAGCACTCAGAATGACTCATCAAATA
droVir3	scaffold_12875:16269324-16269480 +		ANCTCAGCTGTGATAAACCA------GGCGATAAAAGATCCCAAAAAGGTTTGTAGC------AAA-TAAAT----------TGC--AATATTGAT----------ATA----------T-----A----------TTG-TA---------TTCTAAATTGTTG-TCG-----------C-ATTTGCAGCATGCTTATTGATGACAACTCCAACAAGTGTCCGGAGCA---------CGATTCAA----------TA
droMoj3	scaffold_6496:7486092-7486263 -		ANCTCAGCTGTGATAAACCA------GGCGATAAAAGATCCCAAAAAGGTTTGTATTGCAGCTAAAG----G----------AA--A----------ATAGCTAAAAGAA----------GT---T-----A----------TTT-TA---TTT-----TAATGCAATCTGATTTGCT-TG-----------GC-ATTTGCAGCATGCTTATTGATGACAACTCCAACAAGTGTCCGGAGCA---------TGATTCAA----------TA
droGri2	scaffold_15245:5138065-5138234 +		ANCTCAGCTGTGATAAACCA------GGCGATAAAAGATCCCAAAAAGGTGCGTAGT------CGT----A----------GA--A----------ACTGCTGAA-AGA----------TTTA-T-TCGTTGAAGC----------T-----TGAATA-CTT-GAATGTCTG-TCT-----------C-ATTCGCAGCATGCTTATTGATGACAACTCCAACAAGTGTCCGGAGCA---------CGATTCCAA----------TA

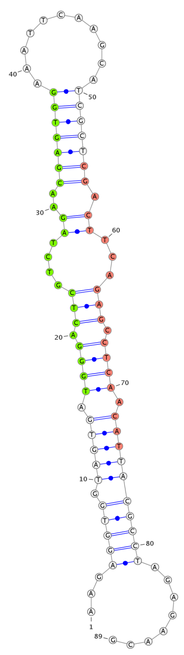
Generated: 09/08/2015 at 10:35 PM

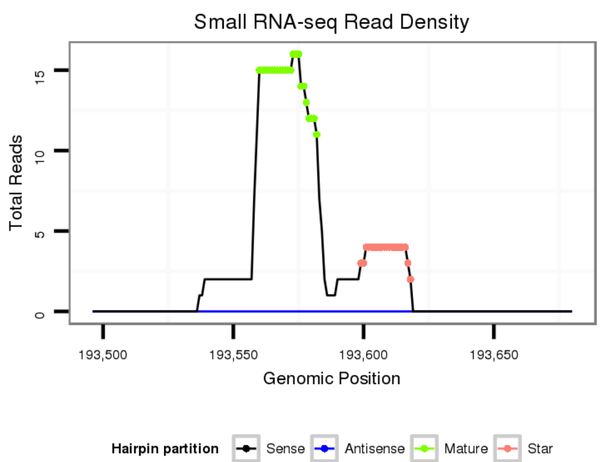
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	0
crit.top3	1
crit.tplop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	0
rescue.candidate	2

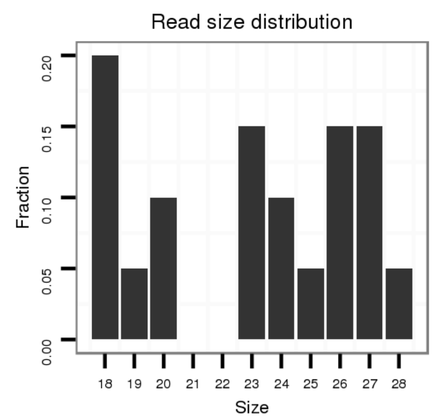
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1847	**scaffold_20:193546-193630 +**	**candidate-rescued**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

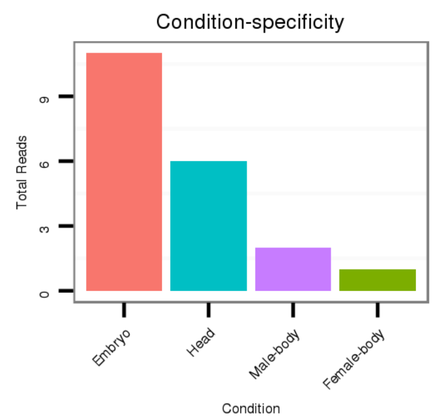
Legend: mature star **mismatch in alignment** mismatch in read

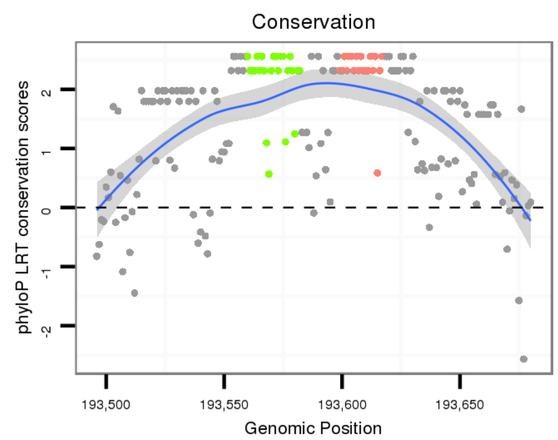
Predicted structure











dse_1847_mature (-25.4)

Show Alternate Folds

Flybase annnotation

intron [Dsec\GM17623-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TAACAAATAAGAAACCATAAGCGGGAACTTGGTCTGAAAGACCCCAAATAAGAGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTCAAGCATCGCTCGACTTCAGAGCCTCAACATTACGCCTAGAGAACGACATCAGGGTTAGATCATTGCGACCCCGCTTAGGAAACGAGAACTGA **********...(((((.(((((.((((.(((....((..(((((((.....)))))))..))...))).))))).)))))))))).....**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V114 embryo**	**V115 head**	**V113 male body**	**M054 female body**
...TGGGACTCGTCTAGAACGAGTGG...	23	0	1	2.00	2	0	1	0	1
...GATGGGACTCGTCTAGAACGAGTGGAA...	27	0	1	2.00	2	2	0	0	0
...GATGGGACTCGTCTAGAA...	18	0	1	2.00	2	1	1	0	0
...CCCCAAATAAGAGGTGGTAGT...	21	0	1	1.00	1	1	0	0	0
...AGCATCGCTCGACTTCAGAGCCTCAAC...	27	0	1	1.00	1	1	0	0	0
...GATGGGACTCGTCTAGAACGAGTGTT...	25	1	1	1.00	1	1	0	0	0
...ACTTCAGAGCCTCAACAT...	18	0	1	1.00	1	1	0	0	0
...CGACTTCAGAGCCTCAACAT...	20	0	1	1.00	1	0	1	0	0
...GATGGGACTCGTCTAGAACGAGTGGAAA...	28	0	1	1.00	1	1	0	0	0
...CGACTTCAGAGCCTCAACA...	19	0	1	1.00	1	1	0	0	0
...TGGGACTCGTCTAGAACGAGTGGA...	24	0	1	1.00	1	1	0	0	0
...ATGGGACTCGTCTAGAACGA...	20	0	1	1.00	1	0	1	0	0
...ATGGGACTCGTCTAGAACGAGTGGAA...	26	0	1	1.00	1	0	0	1	0
...GATGGGACTCGTCTAGAACGAGTGGA...	26	0	1	1.00	1	1	0	0	0
...ATGGGACTCGTCTAGAACGAGTGG...	24	0	1	1.00	1	0	1	0	0
...CCAAATAAGAGGTGGTAGT...	19	0	1	1.00	1	1	0	0	0
...GATGGGACTCGTCTAGAACGAGTGG...	25	0	1	1.00	1	1	0	0	0
...ATGGGACTCGTCTAGAACGAGTG...	23	0	1	1.00	1	0	0	1	0
...GAACGAGTGGAAATTCAAGCATCGCT...	26	0	1	1.00	1	1	0	0	0
...TGGGACTCGTCTAGAACG...	18	0	1	1.00	1	0	1	0	0

Anti-sense strand reads

ATTGTTTATTCTTTGGTATTCGCCCTTGAACCAGACTTTCTGGGGTTTATTCTCCACCATCACTACCCTGAGCAGATCTTGCTCACCTTTAAGTTCGTAGCGAGCTGAAGTCTCGGAGTTGTAATGCGGATCTCTTGCTGTAGTCCCAATCTAGTAACGCTGGGGCGAATCCTTTGCTCTTGACT **********...(((((.(((((.((((.(((....((..(((((((.....)))))))..))...))).))))).)))))))))).....**********	**Read size**	**# Mismatch**	**Hit Count**	**Total Norm**	**Total**	**V114 embryo**	**V115 head**

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_20:193496-193680 +	dse_1847	TAAC-AAATA---AGAAAC---CATA-AGC--GGGAACTTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-ATCAGGG--TTAGATCATTGCGACCCCGCTTAGG-----AAAC----GA----GAAC----------T--GA
droSim2	x:12890274-12890458 +	dsi_32459	TAAC-AAATA---AGAAAC---CATA-AGC--GGGAACTTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTGCGACCCCGCTTAGA-----AACA----GA----AAAT----------T--GA
dm3	chrX:13553556-13553740 +	dme_424	TAAC-A-ATA---AGAAAC---CATA-AGC--GGGAACTTGGTCTGAAAGACCCCA--A---ATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAATGAGTGGAAATTCA-AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-ATCAGGT--TTAGATCATTGCGATCCCCGCTTAGG-----AAAC----GA----GAAC----------T--GA
droEre2	scaffold_4690:13329650-13329839 -	der_1524	TAAA-C-TTT---AGGAAC---TATG-AGC--GGGAACTTGTTCTGAAAGACCCA--A---CTTAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-AACAGCT--TTAGATCATGCGACCCCGCTTAGG-----AATC----GG----GAAATA-GAAC------T--GG
droYak3	X:7836395-7836583 +	dya_1799	TAAC-A-ATTAG-AAATAACAATGTA-AGC--GGGAACTTGTTCTGAAAGACCCAA--A---ATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-AACAGCT--TTAGATCATGCGACCCCGCTTAGG-----AATC----GA----GAAT----------T--GG
droEug1	scf7180000408958:35913-36111 -		----------------G-GAAT---TTTA-AGC--GGGAACTTGTTCTGAAAGACCGAA--AAATAAAAGAAGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-AACAGCT--TTAGATCATGCGACCCCGCTTAGGAGAATAATC----GAGT-T--AAGGACCTGAGGCAGCA--GA
droBia1	scf7180000302041:563671-563853 +		AGC--AAATT---AGGCAC---TGTA-AGC--GGGAACTTGTTCTGAAAGACCCCA--G---ATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AGCGCGCTCG-ACTTCAGAGCCTCAGCATTACGCC-TAGAGAAC-GAC-ATCAGCT--TTAGATCATGCGACCCCGCTTAGG-----CATC----AG----GCAC----------C--GA
droTak1	scf7180000414393:30808-31003 -		CTA--------T---AGGAAC---TGTA-AGC--GGGAACTTGTTCTGAAAGACCAAA--C---TTAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAAATTC--AAGCGTCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-AACAGCT--TTAGATCATGCGACCCCGCTTAGG-----AATC----GAATAT--ATTGCCCACTGGGAACT--GA
droEle1	scf7180000491044:215067-215264 +		TAA--AATT---AGAAAA---TATA-AGC--GGGAACTTGTTCTGAAAGACCTA--A---ATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTC--AAGCATGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGCGAAC-GACAACTAGCT--TTAGATCATGCGACCCCGCTTAGG-----AATC----GA----GAATTGCAGACTGGGATCA--TA
droRho1	scf7180000779510:38391-38579 +		TGA--AATT---AGGAAC---TGTA-AGC--GGGAACTTGTTCTGAAAGACCGTA--A---ATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGCATTTA--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-AACAGCT--TTAGATCATGCGACCCCGCTTAGG-----AACC----GA----GTATTGCGAAC------T--GG
droFic1	scf7180000454073:1442990-1443193 +		TATTCCAAATT---AGAAAC---TTCA-AGC--GGGAACTTGTTCTGAAAGACCAA--AA--TTAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTC--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAACCGAC-AACAGCT--TTAGATCATGCGACCCCGCTTAGG-----AATC----GA----GTACTACGAACTGGGATCTGAGA
droKik1	scf7180000302698:307798-307982 -		CAC--A--AT---------A---CATA-AGC--GGGAACTTGTTCTGAAAGACCCAATACAAAATAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTA--AAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GAC-AACAATT--TTAGATCATGCGACCCCGCTTAGG-----AGTTGTAGGA----GAAT----------T--GA
droAna3	scaffold_13334:472144-472320 +	dan_4039	----------------------A-AGC--GGGAACTTGTTCTGAAAGATCAAA--CAATTTAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTTT-GAGCATCGCTCG-ACTTCAGAGCCTCAACATTACGCCTAGAGAAAAGAC-AACAGCT--TTAGATCATGCCAACCCGCTTAGG-----AAGT--GCGA----GC-C-------T----GAT--AA
droBip1	scf7180000396431:1081223-1081414 -		AAACTAGATA--TAGAA-A---TATATAGC--GGGAACTTGTTCTGAAAGATCCAA--CAG-TGAAG-AGGTGGTAGTGATGGGACTCGTCTAGAACGAGTGGAATTTTG-AAGCATGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGACCAGAC-AACAGCTTTTTAGATCATGACCACCCGCTTGGG----GA----A----GAGCTAC----------T--A
dp5	XL_group3b:100225-100382 +	dps_110	CCAC-AGATG---AGGTGA---CAAA-AGGGTGGGTACTTGTTTTGAAAGAACATA--T---CGAAG-GGTTGGTAGTGATGGGACTCGTCTAGAACGAGCGGAATTTC--AAACATTGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GCA-AGCAGCT--TTCGACCAT--
droPer2	scaffold_56:124031-124187 +	dpe_157	CCAC-AGATG---AGGTGA---CAAA-AGGGTGGGTACTTGTT-TGAAAGAACATA--T---CGAAG-GGTTGGTAGTGATGGGACTCGTCTAGAACGAGCGGAATTTC--AAACATTGCTCG-ACTTCAGAGCCTCAACATTACGCC-TAGAGAAC-GCA-AGCAGCT--TTCGACCAT--
droVir3	scaffold_12970:5369119-5369203 -	dvi_24642	A---A-AGAGGTAGTGATGGGACTCACTAGAACGAGTGGAATATT--AAGCATTGCTCGCACTTCAGAGCCTCAGCATTACGCC-TAGAGAA---------------------------------------
droMoj3	scaffold_6473:4951753-4951833 -	dmo_3154	--GGTAGTGATGGGACTCACTAGAACGAGTGGATTATT--TAGCATTGCTCGCACTTCAGAGCCTCAGCATTACGCC-TAGAGAA---------------------------------------
droGri2	scaffold_15203:9467764-9467849 +	dgr_467	A---A-AGAAGTAGTGATGGGACTCAACTAGAACGAGTGGAATTTTAAAAGCATTGCTCGCACTTCAGAGCCTCAGCATTACGCC-TAGAGA---------------------------------------

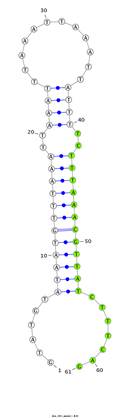
Generated: 09/08/2015 at 07:54 PM

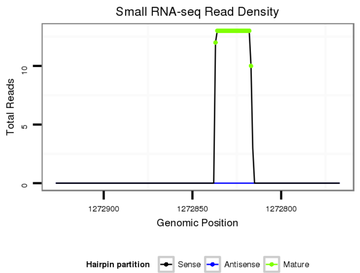
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	2
rescue.candidate	9

