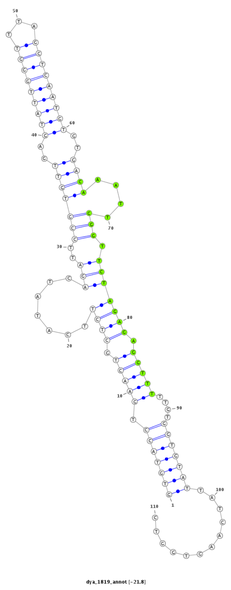
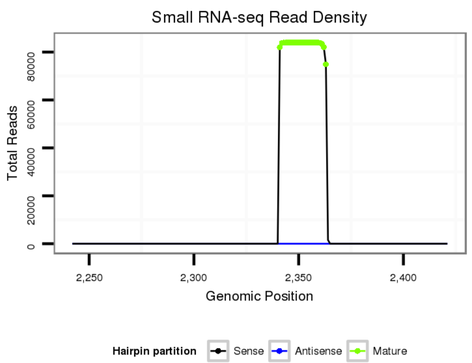
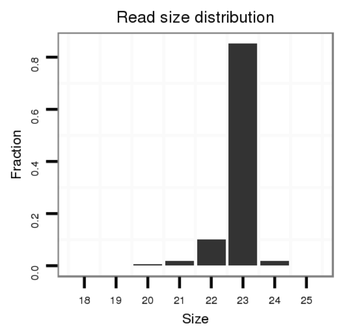
| ID: | Coordinate: | Confidence: | Class: | Genomic Locale: | |
|---|---|---|---|---|---|
| **dya_1819** | **v2_chrUn_157:2292-2371 +** | **Known Ortholog** | **Unknown** | **intergenic** | [View on UCSC Genome Browser [Cornell Mirror]] |

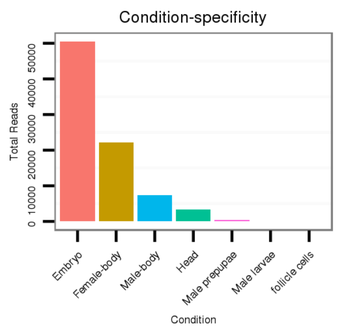
Legend: mature star mismatch in alignment mismatch in read

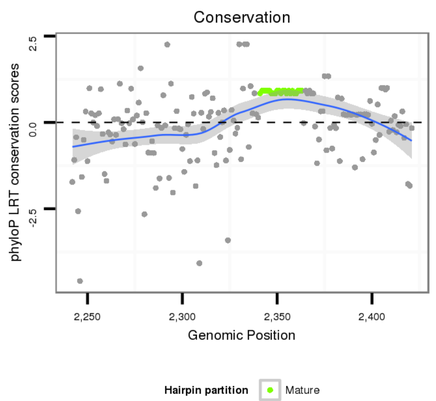
**Predicted structure**






Show Alternate Folds

**Flybase annnotation**

intergenic

**Repeatable elements**

| Name | Class | Family | Strand |
|---|---|---|---|
| FW_DM | LINE | Jockey | - |

| mature | star |
|---|---|
| 1. dya-mir-10 3R:7778053-7778075 +<br>2. dya_110 v2_chrUn_5709:227742-227764 -<br>3. dya_1819 v2_chrUn_1572341-2363 + | |

**Sense Strand Reads**

hide 3p reads  show mid mismatch reads

| TGCAGTACTATCTGCAGCCGTAACAATGGACTCTAGTGTACCTGAACTGCTCTTCATATCAGATTCCGTGTTGAGTATTGGGTTTAGCTCAATGTGTGACAAATTCGGTTCTAGAGAGGTTTTTGTGGTGTATTATCAAGTGGTCGTGAACAAGTTCGTACATATGTATCACCCACTTAA<br>**********(((((((.(((((.((((.....(((..(((((((..((((((((((...)))))))))..))))....)))).)))))))).)))))....)))))))).....**********<br>Legend: mature star mismatch in alignment mismatch in read | Read size | # Mismatch | Hit Count | Total Norm | Total | M056 embryo | M043 female body | V120 male body | M026 head | V046 embryo | V058 head | SRR1275484 Male prepupae | V052 head | SRR1275488 Male larvae | GSM1528802 follicle cells | SRR1275486 Male prepupae |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| .....CAAATTCGGTTCTAGAGAGGTTT..... | 23 | 0 | 3 | 71583.33 | 214750 | 136605 | 52642 | 15257 | 3719 | 2727 | 1915 | 874 | 586 | 395 | 12 | 18 |
| .....CAAATTCGGTTCTAGAGAGGTT..... | 22 | 0 | 3 | 7005.67 | 21017 | 8552 | 5805 | 3402 | 2345 | 168 | 478 | 61 | 160 | 32 | 12 | 2 |
| .....CAAATTCGGTTCTAGAGAGGTTG..... | 23 | 1 | 3 | 2283.00 | 6849 | 6785 | 16 | 7 | 34 | 2 | 4 | 1 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGTTT..... | 22 | 0 | 3 | 1531.33 | 4594 | 327 | 4141 | 89 | 3 | 16 | 13 | 2 | 3 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTTT..... | 24 | 0 | 2 | 1454.00 | 2908 | 1075 | 766 | 862 | 36 | 81 | 57 | 10 | 12 | 6 | 3 | 0 |
| .....CAAATTCGGTTCTAGAGAGGT..... | 21 | 0 | 3 | 1356.67 | 4070 | 964 | 1188 | 1335 | 276 | 34 | 153 | 51 | 49 | 20 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGG..... | 20 | 0 | 3 | 407.67 | 1223 | 110 | 392 | 590 | 49 | 10 | 32 | 25 | 10 | 5 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTG..... | 22 | 1 | 3 | 171.67 | 515 | 470 | 4 | 8 | 29 | 1 | 3 | 0 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGTT..... | 21 | 0 | 3 | 166.00 | 498 | 12 | 459 | 16 | 8 | 1 | 2 | 0 | 0 | 0 | 0 | 0 |
| .....AATTCGGTTCTAGAGAGGTTT..... | 21 | 0 | 3 | 113.00 | 339 | 56 | 252 | 28 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAG..... | 19 | 0 | 3 | 96.33 | 289 | 13 | 69 | 167 | 2 | 3 | 14 | 13 | 7 | 1 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGG..... | 21 | 1 | 3 | 68.67 | 206 | 182 | 1 | 6 | 15 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTTA..... | 24 | 1 | 3 | 64.67 | 194 | 35 | 115 | 29 | 0 | 6 | 6 | 1 | 2 | 0 | 0 | 0 |
| .....ACAAATTCGGTTCTAGAGAGGTTT..... | 24 | 0 | 3 | 50.33 | 151 | 100 | 44 | 3 | 1 | 3 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTG..... | 23 | 1 | 3 | 48.67 | 146 | 126 | 11 | 2 | 5 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTTTT..... | 25 | 0 | 2 | 41.00 | 82 | 16 | 28 | 31 | 1 | 3 | 3 | 0 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGTTTT..... | 23 | 0 | 2 | 37.50 | 75 | 12 | 52 | 9 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTTC..... | 24 | 1 | 3 | 34.33 | 103 | 63 | 15 | 3 | 18 | 1 | 1 | 0 | 2 | 0 | 0 | 0 |
| .....TTCGGTTCTAGAGAGGTTT..... | 19 | 0 | 3 | 31.67 | 95 | 39 | 53 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGT..... | 20 | 0 | 3 | 30.67 | 92 | 0 | 81 | 9 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....TCGGTTCTAGAGAGGTTT..... | 18 | 0 | 3 | 27.00 | 81 | 16 | 65 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....ATTCGGTTCTAGAGAGGTTT..... | 20 | 0 | 3 | 26.00 | 78 | 32 | 39 | 7 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTA..... | 23 | 1 | 3 | 22.67 | 68 | 11 | 41 | 11 | 0 | 0 | 1 | 1 | 3 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGA..... | 18 | 0 | 3 | 17.67 | 53 | 6 | 31 | 5 | 0 | 1 | 4 | 2 | 4 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGG..... | 19 | 0 | 3 | 12.00 | 36 | 0 | 33 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTA..... | 22 | 1 | 3 | 11.33 | 34 | 6 | 16 | 11 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....AATTCGGTTCTAGAGAGGTT..... | 20 | 0 | 3 | 10.33 | 31 | 3 | 22 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGG..... | 21 | 1 | 3 | 9.33 | 28 | 5 | 2 | 2 | 19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....ACAAATTCGGTTCTAGAGAGGTT..... | 23 | 0 | 3 | 9.00 | 27 | 13 | 11 | 0 | 2 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTG..... | 22 | 1 | 3 | 7.00 | 21 | 0 | 17 | 0 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGTTG..... | 22 | 1 | 3 | 6.33 | 19 | 18 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTTAA..... | 25 | 2 | 3 | 5.00 | 15 | 0 | 9 | 4 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGTTTA..... | 23 | 1 | 3 | 4.67 | 14 | 1 | 13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTTTT..... | 26 | 1 | 2 | 4.00 | 8 | 1 | 1 | 5 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AATTCGGTTCTAGAGAGGTTTT..... | 22 | 0 | 2 | 3.00 | 6 | 2 | 2 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGA..... | 21 | 1 | 3 | 3.00 | 9 | 0 | 5 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGTTG..... | 22 | 1 | 3 | 3.00 | 9 | 0 | 9 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....TTCGGTTCTAGAGAGGTTG..... | 19 | 1 | 3 | 2.67 | 8 | 8 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGTTTTT..... | 24 | 0 | 2 | 2.50 | 5 | 0 | 4 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGGG..... | 22 | 2 | 3 | 2.33 | 7 | 7 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AATTCGGTTCTAGAGAGGT..... | 19 | 0 | 3 | 2.33 | 7 | 0 | 7 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....ACAAATTCGGTTCTAGAGAGGTTG..... | 24 | 1 | 3 | 2.33 | 7 | 7 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTGG..... | 23 | 2 | 3 | 2.00 | 6 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGTTA..... | 22 | 1 | 3 | 2.00 | 6 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AATTCGGTTCTAGAGAGG..... | 18 | 0 | 3 | 2.00 | 6 | 1 | 4 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....GACAAATTCGGTTCTAGAGAGGT..... | 23 | 0 | 3 | 1.67 | 5 | 3 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |

**Anti-sense strand reads**

| ACGTCATGATAGACGTCGGCATTGTTACCTGAGATCACATGGACTTGACGAGAAGTATAGTCTAAGGCACAACTCATAACCCAAATCGAGTTACACACTGTTTAAGCCAAGATCTCTCCAAAAACACCACATAATAGTTCACCAGCACTTGTTCAAGCATGTATACATAGTGGGTGAATT<br>**********(((((((.(((((.((((.....(((..(((((((..((((((((((...)))))))))..))))....)))).)))))))).)))))....)))))))).....**********<br>Legend: mature star mismatch in alignment mismatch in read | Read size | # Mismatch | Hit Count | Total Norm | Total | M056 embryo |
|---|---|---|---|---|---|---|

Show Alignment With Reads

**Re-alignment of all predicted orthologs**

| Species | Coordinate | ID | Alignment |
|---|---|---|---|
| droYak3 | v2_chrUn_157:2242-2421 + | dya_1819 | TGCAGTACTATCTGCAGCCGTAACAATGGACTCTAGTGTACCTGAACTGCT----------CTTC----------ATATCAGATTCCG---T--GTTGAGTATTGGGTTTAGCTCAATGTGTGACAAATTCGGTTCTAGAGAGGTTTTTGTGGTGTATTATCAA----------GTGGTCGTGAACAAGTTCGTACATATGTATCACCCACTTAA |
| droEre2 | scaffold_4770:2882455-2882640 - | der-mir-10 | CTACCCT----------GTAGATCCGAATTTGTTTTATAGTAGCTTTAAGGA--CAAATTCGGTTCTAGAGAGGTTTGTGTGGTCAATATCGATCGG-AAA----------AGTGA---AGCTGATGTCAAGCGGAAAAGTGATTTTCATTTAAGTTTAAAGCAAAAAAA----------GTGTCGTGACCAAATTCGTCGATATGTATGACCCACTTGA |
| droSec2 | scaffold_51:183605-183751 - | | AGCGTGTAGCGCATGCGGCCGTAAGAATGGAGTCTAGTAAACCTGCCAAGAT----------CTTT----------TTATCAGATTCAG---T--GTTGAGTTTTAACATTAGCTCAATGGGTGA----------ACGTATATATTTTGTATAG----------CTGAGCAAGTTTGTTTGGTGTGAAA--------TCAA |
| droSim2 | 2r:246841-246939 + | | TGCAGTAGCGCTGCGGCGCAAGAATGGAGTCTAGTGCACCTGTGAGAT----------CTGT----------ATATTAGATTCAT---T--GTTGAGTTTTGGCTTTAGCTCAATGTGTAA---------- |
| dm3 | chr2R:454756-454853 - | | TGCATTACGCGCTGCTTTCGTAAGAATGAATTCCAGTGTACCTGTGAGCT----------CTTT----------ATATCAGATTCAG---T--ATTGCGT-TTGGACTTAACTCAATGTGTGA---------- |
| droEug1 | scf7180000409825:16137-16235 - | | TGAAGCTGAGCTGCAGAGAGCGTAGACTCTGGTGAATTACCAAACCT----------GTCT----------ACGTGCGCTTCAT---T--GTTGAGATGAGGACCTGGCTCAATGTGTGA---------- |
| droBia1 | scf7180000302155:2026136-2026288 + | | CTACCCT----------GTAGATCCGAATTTGTTTTATAGTAGCTTTAAGGA--CAAATTCGGTTCTAGAGAGGTTTGTGTGGTCAATGTCGATCGT-AAAACGCATTTTGAGTGA---AAAAGAAATGGAGTGATAAAGTGAACCG----------SAGAACATGTTTCACGTA--GTAA |
| droTak1 | scf7180000415671:411455-411617 + | | CTACCCT----------GTAGATCCGAATTTGTTTTATAGTAGCTTTAAGGA--CAAATTCGGTTCTAGAGAGGTTTGTGTGGTCAATATCGATCGA-TAAAA-CATTTAAAGTGA---AACTGAAATGAAGTGAAAAAGTGAAACT----------AAAAACGAAATATATAAAAACTAATTCT----------TGTA |
| droEle1 | scf7180000491321:6210-6308 + | | CGAAACTCGAGCGCAGTGACGAGTACGGACTCCAGTGTAGTTACAAAGCT----------GTCT----------ATGTCAGCTTCCT---C--GTTGAGCGAGGACATAGCTCAATATGTGA---------- |
| droRho1 | scf7180000777432:2275-2414 + | | CTACCCT----------GTAGATCCGAATTTGTTTTAGATTAGCTTTAAGGA--CAAATTCGGTTCTAGAGAGGTTTGTGTGGTCCATATCGATCGA-TAAAT-C-----AAAAGA---AGCCGGAATCAAGTGAAAAAGTGAATTT----------SAA--------CATTATATTTAA |
| droFic1 | scf7180000453835:71929-72050 - | | CTACCCT----------GTAGATCCGAATTTGTTTTATAGTAGCTTTAAGGA--CAAATTCGGTTCTAGAGAGGTTTGTGTGGTCAATGTCGATCGA-AAA----------AGTGATCTCAGCTGATATTA----------AA--------GTTTACGAAAC |
| droKik1 | scf7180000299218:340-435 - | | TGAGATTCTGGCTGCAGTCACAAGTACCTCTGCAGTGCGGAGTGGAG--CTCC----------ATGTGCGTTTGAG---T--ATTGAGCTGGGGGCTAGCTCAATGTGGGA---------- |
| droAna3 | scaffold_13480:2595-2754 - | | TGAAGCTCGAGTGCAGAGACGAGTACAGACTCCAGTGATTTAACAAAGCT----------GTCT----------ACGTTGCCTTCCT---C--GTTGAGGTGACGACTTAGCTCCATATGTGA----------GCTAATCTACTTTCTGTAG----------ATAATCCAGTTGGTTTCTTGTGGGGTCCATTTTAATGG----------TTGT |
| droBip1 | scf7180000395821:11295-11425 + | | TGAAGCTCGAGCTGCAGAGACCGTACAGACTCCAGTGATTAAACAAAGCT----------CTGT----------ACGTTGCCTTCAT---C--GTTGAGATGAGGACCTATTTCAATGTGTGC----------GCTAATATAATTTCTGTACTT----------TTGGGGAG----------GCT |
| dp5 | Unknown_singleton_799:1166-1244 - | | TTCATACT------TTGCCGGAAACAGATCTATATA----------TGTTTCGCATTATTCCGTCGGT---CAGGTCTAGGTCCAGTTAATGTG---------- |
| droPer2 | scaffold_183:34478-34530 - | | GAACCGC----------GT----------CGTA----------AGATGCATCTCA---T--GCGAGTATTCGGCCTAGTTTAATCTG---------- |
| droWil2 | scf2_1100000004577:3663082-3663185 - | | TGCATAATTATCTAAACTGAAAACTACAACTTT----------GTT----------CTTT----------ATATTGATTGAAT---TGAATTGAGTTTGAATTTAATTAATAATTTGT----------ATGTTCTACTGAGATTT |
| droVir3 | scaffold_12963:4577171-4577259 - | | TGTGACGTCATGCACAGATTTGACAAGAGATTGTG--------GACAGCT----------TTAT----------ATATGAATTTATT---T--ATTTTTGTTGGGCTTGGCTTAATGTGTG---------- |
| droMoj3 | scaffold_4206:818-926 + | | TAATATGT--ATGCATATTTATGGATTATAATATAAG-----TTAGGGCTCCCGTACTAGAGTACTAGTGA----------TTGGGGGACGCTG---T------TGTTGGGTTTTTGTGAATATATAA---------- |
| droGri2 | scaffold_15074:5711536-5711592 - | | TGCATTTCCATTTCAGCGCCAACTGCTC----------AACTGAT----------CTTT----------ATAAATAATTCCA---T-- |