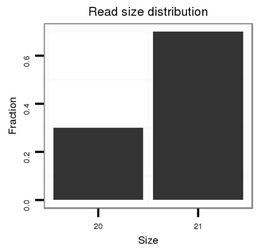
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_392	**scaffold_0:1272817-1272877 -**	**candidate-rescued**	**Mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

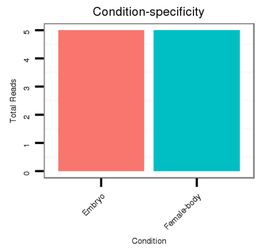
Legend: mature star mismatch in alignment mismatch in read

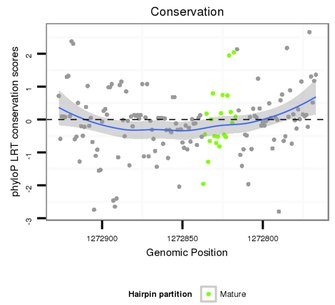
Predicted structure











Show Alternate Folds

Flybase annotation

intron [Dsec/GM24896-in]; CDS [Dsec/GM24896-cds]; CDS [Dsec/GM24896-cds]; utr3 [utr3_minus_5231]

Repeatable elements

Name	Class	Family	Strand
AT_rich	Low_complexity	Low_complexity	+
AT_rich	Low_complexity	Low_complexity	+