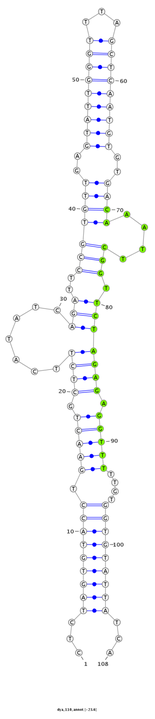
Generated: 08/16/2015 at 02:03 PM

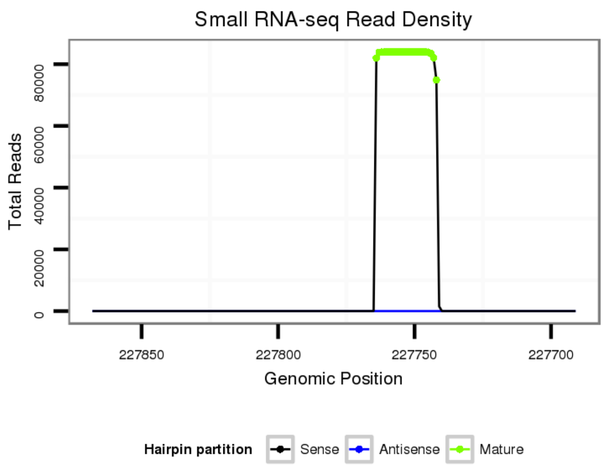
| | PASS/FAIL |
|---|---|
| crit.star | 0 |
| crit.loop | 0 |
| crit.mor | 0 |
| crit.half | 0 |
| crit.total | 1 |
| crit.pairing | 1 |
| crit.top3 | 1 |
| crit.tptop3 | 1 |
| crit.uri | 0 |
| crit.back | 1 |
| rescue.total | 1 |
| rescue.dominant | 1 |
| rescue.known | 12 |
| rescue.confident | 0 |
| rescue.candidate | 2 |

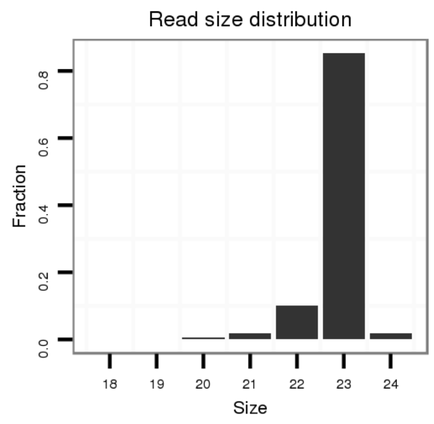
| ID: | Coordinate: | Confidence: | Class: | Genomic Locale: | |
|---|---|---|---|---|---|
| **dya_110** | **v2_chrUn_5709:227741-227818 -** | **confident-exception** | **Canonical miRNA** | **intergenic** | [View on UCSC Genome Browser {Cornell Mirror}] |

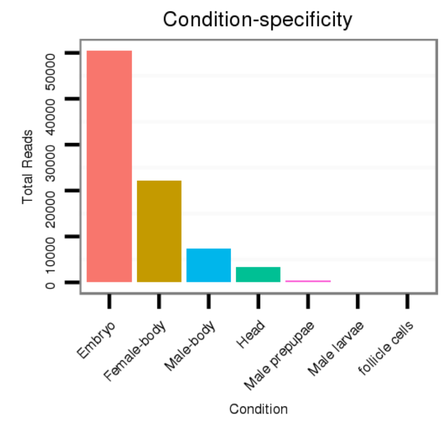
Legend: mature star mismatch in alignment mismatch in read

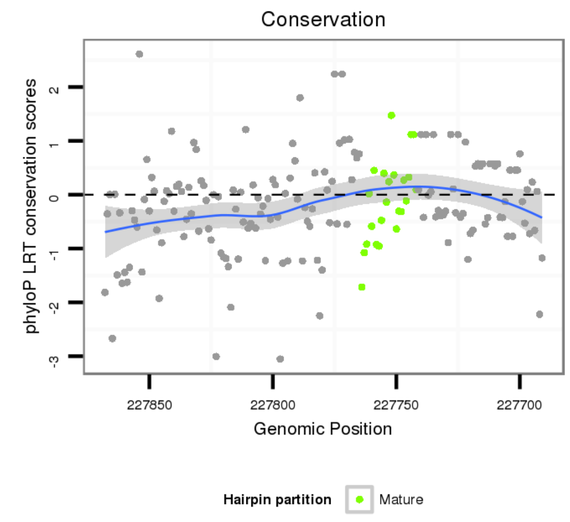
**Predicted structure**






Show Alternate Folds

### Flybase annnotation

intergenic

### Repeatable elements

| Name | Class | Family | Strand |
|---|---|---|---|
| FW_DM | LINE | Jockey | + |

| mature | star |
|---|---|
| 1. dya-mir-10 3R:7778053-7778075 +<br>2. dya_110 v2_chrUn_5709:227742-227764 -<br>3. dya_1819 v2_chrUn_157:2341-2363 + | |

### Sense Strand Reads

hide 3p reads show mid mismatch reads

| GGTGTTGCAGTACTATCTGCAGCCGTAACAATGGACTCTAGTGTACCTGAACTGCTCTTCATATCAGATTCCGTGTTGAGTATTGGGTTTAGCTCAATGTGTGACAAATTCGGTTCTAGAGAGGTTTTTGTGGTGTATTATCAAGTGGTCGTGAACAAGTTCGTACATATGTATCACC ********...(((((((((.(((((.((((.....(((..(((((((..(((((((((...)))))))))..))))....)))).)))))))..)))))....)))))))))...******** | Read size | # Mismatch | Hit Count | Total Norm | Total | M056 embryo | M043 female body | V120 male body | M026 head | V046 embryo | V058 head | SRR1275484 Male prepupae | V052 head | SRR1275488 Male larvae | GSM1528802 follicle cells | SRR1275486 Male prepupae |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| .....CAAATTCGGTTCTAGAGAGGTTT..... | 23 | 0 | 3 | 71583.33 | 214750 | 136605 | 52642 | 15257 | 3719 | 2727 | 1915 | 874 | 586 | 395 | 12 | 18 |
| .....CAAATTCGGTTCTAGAGAGGTT..... | 22 | 0 | 3 | 7005.67 | 21017 | 8552 | 5805 | 3402 | 2345 | 168 | 478 | 61 | 160 | 32 | 12 | 2 |
| .....CAAATTCGGTTCTAGAGAGGTTC..... | 23 | 1 | 3 | 2283.00 | 6849 | 6785 | 16 | 7 | 34 | 2 | 4 | 1 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGTTT..... | 22 | 0 | 3 | 1531.33 | 4594 | 327 | 4141 | 89 | 3 | 16 | 13 | 2 | 3 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTTT..... | 24 | 0 | 2 | 1454.00 | 2908 | 1075 | 766 | 862 | 36 | 81 | 57 | 10 | 12 | 6 | 3 | 0 |
| .....CAAATTCGGTTCTAGAGAGGT..... | 21 | 0 | 3 | 1356.67 | 4070 | 964 | 1188 | 1335 | 276 | 34 | 153 | 51 | 49 | 20 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGG..... | 20 | 0 | 3 | 407.67 | 1223 | 110 | 392 | 590 | 49 | 10 | 32 | 25 | 10 | 5 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTC..... | 22 | 1 | 3 | 171.67 | 515 | 470 | 4 | 8 | 29 | 1 | 3 | 0 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGTT..... | 21 | 0 | 3 | 166.00 | 498 | 12 | 459 | 16 | 8 | 1 | 2 | 0 | 0 | 0 | 0 | 0 |
| .....AATTCGGTTCTAGAGAGGTTT..... | 21 | 0 | 3 | 113.00 | 339 | 56 | 252 | 28 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAG..... | 19 | 0 | 3 | 96.33 | 289 | 13 | 69 | 167 | 2 | 3 | 14 | 13 | 7 | 1 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGC..... | 21 | 1 | 3 | 68.67 | 206 | 182 | 1 | 6 | 15 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTTA..... | 24 | 1 | 3 | 64.67 | 194 | 35 | 115 | 29 | 0 | 6 | 6 | 1 | 2 | 0 | 0 | 0 |
| .....ACAAATTCGGTTCTAGAGAGGTTT..... | 24 | 0 | 3 | 50.33 | 151 | 100 | 44 | 3 | 1 | 3 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTG..... | 23 | 1 | 3 | 48.67 | 146 | 126 | 11 | 2 | 5 | 0 | 1 | 0 | 1 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTTTT..... | 25 | 0 | 2 | 41.00 | 82 | 16 | 28 | 31 | 1 | 3 | 3 | 0 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGTTTT..... | 23 | 0 | 2 | 37.50 | 75 | 12 | 52 | 9 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTTC..... | 24 | 1 | 3 | 34.33 | 103 | 63 | 15 | 3 | 18 | 1 | 1 | 0 | 2 | 0 | 0 | 0 |
| .....TTCGGTTCTAGAGAGGTTT..... | 19 | 0 | 3 | 31.67 | 95 | 39 | 53 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGT..... | 20 | 0 | 3 | 30.67 | 92 | 0 | 81 | 9 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....TCGGTTCTAGAGAGGTTT..... | 18 | 0 | 3 | 27.00 | 81 | 16 | 65 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....ATTCGGTTCTAGAGAGGTTT..... | 20 | 0 | 3 | 26.00 | 78 | 32 | 39 | 7 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTTA..... | 23 | 1 | 3 | 22.67 | 68 | 11 | 41 | 11 | 0 | 0 | 1 | 1 | 3 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGA..... | 18 | 0 | 3 | 17.67 | 53 | 6 | 31 | 5 | 0 | 1 | 4 | 2 | 4 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGG..... | 19 | 0 | 3 | 12.00 | 36 | 0 | 33 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTA..... | 22 | 1 | 3 | 11.33 | 34 | 6 | 16 | 11 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....AATTCGGTTCTAGAGAGGTT..... | 20 | 0 | 3 | 10.33 | 31 | 3 | 22 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGG..... | 21 | 1 | 3 | 9.33 | 28 | 5 | 2 | 2 | 19 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....ACAAATTCGGTTCTAGAGAGGTT..... | 23 | 0 | 3 | 9.00 | 27 | 13 | 11 | 0 | 2 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTG..... | 22 | 1 | 3 | 7.00 | 21 | 0 | 17 | 0 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGTTC..... | 22 | 1 | 3 | 6.33 | 19 | 18 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTTAA..... | 25 | 2 | 3 | 5.00 | 15 | 0 | 9 | 4 | 0 | 0 | 1 | 1 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGTTTA..... | 23 | 1 | 3 | 4.67 | 14 | 1 | 13 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTTTTTT..... | 26 | 1 | 2 | 4.00 | 8 | 1 | 1 | 5 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AATTCGGTTCTAGAGAGGTTTT..... | 22 | 0 | 2 | 3.00 | 6 | 2 | 2 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGTTG..... | 22 | 1 | 3 | 3.00 | 9 | 0 | 9 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGA..... | 21 | 1 | 3 | 3.00 | 9 | 0 | 5 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....TTCGGTTCTAGAGAGGTTG..... | 19 | 1 | 3 | 2.67 | 8 | 8 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGTTTTT..... | 24 | 0 | 2 | 2.50 | 5 | 0 | 4 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AATTCGGTTCTAGAGAGGT..... | 19 | 0 | 3 | 2.33 | 7 | 0 | 7 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....ACAAATTCGGTTCTAGAGAGGTTG..... | 24 | 1 | 3 | 2.33 | 7 | 7 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGGC..... | 22 | 2 | 3 | 2.33 | 7 | 7 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AATTCGGTTCTAGAGAGG..... | 18 | 0 | 3 | 2.00 | 6 | 1 | 4 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....CAAATTCGGTTCTAGAGAGGTCC..... | 23 | 2 | 3 | 2.00 | 6 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AAATTCGGTTCTAGAGAGGTTA..... | 22 | 1 | 3 | 2.00 | 6 | 0 | 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

### Anti-sense strand reads

| CCACAACGTCATGATAGACGTCGGCATTGTTACCTGAGATCACATGGACTTGACGAGAAGTATAGTCTAAGGCACAACTCATAACCCAAATCGAGTTACACACTGTTTAAGCCAAGATCTCTCCAAAAACACCACATAATAGTTCACCAGCACTTGTTCAAGCATGTATACATAGTGG ********...(((((((((.(((((.((((.....(((..(((((((..(((((((((...)))))))))..))))....)))).)))))))..)))))....)))))))))...******** | Read size | # Mismatch | Hit Count | Total Norm | Total | M056 embryo |
|---|---|---|---|---|---|---|

Show Alignment With Reads

### Re-alignment of all predicted orthologs

| Species | Coordinate | ID | Alignment |
|---|---|---|---|
| droYak3 | v2_chrUn_5709:227691-227868 - | dya_110 | GGTGTTGCAGTA----CTATCTGCAGCCGTAACAATGG--------ACTCTAGTGTACCTGAACTGCTC--------TTCATATCAGATTC------CGTGTTGAGTATTGGGTTTAGCTCAATGTGTGACAAATTCGGT--------TCTAGAGAGGTTTTTGTGGTGT-----ATTATCAAGTGGT----------CGTGAACAAGTTC----G-----TACATATGTATCACC |
| droEre2 | scaffold_4784:23548909-23549000 - | | GGTGTTGAAATA----CGAGCTGGC--------AGTGG--------ATTCTAGTGTTGCTGTGGAATTC--------TCTATATCAGATTC------TTTCTTGAGTTGTGGGCTTTAGTAAAGGT----------------------------------------------------------------------------------- |
| droSec2 | scaffold_51:183605-183756 - | | GGTGTAGCTGTA----CGAGATGCTGCCGTAAGAATGG--------ATTCTAGTAACCTGCCAAGATC--------TTTTTATCAGATTC------AGTGTTGAGTTTTAAGATTAGCTCAATGCGTGAACTTATATTTTGTATACCTGAGCAAGTTTGTTGGTGT-----GAAATCAA----------------------------------------------------------------------------------- |
| droSim2 | node_36:3071-3174 - | | GGTGTTGCTTTA----CGAGCTGCTTCCGTAAGAATGG--------ATTCCAGTGTACCTGTGCAGCTC--------TCTATATCAGATTC------AGTATTGTGTTTGGGCTTAGCTCAATGTGTGA---------------------------------------------------------------------------------- |
| dm3 | chr2R:454756-454858 - | | GGTATTTGCATTA----CGAGCTGCTTTCGTAAGAATGA--------ATTCCAGTGTACCTGTGCAGCTC--------TTTATATCAGATTC------AGTATTGCGT-TTGGACTTAACTCAATGTGTGA---------------------------------------------------------------------------------- |
| droEug1 | scf7180000409825:16137-16240 - | | GGTGTTGAAGCT----CAAGCTCCAGAGACGAGTATAG--------ACTCTCGTGAATTACCAAACCTC--------TCTACGTCGGCTTC------ATTGTTGAGATGAGGACCTTGCTCAATGTGTGA---------------------------------------------------------------------------------- |
| droBia1 | scf7180000302155:2026136-2026283 + | | CTACCCTGTAGATCCGA-ATTT----------GTTGTATA------CTAGCTTTAAGGAC----------AAATTCGGT--------TCTAGAGAGGTTTGTGTGGTTC-----AATGTCCATCGTAAAACGCATTTTGAGTGAAAAAGAAATGGAGTGATAAAGTGAACCCGAGAAC-----ATGTTTCAGT |
| droTak1 | scf7180000415671:411455-411606 + | | CTACCCTGTAGATCCGA-ATTT----------GTTTTATA------CTAGCTTTAAGGAC----------AAATTCGGT--------TCTAGAGAGGTTTGTGTGGTTC-----AATATCCATCGATAA-AACATTTAAAGTGAAACTGAAATGAAGTGAAAAAGTGAAACTAAAAACGAAATATATAAAAC |
| droEle1 | scf7180000491321:6205-6308 + | | GGTGTGGAACT----CGAGCGCAGTGACGAGTACGG--------ACTCCAGTGTAGTTACAAAGCTG--------TCTATGTCAGCTTC------GTCGTTGAGCGAGGACATAGCTCAATATGTGA---------------------------------------------------------------------------------- |
| droRho1 | scf7180000779496:8576-8695 + | | GGTGTTGAAACT----TGATCTGCAGAGACGAGTACAG--------ACTCCAGTGAATTAACAAATCTG--------TCTACGTTGGCTTC------ATCGTTGAGATGAGGACTTAGCTCAATGTGTGAGCTAATGTAT---------------------------------------------------------------------------------- |
| droFic1 | scf7180000453835:71933-72050 - | | CTACCCTGTAGATCCGA-ATTT----------GTTTTATA------CTAGCTTTAAGGAC----------AAATTCGGT--------TCTAGAGAGGTTTGTGTGGTTC-----AATGTCCATCGAAAAAGTGATCTC----------AGCTGATATT-----AAACTTTACC |
| droKik1 | scf7180000302735:9167-9270 - | | GGTGTTGAGATC----CTAACTGCAGTCACAAGTTCCT--------CTTCCAGACCGGAGTGGAGGAG--------TCCATGTCCGCTTC------AGTATTGAGCTGGGGGCCTAGCTCAATGTGGGA---------------------------------------------------------------------------------- |
| droAna3 | scaffold_9019:2919-3083 + | | GGTATTGAAGCT----CGAGCTGCAGAGACGAGTACAG--------ACTCCAGTGAATTAACAAAGCTG--------TCTACGTTGGCTTC------CTCGTTGAGGTGACGACTTAGCTCGATATGTGAGCTAATCTACTTTCTGTACATAATCCAGTTGGTTTCTTGTGGGGTCCATTTTAATGGT----------T----------GT |
| droBip1 | scf7180000395035:1474-1577 + | | TGTGTTGAAACT----CGAGCTGCAGAGACGAGTACAG--------ACTCCAGCGCAAATAACAAAACTG--------TCTTCGTTGGCTTC------GTCGCTGAGGTGAGGATTCAGCTCAATGTGTGA---------------------------------------------------------------------------------- |
| dp5 | Unknown_singleton_799:1166-1249 - | | AGAATTTCCATA----CT-------TTCCGGAAACAG--------ATTCTAATATGTTTCGA----------TTATTCCGTGGGT-----CAGGTCTAGGTTGGCAGTTAAATGTG---------------------------------------------------------------------------------- |
| droPer2 | scaffold_183:34478-34530 - | | GAACCGCTC-------------------------------CTAAGACTGCATCT------CATGGCGAGTATTCGGCCTAGTTTAATCTG---------------------------------------------------------------------------------- |
| droWil2 | scf2_1100000004577:3663082-3663190 - | | TTTTTTGCATAA----TTATCTAAACTGAAAACTACAA--------CTTTT----------GTTC--------TTTATATTGATTGA---AT-TGAATTGAGTTTTGAATTTAATTAAATATTTGT------ATGT-------TCTACTGAGA---------- |
| droVir3 | scaffold_13049:2946349-2946433 + | | CGAGTGGCCACA----ATAAGAGCAAGAGCAACAAAG--------TATTTGCACTGCAT--------TCAATGAAAGCA--------TAAAGAAATTCT----------TATCG---------------------------------------------------------------------------------- |
| droMoj3 | scaffold_4206:814-926 + | | TGTATATATGTATCC-ATATCTATGGATATAAATATAAGTTAAGCGCTCGCGTACTAGAGTACTAGTGA--------TTGGGGG---ACGC------TGTG-------TTGGGTTTTTGTGAATATATATACAAC---------------------------------------------------------------------------------- |
| droGri2 | scaffold_15074:5711536-5711597 - | | AATTATGCATTT----CCATTTTCAGCGGCAACTGCTC--------AACTGATC--------TTTATAAATAATTC------CTTCTT---------------------------------------------------------------------------------- |

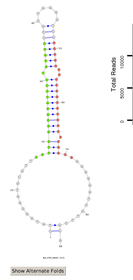
Generated: 09/08/2015 at 07:45 PM

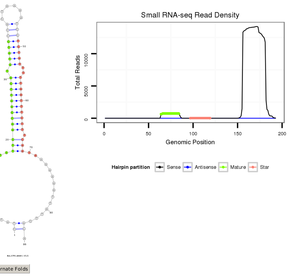
| | PASS/FAIL |
|---|---|
| crit.star | 0 |
| crit.loop | 0 |
| crit.mor | 0 |
| crit.half | 0 |
| crit.total | 1 |
| crit.pairing | 1 |
| crit.top3 | 1 |
| crit.tptop3 | 1 |
| crit.uri | 0 |
| crit.back | 1 |
| rescue.total | 1 |
| rescue.dominant | 1 |
| rescue.known | 12 |
| rescue.confident | 0 |
| rescue.candidate | 2 |

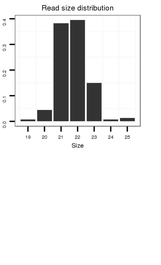
| ID: | Coordinate: | Confidence: | Class: | Genomic Locus: |
|---|---|---|---|---|
| **dya_1793** | **v2_chrUn_1311:45-143 +** | **candidate-rescued** | **Canonical miRNA** | **intergenic** |
| | | | | [View on UCSC Genome Browser (Comfil Mitmit)] |

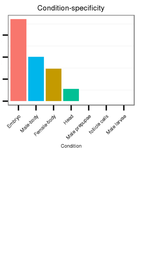
Legend: Loop Star Mature 5 arm in mature Mature 3 arm in mature

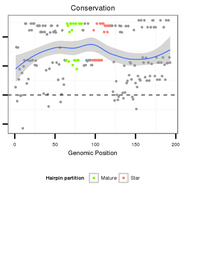
## Predicted structure






Show Alternate Folds

## Flybase annotation

dRNA:Dyak\FBrRNAAGE26302-RA]

## Repeatable elements

| Name | Class | Family | Strand |
|---|---|---|---|
| AT_rich | Low_complexity | Low_complexity | + |

**mature**

1. dya_1793 v2_chrUn_1311:45-143 +
2. v2_chrUn_2920:788-728 +
3. v2_chrUn_1929:235-293 +
4. v2_chrUn_4644:179-199 +
5. v2_chrUn_4933:1063-1023 +
6. v2_chrUn_2147:1-41 +
7. v2_chrUn_2347:62-94 +
8. v2_chrUn_5370:203-223 +
9. v2_chrUn_5306:4414-4361 +
10. v2_chrUn_5762:888-908 +
11. v2_chrUn_2944:2472-2492 +
12. v2_chrUn_2944:2472-2492 +
13. v2_chrUn_2613:7268-7288 +
14. v2_chrUn_2167:926-7846 +
15. v2_chrUn_2944:4355-4375 +
16. v2_chrUn_2763:2951-2911 +
17. v2_chrUn_4475:1-41 +
18. v2_chrUn_5370:1395-1435 +
19. v2_chrUn_3133:52-5242 +
20. v2_chrUn_924:1125-1143 +
21. v2_chrUn_2514:436-456 +
22. v2_chrUn_4130:1030-1030 +
23. v2_chrUn_5306:4414-4361 +
24. v2_chrUn_3472:129-149 +
25. v2_chrUn_3944:8-44 +
26. v2_chrUn_5746:1201-1241 +
27. v2_chrUn_3273:1669-1689 +

**star**

1. dya_1793 v2_chrUn_1311:97-119 +
2. v2_chrUn_2920:743-763 +
3. v2_chrUn_4230:975-997 +
4. v2_chrUn_1739:110-1132 +
5. v2_chrUn_1938:198-220 +
6. v2_chrUn_2147:1-41 +
7. v2_chrUn_4644:101-161 +
8. v2_chrUn_5347:954-978 +
9. v2_chrUn_5370:634-595 +
10. v2_chrUn_3294:4174-4396 +
11. v2_chrUn_3472:98-140 +
12. v2_chrUn_3472:98-140 +
13. v2_chrUn_2364:9-31 +
14. v2_chrUn_4164:187-1189 +
15. v2_chrUn_0614:6856-6898 +
16. v2_chrUn_0615:581-533 +
17. v2_chrUn_2:1-41 +
18. v2_chrUn_5370:1396-1436 +
19. v2_chrUn_3:6:2924-3946 +
20. v2_chrUn_4:87:4873-4893 +
21. v2_chrUn_4933:868-890 +
22. v2_chrUn_2990:90-130 +
23. v2_chrUn_5347:954-978 (5746:1243-1270) +
24. v2_chrUn_3543:2504-2556 +
25. v2_chrUn_6:26:1323-1324 +
26. v2_chrUn_3524:411-421 +

## Sense Strand Reads

Hide 3p reads  Show mid mismatch reads

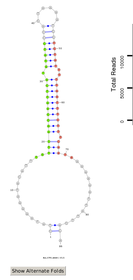
```
TACATAAGTCCTTATGAGAACTAAGACATTTCCCAGCATTTATTTTAGGTATAAAAATACATTTATTGAAGGAATTGATATATCCAGTAAAATCGTATTTTTAATTTCTTTCAATTAAAAAATTATTGACATATATAGAAATAAATTATAAACTCTAAGCGTGATCACTCGGCTCATGGCTCGATG
```