Sense Strand Reads

hide 3p reads | show mid mismatch reads

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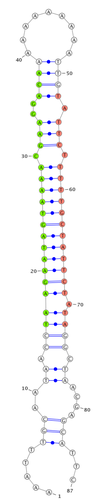
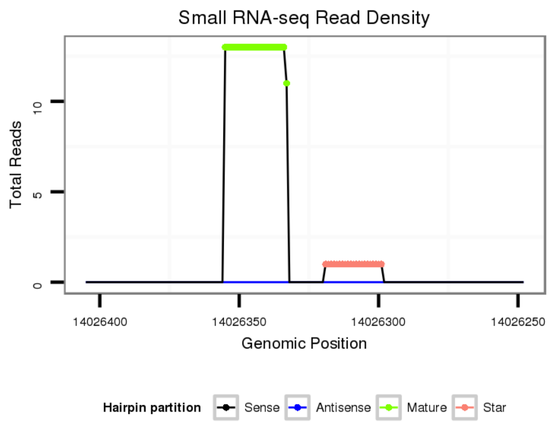
```

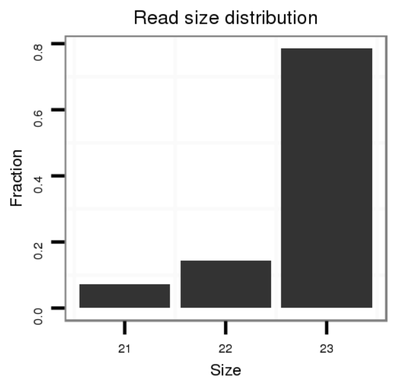
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_339	**scaffold_1:14026298-14026355 -**	**candidate-rescued**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

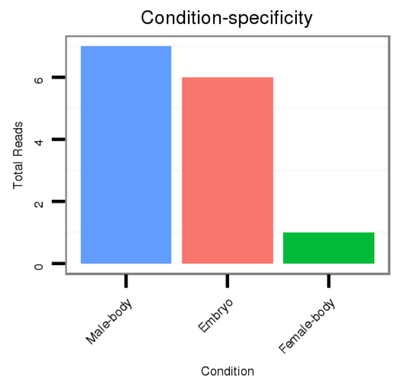
Legend: mature star mismatch in alignment mismatch in read

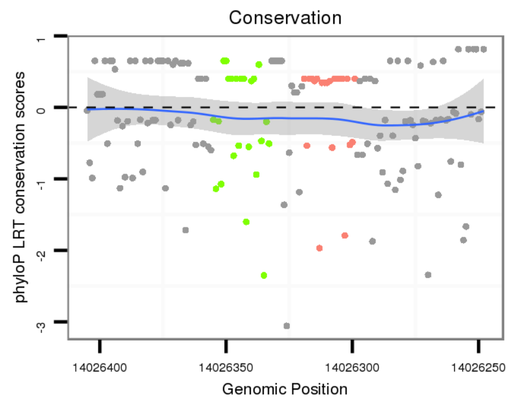
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTGAAAAAAAAAACACAAGAATGTGATATTTCATCAAATTTGCAATAACCTAAGAATAGTAAAACGAAGGACAAAAAAAAAAATTGTATTCTTTTTGCTATTCTATAGGCTAACGAGCATTCCTTAAAATACATATGTACATAAGTGTTTAAAAAAAT **********.....(((..((.((((((((((((((((.((((..((((.........)))))..)))).)))))))))))))).)))).))....)))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V113 male body	V114 embryo	M054 female body
.....TAAGAATAGTAAAACGAAGGACA.....	23	0	1	11.00	11	7	4	0
.....TAAGAATAGTAAAACGAAGGAC.....	22	0	1	2.00	2	0	2	0
.....TATTCTTTTTGCTATTCTATA.....	21	0	1	1.00	1	0	0	1
.....TAAGAATAGTAAAACGAAGGACAT.....	24	1	1	1.00	1	0	0	1

Anti-sense strand reads

AACTTTTTTTTTTGTGTTCTTACACTATAAAGTAGTTTAAACGTTATTGGATTCTTATCATTTGCTTCCTGTTTTTTTTTTTAACATAAGAAAAACGATAAGATATCCGATTGCTCGTAAGGAATTTTATGTATACATGTATTCACAAATTTTTTTA **********.....(((..((.((((((((((((((((.(((..((((.........)))))..)))).)))))))))))))).)))).))....)))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V115 head	M054 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_1:14026248-14026405 -	dse_1856	TTGAAAAA-AAAAA-CA-CAAGAATGTGATATTTC--ATCAAATT-----TGCAATAACCTAAGAATAGTAAAACGAAGGACAAAAAAAA-AAATTGTATTCTTTTTGCTATTCTA----------TAGGCTAACGAGC---------ATTCCTTAAAAT---------ACATATGTACATAAGTGTT-TA-AAAAAAT
droSim2	2r:17041512-17041659 -	dsi_32435	TTGA---AAAAAA-CA-CAAGAATGTGATATTTC--ATCAAATT-----TGCCATAACCTAAGAATAGTAAAACGAAGGCAAAAAAAA-AAATT-TATTCTTTTTGCTATTCTA----------TAGGCTAATGAGC---------ATTCCTTAAAAT---------AACATATGTGTT-TAAAAAAAT
dm3	chr2R:16472042-16472207 -		TTGAAAAA-AAAAA-CA-CAAAAATGTGATATTTC--ATCAC---------TCATCAACTCAAAATAGTAAATCGAAGGCCAAAAAAAT--ATGTATTCTGTTTGCTATTATA----------AAAGTTCACGAGCTAAGCTAACGATTCATTAAAAT------ATGTACATACATATTTAAGTGTT-AAAAAAAAAT
droEre2	scaffold_4845:10618664-10618918 -	der_25	ATAA----ACTAA-TTGT-ACAAAATGTGATATTTT--ATCAAATC-----TGCCATAACATCCAAATACTTAACCGATCATCAAAAACGGT----GTTTCT----GTATTTTACTATATAACTTATTTATGAAGAAGCTTTAGGATTTAATTTTTCCGACAATGCGATCTAGGCGTTTCTATCGCTGAGGTAGTATTGTTTGAAAGATTAAGTTAAAGCGT---------AATCATCAAAATTTTAAAATGTGATAAGTACATAAGTGTG-CCAAAAATAT
droYak3	2R:12724006-12724252 +	dya_34	AAAA----ACTAA-ATGTTAAAAATATATATTTT--ATCAAATG-----TACATAACCTCAAATACTAAACTGATGAGCAAAAAAGC-TA----TTTCTCTTTGTATTCTGCAATG-GATTTATTT-------GCTTTAGGATTTATTTTTTCGGACAATTCAATCTGGGCGTTGCTTTCGCTGAGGTAGTATTGTTTGGAAGACTAAGTTAACGAGC---------ATTCATCTCATTTTGAAATTT---TGTGTTCATCAGTGTG-TTAAAAATAT
droEug1	scf7180000409474:1489651-1489666 +		AA--ATGTG-TT-ACAAATT
droEle1	scf7180000491201:736783-736924 -		AATA----AAAAAA-TT-TAAGAACATGATATTTTGCAAGCAAATTATGTGTGC-------CAATAA-----------CGGTTAAAAAAAT----------GAAGCATTTCAAGAATTTAATTTTTTT-ATAA----------CT---------TGTGCTATAAAG---------AAACACGTAGATAACAATTAAAGAAAAAAT

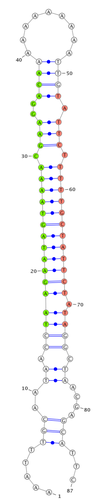
	PASS/FAIL		
crit.star	0	0	0
crit.loop	0	0	0
crit.mor	0	0	0
crit.half	0	0	0
crit.total	0	0	0
crit.pairing	1	1	1
crit.top3	1	1	1
crit.tptop3	1	1	1
crit.uri	0	0	0
crit.back	1	1	1
rescue.total	1	1	1
rescue.dominant	1	1	1
rescue.known	0	0	0
rescue.confident	3	3	2
rescue.candidate	6	6	7

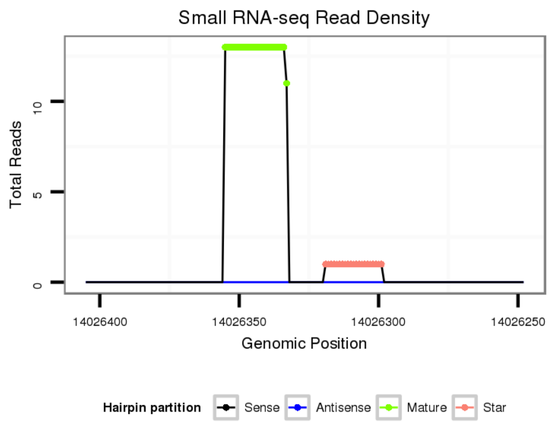
Generated: 09/08/2015 at 08:02 PM

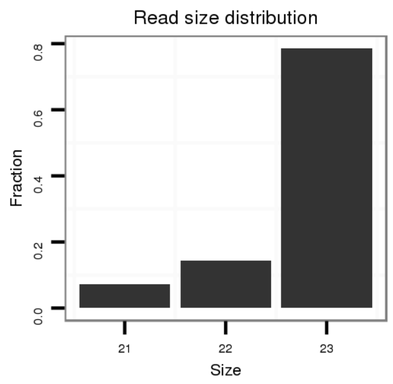
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_339	**scaffold_1:14026298-14026355 -**	**candidate-rescued**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

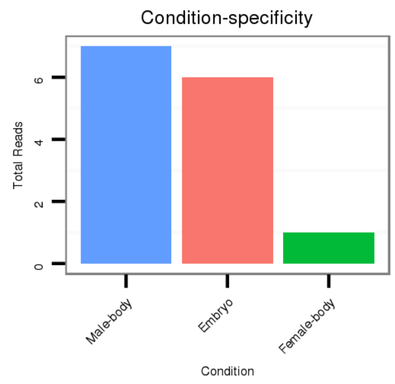
Legend: mature star mismatch in alignment mismatch in read

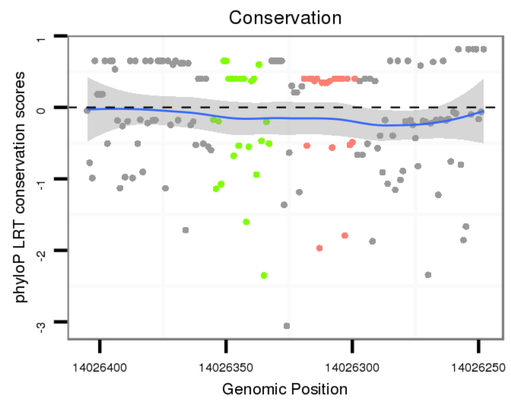
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTGAAAAAAAAAACACAAGAATGTGATATTTCATCAAATTTGCAATAACCTAAGAATAGTAAAACGAAGGACAAAAAAAAAAATTGTATTCTTTTTGCTATTCTATAGGCTAACGAGCATTCCTTAAAATACATATGTACATAAGTGTTTAAAAAAAT **********.....(((..((.((((((((((((((((.((((..((((.........)))))..)))).)))))))))))))).)))).))....)))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V113 male body	V114 embryo	M054 female body
.....TAAGAATAGTAAAACGAAGGACA.....	23	0	1	11.00	11	7	4	0
.....TAAGAATAGTAAAACGAAGGAC.....	22	0	1	2.00	2	0	2	0
.....TATTCTTTTTGCTATTCTATA.....	21	0	1	1.00	1	0	0	1
.....TAAGAATAGTAAAACGAAGGACAT.....	24	1	1	1.00	1	0	0	1

Anti-sense strand reads

AACTTTTTTTTTTGTGTTCTTACACTATAAAGTAGTTTAAACGTTATTGGATTCTTATCATTTGCTTCCTGTTTTTTTTTTTAACATAAGAAAAACGATAAGATATCCGATTGCTCGTAAGGAATTTTATGTATACATGTATTCACAAATTTTTTTA **********.....(((..((.((((((((((((((((.(((..((((.........)))))..)))).)))))))))))))).)))).))....)))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V115 head	M054 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_1:14026248-14026405 -	dse_1856	TTGAAAAA-AAAAA-CA-CAAGAATGTGATATTTC--ATCAAATT-----TGCAATAACCTAAGAATAGTAAAACGAAGGACAAAAAAAA-AAATTGTATTCTTTTTGCTATTCTA----------TAGGCTAACGAGC---------ATTCCTTAAAAT---------ACATATGTACATAAGTGTT-TA-AAAAAAT
droSim2	2r:17041512-17041659 -	dsi_32435	TTGA---AAAAAA-CA-CAAGAATGTGATATTTC--ATCAAATT-----TGCCATAACCTAAGAATAGTAAAACGAAGGCAAAAAAAA-AAATT-TATTCTTTTTGCTATTCTA----------TAGGCTAATGAGC---------ATTCCTTAAAAT---------AACATATGTGTT-TAAAAAAAT
dm3	chr2R:16472042-16472207 -		TTGAAAAA-AAAAA-CA-CAAAAATGTGATATTTC--ATCAC---------TCATCAACTCAAAATAGTAAATCGAAGGCCAAAAAAAT--ATGTATTCTGTTTGCTATTATA----------AAAGTTCACGAGCTAAGCTAACGATTCATTAAAAT------ATGTACATACATATTTAAGTGTT-AAAAAAAAAT
droEre2	scaffold_4845:10618664-10618918 -	der_25	ATAA----ACTAA-TTGT-ACAAAATGTGATATTTT--ATCAAATC-----TGCCATAACATCCAAATACTTAACCGATCATCAAAAACGGT----GTTTCT----GTATTTTACTATATAACTTATTTATGAAGAAGCTTTAGGATTTAATTTTTCCGACAATGCGATCTAGGCGTTTCTATCGCTGAGGTAGTATTGTTTGAAAGATTAAGTTAAAGCGT---------AATCATCAAAATTTTAAAATGTGATAAGTACATAAGTGTG-CCAAAAATAT
droYak3	2R:12724006-12724252 +	dya_34	AAAA----ACTAA-ATGTTAAAAATATATATTTT--ATCAAATG-----TACATAACCTCAAATACTAAACTGATGAGCAAAAAAGC-TA----TTTCTCTTTGTATTCTGCAATG-GATTTATTT-------GCTTTAGGATTTATTTTTTCGGACAATTCAATCTGGGCGTTGCTTTCGCTGAGGTAGTATTGTTTGGAAGACTAAGTTAACGAGC---------ATTCATCTCATTTTGAAATTT---TGTGTTCATCAGTGTG-TTAAAAATAT
droEug1	scf7180000409474:1489651-1489666 +		AA--ATGTG-TT-ACAAATT
droEle1	scf7180000491201:736783-736924 -		AATA----AAAAAA-TT-TAAGAACATGATATTTTGCAAGCAAATTATGTGTGC-------CAATAA-----------CGGTTAAAAAAAT----------GAAGCATTTCAAGAATTTAATTTTTTT-ATAA----------CT---------TGTGCTATAAAG---------AAACACGTAGATAACAATTAAAGAAAAAAT

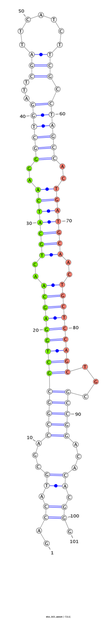
	PASS/FAIL		
crit.star	0	0	0
crit.loop	0	0	0
crit.mor	0	0	0
crit.half	0	0	0
crit.total	0	0	0
crit.pairing	1	1	1
crit.top3	1	1	1
crit.tptop3	1	1	1
crit.uri	0	0	0
crit.back	1	1	1
rescue.total	1	1	1
rescue.dominant	1	1	1
rescue.known	0	0	0
rescue.confident	3	3	2
rescue.candidate	6	6	7

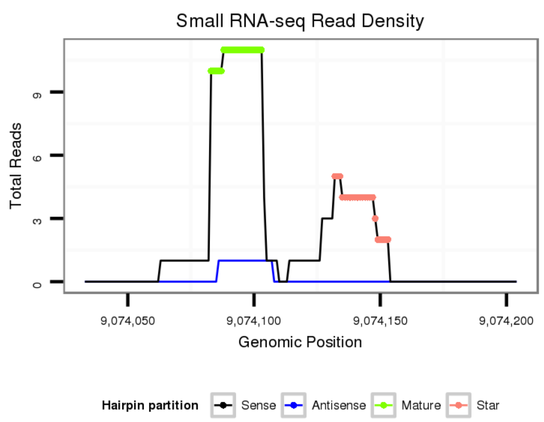
Generated: 09/08/2015 at 08:02 PM

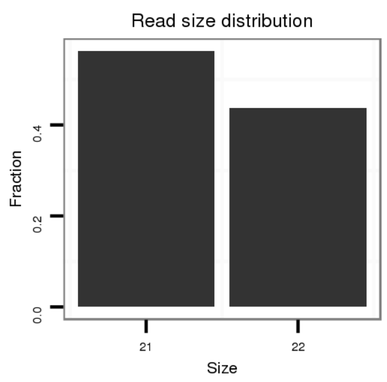
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_163	**scaffold_0:9074083-9074154 +**	**candidate-rescued**	**Canonical miRNA**	**antisense_to_3pUTR**	[View on UCSC Genome Browser {Cornell Mirror}]

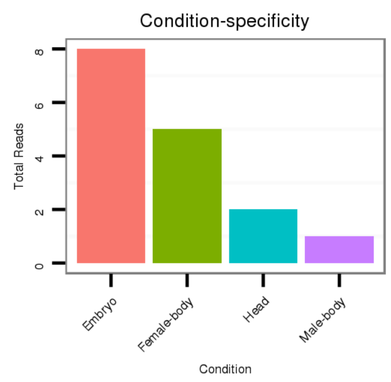
Legend: mature star mismatch in alignment mismatch in read

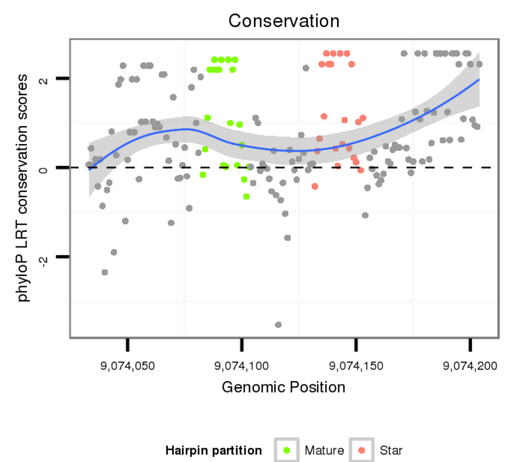
Predicted structure











Show Alternate Folds

Flybase annnotation

Antisense to utr3 [utr3_minus_5980]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AAACACAAAAATGTTTATATTAAAATTTAATCAACGACCATGCGACCGGCGCTGGAGCAACTGCATCAAGGGCTGGATTCGATTCATCTTCGCCTAGCCACTGATGCAACTGCTCCAGCTGCGCCGGACACACGGGCCTCAGCTTGAAAAATATATATATAACTCAACACCG **********..((.((...(((((((((((((((..(((((((..(((((((...(((.....))).)))))))..))))))))..))))))))))...)))))...)).)).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V114 embryo	M054 female body	V115 head	V113 male body
.....GCTGGAGCAACTGCATCAAGG.....	21	0	1	7.00	7	6	0	1	0
.....GCTGGAGCAACTGCATCAAGGG.....	22	0	1	3.00	3	1	1	0	1
.....ACTGATGCAACTGCTCCAGCTG.....	22	0	1	2.00	2	1	1	0	0
.....TCAACGACCATGCGACCGGC.....	20	0	1	1.00	1	1	0	0	0
.....TAGCCACTGATGCAACTGCTCCC.....	23	1	1	1.00	1	0	1	0	0
.....AGCAACTGCATCAAGGGCTGGA.....	22	0	1	1.00	1	0	1	0	0
.....TAGCCACTGATGCAACTGCTC.....	21	0	1	1.00	1	0	1	0	0
.....TAGCCACTGATGCAACTGCTCC.....	22	0	1	1.00	1	0	1	0	0
.....ATTCATCTTCGCCTAGCCACT.....	21	0	1	1.00	1	0	0	1	0

Anti-sense strand reads