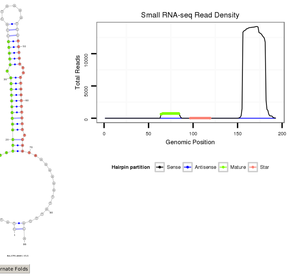
| Read # | Size | Mismatch | Hit Count | Total Norm | Total | V120 male body | V120 female body | M043 follicle cells | M043 female body | V058 head | M026 head | M056 embryo | V052 head | V046 embryo | SRR1275484 Male pregonads | SRR1275485 Male larvae | SRR1275486 Male pregonads |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | GSM1528802 | | | | | | | | | | | |
| 26 | 0 | | 20 | 7843.75 | 156875 | 120737 | 13571 | 4323 | 7163 | 6650 | 1335 | 2956 | 134 | 7 | 4 | 0 | 0 |
| 21 | 0 | | 20 | 1203.60 | 24072 | 12503 | 4326 | 2979 | 1618 | 595 | 1388 | 415 | 46 | 2 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 723.45 | 14469 | 9 | 9311 | | 313 | 2801 | 441 | 275 | 1291 | 28 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 7352.94 | 12797 | 1832 | 952 | | 327 | 473 | 546 | 152 | 164 | 9 | 1 | 1 | 0 |
| 25 | 0 | | 20 | 511.95 | 10221 | 3068 | 4608 | | 831 | 415 | 516 | 536 | 153 | 89 | 3 | 2 | 0 |
| 25 | 0 | | 20 | 464.26 | 8886 | 583 | 7839 | | 0 | 0 | 424 | 40 | 0 | 46 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 251.35 | 5027 | 2080 | 0 | | 1350 | 360 | 12 | 0 | 66 | 1158 | 0 | 1 | 0 |
| 20 | 0 | | 20 | 240.90 | 4858 | 1000 | 0 | | 213 | 157 | 1474 | 38 | 2102 | 2 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 204.45 | 4093 | 0 | 4084 | | 0 | 0 | 0 | 0 | 0 | 0 | 4 | 0 | 0 |
| 30 | 0 | | 20 | 179.49 | 3590 | 1576 | 0 | | 895 | 249 | 229 | 0 | 0 | 0 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 159.89 | 2878 | 2372 | 265 | | 33 | 29 | 159 | 3 | 6 | 1 | 5 | 0 | 0 |
| 23 | 0 | | 20 | 149.05 | 2981 | 1284 | 972 | | 370 | 207 | 8 | 0 | 90 | 45 | 1 | 1 | 1 |
| 24 | 0 | | 20 | 135.70 | 2714 | 704 | 1642 | | 232 | 104 | 19 | 45 | 45 | 14 | 0 | 2 | 1 |
| 21 | 0 | | 20 | 125.35 | 2507 | 497 | 485 | | 927 | 306 | 20 | 115 | 147 | 6 | 4 | 0 | 0 |
| 18 | 0 | | 20 | 121.72 | 2191 | 1256 | 494 | | 127 | 45 | 120 | 128 | 19 | 2 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 121.00 | 2420 | 409 | 1194 | | 649 | 26 | 25 | 94 | 17 | 4 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 90.40 | 1892 | 99 | 5 | | 293 | 23 | 12 | 1293 | 2 | 258 | 3 | 0 | 0 |
| 26 | 1 | | 20 | 91.55 | 1831 | 155 | 1 | | 2 | 15 | 1228 | 424 | 4 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 76.05 | 1521 | 0 | 272 | | 583 | 407 | 16 | 27 | 0 | 16 | 0 | 0 | 0 |
| 25 | 0 | | 20 | 71.70 | 1434 | 414 | 370 | | 311 | 35 | 46 | 31 | 24 | 3 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 18.98 | 1279 | 1223 | 6 | | 0 | 40 | 10 | 0 | 0 | 0 | 0 | 0 | 0 |
| 17 | 0 | | 20 | 66.45 | 1333 | 0 | 1195 | | 0 | 136 | 0 | 0 | 0 | 0 | 2 | 0 | 0 |
| 20 | 0 | | 20 | 65.76 | 1314 | 56 | 101 | | 441 | 0 | 202 | 134 | 369 | 13 | 0 | 0 | 0 |
| 25 | 0 | | 20 | 63.80 | 1276 | 6 | 1252 | | 11 | 0 | 0 | 4 | 3 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 57.50 | 1035 | 16 | 744 | | 43 | 128 | 13 | 50 | 39 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 50.47 | 912 | 268 | 313 | | 98 | 27 | 59 | 130 | 6 | 11 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 48.46 | 972 | 513 | 157 | | 87 | 55 | 53 | 70 | 32 | 5 | 2 | 0 | 0 |
| 28 | 0 | | 20 | 48.45 | 969 | 7 | 936 | | 0 | 0 | 10 | 17 | 1 | 0 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 35.95 | 719 | 158 | 327 | | 51 | 52 | 19 | 85 | 103 | 29 | 1 | 0 | 0 |
| 22 | 0 | | 20 | 34.15 | 683 | 157 | 0 | | 206 | 83 | 0 | 97 | 24 | 115 | 0 | 1 | 0 |
| 30 | 0 | | 20 | 18.32 | 681 | 12 | 589 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 29.00 | 580 | 3 | 577 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 31 | 0 | | 20 | 28.00 | 560 | 0 | 560 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 26.45 | 529 | 142 | 0 | | 183 | 0 | 29 | 0 | 11 | 162 | 1 | 1 | 0 |
| 23 | 0 | | 20 | 23.45 | 469 | 195 | 159 | | 44 | 30 | 14 | 15 | 11 | 1 | 0 | 0 | 0 |
| 29 | 0 | | 18 | 22.61 | 407 | 228 | 137 | | 1 | 0 | 21 | 20 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 21.80 | 436 | 49 | 132 | | 216 | 5 | 26 | 4 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 18.60 | 372 | 19 | 353 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 17 | 0 | | 20 | 17.70 | 354 | 154 | 1 | | 64 | 50 | 4 | 41 | 15 | 0 | 0 | 0 | 0 |
| 17 | 0 | | 20 | 16.55 | 331 | 0 | 331 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 16.44 | 296 | 103 | 46 | | 46 | 16 | 10 | 47 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 16.40 | 328 | 2 | 297 | | 20 | 1 | 0 | 6 | 1 | 1 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 16.39 | 295 | 0 | 295 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 15.50 | 310 | 112 | 0 | | 60 | 15 | 0 | 123 | 0 | 0 | 0 | 0 | 0 |
| 25 | 0 | | 20 | 15.35 | 307 | 43 | 247 | | 15 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 15.05 | 301 | 25 | 144 | | 43 | 14 | 0 | 60 | 5 | 4 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 14.80 | 267 | 45 | 181 | | 24 | 4 | 0 | 8 | 0 | 5 | 0 | 0 | 0 |
| 27 | 0 | | 18 | 14.78 | 266 | 97 | 92 | | 34 | 5 | 16 | 31 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 14.45 | 289 | 5 | 284 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 14.25 | 285 | 8 | 36 | | 42 | 36 | 9 | 112 | 13 | 2 | 0 | 0 | 0 |
| 27 | 0 | | 20 | 13.80 | 276 | 18 | 258 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | | 18 | 13.12 | 263 | 247 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 13.70 | 274 | 18 | 92 | | 79 | 18 | 1 | 61 | 4 | 1 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 13.35 | 267 | 8 | 244 | | 11 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 |
| 26 | 1 | | 20 | 12.30 | 246 | 19 | 1 | | 0 | 7 | 237 | 0 | 2 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 10.30 | 206 | 56 | 0 | | 148 | 28 | 0 | 22 | 2 | 0 | 0 | 1 | 0 |
| 20 | 0 | | 20 | 10.25 | 265 | 78 | 0 | | 57 | 0 | 3 | 61 | 3 | 63 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 10.21 | 249 | 4 | 40 | | 51 | 42 | 17 | 39 | 13 | 33 | 0 | 0 | 0 |
| 15 | 0 | | 20 | 10.05 | 261 | 0 | 261 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 10.00 | 254 | 54 | 0 | | 45 | 36 | 13 | 73 | 0 | 22 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 12.75 | 255 | 40 | 51 | | 23 | 29 | 11 | 87 | 9 | 5 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 12.23 | 245 | 41 | 0 | | 110 | 38 | 0 | 26 | 21 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 12.20 | 244 | 101 | 0 | | 0 | 8 | 0 | 71 | 3 | 61 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 11.85 | 237 | 70 | 0 | | 59 | 42 | 0 | 0 | 21 | 45 | 0 | 0 | 0 |
| 27 | 0 | | 20 | 11.80 | 236 | 6 | 203 | | 10 | 1 | 7 | 9 | 0 | 0 | 0 | 0 | 0 |
| 27 | 0 | | 18 | 11.47 | 210 | 46 | 0 | | 0 | 1 | 109 | 54 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 18 | 11.56 | 208 | 103 | 35 | | 25 | 23 | 2 | 8 | 11 | 1 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 11.35 | 231 | 45 | 32 | | 38 | 15 | 0 | 69 | 17 | 0 | 0 | 1 | 0 |
| 21 | 0 | | 20 | 11.35 | 227 | 15 | 0 | | 49 | 27 | 0 | 17 | 15 | 64 | 0 | 0 | 0 |
| 19 | 0 | | 17 | 11.28 | 192 | 23 | 153 | | 3 | 2 | 9 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 18 | 11.22 | 202 | 5 | 180 | | 6 | 3 | 1 | 6 | 1 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 10.55 | 211 | 78 | 0 | | 52 | 30 | 0 | 38 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 10.00 | 180 | 80 | 34 | | 30 | 0 | 7 | 29 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 9.85 | 197 | 35 | 0 | | 48 | 28 | 16 | 36 | 11 | 3 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 9.80 | 196 | 45 | 19 | | 23 | 22 | 6 | 61 | 14 | 6 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 9.28 | 167 | 115 | 9 | | 22 | 8 | 3 | 1 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 8.75 | 175 | 19 | 57 | | 61 | 4 | 2 | 23 | 3 | 6 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 8.25 | 165 | 5 | 25 | | 60 | 9 | 4 | 58 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 8.25 | 165 | 0 | 0 | | 133 | 0 | 0 | 32 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 8.22 | 148 | 22 | 9 | | 76 | 20 | 0 | 10 | 0 | 10 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 8.15 | 163 | 4 | 15 | | 79 | 24 | 2 | 11 | 23 | 3 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 8.05 | 161 | 3 | 132 | | 2 | 2 | 5 | 1 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 7.60 | 152 | 0 | 0 | | 139 | 0 | 0 | 11 | 0 | 2 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 7.40 | 152 | 19 | 21 | | 90 | 14 | 0 | 4 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 7.55 | 151 | 56 | 0 | | 41 | 30 | 1 | 2 | 15 | 6 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 7.35 | 147 | 147 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 7.25 | 145 | 2 | 143 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 7.10 | 142 | 33 | 0 | | 54 | 37 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 18 | 7.06 | 127 | 29 | 95 | | 0 | 0 | 1 | 2 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 6.35 | 127 | 15 | 0 | | 12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 6.35 | 127 | 15 | 0 | | 11 | 2 | 79 | 16 | 0 | 3 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 6.25 | 125 | 2 | 0 | | 54 | 9 | 1 | 55 | 4 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 19 | 6.14 | 117 | 58 | 21 | | 20 | 12 | 2 | 3 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 6.10 | 122 | 42 | 18 | | 34 | 0 | 0 | 9 | 13 | 6 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 6.10 | 122 | 0 | 30 | | 29 | 18 | 24 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 19 | 6.05 | 115 | 25 | 35 | | 24 | 15 | 0 | 10 | 4 | 2 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 5.95 | 119 | 3 | 99 | | 12 | 1 | 1 | 3 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 5.95 | 119 | 27 | 47 | | 8 | 8 | 9 | 13 | 4 | 3 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 5.90 | 118 | 0 | 0 | | 66 | 0 | 5 | 0 | 0 | 18 | 0 | 0 | 0 |
| 27 | 0 | | 17 | 5.88 | 100 | 57 | 10 | | 13 | 1 | 10 | 9 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 5.85 | 117 | 0 | 117 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 5.80 | 116 | 40 | 20 | | 17 | 22 | 0 | 3 | 11 | 3 | 0 | 0 | 0 |
| 27 | 0 | | 20 | 5.80 | 116 | 8 | 0 | | 53 | 4 | 0 | 50 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 5.80 | 116 | 45 | 27 | | 21 | 7 | 1 | 10 | 4 | 1 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 5.80 | 116 | 4 | 82 | | 3 | 2 | 4 | 2 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 5.75 | 115 | 4 | 78 | | 14 | 3 | 4 | 12 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 18 | 5.78 | 104 | 6 | 92 | | 0 | 2 | 0 | 0 | 4 | 0 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 5.60 | 112 | 2 | 38 | | 46 | 18 | 0 | 2 | 4 | 2 | 0 | 0 | 0 |
| 21 | 0 | | 18 | 5.78 | 104 | 6 | 82 | | 3 | 2 | 4 | 2 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 5.45 | 109 | 0 | 56 | | 11 | 12 | 4 | 20 | 4 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 5.45 | 109 | 15 | 20 | | 45 | 3 | 0 | 5 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 5.40 | 108 | 41 | 0 | | 25 | 25 | 0 | 3 | 8 | 6 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.35 | 107 | 28 | 0 | | 35 | 17 | 0 | 13 | 12 | 2 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.35 | 107 | 0 | 0 | | 88 | 2 | 0 | 17 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 18 | 5.28 | 95 | 12 | 0 | | 35 | 17 | 4 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 18 | 5.28 | 95 | 3 | 0 | | 21 | 43 | 4 | 13 | 10 | 1 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.25 | 105 | 0 | 105 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.15 | 103 | 48 | 0 | | 13 | 15 | 0 | 9 | 8 | 10 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.05 | 101 | 12 | 0 | | 39 | 6 | 0 | 42 | 0 | 2 | 0 | 0 | 0 |
| 16 | 0 | | 20 | 5.05 | 101 | 0 | 101 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.95 | 99 | 5 | 89 | | 4 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.95 | 99 | 28 | 37 | | 12 | 9 | 3 | 6 | 4 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 4.84 | 92 | 92 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 4.80 | 96 | 8 | 10 | | 56 | 13 | 1 | 3 | 4 | 1 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 4.65 | 93 | 4 | 47 | | 7 | 0 | 13 | 2 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 4.60 | 92 | 4 | 83 | | 0 | 1 | 2 | 2 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 4.60 | 92 | 0 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 4.50 | 90 | 40 | 16 | | 12 | 12 | 0 | 4 | 6 | 2 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 4.50 | 90 | 2 | 3 | | 52 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 4.40 | 88 | 10 | 0 | | 52 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.35 | 87 | 20 | 0 | | 32 | 21 | 0 | 5 | 8 | 1 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.35 | 87 | 4 | 47 | | 24 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 4.30 | 86 | 20 | 0 | | 49 | 0 | 1 | 13 | 3 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 4.25 | 76 | 29 | 16 | | 13 | 5 | 3 | 8 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 4.20 | 84 | 19 | 18 | | 26 | 0 | 1 | 9 | 11 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 4.05 | 81 | 0 | 0 | | 21 | 18 | 0 | 14 | 0 | 28 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 4.05 | 81 | 2 | 24 | | 24 | 2 | 6 | 21 | 1 | 1 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 4.00 | 80 | 3 | 12 | | 39 | 4 | 0 | 11 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.00 | 80 | 26 | 0 | | 11 | 17 | 0 | 5 | 11 | 10 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.95 | 79 | 7 | 45 | | 22 | 0 | 1 | 1 | 2 | 1 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.95 | 79 | 7 | 45 | | 22 | 0 | 1 | 1 | 2 | 1 | 0 | 0 | 0 |
| 21 | 0 | | 18 | 3.94 | 71 | 15 | 43 | | 7 | 2 | 3 | 1 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 3.85 | 77 | 1 | 0 | | 27 | 5 | 9 | 31 | 3 | 1 | 0 | 0 | 0 |
| 31 | 0 | | 20 | 3.75 | 75 | 0 | 75 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 3.70 | 74 | 1 | 3 | | 37 | 20 | 2 | 4 | 7 | 0 | 0 | 0 | 0 |
| 18 | 0 | | 18 | 3.47 | 66 | 1 | 50 | | 4 | 3 | 4 | 2 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.45 | 73 | 3 | 66 | | 3 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.45 | 73 | 1 | 4 | | 32 | 3 | 5 | 27 | 0 | 3 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.45 | 73 | 15 | 0 | | 32 | 10 | 0 | 5 | 8 | 3 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 3.45 | 73 | 2 | 49 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 3.45 | 73 | 0 | 43 | | 11 | 3 | 1 | 13 | 0 | 1 | 0 | 1 | 0 |
| 29 | 0 | | 20 | 3.40 | 72 | 0 | 0 | | 25 | 5 | 22 | 24 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 17 | 3.59 | 61 | 48 | 0 | | 9 | 1 | 2 | 1 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 3.50 | 63 | 0 | 63 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | | 18 | 3.50 | 63 | 60 | 3 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 16 | 0 | | 20 | 3.45 | 69 | 0 | 65 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 3.40 | 68 | 52 | 0 | | 8 | 1 | 0 | 7 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.35 | 67 | 0 | 0 | | 21 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 28 | 1 | | 20 | 3.30 | 66 | 6 | 0 | | 54 | 0 | 0 | 4 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 19 | 3.16 | 60 | 41 | 2 | | 2 | 2 | 2 | 2 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 3.15 | 63 | 15 | 13 | | 8 | 13 | 0 | 10 | 0 | 4 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.05 | 61 | 9 | 24 | | 14 | 0 | 4 | 0 | 0 | 0 | 0 | 1 | 0 |
| 18 | 0 | | 20 | 3.05 | 61 | 0 | 53 | | 0 | 7 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.00 | 60 | 0 | 57 | | 0 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.00 | 60 | 0 | 0 | | 57 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.00 | 60 | 2 | 0 | | 57 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 23 | 0 | | 18 | 2.94 | 53 | 4 | 22 | | 18 | 2 | 1 | 5 | 1 | 1 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 2.85 | 57 | 0 | 0 | | 17 | 0 | 0 | 0 | 0 | 40 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.80 | 56 | 0 | 0 | | 23 | 0 | 0 | 13 | 0 | 20 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 2.85 | 57 | 1 | 52 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 2.82 | 48 | 38 | 12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 2.80 | 56 | 4 | 18 | | 26 | 2 | 0 | 2 | 0 | 2 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 2.75 | 55 | 3 | 40 | | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 2.70 | 54 | 1 | 14 | 0 | 0 | 16 | 4 | 12 | 7 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.70 | 54 | 0 | 0 | 0 | 37 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 2.70 | 54 | 0 | 0 | 0 | 48 | 0 | 0 | 4 | 0 | 2 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 2.65 | 53 | 51 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 2.65 | 53 | 2 | 0 | 18 | 0 | 0 | 27 | 1 | 5 | 0 | 0 | 0 | 0 |
| 25 | 0 | | 18 | 2.68 | 47 | 23 | 11 | 9 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 27 | 0 | | 20 | 2.60 | 52 | 0 | 43 | 0 | 9 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.60 | 52 | 0 | 0 | 0 | 4 | 8 | 0 | 28 | 0 | 12 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 2.60 | 52 | 26 | 9 | 12 | 2 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| 32 | 0 | | 20 | 2.55 | 51 | 7 | 25 | 14 | 0 | 0 | 0 | 0 | 0 | 5 | 0 | 0 | 0 |
| 32 | 0 | | 20 | 2.55 | 51 | 0 | 51 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 2.55 | 51 | 16 | 9 | 20 | 3 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 2.55 | 51 | 0 | 0 | 50 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 2.50 | 50 | 1 | 16 | 27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.45 | 49 | 22 | 11 | 2 | 4 | 0 | 1 | 7 | 2 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 2.45 | 49 | 41 | 0 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 2.40 | 48 | 7 | 0 | 23 | 0 | 11 | 3 | 3 | 1 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.40 | 48 | 13 | 0 | 0 | 16 | 0 | 13 | 6 | 0 | 0 | 0 | 0 | 0 |
| 31 | 0 | | 20 | 2.40 | 48 | 0 | 48 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.40 | 48 | 0 | 0 | 17 | 3 | 0 | 12 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 2.40 | 48 | 0 | 0 | 29 | 2 | 0 | 16 | 0 | 1 | 0 | 0 | 0 | 0 |
| 25 | 0 | | 20 | 2.35 | 47 | 2 | 32 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 