TTTGTGTTTTTACAAATATAATTTTAAATTAGTTGCTGGTACGCTGGCCGCGACCTCGTTGACGTAGTTCCCGACCTAAGCTAAGTAGAAGCGGATCGGTGACTACGTTGACGAGGTCGACGCGGCCTGTGTGCCCGGAGTCGAACTTTTATATATATATTGAGTTGTGGC **********..((.((...(((((((((((((((..(((((((..(((((((...(((.....))).)))))))..))))))))..))))))))))...)))))...)).)).**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V115 head	M054 female body
.....CCTCGTTGACGTAGTTCCCGAC.....	22	0	1	1.00	1	1	0

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_0:9074033-9074204 +	dse_163	AA----------ACACAAAAATG----TTTATATTAAAATTTAATCAACGACCAT-G-CGACCGGCGCTGGAGCAACTGCATCAAGG-GCTGGATTC----------GA-TTCATC--------TTCGCCTAGCCACTGATGCAACTGCTCCAGCTGCGCCGGAC--ACACGGG--CCTCA-GC--TTGAA----------AAATAT----ATATATAACTCAACACCG
droSim2	31:16596499-16596670 +	dsi_32454	AA----------ACACAAAAATG----TTTATATTAAAATTTAATCAACGACCAT-G-CGACCGGCGCTGGAGCAACTGCATCAAGG-GCTGGATTC----------GA-TCCATC--------TTCGCCAAACCACTGATGCAACTACTCCAGCTACGCCGGAC--ACACGGG--CCTCA-TC--TTGAA----------AAATAT----ATATATAACTCAACACCG
dm3	chr3L:17013432-17013603 +	dme_266	AA----------ACACAAAATG----TTTATATTAAAATTTAATCAACGAGTGT-G-CGACCGGCGCTGGAGCAACTGCATCAAGG-GCTTGATTC----------GA-TCCATC--------TTCGCCAAGCCACTGATGCAACTGCTCCAGCTGCGCCGGGC--ACACGGG--CCTCA-GC--TTGAA----------AAATAT----ATATATAACTCAACACCG
droEre2	scaffold_4784:16829206-16829376 -		AA----------CACACAATACA----TTTATATTAAAATTTAATCAACGTCCGT-G-CGACCGGCGCATGGAGCAAATGCATCAAGG-GCTGGATTC----------GA-GCCATC--------TGGGCCAGTCACTGATGCAGCTGCTCCATCTGCGCCGGAC--GCACGGG--CCTCA-GC--TTGAA----------AAATAT----ATATATAACCCAACACCG
droYak3	3L:17060466-17060636 -	dya_1791	AA----------ACACAAATATG----TTTATATTAAAATTTAATCAACGTCCGT-G-CGCCGGCGCTGGAGCAACTGCATCAAGG-GCTGGATTC----------GA-TCCATC--------TTGGCCAGCACTGATGCAGTGCTCCAGCTGGACCGGAC--GCACGAG--CCTCA-GC--TTGAA----------AAATAT----ATATATAACTCAACACCG
droEug1	scf7180000409711:321990-322162 -		AA----------ACACTGATATA----TTTGTATTAAAATTTACTTAAGTCCCAT-G-CTTCCAGCGCTGGAGCAACTGCACCAACC-GCTGGATTC----------AA-TGCCTT--------TTGGCCAGCCGCTGATGCAGGTACTCCAGCTGGCCGAAC--GCACCGG--TCTCA-GC--TTGAA----------AAATAT--ATATATAACTCAACACCG
droBia1	scf7180000302428:3096440-3096610 -		AC----------ACTAGGATATA----TTTATATTAAAATTTACTCAACGTCCGG-G-CTGCCGGCGCTGGAGCAACTGCACAGTC-GTTGCGCTTG----------GA-TACCC--------TTAGCCAGCCACTGATGCAGTGCTCCAACTGGCCGGTC--GCACCGG--TCTCA-GC--TTGAA----------AAATAT----ATATATAACTCAACACCG
droTak1	scf7180000415352:343071-343245 -		CA----------AAGCAGGTGTA----TTTCTATTAAAATTTACTCAACGTCCGT-G-CGCCGGCGCTGGAGCAACTGCACAGCC-GCTGGATGTC----------GA-ATCGTGTAGCT-----CC-CGCAGCCACGATGCAGTGCTCCAACTGACCGGAC--GCACGGG--TCTCA-GC--TTGAA----------AAATAT--ATATATAACTCAACACCG
droEle1	scf7180000491255:3452249-3452431 +		CA----------ACACAATTACA----TTTTTATTACAATTTACTCAACGTCCGG-G-CTGCCGGCGCTGGAGCAACTGCATCGACC-GCTGGATCC----------CA-TTGCTG--------TTGGCCAGCCACGATGCAGTGCTCCAGCTGCGCCGGAA--GCACGGG--TCTCA-GC--TTGAAAAATATTTTATTATATAT----ATATGTAACTCAACACCG
droRho1	scf7180000779902:48424-48594 -		CA----------ACACTGTTAAA----TTTCTATTACAATTTACTCAACGACCGG-A-CTGCCGGCGCTGGAGCAACTGCACATTC-GCTGGATCC----------GA-TAGCGT--------TTGGCCAGCCACTGATGCAGCTGCTCCAGCAGCGCCGGAA--GCACGGG--TCTCA-GC--TTGAA----------AAATAT----ATATATAACTCAACACCG
droFic1	scf7180000454107:485601-485776 +		AAC----------CA----------ACACACTTAAA----TTTCTATTACAATTTACTCAACGACCGT-G-CGCCGGCGCTGGAGCAACTGCACCAACC-TGTGGATCA----------GC-GCCCGT--------TCGGCCAGCCACTGATGCAGTTGCTCCGGCCGGACCGGAC--GCACGGGTTCTTCACGC--TTGAA----------AAATAT----ATATATAACTCAACACCG
droKik1	scf7180000302486:860861-861026 +		AA----------ATTTGACTACA----TTTCAATTACAATTTACTCAACGCCGC-T-CTTCCGACACTGGAGCAGTTACACGAAATC-GGTGGC---------A-TAGCCT--------TCCGCCAGCGTCTGCTGCAGCTGCTCCAGGAGG---GAAA--AAGCGGG--TCTCA-GTTTTTGGA----------AAATAT----ATACATAACGCAACACCG
droAna3	scaffold_13337:13605815-13606044 -		AAAAAATTTAAAAATATTTCTTAAATTACAAAACAGGAGGAGGCCACTAACAGATTATTTTCAATTAAAATTTACTCAACGCCCTTCGTGTTCCGACACTGGAGCAACTGCACGCACCC-ACCGGAGCA----------CCATACCTGC--AA---TACC--------TTGT-CCAGTGGCTGCTGCAGTTGCTCCAACTGGACCGGAA--GCACCGG--GCTGT-GC--TTGAA----------AAATATATATATATAACTCAACACCG
droBip1	scf7180000395832:550950-551136 -		AA----------C-CCTCACATATTATTTTCAATTAAAATTTACTCAACACCCTT-GACTTCCGACGCTGGAGCAACTGCACGCTCCC-CTGGAGCA----------CCAAATCTGC--AA-T-AACT--------CTGC-CCAGCGGCTGCTGCAGTTGCTCCAACTGGACCGGAA--GCACCGG--GCTGT-GC--TTGAA----------AAATATATATATATAACTCAACACCG
dp5	XR_group8:696625-696794 -	dps_3843	AA----------ACACACAGACA----TTTGGTTCAGCAATTTACAC--TG-----A--G-CCG--ACTGGAGCAGCTGCACCAACT-GGTGACTAC----------GCC--CAGAGGACTGTGTAGTACAGCGT-------GGGTGCTGCAGCTGCTCCAGCGGCAGGCGCAATGCAAAAA--TTTA-TT--CTAA----------AAATAT----ACATGTAACTCAACACCG
droPer2	scaffold_32:787508-787677 +	dpe_2517	AA----------ACACACAGACA----TTTGGTTCAGCAATTTACAC--TG-----A--G-CCG--ACTGGAGCAGCTGCACCAACT-GGTGACTAC----------GCC--CAGAGGACTGTTTAGTACAGCGT-------GGGTGCTGCAGCTGCTCCAGCGGCAGGCGCAATGCAAAAA--TTTA-TT--CTAA----------AAATAT----ACATGTAACTCAACACCG
droVir3	scaffold_13049:10145207-10145369 -		--GGGCGCTGGAGCAGGTGCAACACGC-ACTGAACCAAATCCTGGCACAAATGGGCAAGCCATCCATATGGAC--C--AGCAC--------TTGT-CCAGGAATTCCTGCATCATGCTAGGGCTGCCGCGCCT--ACGGAGC--TCTTTT-AC--TTGGA----------ATCAATTAAAAATATAACTTAACGCAG
droMoj3	scaffold_6680:10650124-10650300 +	dmo_3162	GT----------T----------A----TTT------TACTTGCTCAA-------A--A----GGGCGCTGGAGCATGTGCACCAACAAGCTGCAGTAGACGCTGGGTC--ATGGGAACGTCATCCATGGGTAC--CA-GGGAAT--------TTGT-GCAGGTTCTGCTGCATCATGCTTCAGCTGACGCCTTA--TCAGAGC--TCTTTACT--TTGAA----------TCAAAT-AAAAAATATAACTTAAC---G
droGri2	scaffold_15110:20710591-20710663 -		--GGGCGCTGGAGCAGGTGCAACACGC-ACTGAACCAAATCCTGGCACAAATGGGCAAGCCATCCATATGGAC--C--AGCAC--------TTGT-CCAGGAATTCCTGCATCATGCTAGGGCTGCCGCGCCT--ACGGAGC--TCTTTT-AC--TTGGA----------ATCAATTAAAAATATAACTTAACGTAG

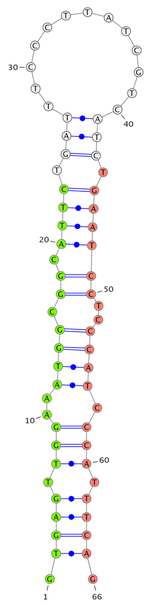
Generated: 09/08/2015 at 07:54 PM

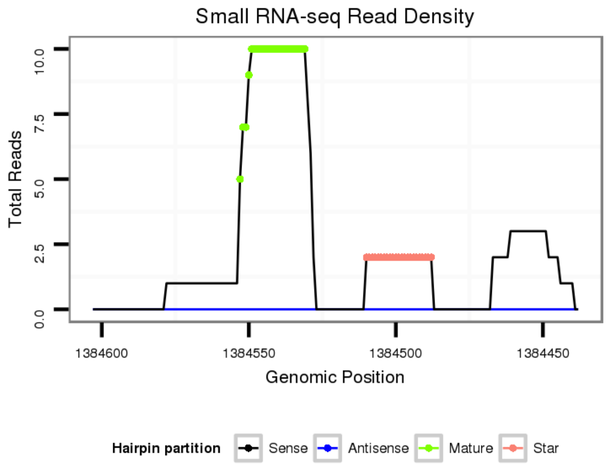
PASS/FAIL	
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	0
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	2

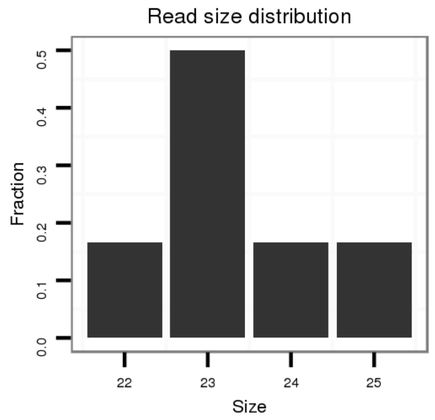
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_989	**scaffold_2:1384488-1384553 -**	**confident-exception**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

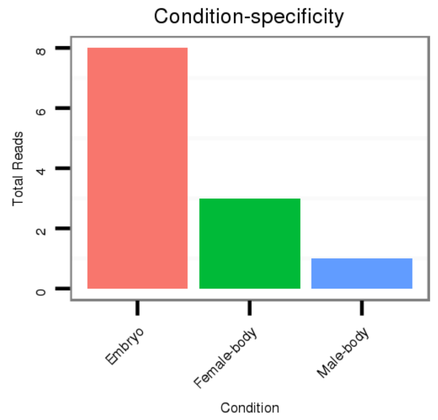
Legend: mature star mismatch in alignment mismatch in read

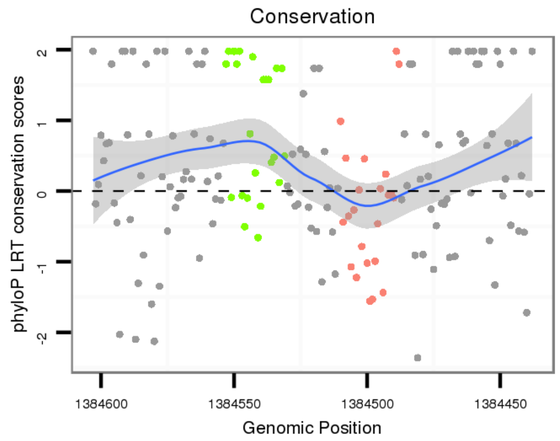
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dsec\GM14218-in]; CDS [Dsec\GM14218-cds]; CDS [Dsec\GM14218-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TCCTGGGCAGGAAAATAACAGACGTATTGGAGACCATCACCCACAGAAGCGTGAGTTGGAAATGGCGGCATTCTGATTTCCCTTATCGTCATCTGAATCCTCCCATCCCATTTCAGATCCCATCATCATTGCCGATCAAGATATGCTTCGTCTGCACCTCCACATT	Read size	# Mismatch	Hit Count	Total Norm	Total	V114 embryo	M054 female body	V113 male body	V115 head
**********.(((((.(((..(((((.((.(((((.(((.....)))).))))))..)))))..))))..))))..**********									
.....AATCCTCCCATCCCATTTCAGT.....	22	1	1	5.00	5	4	0	0	1
.....ATCCTCCCATCCCATTTCAGT.....	21	1	1	3.00	3	3	0	0	0
.....GTGAGTTGGAAATGGCGGCATTC.....	23	0	1	2.00	2	2	0	0	0
.....GTGAGTTGGAAATGGCGGCATTCTG.....	25	0	1	2.00	2	2	0	0	0
.....TGAATCCTCCCATCCCATTTCAG.....	23	0	1	2.00	2	0	2	0	0
.....GTGAGTTGGAAATGGCGGCATTTT.....	23	1	1	1.00	1	0	0	0	1
.....AGTTGGAAATGGCGGCATTCTG.....	22	0	1	1.00	1	0	0	1	0
.....GTGAGTTGGAAATGGCGGCATTCT.....	24	0	1	1.00	1	1	0	0	0
.....ATGCTTCGTCTGCACCTCCACA..	22	0	1	1.00	1	1	0	0	0
.....AGTTGGAAATGGCGGCATTCTGA.....	23	0	1	1.00	1	0	1	0	0
.....ATTGGAGACCATCACCCACAGAAGC.....	25	0	1	1.00	1	1	0	0	0
.....TGAGTTGGAAATGGCGGCATTCTGT.....	25	1	1	1.00	1	1	0	0	0
.....CAAGATATGCTTCGTCTGCACCT.....	23	0	1	1.00	1	1	0	0	0
.....GTTGGAAATGGCGGCATTCTGA.....	22	0	1	1.00	1	1	0	0	0
.....TGAGTTGGAAATGGCGGCATTCT.....	23	0	1	1.00	1	1	0	0	0
.....TGAGTTGGAAATGGCGGCATTCTG.....	24	0	1	1.00	1	1	0	0	0
.....CAAGATATGCTTCGTCTGC.....	19	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

AGGACCCGTCCTTTTATTGTCTGCATAACCTCTGGTAGTGGGTGTCTTCGCACTCAACCTTTACCGCCGTAAGACTAAAGGGAATAGCAGTAGACTTAGGAGGGTAGGGTAAAGTCTAGGGTAGTAGTAACGGCTAGTTCTATACGAAGCAGACGTGGAGGTGTAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V113 male body
**********.(((((.(((..(((((.((.(((((.(((.....)))).))))))..)))))..))))..))))..**********						

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_2:1384438-1384603 -	dse_989	TCC---TGGGCAGGAAAATAACAGACGTATTGGAGACCATCACCCACAGAAGCGTGAGTTG----------G-AAA-----TGGCGGCATTCTGA-TTTCCCT-TATCGTC-ATCTG------AATCCTCC------C-----ATCCCATTTCAGATCCCATCATCATTGCCGATCAAGATATGCTTCGTCTGCACCTCCACATT
droSim2	3L:1265272-1265437 -	dsi_14614	TCC---TGGGCAGGAAAATAACAGACGTACTGGAGACCATCACCCACAGAAGCGTGAGTTG----------G-AAA-----TGGCGGCATTCTGA-TTTCCCT-TCTCGTC-ATCTG------AATCCTCC------C-----ATCCCATTTCAGATCCCAGCATCATTGCCGATCAAGATATGCTTCGTCTGCACCTCCACATT
dm3	chr3L:1341812-1341977 -	dme_473	TCC---TGGGCAGGAAAATAACAGACGTACTGGAGACCATCACCCACAGAAGCGTGAGTTG----------G-AAA-----TGGCGGCATTCTGA-TTTCCCT-TCTCGTC-ATCTA------AATCATCC------C-----ATCCCATTTCAGATCCCATCATCCTTGCCCATCAAGATATGCTTCGTCTGCACCTCCACATT