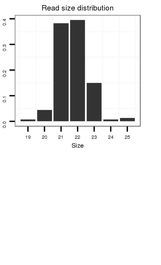
| ID: | Coordinate: | Confidence: | Class: | Genomic Locus: |
|---|---|---|---|---|
| **dya_1793** | **v2_chrUn_1311:45-143 +** | **candidate-rescued** | **Canonical miRNA** | **intergenic** |
| | | | | [View on UCSC Genome Browser (Comfil Mitmit)] |

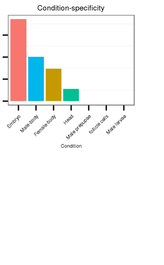
Legend: Loop Star Mature 5 arm in mature Mature 3 arm in mature

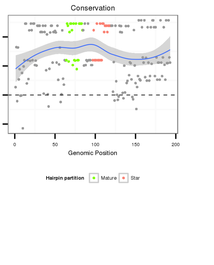
## Predicted structure






Show Alternate Folds

## Flybase annotation

dRNA:Dyak\FBrRNAAGE26302-RA]

## Repeatable elements

| Name | Class | Family | Strand |
|---|---|---|---|
| AT_rich | Low_complexity | Low_complexity | + |

**mature**

1. dya_1793 v2_chrUn_1311:45-143 +
2. v2_chrUn_2920:788-728 +
3. v2_chrUn_1929:235-293 +
4. v2_chrUn_4644:179-199 +
5. v2_chrUn_4933:1063-1023 +
6. v2_chrUn_2147:1-41 +
7. v2_chrUn_2347:62-94 +
8. v2_chrUn_5370:203-223 +
9. v2_chrUn_5306:4414-4361 +
10. v2_chrUn_5762:888-908 +
11. v2_chrUn_2944:2472-2492 +
12. v2_chrUn_2944:2472-2492 +
13. v2_chrUn_2613:7268-7288 +
14. v2_chrUn_2167:926-7846 +
15. v2_chrUn_2944:4355-4375 +
16. v2_chrUn_2763:2951-2911 +
17. v2_chrUn_4475:1-41 +
18. v2_chrUn_5370:1395-1435 +
19. v2_chrUn_3133:52-5242 +
20. v2_chrUn_924:1125-1143 +
21. v2_chrUn_2514:436-456 +
22. v2_chrUn_4130:1030-1030 +
23. v2_chrUn_5306:4414-4361 +
24. v2_chrUn_3472:129-149 +
25. v2_chrUn_3944:8-44 +
26. v2_chrUn_5746:1201-1241 +
27. v2_chrUn_3273:1669-1689 +

**star**

1. dya_1793 v2_chrUn_1311:97-119 +
2. v2_chrUn_2920:743-763 +
3. v2_chrUn_4230:975-997 +
4. v2_chrUn_1739:110-1132 +
5. v2_chrUn_1938:198-220 +
6. v2_chrUn_2147:1-41 +
7. v2_chrUn_4644:101-161 +
8. v2_chrUn_5347:954-978 +
9. v2_chrUn_5370:634-595 +
10. v2_chrUn_3294:4174-4396 +
11. v2_chrUn_3472:98-140 +
12. v2_chrUn_3472:98-140 +
13. v2_chrUn_2364:9-31 +
14. v2_chrUn_4164:187-1189 +
15. v2_chrUn_0614:6856-6898 +
16. v2_chrUn_0615:581-533 +
17. v2_chrUn_2:1-41 +
18. v2_chrUn_5370:1396-1436 +
19. v2_chrUn_3:6:2924-3946 +
20. v2_chrUn_4:87:4873-4893 +
21. v2_chrUn_4933:868-890 +
22. v2_chrUn_2990:90-130 +
23. v2_chrUn_5347:954-978 (5746:1243-1270) +
24. v2_chrUn_3543:2504-2556 +
25. v2_chrUn_6:26:1323-1324 +
26. v2_chrUn_3524:411-421 +

## Sense Strand Reads

Hide 3p reads  Show mid mismatch reads

```
TACATAAGTCCTTATGAGAACTAAGACATTTCCCAGCATTTATTTTAGGTATAAAAATACATTTATTGAAGGAATTGATATATCCAGTAAAATCGTATTTTTAATTTCTTTCAATTAAAAAATTATTGACATATATAGAAATAAATTATAAACTCTAAGCGTGATCACTCGGCTCATGGCTCGATG
```

| Read # | Size | Mismatch | Hit Count | Total Norm | Total | V120 male body | V120 female body | M043 follicle cells | M043 female body | V058 head | M026 head | M056 embryo | V052 head | V046 embryo | SRR1275484 Male pregonads | SRR1275485 Male larvae | SRR1275486 Male pregonads |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | GSM1528802 | | | | | | | | | | | |
| 26 | 0 | | 20 | 7843.75 | 156875 | 120737 | 13571 | 4323 | 7163 | 6650 | 1335 | 2956 | 134 | 7 | 4 | 0 | 0 |
| 21 | 0 | | 20 | 1203.60 | 24072 | 12503 | 4326 | 2979 | 1618 | 595 | 1388 | 415 | 46 | 2 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 723.45 | 14469 | 9 | 9311 | | 313 | 2801 | 441 | 275 | 1291 | 28 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 7352.94 | 12797 | 1832 | 952 | | 327 | 473 | 546 | 152 | 164 | 9 | 1 | 1 | 0 |
| 25 | 0 | | 20 | 511.95 | 10221 | 3068 | 4608 | | 831 | 415 | 516 | 536 | 153 | 89 | 3 | 2 | 0 |
| 25 | 0 | | 20 | 464.26 | 8886 | 583 | 7839 | | 0 | 0 | 424 | 40 | 0 | 46 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 251.35 | 5027 | 2080 | 0 | | 1350 | 360 | 12 | 0 | 66 | 1158 | 0 | 1 | 0 |
| 20 | 0 | | 20 | 240.90 | 4858 | 1000 | 0 | | 213 | 157 | 1474 | 38 | 2102 | 2 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 204.45 | 4093 | 0 | 4084 | | 0 | 0 | 0 | 0 | 0 | 0 | 4 | 0 | 0 |
| 30 | 0 | | 20 | 179.49 | 3590 | 1576 | 0 | | 895 | 249 | 229 | 0 | 0 | 0 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 159.89 | 2878 | 2372 | 265 | | 33 | 29 | 159 | 3 | 6 | 1 | 5 | 0 | 0 |
| 23 | 0 | | 20 | 149.05 | 2981 | 1284 | 972 | | 370 | 207 | 8 | 0 | 90 | 45 | 1 | 1 | 1 |
| 24 | 0 | | 20 | 135.70 | 2714 | 704 | 1642 | | 232 | 104 | 19 | 45 | 45 | 14 | 0 | 2 | 1 |
| 21 | 0 | | 20 | 125.35 | 2507 | 497 | 485 | | 927 | 306 | 20 | 115 | 147 | 6 | 4 | 0 | 0 |
| 18 | 0 | | 20 | 121.72 | 2191 | 1256 | 494 | | 127 | 45 | 120 | 128 | 19 | 2 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 121.00 | 2420 | 409 | 1194 | | 649 | 26 | 25 | 94 | 17 | 4 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 90.40 | 1892 | 99 | 5 | | 293 | 23 | 12 | 1293 | 2 | 258 | 3 | 0 | 0 |
| 26 | 1 | | 20 | 91.55 | 1831 | 155 | 1 | | 2 | 15 | 1228 | 424 | 4 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 76.05 | 1521 | 0 | 272 | | 583 | 407 | 16 | 27 | 0 | 16 | 0 | 0 | 0 |
| 25 | 0 | | 20 | 71.70 | 1434 | 414 | 370 | | 311 | 35 | 46 | 31 | 24 | 3 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 18.98 | 1279 | 1223 | 6 | | 0 | 40 | 10 | 0 | 0 | 0 | 0 | 0 | 0 |
| 17 | 0 | | 20 | 66.45 | 1333 | 0 | 1195 | | 0 | 136 | 0 | 0 | 0 | 0 | 2 | 0 | 0 |
| 20 | 0 | | 20 | 65.76 | 1314 | 56 | 101 | | 441 | 0 | 202 | 134 | 369 | 13 | 0 | 0 | 0 |
| 25 | 0 | | 20 | 63.80 | 1276 | 6 | 1252 | | 11 | 0 | 0 | 4 | 3 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 57.50 | 1035 | 16 | 744 | | 43 | 128 | 13 | 50 | 39 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 50.47 | 912 | 268 | 313 | | 98 | 27 | 59 | 130 | 6 | 11 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 48.46 | 972 | 513 | 157 | | 87 | 55 | 53 | 70 | 32 | 5 | 2 | 0 | 0 |
| 28 | 0 | | 20 | 48.45 | 969 | 7 | 936 | | 0 | 0 | 10 | 17 | 1 | 0 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 35.95 | 719 | 158 | 327 | | 51 | 52 | 19 | 85 | 103 | 29 | 1 | 0 | 0 |
| 22 | 0 | | 20 | 34.15 | 683 | 157 | 0 | | 206 | 83 | 0 | 97 | 24 | 115 | 0 | 1 | 0 |
| 30 | 0 | | 20 | 18.32 | 681 | 12 | 589 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 29.00 | 580 | 3 | 577 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 31 | 0 | | 20 | 28.00 | 560 | 0 | 560 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 26.45 | 529 | 142 | 0 | | 183 | 0 | 29 | 0 | 11 | 162 | 1 | 1 | 0 |
| 23 | 0 | | 20 | 23.45 | 469 | 195 | 159 | | 44 | 30 | 14 | 15 | 11 | 1 | 0 | 0 | 0 |
| 29 | 0 | | 18 | 22.61 | 407 | 228 | 137 | | 1 | 0 | 21 | 20 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 21.80 | 436 | 49 | 132 | | 216 | 5 | 26 | 4 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 18.60 | 372 | 19 | 353 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 17 | 0 | | 20 | 17.70 | 354 | 154 | 1 | | 64 | 50 | 4 | 41 | 15 | 0 | 0 | 0 | 0 |
| 17 | 0 | | 20 | 16.55 | 331 | 0 | 331 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 16.44 | 296 | 103 | 46 | | 46 | 16 | 10 | 47 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 16.40 | 328 | 2 | 297 | | 20 | 1 | 0 | 6 | 1 | 1 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 16.39 | 295 | 0 | 295 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 15.50 | 310 | 112 | 0 | | 60 | 15 | 0 | 123 | 0 | 0 | 0 | 0 | 0 |
| 25 | 0 | | 20 | 15.35 | 307 | 43 | 247 | | 15 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 15.05 | 301 | 25 | 144 | | 43 | 14 | 0 | 60 | 5 | 4 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 14.80 | 267 | 45 | 181 | | 24 | 4 | 0 | 8 | 0 | 5 | 0 | 0 | 0 |
| 27 | 0 | | 18 | 14.78 | 266 | 97 | 92 | | 34 | 5 | 16 | 31 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 14.45 | 289 | 5 | 284 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 14.25 | 285 | 8 | 36 | | 42 | 36 | 9 | 112 | 13 | 2 | 0 | 0 | 0 |
| 27 | 0 | | 20 | 13.80 | 276 | 18 | 258 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | | 18 | 13.12 | 263 | 247 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 13.70 | 274 | 18 | 92 | | 79 | 18 | 1 | 61 | 4 | 1 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 13.35 | 267 | 8 | 244 | | 11 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 |
| 26 | 1 | | 20 | 12.30 | 246 | 19 | 1 | | 0 | 7 | 237 | 0 | 2 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 10.30 | 206 | 56 | 0 | | 148 | 28 | 0 | 22 | 2 | 0 | 0 | 1 | 0 |
| 20 | 0 | | 20 | 10.25 | 265 | 78 | 0 | | 57 | 0 | 3 | 61 | 3 | 63 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 10.21 | 249 | 4 | 40 | | 51 | 42 | 17 | 39 | 13 | 33 | 0 | 0 | 0 |
| 15 | 0 | | 20 | 10.05 | 261 | 0 | 261 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 10.00 | 254 | 54 | 0 | | 45 | 36 | 13 | 73 | 0 | 22 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 12.75 | 255 | 40 | 51 | | 23 | 29 | 11 | 87 | 9 | 5 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 12.23 | 245 | 41 | 0 | | 110 | 38 | 0 | 26 | 21 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 12.20 | 244 | 101 | 0 | | 0 | 8 | 0 | 71 | 3 | 61 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 11.85 | 237 | 70 | 0 | | 59 | 42 | 0 | 0 | 21 | 45 | 0 | 0 | 0 |
| 27 | 0 | | 20 | 11.80 | 236 | 6 | 203 | | 10 | 1 | 7 | 9 | 0 | 0 | 0 | 0 | 0 |
| 27 | 0 | | 18 | 11.47 | 210 | 46 | 0 | | 0 | 1 | 109 | 54 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 18 | 11.56 | 208 | 103 | 35 | | 25 | 23 | 2 | 8 | 11 | 1 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 11.35 | 231 | 45 | 32 | | 38 | 15 | 0 | 69 | 17 | 0 | 0 | 1 | 0 |
| 21 | 0 | | 20 | 11.35 | 227 | 15 | 0 | | 49 | 27 | 0 | 17 | 15 | 64 | 0 | 0 | 0 |
| 19 | 0 | | 17 | 11.28 | 192 | 23 | 153 | | 3 | 2 | 9 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 18 | 11.22 | 202 | 5 | 180 | | 6 | 3 | 1 | 6 | 1 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 10.55 | 211 | 78 | 0 | | 52 | 30 | 0 | 38 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 10.00 | 180 | 80 | 34 | | 30 | 0 | 7 | 29 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 9.85 | 197 | 35 | 0 | | 48 | 28 | 16 | 36 | 11 | 3 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 9.80 | 196 | 45 | 19 | | 23 | 22 | 6 | 61 | 14 | 6 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 9.28 | 167 | 115 | 9 | | 22 | 8 | 3 | 1 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 8.75 | 175 | 19 | 57 | | 61 | 4 | 2 | 23 | 3 | 6 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 8.25 | 165 | 5 | 25 | | 60 | 9 | 4 | 58 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 8.25 | 165 | 0 | 0 | | 133 | 0 | 0 | 32 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 8.22 | 148 | 22 | 9 | | 76 | 20 | 0 | 10 | 0 | 10 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 8.15 | 163 | 4 | 15 | | 79 | 24 | 2 | 11 | 23 | 3 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 8.05 | 161 | 3 | 132 | | 2 | 2 | 5 | 1 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 7.60 | 152 | 0 | 0 | | 139 | 0 | 0 | 11 | 0 | 2 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 7.40 | 152 | 19 | 21 | | 90 | 14 | 0 | 4 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 7.55 | 151 | 56 | 0 | | 41 | 30 | 1 | 2 | 15 | 6 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 7.35 | 147 | 147 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 7.25 | 145 | 2 | 143 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 7.10 | 142 | 33 | 0 | | 54 | 37 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 18 | 7.06 | 127 | 29 | 95 | | 0 | 0 | 1 | 2 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 6.35 | 127 | 15 | 0 | | 12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 6.35 | 127 | 15 | 0 | | 11 | 2 | 79 | 16 | 0 | 3 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 6.25 | 125 | 2 | 0 | | 54 | 9 | 1 | 55 | 4 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 19 | 6.14 | 117 | 58 | 21 | | 20 | 12 | 2 | 3 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 6.10 | 122 | 42 | 18 | | 34 | 0 | 0 | 9 | 13 | 6 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 6.10 | 122 | 0 | 30 | | 29 | 18 | 24 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 19 | 6.05 | 115 | 25 | 35 | | 24 | 15 | 0 | 10 | 4 | 2 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 5.95 | 119 | 3 | 99 | | 12 | 1 | 1 | 3 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 5.95 | 119 | 27 | 47 | | 8 | 8 | 9 | 13 | 4 | 3 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 5.90 | 118 | 0 | 0 | | 66 | 0 | 5 | 0 | 0 | 18 | 0 | 0 | 0 |
| 27 | 0 | | 17 | 5.88 | 100 | 57 | 10 | | 13 | 1 | 10 | 9 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 5.85 | 117 | 0 | 117 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 5.80 | 116 | 40 | 20 | | 17 | 22 | 0 | 3 | 11 | 3 | 0 | 0 | 0 |
| 27 | 0 | | 20 | 5.80 | 116 | 8 | 0 | | 53 | 4 | 0 | 50 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 5.80 | 116 | 45 | 27 | | 21 | 7 | 1 | 10 | 4 | 1 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 5.80 | 116 | 4 | 82 | | 3 | 2 | 4 | 2 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 5.75 | 115 | 4 | 78 | | 14 | 3 | 4 | 12 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 18 | 5.78 | 104 | 6 | 92 | | 0 | 2 | 0 | 0 | 4 | 0 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 5.60 | 112 | 2 | 38 | | 46 | 18 | 0 | 2 | 4 | 2 | 0 | 0 | 0 |
| 21 | 0 | | 18 | 5.78 | 104 | 6 | 82 | | 3 | 2 | 4 | 2 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 5.45 | 109 | 0 | 56 | | 11 | 12 | 4 | 20 | 4 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 5.45 | 109 | 15 | 20 | | 45 | 3 | 0 | 5 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 5.40 | 108 | 41 | 0 | | 25 | 25 | 0 | 3 | 8 | 6 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.35 | 107 | 28 | 0 | | 35 | 17 | 0 | 13 | 12 | 2 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.35 | 107 | 0 | 0 | | 88 | 2 | 0 | 17 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 18 | 5.28 | 95 | 12 | 0 | | 35 | 17 | 4 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 18 | 5.28 | 95 | 3 | 0 | | 21 | 43 | 4 | 13 | 10 | 1 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.25 | 105 | 0 | 105 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.15 | 103 | 48 | 0 | | 13 | 15 | 0 | 9 | 8 | 10 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.05 | 101 | 12 | 0 | | 39 | 6 | 0 | 42 | 0 | 2 | 0 | 0 | 0 |
| 16 | 0 | | 20 | 5.05 | 101 | 0 | 101 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.95 | 99 | 5 | 89 | | 4 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.95 | 99 | 28 | 37 | | 12 | 9 | 3 | 6 | 4 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 4.84 | 92 | 92 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 4.80 | 96 | 8 | 10 | | 56 | 13 | 1 | 3 | 4 | 1 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 4.65 | 93 | 4 | 47 | | 7 | 0 | 13 | 2 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 4.60 | 92 | 4 | 83 | | 0 | 1 | 2 | 2 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 4.60 | 92 | 0 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 4.50 | 90 | 40 | 16 | | 12 | 12 | 0 | 4 | 6 | 2 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 4.50 | 90 | 2 | 3 | | 52 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
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| 20 | 0 | | 20 | 4.35 | 87 | 20 | 0 | | 32 | 21 | 0 | 5 | 8 | 1 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.35 | 87 | 4 | 47 | | 24 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 4.30 | 86 | 20 | 0 | | 49 | 0 | 1 | 13 | 3 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 4.25 | 76 | 29 | 16 | | 13 | 5 | 3 | 8 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 4.20 | 84 | 19 | 18 | | 26 | 0 | 1 | 9 | 11 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 4.05 | 81 | 0 | 0 | | 21 | 18 | 0 | 14 | 0 | 28 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 4.05 | 81 | 2 | 24 | | 24 | 2 | 6 | 21 | 1 | 1 | 0 | 0 | 0 |
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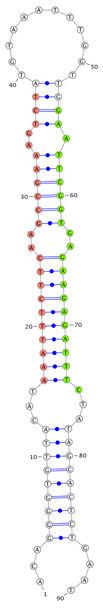
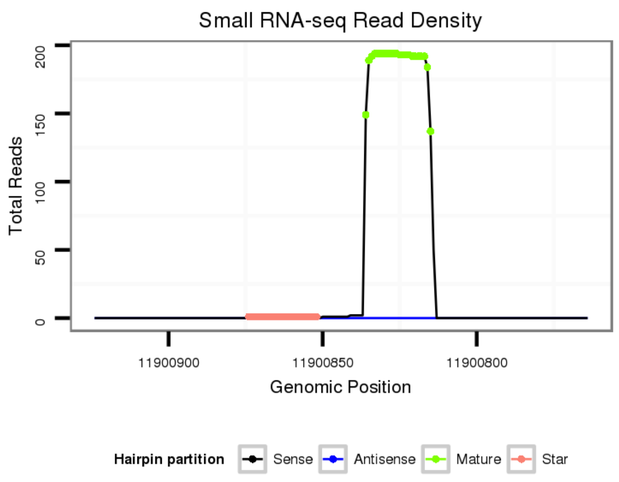
| 20 | 0 | | 20 | 4.00 | 80 | 26 | 0 | | 11 | 17 | 0 | 5 | 11 | 10 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.95 | 79 | 7 | 45 | | 22 | 0 | 1 | 1 | 2 | 1 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.95 | 79 | 7 | 45 | | 22 | 0 | 1 | 1 | 2 | 1 | 0 | 0 | 0 |
| 21 | 0 | | 18 | 3.94 | 71 | 15 | 43 | | 7 | 2 | 3 | 1 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 3.85 | 77 | 1 | 0 | | 27 | 5 | 9 | 31 | 3 | 1 | 0 | 0 | 0 |
| 31 | 0 | | 20 | 3.75 | 75 | 0 | 75 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 3.70 | 74 | 1 | 3 | | 37 | 20 | 2 | 4 | 7 | 0 | 0 | 0 | 0 |
| 18 | 0 | | 18 | 3.47 | 66 | 1 | 50 | | 4 | 3 | 4 | 2 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.45 | 73 | 3 | 66 | | 3 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.45 | 73 | 1 | 4 | | 32 | 3 | 5 | 27 | 0 | 3 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.45 | 73 | 15 | 0 | | 32 | 10 | 0 | 5 | 8 | 3 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 3.45 | 73 | 2 | 49 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 3.45 | 73 | 0 | 43 | | 11 | 3 | 1 | 13 | 0 | 1 | 0 | 1 | 0 |
| 29 | 0 | | 20 | 3.40 | 72 | 0 | 0 | | 25 | 5 | 22 | 24 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 17 | 3.59 | 61 | 48 | 0 | | 9 | 1 | 2 | 1 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 3.50 | 63 | 0 | 63 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | | 18 | 3.50 | 63 | 60 | 3 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 16 | 0 | | 20 | 3.45 | 69 | 0 | 65 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 3.40 | 68 | 52 | 0 | | 8 | 1 | 0 | 7 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.35 | 67 | 0 | 0 | | 21 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 28 | 1 | | 20 | 3.30 | 66 | 6 | 0 | | 54 | 0 | 0 | 4 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 19 | 3.16 | 60 | 41 | 2 | | 2 | 2 | 2 | 2 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 3.15 | 63 | 15 | 13 | | 8 | 13 | 0 | 10 | 0 | 4 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.05 | 61 | 9 | 24 | | 14 | 0 | 4 | 0 | 0 | 0 | 0 | 1 | 0 |
| 18 | 0 | | 20 | 3.05 | 61 | 0 | 53 | | 0 | 7 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.00 | 60 | 0 | 57 | | 0 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.00 | 60 | 0 | 0 | | 57 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.00 | 60 | 2 | 0 | | 57 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 23 | 0 | | 18 | 2.94 | 53 | 4 | 22 | | 18 | 2 | 1 | 5 | 1 | 1 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 2.85 | 57 | 0 | 0 | | 17 | 0 | 0 | 0 | 0 | 40 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.80 | 56 | 0 | 0 | | 23 | 0 | 0 | 13 | 0 | 20 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 2.85 | 57 | 1 | 52 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 2.82 | 48 | 38 | 12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 2.80 | 56 | 4 | 18 | | 26 | 2 | 0 | 2 | 0 | 2 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 2.75 | 55 | 3 | 40 | | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 2.70 | 54 | 1 | 14 | 0 | 0 | 16 | 4 | 12 | 7 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.70 | 54 | 0 | 0 | 0 | 37 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 2.70 | 54 | 0 | 0 | 0 | 48 | 0 | 0 | 4 | 0 | 2 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 2.65 | 53 | 51 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 2.65 | 53 | 2 | 0 | 18 | 0 | 0 | 27 | 1 | 5 | 0 | 0 | 0 | 0 |
| 25 | 0 | | 18 | 2.68 | 47 | 23 | 11 | 9 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 27 | 0 | | 20 | 2.60 | 52 | 0 | 43 | 0 | 9 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.60 | 52 | 0 | 0 | 0 | 4 | 8 | 0 | 28 | 0 | 12 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 2.60 | 52 | 26 | 9 | 12 | 2 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| 32 | 0 | | 20 | 2.55 | 51 | 7 | 25 | 14 | 0 | 0 | 0 | 0 | 0 | 5 | 0 | 0 | 0 |
| 32 | 0 | | 20 | 2.55 | 51 | 0 | 51 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 2.55 | 51 | 16 | 9 | 20 | 3 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 2.55 | 51 | 0 | 0 | 50 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 2.50 | 50 | 1 | 16 | 27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.45 | 49 | 22 | 11 | 2 | 4 | 0 | 1 | 7 | 2 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 2.45 | 49 | 41 | 0 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 2.40 | 48 | 7 | 0 | 23 | 0 | 11 | 3 | 3 | 1 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.40 | 48 | 13 | 0 | 0 | 16 | 0 | 13 | 6 | 0 | 0 | 0 | 0 | 0 |
| 31 | 0 | | 20 | 2.40 | 48 | 0 | 48 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.40 | 48 | 0 | 0 | 17 | 3 | 0 | 12 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 2.40 | 48 | 0 | 0 | 29 | 2 | 0 | 16 | 0 | 1 | 0 | 0 | 0 | 0 |
| 25 | 0 | | 20 | 2.35 | 47 | 2 | 32 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 