droEre2	scaffold_4784:1324682-1324846 -		TCC---TGGGCAGGAAAATTACAGACGTACTGGAGACCATCACCCACAGAAGCGTGAGTTG----------G-AAA-----GGGCGGCATTCTGA-TTTCTCAATCTTAATCT-----CGAATCATCT------T-----GCCCTCTTTCAGATCCCAGCATCGTTGCCCATCAAGATATGCTTCGTCTGTACCTCCACATT
droYak3	3L:1300727-1300891 -		TCC---TGGGCAGGAAAATTACAGATGTACTAGAGACCATCACACACAGAAGCGTGAGTTG----------G-AAA-----AGGCGGCATTCTGA-TTTCCCAATCTTAATCT-----CAAATCATCT------C-----GCCGCTTTCAGATCCCATCATCGTTGCCCATCAAGATATGCTTCGTCTGCACCTCCACATT
droEug1	scf7180000409007:165676-165835 -		TTC---TGGACAAAAAATGATAGAAATACTGGAGACCATTACACACAGAAGCGTTAGTTA----------A-AAA-----GAGCGGCATTCTGA-TTTCCCAATCTGACCC-----CGACC-----C-----TTTCCCTTTCAGATCCCGGCCAACGCTCGTATTAAGATTTGCTTCCTTTGCCATGTTCATT
droBia1	scf7180000300910:1446654-1446820 -		TTG---TGGGCACAAAGTCGTGGACTTGCTGGAGGCCATCACCCACAAGAGCGTGAGTTG----------G-GCC-----GCGCGGCATTCCTA-TCTCCAGATCTGATCC-----CAATC--CATTCCCTT-----CACCCCTTTCAGATCCCAGCCAACGCCAACGTCAAGATATGCTTCATCTGTGCCGTCGGGCTT
droTak1	scf7180000414671:329963-330127 -		TTG---TGGGCACCAAAATGGTAGACATACTGGAGCCCATCACCCACAAGAGCGTGAGTTT----------G-AAA-----GAGCGGCATTCCGA-ATTCCCTTTCTATC-ACCTA------ACTTTTT------------GACCTCTTTAGATCCCAGCAATGCGCCCATTAAGATATGCTTCATCTGCGCCTCGGGCTT
droEle1	scf7180000491249:4280450-4280634 +		TCGCCCATGGGCCGCAAAATTGTGGTCTGCTGGAGATCCGTCACGCACAGCAACGTAAGTGG----------A-AAA-----AGGCGGTATTCTGA-TTTCCCAATCTTACTTGACTGACCCCCGCC--CTT-CCCCCTCCACATCCCCTTTCAGCACCCGCCAACGCGCCGTAAGGCTATGCTTCCATTGCCCCTCCAATTT
droRho1	scf7180000779696:6192-6352 +		TCG---TGGGCCGTAAAATTGTGGACCTGCTGGAGACAATCACCCACAAAACGTGAGTAG----------A-AAA-----AGGCGGTATTCTGA-TTTCCTATATCTG---T-TCTG------ACCGTCC-------------TCCTCCTCTCAGCTCCCGATAAACTTGGCCCTGAAGCTGTGCTTCCTGTGCCCATCCACCAT
droFic1	scf7180000454113:738145-738307 +		TTG---TGGGCAGAAATTGATAGACATTCTGCCCGCCTCTCCCACAGAAGCGTGAGTTA----------G-AAA-----AGGCGGCACTCTGA-ATTCCCAATTTGACCC-----CT--TCTTCT------A-----TCCCCTTTTAGCTGCCGGCCAACTTGCCGATCAAGCTATGCTTCCTGTGCCCCTCTAGTTT
droKik1	scf7180000302577:378184-378368 -		TTG---TGGGCTACAACATGCTCGAAGTTTTGCAAATAATCACCCACAAAGACGTGAGTACAGCACC----------CCAGC----------CA-AAA-----GGGCGGCATTCTGATTT-CTAATTTAATC-TATTG------ACCTATTTTTGCCGT-----GTGCCCTTCCAGTTGCCTGCTAACCTGGCCGTAAAAGTATGCTTCATGTGCCTTCCAACCT
droAna3	scaffold_13337:6571368-6571537 +		TCG---TCAGCCGGAAAGTGTTGGAACTGCTTGAGATCATTAACTCACAAAAACGTGAGTACTTGTCCCC----------A-AAA-----AGGCGCAATCTTA-GCA-CCAATATGATTT-----TAATT--TCT------C-----CTTCTGTCCTAGCTGCCCAATAATGTGGGCTTCAAGCTATGCTTTCTGTGCCCCTCCAGCCT
droBip1	scf7180000396709:303017-303187 +		TCG---TCAGCCGGAAAGTACTGGAGCTACTTGAGATCATTAACTCACAAAAACGTGAGTACT----------GTCCCCCA-AAA-----AGGCGCAATCTT-TGACCGAATTTGATTA-----AA--ATGTCT------C-----CCGATTCGACAGCTGCCCAATAATGTGGGCTTCAAGCTATGCTTCCTATGCCCTCCACACCT
dp5	XR_group8:766988-767159 +		TTT---ACGGCAACAAACTTACGCGACGTTCTGCACGCCATCACACAACGCCATGTAAGTACAGGCTATGGAAAATAACAAAAACAAAAATATGGCCCTCTGATAATTGGGGA----------------------------C-----ACTTTATTTCAGATTCCCACCACTTCGGCCATCAAGGTGTGCTTCATTTGTTTCTTCAAATT
droPer2	scaffold_32:715756-715927 -		TTT---ACGGCAACAAACTTACGCGACATTCTGCACGCCATCACACAACGCCATGTAAGTACAGGCTATGGAAAATAACAAAAACAAAAATATGGCCCTCTGATAATTGGGGA----------------------------C-----ACTTTATTTCAGATTCCCACCACTTCGGCCATCAAGGTGTGCTTCATTTGTTTCTTCAAATT

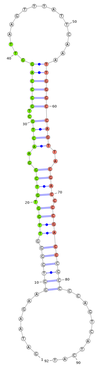
Generated: 09/08/2015 at 07:02 PM

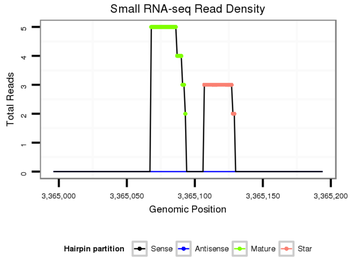
	PASS/FAIL
crit.star	1
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	1

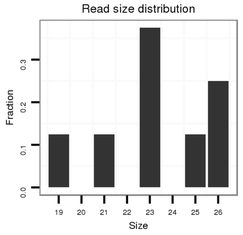
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_1836	**scaffold_3:3365046-3365144 +**	**candidate-rescued**	**Canonical miRNA**	**antisense_to_intron**	[View on UCSC Genome Browser [Cornell Mirror]]

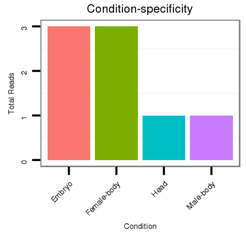
Legend: mature star mismatch in alignment mismatch in read

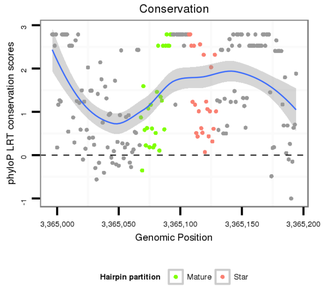
Predicted structure











Show Alternate Folds

Flybase annotation

Antisense to intron [Dsec/GM13290-in]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M054 female body	V114 embryo	V113 male body	V115 head
ATGTGGGAATAAACGCCGTATTCTTCGGGGATAAGGTGGGGGTGCTGTTCCGTTGATGATAAGAAGGTGGGGTTGGTGTCGGAACTGCTGCCCAGGTTAAGTTTATTCAAATTGGGCCAGTTACGACCCCGACGCCGCCCCAGTCATCATCATCATTGTTTGGCCCAGGGGCAACATTATGCCACGCCCCCTGCAACCGC									
.....(((((.(((((.(((((..(((((.....))))))))))..)))))).)))))..))))).)))))))))).....									
.....TTGGTGTCGGAACTGCTGCCCAGGTT.....	26	0	1	2.00	2	0	1	1	0
.....TTGGGCCAGTTACGACCCCGACC.....	23	0	1	2.00	2	2	0	0	0
.....TTGGTGTCGGAACTGCTGC.....	19	0	1	1.00	1	0	0	0	1
.....TTGGTGTCGGAACTGCTGCCCAGG.....	23	0	1	1.00	1	0	1	0	0
.....TTGGTGTCGGAACTGCTGCCCAGGT.....	25	0	1	1.00	1	0	1	0	0
.....TGGGCCAGTTACGACCCCGAG.....	21	1	1	1.00	1	1	0	0	0
.....TTGGGCCAGTTACGACCCCGA.....	21	0	1	1.00	1	1	0	0	0
.....TTGGGCCAGTTACGACCCCGAG.....	23	1	1	1.00	1	0	1	0	0
.....TTGGGCCAGTTACGACCCCGAG.....	22	1	1	1.00	1	0	0	0	1

Anti-sense strand reads

	Read size	# Mismatch	Hit Count	Total Norm	Total	M054 female body	V114 embryo
TACACCCTTATTTGCGGCATAAGAAGCCCCTATTCCACCCCACGACAAGGCAACTACTATTCTTCCACCCCAACCACACGCCTTGACGACGGGTCCAATTCAAATAAGTTTAACCCGGTCAATGCTGGGGCTGGGCGGGGTCAGTAGTAGTAGTAACAAACCGGGTCCCCGTTGTAATACGGTGCGGGGGACGTTGGCG							
**********.....(((((((.(((((.(((((..(((((((.....)))))))))..)))))).)))))..))))).)))))))))).....**							

Show Alignment With Reads

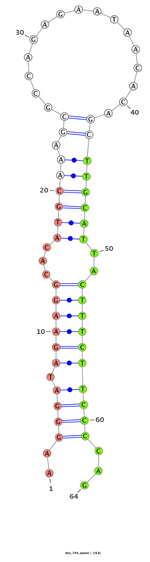
Re-alignment of all predicted orthologs

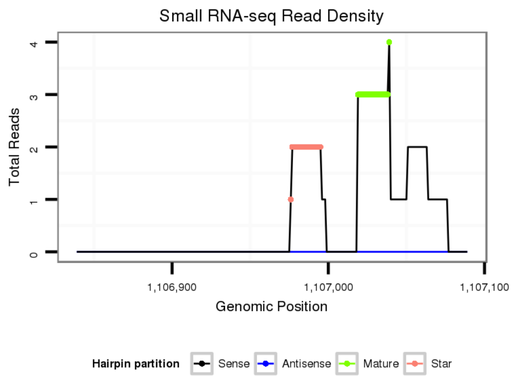
Species	Coordinate	ID	Alignment
droSec2	scaffold_3:3364996-3365194 +	dse_1836	ATGTGGGAATAAACGCCGTATT--CTTCGG----GG----------ATAA----------GG--TGGG-GGTGCTGTTCC----------GTTGATGATAA------GAAGGTGGGGCTGGTTACGACCCCGACGCCGCCCCAGTCATCATCATCATTGTTTGGCCCAGGGGCAACATTATGCCACGCCCCCTGCAACCGC
droSim2	2L:7597071-7597269 +	dsi_32441	ATGTGGGAATAAACGCCGTATT--CTTCGG----GG----------ATAA----------GG--TGGG-GGTGCTGTTCC----------GTTGATGATAA------GAAGGTGGGGCTGGTTACGACCCCGACGCCGCCCCAGTCATCATCATCATTGTTTGGCCCAGGGGCAACATTATGCCACGCCCCCTGCAACCGC
dm3	chr2L:7850626-7850824 +		ATGTGGGAATAAACGCCGTATT--CTTCGG----GG----------ATAA----------GG--TGGG-GGTGCTGTTCC----------GTTGATGATAA------GAAGGTGGGGCTGGTTACGACCCCGACGCCGCCCCAGTCATCATCATCATTGTTTGGCCCAGGGGCAACATTATGCCACGCCCCCTGCAACCGC
droEre2	scaffold_4929:16772171-16772375 +	der_190	ATGTGGGAATAAACGCCGTATT--CTTCGG----GG----------ATAA----------GG--TGGG-GCGCTGTTCC----------GTTGATGATAA------GAAGGTGGGGCTGGTTACGACCCCGACGCCGCCCCAGTCATCATCATCATTGTTTGGCCCAGGGGCAACATTATGCCACGCCCCCTGCAACCGC
droYak3	2L:5046038-5046268 -		ATGTGGGAATAAACGCCGTATT--CTTCGG----GG----------ATAA----------GG--TGGG-GGTGCTGTTCC----------GTTGATGATAA------GAAGGTGGGGCTGGTTACGACCCCGACGCCGCCCCAGTCATCATCATCATTGTTTGGCCCAGGGGCAACATTATGCCACGCCCCCTGCAACCGC
droEug1	scf1800004893463:893461-893686 -		ATGTGGGAATAAACGCCGTATT--CTTCGG----GGAAGTCTC----------ATA----------TA--TA-A--AGAC----------AGAGAGAGTAA----CA-TGGG-GC-C-----C----------G--GTATGATGATAA------GGCATGGGGCTGGTTACGACCCCGACGCCGCCCCAGTCATCATCATCATTGTTTGGCCCAGGGGCAACATTATGCCACGCCCCCTGCAACCGC
droBia1	scf1800003301518:690148-690339 +		ATGTGGGAATAAACGCCGTATT--CTTCGG----GG----------ATAA----------A-AGCGGG-GC--------GTTGATGATA------GACGGTGGGGCTGGTTACGACCCCGACGCCGCCCCAGTCATCATCATCATTGTTTGGCCCAGGGGCAACATTACGCCACGCCCCCTGCAACCGC
droTak1	scf1800004415876:487759-487951 -		ATGTGGGAATAAACGCCGTATT--CTTCGG----GG----------ATAA----------GG--TGGG-GGTGCTGTTCC----------GTTGATGATAA------GAAGGTGGGGCTGGTTACGACCCCGACGCCGCCCCAGTCATCATCATCATTGTTTGGCCCAGGGGCAACATTATGCCACGCCCCCTGCAACCGC
droEle1	scf1800004491028:1167920-1168118 +		ATGTGGGAATAAACGCCGTATT--CTTCGG----GG----------ATAA----------GG--TGGG-GC--------GTTGATGATAA------GACGTGGGGCTGGTTACGACCCCGACGCCGCCCCAGTCATCATCATCATTGTTTGGCCCAGGGGCAACATTATGCCACGCCCCCTGCAACCGC
droRho1	scf1800000778576:3664-3856 +		ATGTGGGAATAAACGCCGTATT--CTTCGG----GGAAGTCTC----------ATA----------GG--TGGG-GC--------GTTGATGATAA------GACGTGGGGCTGGTTACGACCCCGACGCCGCCCCAGTCATCATCATCATTGTTTGGCCCAGGGGCAACATTACGCCACGCCCCCTGCAACCGC
droFic1	scf1800004454115:654156-654402 +		ATGTGGGAATAAACGCCGTATT--CTTCGG----GGAAGTCCGGATGCCAATGCGGATGCCAATGCGGCATAACGGGGGGTGCGGGGGGCGGATGTTGAT----------ATA----------GA----GGGGCTGGTTACGACCCCGACGCCGCCCCAGTCATCATCATCATTGTTTGGCCCAGGGGCAACATTACGCCATGCCACGCCCCCTGCTCCCTG----------TGCCGCC
droKik1	scf1800000302570:197659-197912 -		ATGTGGGAATAAACGCCGTATT--CTTCGG----GG----------ATAA----------TGTGA----GC--TGGG-GCGCTGCCC----------TCAAGTGATGATAA------GACGGCGGCTGGTTACGACCCCGACGCCGCCCCAGTCATCATCATCATTGTTTGGCCCAGGGGCAACATTACGCCACGCCCCCTGTCCACGTCCCGGCTGTCCACGCCCCCTGCTCCCTG----------TGCCGCC
droAna3	scaffold_12943:11454011-11454230 -		ATGTGGGAATAAACGCCGTATT--CTTCGG----GGGAGTTTC----------ATA----------TGTTGATA--AGAC----------GC--TGGG-GC--------GTTGATGATAA------GACGTGGGGCTGGTTACGACCCCGACGCCGCCCCAGTCATCATCATCATTGTTTGGCCCAGGGGCAACATTACCTCGTGCACGCCTCCCG----------T----------CATCCTGGCGGATCCTGCCTGCCCCG