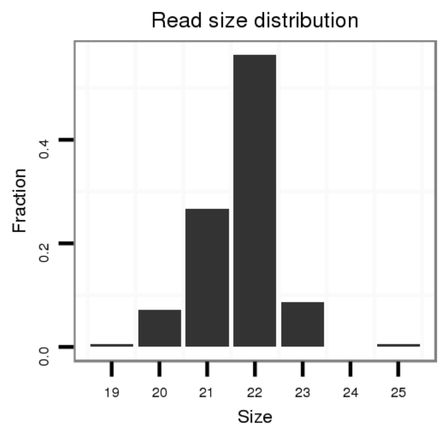
| ID: | Coordinate: | Confidence: | Class: | Genomic Locale: | |
|---|---|---|---|---|---|
| **dya_55** | **X:11900814-11900874 -** | **candidate-rescued** | **Testes-restricted** | **antisense_to_intron** | [View on UCSC Genome Browser {Cornell Mirror}] |

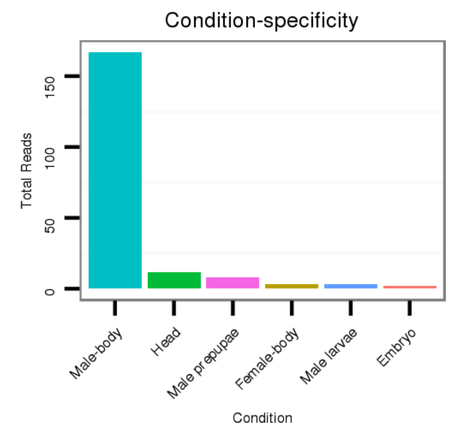
Legend: mature star mismatch in alignment mismatch in read

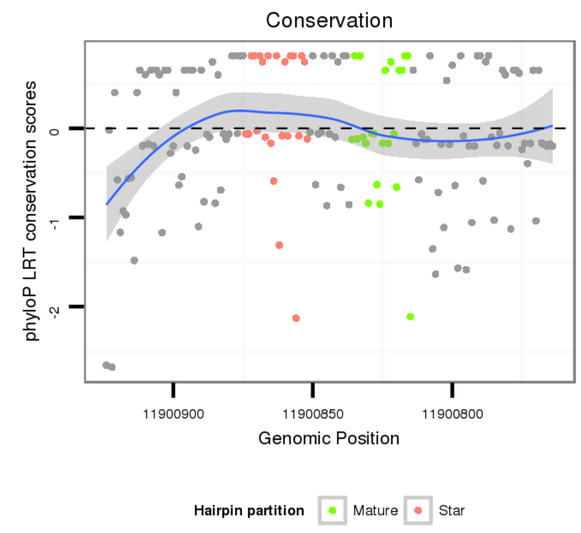
**Predicted structure**






Show Alternate Folds

**Flybase annotation**

Antisense to intron [Dyak\GE17381-in]

No Repeatable elements found

**Sense Strand Reads**

hide 3p reads show mid mismatch reads

TAAAGACAAAGATGGATGAGGTTGGATGAGATTGTACAGGGGTGTTACATAAATTTCTTCAAGCCGAAAGTCTATGTAAATTTGGTTGGAATTCGGTGAGAAGAGATTTCTATAGCACTCTGAATAGAGCCTGAATCTTCCAAGCTAATCAGTTGAAAGTC

| ********** | Read size | # Mismatch | Hit Count | Total Norm | Total | V120 male body | M026 head | SRR1275484 Male prepupae | V058 head | M043 female body | SRR1275488 Male larvae | V052 head | M056 embryo |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| .....GAATTCGGTGAGAAGAGATTTC..... | 22 | 0 | 1 | 80.00 | 80 | 57 | 7 | 7 | 1 | 3 | 2 | 1 | 2 |
| .....GAATTCGGTGAGAAGAGATTT..... | 21 | 0 | 1 | 44.00 | 44 | 43 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| .....AATTCGGTGAGAAGAGATTTCT..... | 22 | 0 | 1 | 30.00 | 30 | 28 | 0 | 0 | 2 | 0 | 0 | 0 | 0 |
| .....GAATTCGGTGAGAAGAGATTTT..... | 22 | 1 | 1 | 20.00 | 20 | 19 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| .....GAATTCGGTGAGAAGAGATTTCT..... | 23 | 0 | 1 | 16.00 | 16 | 16 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....GAATTCGGTGAGAAGAGATT..... | 20 | 0 | 1 | 7.00 | 7 | 7 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AATTCGGTGAGAAGAGATTTC..... | 21 | 0 | 1 | 6.00 | 6 | 4 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....AATTCGGTGAGAAGAGATTT..... | 20 | 0 | 1 | 3.00 | 3 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....GAATTCGGTGAGAAGAGATTTCA..... | 23 | 1 | 1 | 2.00 | 2 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....TTCGGTGAGAAGAGATTTCT..... | 20 | 0 | 1 | 2.00 | 2 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....ATTCGGTGAGAAGAGATTTCT..... | 21 | 0 | 1 | 2.00 | 2 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....GGTTGGAATTCGGTGAGAAG..... | 20 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AATTCGGTGAGAAGAGATTTA..... | 21 | 1 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| .....ATTCGGTGAGAAGAGATTTC..... | 20 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....TGTAAATTTGGTTGGAATTCGGTGA..... | 25 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AATTCGGTGAGAAGAGATT..... | 19 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AAATTTCTTCAAGCCGAAAGTCT..... | 23 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

**Anti-sense strand reads**

ATTTCTGTTTCTACCTACTCCAACCTACTCTAACATGTCCCCACAATGTATTTAAAGAAGTTCGGCTTTCAGATACATTTAAACCAACCTTAAGCCACTCTTCTCTAAAGATATCGTGAGACTTATCTCGGACTTAGAAGGTTCGATTAGTCAACTTTCAG

| ********** | 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 |
|---|---|---|---|
| droYak3 | X:11900764-11900924 - | dya_55 | TAAAGACAAAGATGGATGAGGTTGGATGAGATTGTA-----CAGGGGTGTTACATAAATTTCTTCAAGCCGAAAGTCTATGTAAATTTGGTTGGAATTCGGTGAGAAGAGATTTCTATAGCACTCTGAATAGAGCCTGAATCTTCCAAGCTAA----------TCAGTTGAAAGTC |
| droEre2 | scaffold_4690:9673150-9673307 + | der_57 | CACAG---AGTATGGATGAGGTTGGATGAGATTTTA-----CAGGGCTGTTACATAAATCTCTTCAAGCCGAACGTCTATGTAAGTTTGGTTGGAATTCTGTGAGAAGAGATTTCTATAGCATCCTGAATACAGTCGGAATCTTCCAAGCTAA----------TCAGTTGAATGTC |
| droSec2 | scaffold_8:1718425-1718579 + | dse_116 | CAAAT---GGAATGGATGAGATTGGAAAAGATTGTG-----TAGAGGTGTTACATAAATTTCTTCAAGCCGAACGTCTTTGTTAATTTGATTAGAATTCTGTGCGAAGAAATTTTTATAGCATCTTA---AGAGCCTGAATCTTTCGAGCCAA----------TCAGTTGAGAGTC |
| droSim2 | x:18325711-18325868 + | dsi_203 | TCCATCTTGGAATGGATGAGATTGGAAAAGATTGTG-----TAGAGGTGTTACATAAATTTCTTCAAACCGAAGCGTCTTTGTTAATTTGATTAGAATTCTGTGCGAAGAAATTTTTATAGCATCTTA---AGAGCCTGAATCTTTCGAGCCAA----------TCAGTTAAAAGTC |
| dm3 | chrX:19436179-19436341 + | | CAAAT---GGAATGGATAAGATTGGATAAGATTGTGTAAGATAGGGTTGTTATATAAATTTCTTCAAACCGAAAGTCTTTGTTAGTTTGATTAGAATTCTATGCGATGAAATTTGTATAGCATCCTT---TGAGTCTGAATCTTTCGAGTCAATCAGA----------TGATGAAAGTC |
| droEug1 | scf7180000409109:15701-15825 - | | GA----------TAGTTGAGCTTTA---AAATGTTA-----CAGT-GCTTTACATAAATTCTTTTAATCGAAAATCCATATAAATTTGGTTTGAGTTTTGCAGA--GGA--TTG--CAGAAAAT---ATAAAGTTGAAACTGCCAAGCCAA----------
| droEle1 | scf7180000490709:12017-12153 + | | TAT----------T-----CCGGGGTGCTACATAGATTTCGTTCAACCAAATGTCCATTCAAACTGGATTGTAGTGTGGTTGAAAGAGATTTCTGAGTCACGCAGATTGTAA----AACCTTGGA------TATTTATGATTAAAATAATTACTTTAAAAAT |

Generated: 09/08/2015 at 1:57 PM

| PASSFAIL | |
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| crit.loop | 0 |
| crit.mor | 0 |
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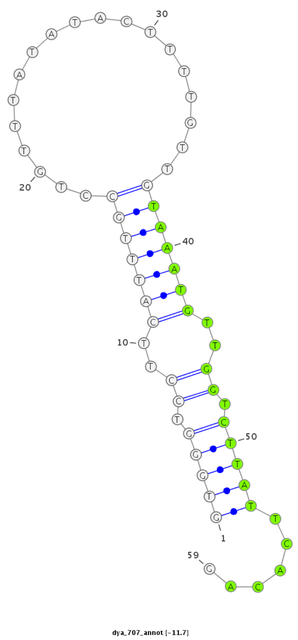
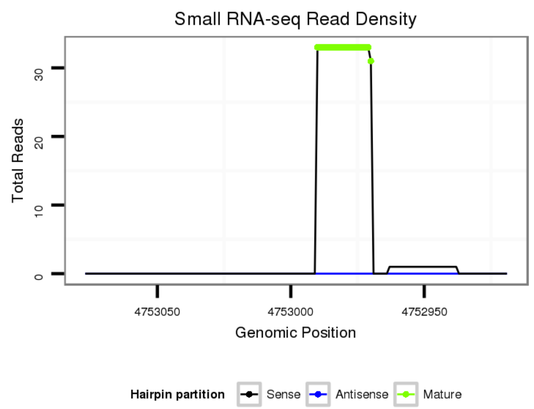
| crit.tptop3 | 1 |
| crit.uri | 0 |
| crit.back | 1 |
| rescue.total | 1 |
| rescue.dominant | 1 |
| rescue.known | 0 |
| rescue.confident | 3 |
| rescue.candidate | 1 |

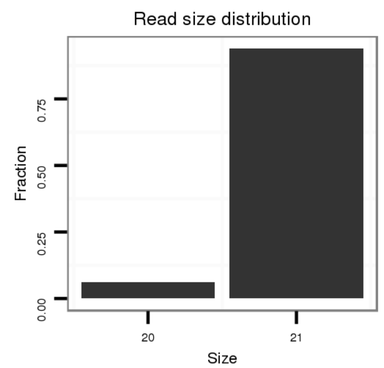
| ID: | Coordinate: | Confidence: | Class: | Genomic Locale: | |
|---|---|---|---|---|---|
| **dya_707** | **3L:4752969-4753027 -** | **candidate-rescued** | **Mirtron** | **intron** | [View on UCSC Genome Browser {Cornell Mirror}] |

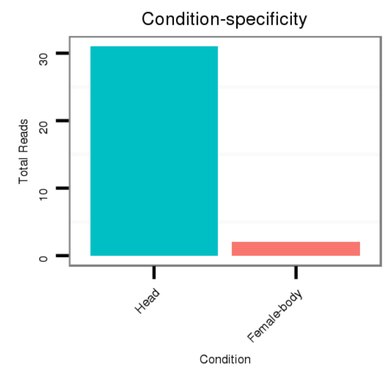
Legend: mature star mismatch in alignment mismatch in read

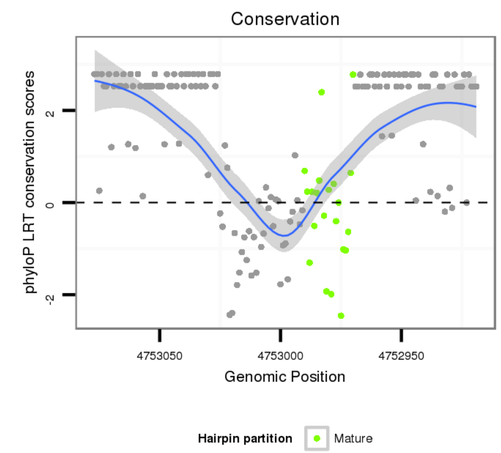
**Predicted structure**




Show Alternate Folds

**Flybase annnotation**

intron [Dyak\GE20641-in]; CDS [Dyak\GE20641-cds]; CDS [Dyak\GE20641-cds]

No Repeatable elements found

**Sense Strand Reads**

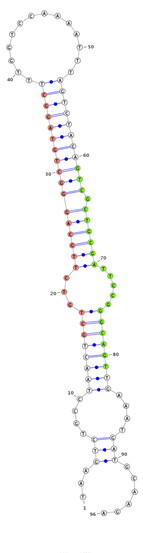
hide 3p reads show mid mismatch reads

```
                                                
```