droBip1	scf1800003396728:1749692-1749932 +		ATGTGGGAATAAACGCCGTATT--CTTCGG----GGGAGTTTC----------ATA----------TGTTGATA--AGAC----------GC--TGG-GC--------GTTGATGATAA------GAAATGGGCTAT--------TGGGA----------ATGTCGGAACT-----G----CTGCCCAGGTTAAGTTTATTCAAATTGGGCCAGTTA-A------CGACCCCG------ACCGTGCACGCCTCCGC-G----------CCAATCCCCCTGTCCTGGCGGATCCTGGCCCCCGGCACAGACC----ACGC
dp5	4_group1:5445634-5445900 -		ATGTGGAATAAACGCCGTATT--CTTCGA----GG----------ATAA----------GG--TGGG-GC--------GTTGATGATAA------GACGGCGACTGAGAACCAGAGGAGAACCAGAGAGGCGAGAGGAGG--GC--TGA----------ATGTGGC-GGGAGGGAG-TATGTGGC-TGAGC-TGGCATGGGGCATTATGGAAGG------AACACT-----G----CTGCCAGGTTAAGTTTATTCAAATTGTGCCAGTT-A------CGACCCCG------ACCGTGCACGCCTCCGC-G----------CCATCCCCCTGTCCTGGCGGATCCTGGCCCCCGGCACAGACC----ACGC
droPer2	scaffold_11693635I-6936617 -		ATGTGGAATAAACGCCGTATT--CTTCGA----GG----------ATAA----------GG--TGGG-GC--------GTTGATGATAA------GACGGCGACTGAGAACCAGAGGAGAACCAGAGAGGCGAGAGGAGG--GC--TGA----------ATGTGGC-GGGAGGGAG-TATGTGGC-TGAGC-TGGCATGGGGCATTTGGAAGG------AACACT-----G----CTGCCAGGTTAAGTTTATTCAAATTGTGCCAGTT-A------CGACCCCG------ACCGTGCACGCCTCCGC-G----------CCATCCCCCTGTCCTGGCGGATCCTGGCCCCCGGCACAGACC----ACGC
droWil2	scf2_11000000045I6:3485059-3485237 -		ATGTGGAATAAACGCCGTATT--CTTCGA----GG----------ATAA----------GG--TGGG-GC--------GTTGATGATAA------GAGGGGCGTGAGGCGG---CGA-TGTCGCCA----------GTTGGGC----------GA----------GTGCGG----------GCGTGCAAGGTTAAGTTTATTCAAATTGGGCC----C----------CGTCACGTCCCCCTGTCCACGCCCCCTGCAACCGC
droVir3	scaffold_12963:8616447-8616616 +		ATGTGGGAATAAACGCCGTATT--CTTCGA----GG----------ATAA----------CAGTCATTGGCGATGGC---G----------C----------TGTAC----AAACGGGGGG

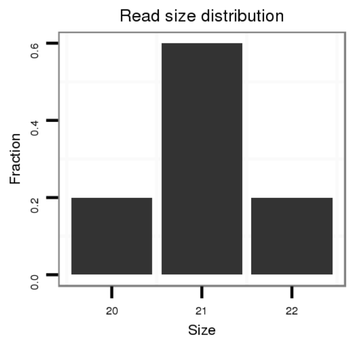
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_744	**scaffold_10:1106889-1107039 +**	**candidate-rescued**	**5p_tailed_mirtron**	**intron**	[View on UCSC Genome Browser [Cornell Mirror]]

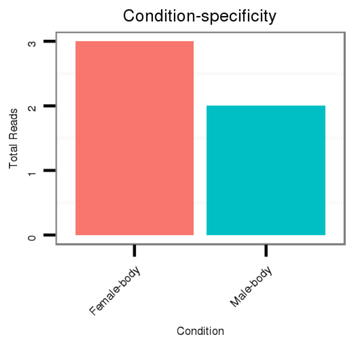
Legend: mature star mismatch in alignment mismatch in read

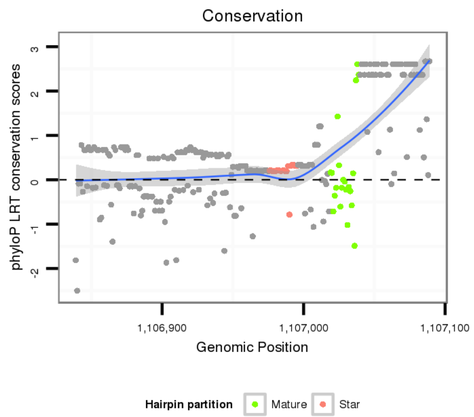
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dsec\GM19133-in]; CDS [Dsec\GM19133-cds]; utr5 [utr5_plus_13574]; utr5 [utr5_plus_13575]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

GGGATCGGATCGATTGCTTGCGGTGTGTGTGCAATCAGGAGGTGGGGCGATGGTCGCTGGTCACCGTGTCGGGTGGAGCACAGATGGTGGCCAGAGTAGAGCTTACAGAGCTCGACCTCCCTCTTTGCTGCCGATAGAAGGGATAGAAGGCACATGCAAAGCGCCAGAGAATAACACAGCTTGCATTACTTTCTTCCCCAGCTTCACGACGTCTTGCAAACGGCTGAAAATGGAGAAGACTCCCCGGTACA	Read size	# Mismatch	Hit Count	Total Norm	Total	V114 embryo	M054 female body	V115 head	V113 male body
**********..((((.(((((((...(((((((.((.....................)))))))))..))))))))))...**********	22	1	1	6.00	6	4	2	0	0
.....TTGCATTACTTTCTTCCCCAG.....	21	0	1	3.00	3	0	3	0	0
.....TTGCATTACTTTCTTCCCCAGA.....	22	1	1	1.00	1	0	1	0	0
.....AAGGGATAGAAGGCACATGC.....	20	0	1	1.00	1	0	0	0	1
.....AGGGATAGAAGGCACATGCAAA.....	22	0	1	1.00	1	0	0	0	1
.....CTTGCAAACGGCTGAAAATGGAGAAG.....	26	0	1	1.00	1	1	0	0	0
.....GCTTCACGACGTCTTGCAAACGGCT.....	25	0	1	1.00	1	1	0	0	0

Anti-sense strand reads

CCCTAGCCTAGCTAACGAACGCCACACACACGTTAGTCCTCCACCCCGCTACCAGCGACCAGTGGCACAGCCCACCTCGTGTCTACCACCGGTCTCATCTCGAATGTCTCGAGCTGGAGGGAGAAACGACGGCTATCTTCCCTATCTTCCGTGTACGTTTCGCGGTCTCTTATTGTGTCGAACGTAATGAAAGAAGGGGTCGAAGTGCTGCAGAACGTTTGCCGACTTTTACCTCTTCTGAGGGGCCATGT	Read size	# Mismatch	Hit Count	Total Norm	Total	V114 embryo	V113 male body	M054 female body
**********..((((.(((((((...(((((((.((.....................)))))))))..))))))))))...**********	22	1	1	6.00	6	4	2	0	0

Show Alignment With Reads

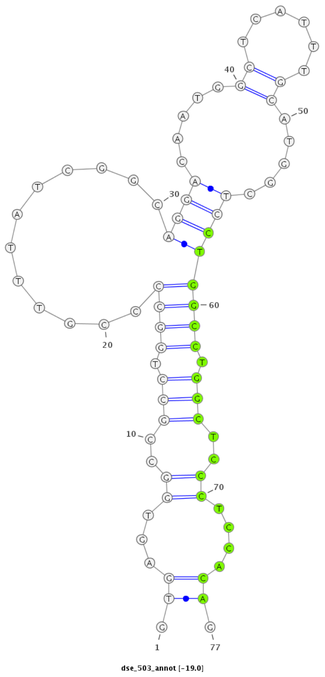
Re-alignment of all predicted orthologs

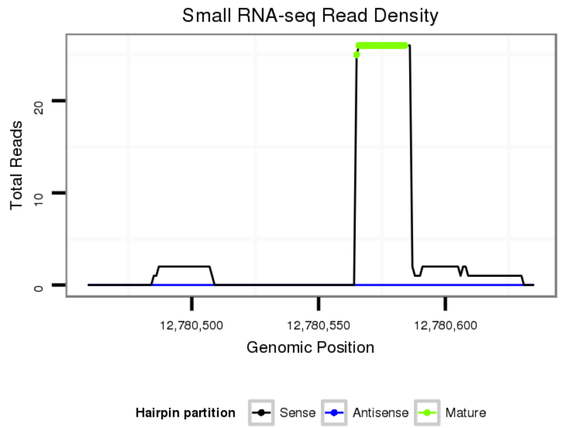
Species	Coordinate	ID	Alignment
droSec2	scaffold_10:1106839-1107089 +	dse_744	G-GGATCGGATCGATTGCTTGC-GGTGTGTGTGCAATCAGGAGG----TGGGGC--GATGGTCGCTGGTCACCGTGTC---------GGGTGGAGCACAGATGGTGG----------CCAGAGTAGAGCTT----------ACAGAGCTCGACCT----CCCTCTTTGCTGCCGATAGAAGGGATAGAAGGCACATGCAAAGCGCCAGAGAA------TAACACAGCTTGCATT------ACT-TTCTT------CCCCAGCTTCACGACG------TCTTGCAAACGGCTGAAAATGGAGAAGACTCCCCGGTACA
droSim2	x:1162509-1162758 +	dsi_25795	G-GGATCGGATCGATTGCTAGG-GGTGTGTGTGCAATCAGGAGG----TGGGGC--GATGGTCGCTGGTCACGTGTC---------GGGTGGAGCACAGATGGTGG----------CCAGAGTAGAGCTT----------ATAGAGCTCGACCT----CCCTCTTTGCTGCCGATAGAAGGGATAGAAGGCACATGCAAAGCGCCAGAGAA------TAACACAGTTGCATT------ACT-TTCTT------CCCCAGCTTCACGACG------TCTTGCAAACGGCTGAAAATGGAGAAGACTCCCCGGTACA
dm3	chrX:1283442-1283683 +	dme_471	G-GGATCGGATCGATTGCTAGG-GGTGTGTGTTCAATCAGGAGG----TGGGGC--GATGGTCGCTGGTCAGTGTGTCGCTGGTCACTGTGTGGAGCACAGATGGTGG----------CCA----------CTTCGCCCCTCTTTGCTGCCGATAGAAGGGATAGAAGGCCATGCAAAGCTCCAGAGAA------TAACACAGTGCTGCATT------ACT-TTCTCG------CCCCAGCTTCACGACG------TCTTGCAAACGGTTGAAAATGGAGAAGACTCCCCGGTACA
droEre2	scaffold_4644:1267479-1267681 +		G-GGATCGGATCGATTGCGAGG-GATGCTGCGCAATCAGGAGG----TGGGA-----------------------CACAG------------------CAGAGTCGAGCTTTCGTTCCCCCATAGA--TTAACCC----CCC-------------------------CACATGCAAAGCGCCAAAAAGCAGAGTTAACTCAGTTGCATTTTGCATTGCT-TTTTT------CCCCAGCTTCACGACG------TCTTGCAAACGGCTGAAAATGGAGAAGACTCCCCGGTACA
droYak3	X:1189688-1189692 +		G-GTAT---------------------------

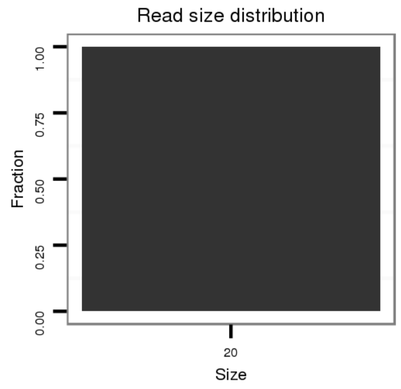
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_503	**scaffold_0:12780509-12780585 +**	**candidate-rescued**	**Mirtron**	**intron**	[View on UCSC Genome Browser {Cornell Mirror}]

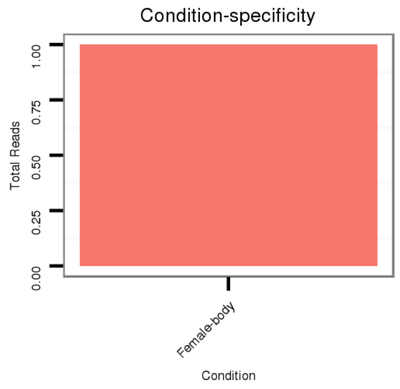
Legend: mature star mismatch in alignment mismatch in read

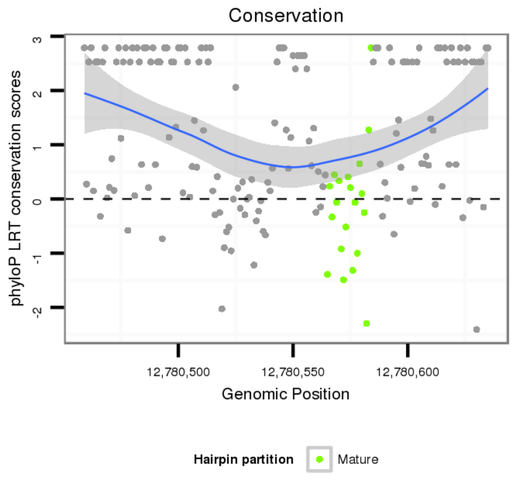
Predicted structure











Show Alternate Folds

Flybase annnotation

intron [Dsec\GM25939-in]; CDS [Dsec\GM25939-cds]; CDS [Dsec\GM25939-cds]

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

AACTGCGCGATGTGGTGGATCTCACCTTCGTGCCGTTCGGAAAGTCTCAGGTGAGTGGCCGCCTGGCCCCGTTTATCGGCAGGACAATGGCTCATTTGCATGGCTCCTGGCCTGGCTCCCTCCACAGTTCGTTACCCAGGGCTCCGAGGTGACGTTCACCTGCCATCACGGACCGAA	Read size	# Mismatch	Hit Count	Total Norm	Total	V114 embryo	V115 head	M054 female body	V113 male body
**********.((...((..((((.((((.....(((((.....((.....)).....)))))))).))))..)).)).**********									
.....CTGGCCTGGCTCCCTCCACAGT.....	22	0	1	23.00	23	14	5	1	3
.....CTGGCCTGGCTCCCTCCACAGTA.....	23	1	1	1.00	1	0	1	0	0
.....TACCCAGGGCTCCGAGGT.....	18	0	1	1.00	1	0	1	0	0
.....CTGGCCTGGCTCCCTCCACAGTT.....	23	0	1	1.00	1	0	1	0	0
.....GTTCGTTACCCAGGGCTCCGA.....	21	0	1	1.00	1	0	0	1	0
.....TTCGTGCCGTTCGGAAAGTCTCA.....	23	0	1	1.00	1	0	1	0	0
.....GTGACGTTCACCTGCCATCACGGA.....	24	0	1	1.00	1	0	0	1	0
.....CTGGCCTGGCTCCCTCCACA.....	20	0	1	1.00	1	0	0	1	0
.....CGTGCCGTTCGGAAAGTCTCAG.....	22	0	1	1.00	1	1	0	0	0
.....CTGGCCTGGCTCCCTCCACT.....	20	1	1	1.00	1	0	1	0	0
.....TGGCCTGGCTCCCTCCACAGT.....	21	0	1	1.00	1	0	0	1	0

Anti-sense strand reads

TTGACGCGCTACACCACCTAGAGTGGAAGCACGGCAAGCCTTTCAGAGTCCACTCACCGGCGGACCGGGGCAAATAGCCGTCCTGTTACCGAGTAAACGTACCGAGGACCGGACCGAGGGAGGTGTCAAGCAATGGGTCCCGAGGCTCCACTGCAAGTGGACGGTAGTGCCTGGCTT	Read size	# Mismatch	Hit Count	Total Norm	Total	M054 female body	V115 head	V113 male body
**********.((...((..((((.((((.....(((((.....((.....)).....)))))))).))))..)).)).**********									
.....TATGCAAGTGGACGGTAGT.....	19	2	1	1.00	1	0	1	0	
.....ATGCAAGTGGACGGTAGT.....	18	1	1	1.00	1	1	0	0	

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_0:12780459-12780635 +	dse_503	AACTGCGCGATGTGGTGGATCTCACCTTCGTGCCGTTCGGAAAGTCTCAGGTGAGTGG-----CCG--------CCTGG---CCC--CGTTTA----TCGGCAGGACAATGGC----------TCATTTGCATGGCTCCTG-GCC------TGGCTC-----CCTCCACAGTTCGTTACCCAGGGCTCCGAGGTGACGTTCACCTGCCATCACGGACCGAA
droSim2	3r:11954798-11954974 +	dsi_17325	AACTGCGCGATGTAGTGGAACTCACCTTCGTGCCGTTCGGAAAGTCTCAGGTGAGTGG-----CCG--------CCTGG---CCC--CGTTTA----TCGGCAGGACAATGGC----------TCATTTGCATGGCTCCTG-GCC------TGGCTC-----CCTCCACAGTTCGTTACCCAGGGCTCCGAGGTGACGTTCACCTGCCATCACGGACCGAA
dm3	chr3R:9225105-9225281 -	dme_472	AACTGCGCGATGTGGTGGAACTCAGTTCGTGCCATTCGGAAAGTCTCAGGTGAGTGG-----CCC--------TCTGG---GAC--CGTTTA----TCGGCAGGACAATGGC----------TCATTTGCATGGCTCCTG-GCC------TGGCTC-----CCTCCACAGTTCGTTACCCAGGGCTCCGAGTGACGTTCACCTGCCACCACGGACCGAA
droEre2	scaffold_4770:12416721-12416905 +		AGCTGCGTGATGTGGTGGAACTCACCTTCGTACCATTCGGAAAGTCTCAGGTGAGTGG-----CCCCGTGGCCCCTTGG---CCC--CGTTTA----TCGGCAGGACAATGGC----------TCATTTGCATGGCTCCTG-GCC------TGGCTT-----CCTCCCCAGTTCTTACCCAGGGCTCCGAGGTGACGTTCACCTGCCACCACGGCCGAA
droYak3	3R:13532111-13532287 -		AACTGCGCGACGTGGTGGAGCTCACCTTCGTGCCGTTCGGAAAGTCTCAGGTGAGTGG-----CCC--------CTTGG---CCC--CGTTTG----TCGGCAGGACAATGGC----------TCATTTGCATGGCCCTG-GCC------TGGCTT-----CCTCGCCAGTTCGTTACCCAGGGCTCCGAGGTGACGTTCACCTGCCACCACGGACCGAA
droEug1	scf7180000409802:779071-779246 +		AGCTTCGTGATGTGGTGGAACTCACCTTCGTGCCATTCGGAAAGTCAACAGTGAGTGG-----CAC--------A-TAA---CCC--CGTTTA----ACGCCAGGACAATGGC----------TCATTTGCATGGCTCTTT-TAC------TTGCTC-----CTTCCACAGTTCGTCACTCAGGGCTCCGAGGTGACGTTAACCTGCCATCATGGACCGAA
droBia1	scf7180000302402:1930668-1930842 -		AGCTGCGCGATGTGGTGGAACTCACCTTCGTGCCGTTCGGAAAGTCCGAGGTGAGTGG-----CCC--------C-TAG---CCC--CGTTTA----CCGGCAGGACAATGGC----------TCATTTGCATGGTTCTCTTCC------CTTCTT-----GCTCCTCAGTTCGTAACCCAGGGCGCCGAGGTGACGTTCACCTGCCACCACGGCCGAA
droTak1	scf7180000410308:24148-24327 +		AGCTGCGCGATGTGGTGGAACTCACCTTCGTGCCGTTCGGAAAGTCTCAGGTGAGTGG-----CCA--------C-TAG---CCCCTTCGTTTG----TCGGCAGGACAATGGC----------TCATTTGCATGGCTGTTT-T-T------GGGCTCCTT--GCTCGCCAGTTGTTCACCCAGGGCGCCGAGACGTGGTTCACCTGCCACCACGGACCGAA
droEle1	scf7180000491261:21560-21735 +		AGCTGCGCGATGTGGTGGAACTCACCTTCGTGCCGTTCGGAAAGTCTCAGGTGAGTGG-----CCA--------T-TAG---CCT--CGTTCA----TCGGCAGGACAATGGC----------TCATTTGCATGGCTCTTT-TGC------TTGCTT-----CCTCCGCAGTTGTTCACTCAGGGCTCCGAGGTGACGTTCACCTGCCACCACGGTCCGAA
droRho1	scf7180000779659:488792-488967 +		AGCTGCGCGATATGGTGGAACTCACCTTCGTGCCGTTCGGAAAGTCTCAGGTGAGTGG-----CCA--------C-CGG---CCC--GAAATA----TCGGTAGGACAATGGC----------TCATTTGCATGGCTCGTTT-TCC------CTGCTC-----GTTCCCAGTTGTTCACCCAGGGCTCCGAGGTGACGTTCAGATGCCACCACGGTCCGAA
droFic1	scf7180000453906:276390-276565 +		AGCTGCGCGATGTGGTGGAGCTCACCTTCGTGCCGTTCGGAAAGTCTCAGGTGAGTGG-----CCC--------C--GA---CCT--C-CTCTT----TCGGCAGGACAATGGC----------TCATTTGCATGGCTCCTGTTCC------TCGCTC-----GTTCCGCAGTTGTTCACCCAGGGCTCCGAGGTGACGTTCACCTGCCACCACGGTCCAAA
droKik1	scf7180000302392:602379-602555 +		AGCTGCGCGATGTGGTGGACCTCACCTTGGTGCCTTTCGGAAAGTCTCAGGTGAGTGT----GAGCCCG----AACCCTTACGTT--GATTTTTCCTCCGGCTGGACAATGGC----------TCATTTGCATGGTT----T----T----T-----T-TGGTAGTTGTTACCCAGGGCGCCGAGGTGACCTTCACCTGCCACCATGGGCCGAA
droAna3	scaffold_13340:1784396-1784575 -		AGCTGCGCGATGTGGTGGAACTCACCTTTGTTGCCTTTCGGAAAATCTCAGGTGAGTAT-----CCT--------CTCTG---CCT--GATTTT----TACCAAGGACAATAGC----------TCATTTGCATGGCTCATT-TGC------GAACTTTTT--CCTTTGCAGTTGTTCTACGCAAGGCTCTGAGGTTACCTTCACCTGCCATCACGGCCCCAA
droBip1	scf7180000396712:2550382-2550561 +		AGCTTACGAGAGGTGGTGGACCTGACCTTCGTTGCCTTTCGGAAAATCTCAGGTGAGTAT-----CCC--------CTCTG---CCT--TACTTT----TGCCAAGACAATAGC----------TCATTTGCATGGCTGTTT-TGC------GAGCCTTTT--GGTTTTCAGTTGTTCTACTCAGGGCTCTGAGGTTACTTTTACCTGCCATCACGGCCCGAA
dp5	2:9884759-9884934 +		AGCTGCGCGATGTGGTGGATCTCACATTTGTGCCGTTCGGCAAGTCCCAGGTGAGTGCTGTGGCAG--------G-GG---CCA--CGGGGG----CGACTAGGACAATGGC----------TCATTTGCATCGCTATCT-----------GTTTG-----CCCCGGCAGTTGTTCACGCAGGGCGCCGAGGTGACCTTCACCTGCCACCATGGACCGAA
droPer2	scaffold_0:10599465-10599640 -		AGCTGCGCGATGTGGTGGATCTCACATTTGTGCCGTTCGGCAAGTCCCAGGTGAGTGCTGTGGCAG--------C-GG---CCA--CGGGGG----CGACCAGGACAATGGC----------TCATTTGCATCGCTATCT-----------GTTTG-----CCCCGGCAGTTGTTCACGCAGGGCGCCGAGGTGACCTTCACCTGCCACCATGGACCGAA
droWil2	scf2_1100000004943:6296384-6296566 -		AACTCCGTGATGTGGTCGAACTCACATTTGTGCCTTTGGCAAATCTCAGGTAAGTGC-----CAA--------T-TGG---CCC--------------A-CAGTAGGCCAATGTG----------TAACGAATTGTGTGGAA----TAAATGCTCATTTGCATATCGCTTT-C--------G-----GTCTGCCAGTTGTCCACGATGGGCGCCGAGGTGACTTTCAGTTGTCATCATGGTCCAAA
droVir3	scaffold_12855:2926783-2926953 +	dvi_3656	AGCTGCGTGATGCGGTCGAACTCACATTTGTGCCTTTGGCAAGTCCCAGGTGAGTGA-----ACG--------AAA--T---CCC--CGTTT----TAGGCCAACAATGCC----------TCATTTGTGACACATTCA-CAT------TTGCA------TCCATGCAGTTGCACACACAAGGCGCTGAGGTGACCTTTACCTGCCATCATGGTCCGAA
droMoj3	scaffold_6540:10279199-10279385 -		AGCTGCGTGACCTTCGTCGAACTCACATTTGTGCCCTTTGGCAAATCCCAGGTGAGTCC-----CCC--------CCCCC---CCC--CCCCCC----CC--AATGGAACAATGCCTCATTTGTCACACTGGCGCACTAACTAACTC----AAACTCTTCAT--T----------TCTCCATTTC---GCATTT-----CCCACACGCAGTTTTTCACACAAGGCTCGGAGGTGACCTTCACCTGCCACCACGGCCCCAA
droGri2	scaffold_14906:3740852-3741024 -		AGCTGCGCGAATCTGTCGAACTCACATTTGTGCCCTTTGGCAAATCCCAGGTGAGTTG-----AA--------CCCCC---CCC--CCCCCC----CAGCAAACACAATGCC----------TCATTTGTCTAAAATATG-CATTTACACGCACTGCATGCTTTATTCACGTTTGTCACACAAGGCGCCGAAACAATGTTCACCTGTCATCATGGCCGAA

Generated: 09/08/2015 at 07:04 PM

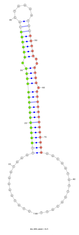
	PASS/FAIL
crit.star	0
crit.loop	0
crit.mor	0
crit.half	0
crit.total	0
crit.pairing	1
crit.top3	1
crit.tptop3	1
crit.uri	1
crit.back	1
rescue.total	1
rescue.dominant	1
rescue.known	0
rescue.confident	1
rescue.candidate	1

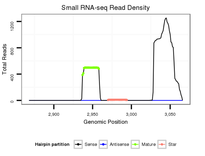
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dse_1841	**scaffold_2529:2918-3016 +**	**candidate-rescued**	**Canonical miRNA**	**intergenic**

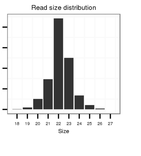
[View on UCSC Genome Browser (Cramd Mmm1)]

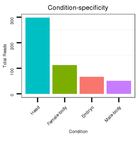
Legend: mature star mismatch in the mature mismatch in the star

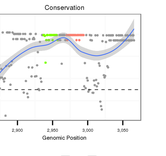
Predicted structure











Show Alternate Folds

Flybase annotation

dRNA:[Dsec]:FAMN:AAGGV000:RA]

No flyanotble element found

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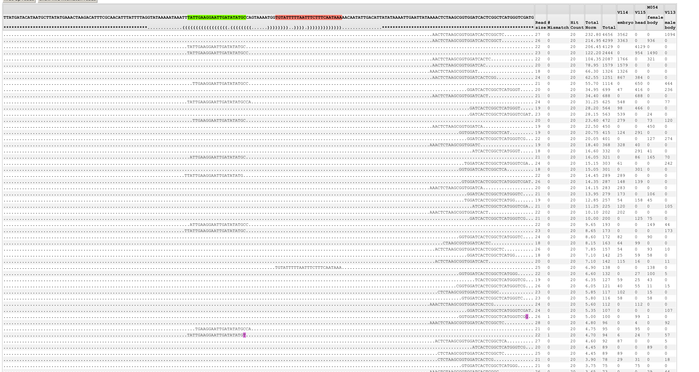
Sense Strand Reads

hide 3p reads | show mid mismatch reads



Anti-sense strand reads

No more available in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	SS	Alignment
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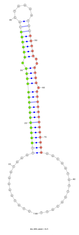
Generated 09/08/2015 at 07:56 PM

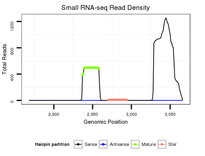
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dse_1841	**scaffold_2529:2918-3016 +**	**candidate-rescued**	**Canonical miRNA**	**intergenic**

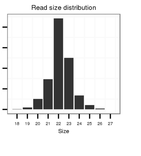
[View on UCSC Genome Browser (Cramd Mmm1)]

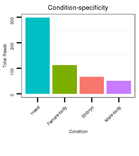
Legend: mature star mismatch in the mature mismatch in the star

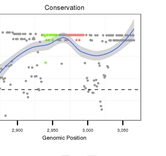
Predicted structure











Show Alternate Folds

Flybase annotation

dRNA:[Dsec]:FAMN:AAGGV000:RA]

No flyanotble element found

names	star
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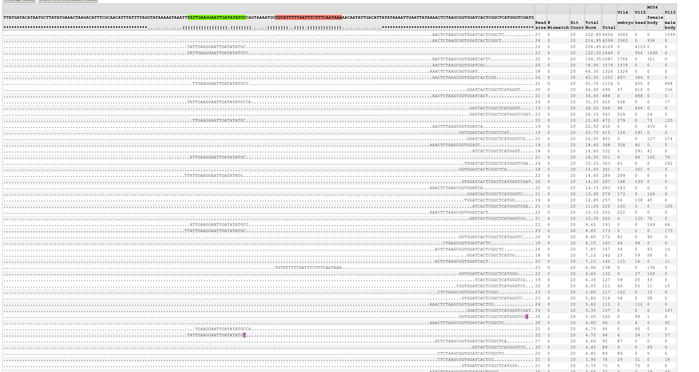
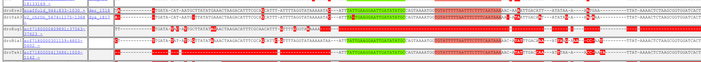
Sense Strand Reads

hide 3p reads | show mid mismatch reads



Anti-sense strand reads



No meta annotation in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment

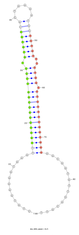
Generated 09/08/2015 at 07:56 PM

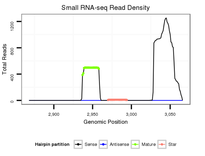
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
dse_1841	**scaffold_2529:2918-3016 +**	**candidate-rescued**	**Canonical miRNA**	**intergenic**

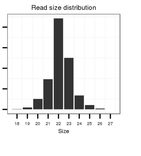
[View on UCSC Genome Browser (Cramd Mmm1)]

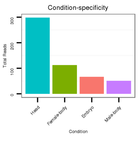
Legend: mature star mismatch in the mature mismatch in the star

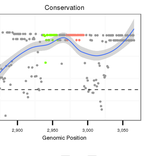
Predicted structure











Show Alternate Folds

Flybase annotation

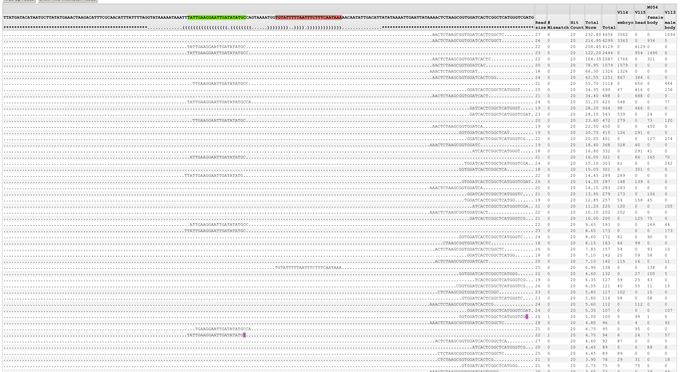
dRNA:[Dsec]:FAMN:AAGGV000:RA]

No flyanotble element found

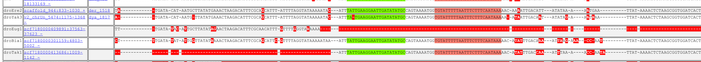
names	star
1. scaffold_39997301-3355 - 2. scaffold_39997301-3355 + 3. scaffold_9669324-3285 - 4. scaffold_13091218-3339 - 5. scaffold_13091218-3339 + 6. scaffold_71958324-3343 - 7. scaffold_4881988-3929 - 8. scaffold_28261328-3467 - 9. scaffold_8107747-3492 - 10. scaffold_8107747-3492 + 11. scaffold_8495488-916 - 12. scaffold_8404413-3456 - 13. scaffold_8404413-3456 + 14. scaffold_8627184-1285 - 15. scaffold_13039128-3412 - 16. scaffold_13039128-3412 + 17. scaffold_2861879-3382 - 18. scaffold_12857484-882 - 19. scaffold_12857484-882 + 20. scaffold_13084-3443 - 21. scaffold_3066158-3761 - 22. scaffold_4364298-3352 - 23. scaffold_7389184-3384 - 24. scaffold_7389184-3384 + 25. scaffold_31631881-3398 - 26. scaffold_30320160-381 - 27. scaffold_30320160-381 + 28. scaffold_7555651-3421 - 29. scaffold_3655128-139 - 30. scaffold_3655128-139 + 31. scaffold_8695392-4454 - 32. scaffold_6354-8932-3873 - 33. scaffold_8457282-3286 - 34. scaffold_18086-388-387 - 35. scaffold_18086-388-387 + 36. scaffold_31299728-3781 - 37. scaffold_1557171-94 - 38. scaffold_1557171-94 + 39. scaffold_12638-928-329 - 40. scaffold_13379326-3477 - 41. scaffold_13379326-3477 + 42. scaffold_4778799-820 - 43. scaffold_7865-8845-3866 - 44. scaffold_33331482-3383 - 45. scaffold_7864-843-3866 - 46. scaffold_7864-843-3866 + 47. scaffold_8273-8825-3946 - 48. scaffold_6447-452-473 - 49. scaffold_6447-452-473 + 50. scaffold_8638185-3228 - 51. scaffold_7027-2295-3280 - 52. scaffold_7027-2295-3280 + 53. scaffold_31892307-838 - 54. scaffold_33354-684-422 - 55. dse_1841 scaffold_2529:2951-3908 - 56. scaffold_8602-1668-3387 - 57. scaffold_8602-1668-3387 + 58. scaffold_7140-763-786 - 59. scaffold_7795-8128-3449 - 60. scaffold_7795-8128-3449 + 61. scaffold_6266-574-1997 - 62. scaffold_18073446-647 - 63. scaffold_18073446-647 +	1. dse_1841 scaffold_2529:2938-2986 + 2. scaffold_39997301-3355 - 3. scaffold_39997301-3355 + 4. scaffold_13047440-364 + 5. scaffold_71958324-3343 - 6. scaffold_71958324-3343 + 7. scaffold_30364-5256 -3280 + 8. scaffold_28261328-3467 - 9. scaffold_28261328-3467 + 10. scaffold_8107747-3492 - 11. scaffold_8107747-3492 + 12. scaffold_8457282-3286 - 13. scaffold_8457282-3286 + 14. scaffold_8627184-1285 - 15. scaffold_13039128-3412 - 16. scaffold_13039128-3412 + 17. scaffold_2861879-3382 - 18. scaffold_12857484-882 - 19. scaffold_12857484-882 + 20. scaffold_13084-3443 - 21. scaffold_3066158-3761 - 22. scaffold_4364298-3352 - 23. scaffold_7389184-3384 - 24. scaffold_7389184-3384 + 25. scaffold_31631881-3398 - 26. scaffold_30320160-381 - 27. scaffold_30320160-381 + 28. scaffold_7555651-3421 - 29. scaffold_3655128-139 - 30. scaffold_3655128-139 + 31. scaffold_8695392-4454 - 32. scaffold_6354-8932-3873 - 33. scaffold_8457282-3286 - 34. scaffold_18086-388-387 - 35. scaffold_18086-388-387 + 36. scaffold_31299728-3781 - 37. scaffold_1557171-94 - 38. scaffold_1557171-94 + 39. scaffold_12638-928-329 - 40. scaffold_13379326-3477 - 41. scaffold_13379326-3477 + 42. scaffold_4778799-820 - 43. scaffold_7865-8845-3866 - 44. scaffold_33331482-3383 - 45. scaffold_7864-843-3866 - 46. scaffold_7864-843-3866 + 47. scaffold_8273-8825-3946 - 48. scaffold_6447-452-473 - 49. scaffold_6447-452-473 + 50. scaffold_8638185-3228 - 51. scaffold_7027-2295-3280 - 52. scaffold_7027-2295-3280 + 53. scaffold_31892307-838 -

Sense Strand Reads

hide 3p reads | show mid mismatch reads



Anti-sense strand reads



No meta annotation in table

Show Alignment With Reads

Re-alignment of all predicted orthologs

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Generated 09/08/2015 at 07:56 PM

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
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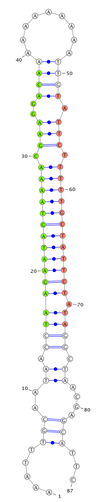
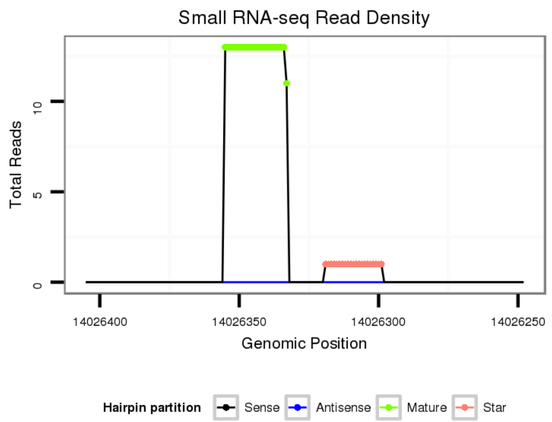
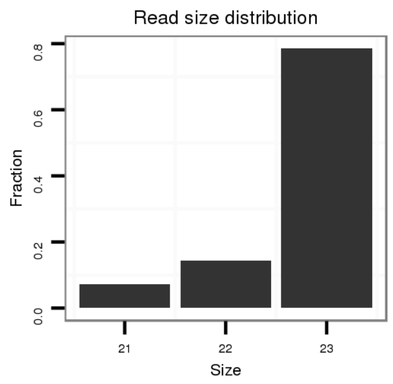
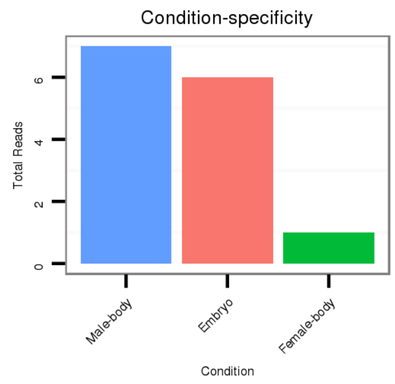
Legend: mature star mismatch in alignment mismatch in read

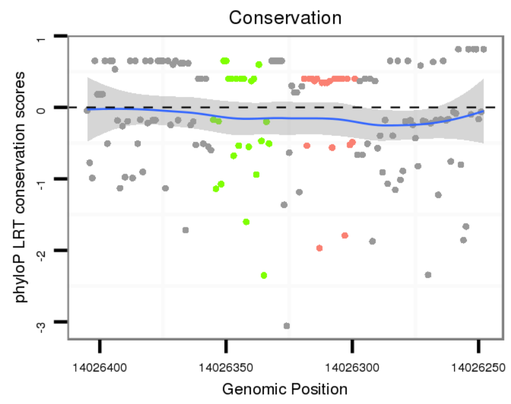
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTGAAAAAAAAAACACAAGAATGTGATATTTCATCAAATTTGCAATAACCTAAGAATAGTAAAACGAAGGACAAAAAAAAAAATTGTATTCTTTTTGCTATTCTATAGGCTAACGAGCATTCCTTAAAATACATATGTACATAAGTGTTTAAAAAAAT **********.....(((..((.((((((((((((((((.((((..((((.........)))))..)))).)))))))))))))).)))).))....)))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V113 male body	V114 embryo	M054 female body
.....TAAGAATAGTAAAACGAAGGACA.....	23	0	1	11.00	11	7	4	0
.....TAAGAATAGTAAAACGAAGGAC.....	22	0	1	2.00	2	0	2	0
.....TATTCTTTTTGCTATTCTATA.....	21	0	1	1.00	1	0	0	1
.....TAAGAATAGTAAAACGAAGGACAT.....	24	1	1	1.00	1	0	0	1

Anti-sense strand reads

AACTTTTTTTTTTGTGTTCTTACACTATAAAGTAGTTTAAACGTTATTGGATTCTTATCATTTGCTTCCTGTTTTTTTTTTTAACATAAGAAAAACGATAAGATATCCGATTGCTCGTAAGGAATTTTATGTATACATGTATTCACAAATTTTTTTA **********.....(((..((.((((((((((((((((.(((..((((.........)))))..)))).)))))))))))))).)))).))....)))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V115 head	M054 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
droSec2	scaffold_1:14026248-14026405 -	dse_1856	TTGAAAAA-AAAAA-CA-CAAGAATGTGATATTTC--ATCAAATT-----TGCAATAACCTAAGAATAGTAAAACGAAGGACAAAAAAAA-AAATTGTATTCTTTTTGCTATTCTA----------TAGGCTAACGAGC---------ATTCCTTAAAAT---------ACATATGTACATAAGTGTT-TA-AAAAAAT
droSim2	2r:17041512-17041659 -	dsi_32435	TTGA---AAAAAA-CA-CAAGAATGTGATATTTC--ATCAAATT-----TGCCATAACCTAAGAATAGTAAAACGAAGGCAAAAAAAA-AAATT-TATTCTTTTTGCTATTCTA----------TAGGCTAATGAGC---------ATTCCTTAAAAT---------AACATATGTGTT-TAAAAAAAT
dm3	chr2R:16472042-16472207 -		TTGAAAAA-AAAAA-CA-CAAAAATGTGATATTTC--ATCAC---------TCATCAACTCAAAATAGTAAATCGAAGGCCAAAAAAAT--ATGTATTCTGTTTGCTATTATA----------AAAGTTCACGAGCTAAGCTAACGATTCATTAAAAT------ATGTACATACATATTTAAGTGTT-AAAAAAAAAT
droEre2	scaffold_4845:10618664-10618918 -	der_25	ATAA----ACTAA-TTGT-ACAAAATGTGATATTTT--ATCAAATC-----TGCCATAACATCCAAATACTTAACCGATCATCAAAAACGGT----GTTTCT----GTATTTTACTATATAACTTATTTATGAAGAAGCTTTAGGATTTAATTTTTCCGACAATGCGATCTAGGCGTTTCTATCGCTGAGGTAGTATTGTTTGAAAGATTAAGTTAAAGCGT---------AATCATCAAAATTTTAAAATGTGATAAGTACATAAGTGTG-CCAAAAATAT
droYak3	2R:12724006-12724252 +	dya_34	AAAA----ACTAA-ATGTTAAAAATATATATTTT--ATCAAATG-----TACATAACCTCAAATACTAAACTGATGAGCAAAAAAGC-TA----TTTCTCTTTGTATTCTGCAATG-GATTTATTT-------GCTTTAGGATTTATTTTTTCGGACAATTCAATCTGGGCGTTGCTTTCGCTGAGGTAGTATTGTTTGGAAGACTAAGTTAACGAGC---------ATTCATCTCATTTTGAAATTT---TGTGTTCATCAGTGTG-TTAAAAATAT
droEug1	scf7180000409474:1489651-1489666 +		AA--ATGTG-TT-ACAAATT
droEle1	scf7180000491201:736783-736924 -		AATA----AAAAAA-TT-TAAGAACATGATATTTTGCAAGCAAATTATGTGTGC-------CAATAA-----------CGGTTAAAAAAAT----------GAAGCATTTCAAGAATTTAATTTTTTT-ATAA----------CT---------TGTGCTATAAAG---------AAACACGTAGATAACAATTAAAGAAAAAAT

	PASS/FAIL		
crit.star	0	0	0
crit.loop	0	0	0
crit.mor	0	0	0
crit.half	0	0	0
crit.total	0	0	0
crit.pairing	1	1	1
crit.top3	1	1	1
crit.tptop3	1	1	1
crit.uri	0	0	0
crit.back	1	1	1
rescue.total	1	1	1
rescue.dominant	1	1	1
rescue.known	0	0	0
rescue.confident	3	3	2
rescue.candidate	6	6	7

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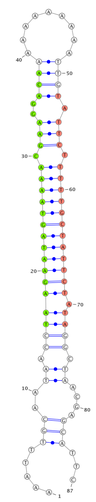
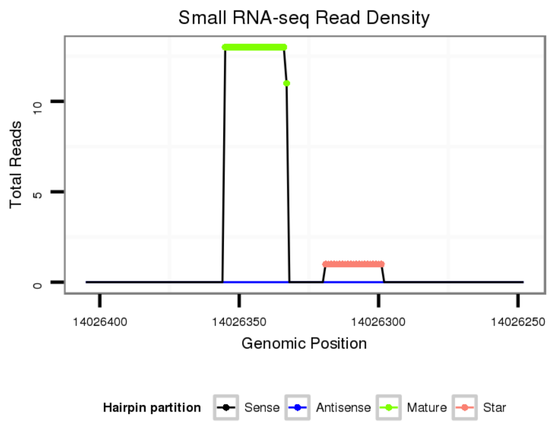
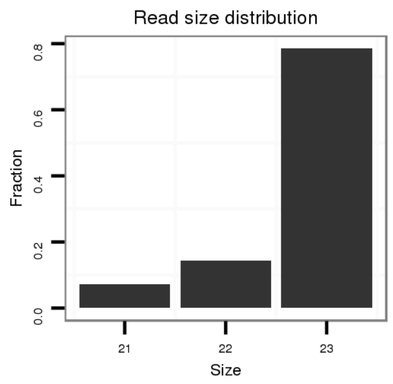
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dse_339	**scaffold_1:14026298-14026355 -**	**candidate-rescued**	**Testes-restricted**	**intergenic**	[View on UCSC Genome Browser {Cornell Mirror}]

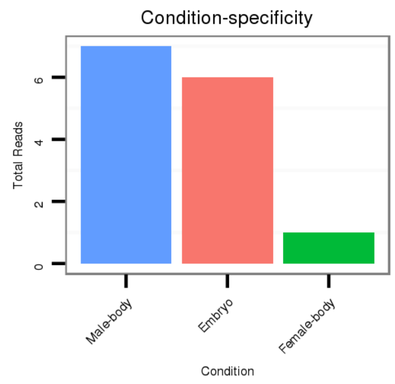
Legend: mature star mismatch in alignment mismatch in read

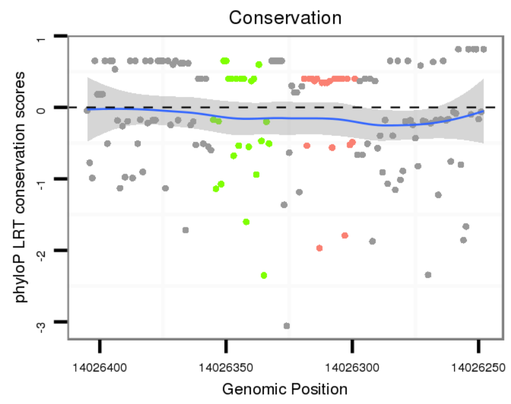
Predicted structure











Show Alternate Folds

Flybase annnotation

intergenic

No Repeatable elements found

Sense Strand Reads

hide 3p reads | show mid mismatch reads

TTGAAAAAAAAAACACAAGAATGTGATATTTCATCAAATTTGCAATAACCTAAGAATAGTAAAACGAAGGACAAAAAAAAAAATTGTATTCTTTTTGCTATTCTATAGGCTAACGAGCATTCCTTAAAATACATATGTACATAAGTGTTTAAAAAAAT **********.....(((..((.((((((((((((((((.((((..((((.........)))))..)))).)))))))))))))).)))).))....)))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V113 male body	V114 embryo	M054 female body
.....TAAGAATAGTAAAACGAAGGACA.....	23	0	1	11.00	11	7	4	0
.....TAAGAATAGTAAAACGAAGGAC.....	22	0	1	2.00	2	0	2	0
.....TATTCTTTTTGCTATTCTATA.....	21	0	1	1.00	1	0	0	1
.....TAAGAATAGTAAAACGAAGGACAT.....	24	1	1	1.00	1	0	0	1

Anti-sense strand reads

AACTTTTTTTTTTGTGTTCTTACACTATAAAGTAGTTTAAACGTTATTGGATTCTTATCATTTGCTTCCTGTTTTTTTTTTTAACATAAGAAAAACGATAAGATATCCGATTGCTCGTAAGGAATTTTATGTATACATGTATTCACAAATTTTTTTA **********.....(((..((.((((((((((((((((.(((..((((.........)))))..)))).)))))))))))))).)))).))....)))...**********	Read size	# Mismatch	Hit Count	Total Norm	Total	V115 head	M054 female body

Show Alignment With Reads

Re-alignment of all predicted orthologs

Species	Coordinate	ID	Alignment
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droSim2	2r:17041512-17041659 -	dsi_32435	TTGA---AAAAAA-CA-CAAGAATGTGATATTTC--ATCAAATT-----TGCCATAACCTAAGAATAGTAAAACGAAGGCAAAAAAAA-AAATT-TATTCTTTTTGCTATTCTA----------TAGGCTAATGAGC---------ATTCCTTAAAAT---------AACATATGTGTT-TAAAAAAAT
dm3	chr2R:16472042-16472207 -		TTGAAAAA-AAAAA-CA-CAAAAATGTGATATTTC--ATCAC---------TCATCAACTCAAAATAGTAAATCGAAGGCCAAAAAAAT--ATGTATTCTGTTTGCTATTATA----------AAAGTTCACGAGCTAAGCTAACGATTCATTAAAAT------ATGTACATACATATTTAAGTGTT-AAAAAAAAAT
droEre2	scaffold_4845:10618664-10618918 -	der_25	ATAA----ACTAA-TTGT-ACAAAATGTGATATTTT--ATCAAATC-----TGCCATAACATCCAAATACTTAACCGATCATCAAAAACGGT----GTTTCT----GTATTTTACTATATAACTTATTTATGAAGAAGCTTTAGGATTTAATTTTTCCGACAATGCGATCTAGGCGTTTCTATCGCTGAGGTAGTATTGTTTGAAAGATTAAGTTAAAGCGT---------AATCATCAAAATTTTAAAATGTGATAAGTACATAAGTGTG-CCAAAAATAT
droYak3	2R:12724006-12724252 +	dya_34	AAAA----ACTAA-ATGTTAAAAATATATATTTT--ATCAAATG-----TACATAACCTCAAATACTAAACTGATGAGCAAAAAAGC-TA----TTTCTCTTTGTATTCTGCAATG-GATTTATTT-------GCTTTAGGATTTATTTTTTCGGACAATTCAATCTGGGCGTTGCTTTCGCTGAGGTAGTATTGTTTGGAAGACTAAGTTAACGAGC---------ATTCATCTCATTTTGAAATTT---TGTGTTCATCAGTGTG-TTAAAAATAT
droEug1	scf7180000409474:1489651-1489666 +		AA--ATGTG-TT-ACAAATT
droEle1	scf7180000491201:736783-736924 -		AATA----AAAAAA-TT-TAAGAACATGATATTTTGCAAGCAAATTATGTGTGC-------CAATAA-----------CGGTTAAAAAAAT----------GAAGCATTTCAAGAATTTAATTTTTTT-ATAA----------CT---------TGTGCTATAAAG---------AAACACGTAGATAACAATTAAAGAAAAAAT

	PASS/FAIL		
crit.star	0	0	0
crit.loop	0	0	0
crit.mor	0	0	0
crit.half	0	0	0
crit.total	0	0	0
crit.pairing	1	1	1
crit.top3	1	1	1
crit.tptop3	1	1	1
crit.uri	0	0	0
crit.back	1	1	1
rescue.total	1	1	1
rescue.dominant	1	1	1
rescue.known	0	0	0
rescue.confident	3	3	2
rescue.candidate	6	6	7

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