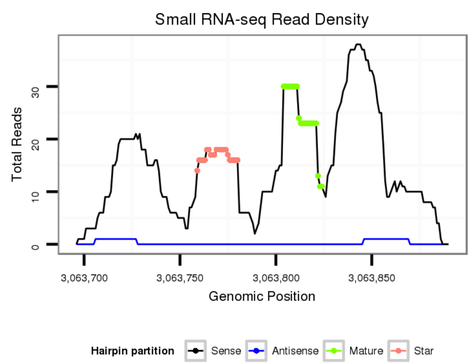
| ID: | Coordinate: | Confidence: | Class: | Genomic Locale: | |
|---|---|---|---|---|---|
| **dya_1801** | **2L:3063746-3063840 +** | **candidate-rescued** | **Canonical miRNA** | **3pUTR** | [View on UCSC Genome Browser (Cornell Mirror)] |

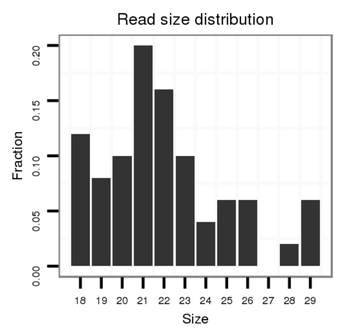
Legend: mature star mismatch in alignment mismatch in read

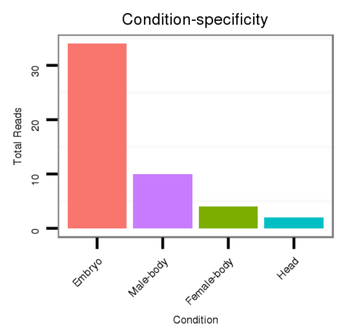
**Predicted structure**

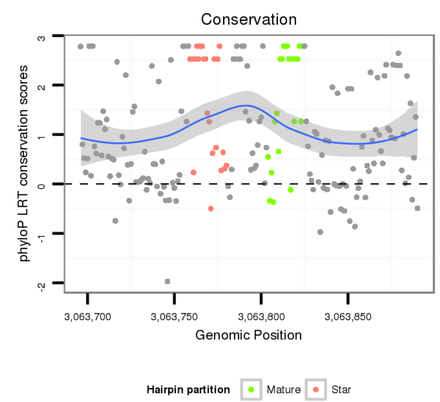


Show Alternate Folds




**Flybase annnotation**

utr3 [utr3_plus_232]

No Repeatable elements found

**Sense Strand Reads**

hide 3p reads  show mid mismatch reads

| ATCCCAGTTACGCACAGCTAGAAGAGATCGGATCGGCGTCGATCGGATTAAGTCTGCCTAACTGCTGTCTTGCAGGGCTGTAGGCTTTGGTCCAAAATTTAGTCTACAGTCGCTGCGATTCCGGGCAGTTGAAATGATGCAAGATGAAAGAGAGCCCGGTCCATAACACTTAACGCTTTGTGCACCGTACAATTC | Read size | # Mismatch | Hit Count | Total Norm | Total | M056 embryo | V120 male body | V046 embryo | M043 female body | M026 head | V052 head |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **********...(((.(....(((((((.(((((((((((((((((.....)))))))))))).))))))).....)))))))))....))).....********** | | | | | | | | | | | |
| .....GTCGCTGCGATTCCGGGCAGT..... | 21 | 0 | 1 | 6.00 | 6 | 3 | 2 | 0 | 1 | 0 | 0 |
| .....GTCGCTGCGATTCCGGGC..... | 18 | 0 | 1 | 6.00 | 6 | 5 | 0 | 0 | 0 | 1 | 0 |
| .....ATGCAAGATGAAAGAGAGCCCGGTC..... | 25 | 0 | 1 | 5.00 | 5 | 3 | 1 | 0 | 1 | 0 | 0 |
| .....GCTGTCTTGCAGGGCTGTAGGC..... | 22 | 0 | 1 | 4.00 | 4 | 2 | 2 | 0 | 0 | 0 | 0 |
| .....GATGCAAGATGAAAGAGAGCCCGGT..... | 25 | 0 | 1 | 3.00 | 3 | 1 | 2 | 0 | 0 | 0 | 0 |
| .....AACTGCTGTCTTGCAGGGCTGTAGGC..... | 26 | 0 | 1 | 3.00 | 3 | 2 | 0 | 1 | 0 | 0 | 0 |
| .....TTTAGTCTACAGTCGCTGC..... | 19 | 0 | 1 | 2.00 | 2 | 1 | 0 | 0 | 1 | 0 | 0 |
| .....AGCTAGAAGAGATCGGATCGGC..... | 22 | 0 | 1 | 2.00 | 2 | 2 | 0 | 0 | 0 | 0 | 0 |
| .....GCACAGCTAGAAGAGATCGGATC..... | 23 | 0 | 1 | 2.00 | 2 | 2 | 0 | 0 | 0 | 0 | 0 |
| .....AGAAGAGATCGGATCGGC..... | 18 | 0 | 1 | 2.00 | 2 | 2 | 0 | 0 | 0 | 0 | 0 |
| .....GTCGCTGCGATTCCGGGCAGTT..... | 22 | 0 | 1 | 2.00 | 2 | 1 | 0 | 0 | 1 | 0 | 0 |
| .....GATGAAAGAGAGCCCGGTC..... | 19 | 0 | 1 | 2.00 | 2 | 1 | 1 | 0 | 0 | 0 | 0 |
| .....CTACAGTCGCTGCGATTCCGGGC..... | 23 | 0 | 1 | 2.00 | 2 | 1 | 1 | 0 | 0 | 0 | 0 |
| .....GATTCCGGGCAGTTGAAATG..... | 20 | 0 | 1 | 2.00 | 2 | 1 | 0 | 1 | 0 | 0 | 0 |
| .....GATGCAAGATGAAAGAGAGCCC..... | 22 | 0 | 1 | 2.00 | 2 | 2 | 0 | 0 | 0 | 0 | 0 |
| .....CTTGCAGGGCTGTAGGCTTTGGTCC..... | 25 | 0 | 1 | 2.00 | 2 | 1 | 1 | 0 | 0 | 0 | 0 |
| .....ATTTAGTCTACAGTCGCTGC..... | 20 | 0 | 1 | 2.00 | 2 | 0 | 0 | 2 | 0 | 0 | 0 |
| .....CATAACACTTAACGCTTTGT..... | 20 | 0 | 1 | 2.00 | 2 | 1 | 1 | 0 | 0 | 0 | 0 |
| .....AATTTAGTCTACAGTCGCTGC..... | 21 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....ATTTAGTCTACAGTCGCTGCG..... | 21 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....AAATTTAGTCTACAGTCGCTGC..... | 22 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....TAGAAGAGATCGGATCGGCGTCGATC..... | 26 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....AAATGATGCAAGATGAAAGA..... | 20 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....TGCTGTCTTGCAGGGCTGTAGGC..... | 23 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 1 | 0 | 0 |
| .....AAGATGAAAGAGAGCCCGGT..... | 20 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....GCAAGATGAAAGAGAGCCCGGTC..... | 23 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....AGAGATCGGATCGGCGTCGATCGGATT..... | 27 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....GTCGCTGCGATTCCGGGCA..... | 19 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| .....AGAAGAGATCGGATCGGCGTCGATCGGAT..... | 29 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....AGAAGAGATCGGATCGGCGTCGATCG..... | 26 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....GATGCAAGATGAAAGAGAGCCCGGTC..... | 26 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....TGAAATGATGCAAGATGAAAGAGA..... | 24 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....GCTAGAAGAGATCGGATCGGCT..... | 22 | 1 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| .....AAGAGATCGGATCGGCGTCGAT..... | 22 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....TACAGTCGCTGCGATTCCGGGCA..... | 23 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....GTCGCTGCGATTCCGGGCAGTG..... | 22 | 1 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....GATGAAAGAGAGCCCGGTCCATAACACTTA..... | 30 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .TCCCAGTTACGCACAGCTAGAA..... | 22 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 1 | 0 | 0 |
| .....CGGCGTCGATCGGATTAAGTCTGC..... | 24 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....TGAAATGATGCAAGATGAAA..... | 20 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....TTAACGCTTTGTGCACCGTAC..... | 21 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....AAATGATGCAAGATGAAAGAGAGCCCGGT..... | 29 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....ATGATGCAAGATGAAAGAGAGCCCG..... | 25 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....CGGATTAAGTCTGCCTAACT..... | 20 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....AGGGCTGTAGGCTTTGGTC..... | 19 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....ATGAAAGAGAGCCCGGTCC..... | 19 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....CAGTCGCTGCGATTCCGGGC..... | 20 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....AAAATTTAGTCTACAGTCGCTGC..... | 23 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....AACACTTAACGCTTTGTGCACCGT..... | 24 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....CATAACACTTAACGCTTTGTGCACC..... | 25 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....ATAACACTTAACGCTTTGTGCACCGT..... | 26 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....AGTTACGCACAGCTAGAAGAGATCGGATC..... | 29 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....GAGATCGGATCGGCGTCGAT..... | 20 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| .....TACAGTCGCTGCGATTCCGGGCAGT..... | 25 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| .....GATGAAAGAGAGCCCGGTCC..... | 20 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....GATGAAAGAGAGCCCGGTCCATAAC..... | 25 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....TGAAATGATGCAAGATGAAAGA..... | 22 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....AACTGCTGTCTTGCAGGGCTG..... | 21 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....CAAAATTTAGTCTACAGTCGCTGC..... | 24 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....AAAGAGAGCCCGGTCCATAAC..... | 21 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....CACTTAACGCTTTGTGCACCGTAC..... | 24 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| .....GGCGTCGATCGGATTAAGT..... | 19 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....AAATGATGCAAGATGAAAG..... | 19 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| .....CTTAACGCTTTGTGCACCGTACA..... | 23 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| .....GAAATGATGCAAGATGAAAGAGA..... | 23 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....CTGTCTTGCAGGGCTGTAGGCTTTGGTCC..... | 29 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....TGAAATGATGCAAGATGAAAGAGAGCCC..... | 28 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....AGATGAAAGAGAGCCCGGTCC..... | 21 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....GATGCAAGATGAAAGAGAGCCCGGTCCAG..... | 29 | 1 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....ATCGGATTAAGTCTGCCTAACTGCTGTCT..... | 29 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| .....ATGCAAGATGAAAGAGAGCCCGGTCC..... | 26 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....GATGCAAGATGAAAGAGAGCCCGGG..... | 25 | 1 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....AGTTACGCACAGCTAGAAGA..... | 20 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 1 | 0 | 0 |
| .....AGAGCCCGGTCCATAACACT..... | 20 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| .....AGCTAGAAGAGATCGGATC..... | 19 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....CTGTCTTGCAGGGCTGTAGGC..... | 21 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....ATAACACTTAACGCTTTGTGCACCGTAC..... | 28 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....TGAAATGATGCAAGATGAAAGAGAGCC..... | 27 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....CTAACTGCTGTCTTGCAGGGCT..... | 22 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....AAATGATGCAAGATGAAAGAGAGCC..... | 25 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....AGAAGAGATCGGATCGGCGTCGATC..... | 25 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....TTTAGTCTACAGTCGCTGCGATTCCGGGC..... | 29 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....GAGATCGGATCGGCGTCGATC..... | 21 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....CAAGATGAAAGAGAGCCCGGTCC..... | 23 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....CAAGATGAAAGAGAGCCCGGTC..... | 22 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 1 | 0 | 0 |
| .....GATCGGATCGGCGTCGATCGGAT..... | 23 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| .....AGAGATCGGATCGGCGTCGAT..... | 21 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| .....AGAGATCGGATCGGCGTCGAG..... | 21 | 1 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....TGCAAGATGAAAGAGAGC..... | 18 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....AGAGATCGGATCGGCGTCGATC..... | 22 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....ATGCAAGATGAAAGAGAGCCCGGG..... | 24 | 1 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....AATGATGCAAGATGAAAGAGAGCCCGGT..... | 28 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....GTCGATCGGATTAAGTCTGC..... | 20 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....ATCGGCGTCGATCGGATTAAGTCTGC..... | 26 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....CACAGCTAGAAGAGATCGGA..... | 20 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....GCTGTCTTGCAGGGCTGTAGGCTTTGGTC..... | 29 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....ACACTTAACGCTTTGTGCACCGT..... | 23 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....CTGCTGTCTTGCAGGGCTGTAGGC..... | 24 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....TGAAATGATGCAAGATGAAAGAGAGCCCG..... | 29 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....GCTGTCTTGCAGGGCTGTAGGCTTTGGT..... | 28 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |

**Anti-sense strand reads**

| TAGGGTCAATGCGTGTCGATCTTCTCTAGCCTAGCCGCAGCTAGCCTAATTCAGACGGATTGACGACAGAACGTCCCGACATCCGAAACCAGGTTTTAAATCAGATGTCAGCGACGCTAAGGCCCGTCAACTTTACTACGTTCTACTTTCTCTCGGGCCAGGTATTGTGAATTGCGAAACACGTGGCATGTTAAG | Read size | # Mismatch | Hit Count | Total Norm | Total | M026 head |
|---|---|---|---|---|---|---|
| **********...(((.(....(((((((.(((((((((((((((((.....)))))))))))).))))))).....)))))))))....))).....********** | | | | | | |
| .....TCTCGGGCCAGGTATTGTGAATTG..... | 24 | 0 | 1 | 1.00 | 1 | 1 |
| .....GCGTGTCGATCTTCTCTAGCCT..... | 22 | 0 | 1 | 1.00 | 1 | 1 |

Show Alignment With Reads

**Re-alignment of all predicted orthologs**

| Species | Coordinate | ID | Alignment |
|---|---|---|---|
| droYak3 | 2L:3063696-3063890 + | dya_1801 | ATCCC----------AGTT--ACG----CACAGCTAGAA--GAGA----------TCGGATCGGCGTCGATCGGAT----------TAAGTCT-GCC--TAACTGCTGTCTTGCAGGG-CT--GTAGGC---TTTGGTCCAAA---ATTT-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGAAA-TGATGCAA-GATGAAAGAGAGCCC---GGTCCATAACACTTAACGCTT--TGTGCACC-GT---------ACAATTC---------- |
| droEre2 | scaffold_4929:3115440-3115632 + | der_1527 | ATCCC----------AGTT--ACG----CACAGCTAGAA--GAGA----------TCGGATTGGCGTCAATCGGAT----------TGATCT-GCC--TAACTGCTGTCTTGCAGGG-CT--GTAGGC---TTCGGTCCAAA---ATTT-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGAAA-TGATGCAA-GATGACAG---GCCC---AGTCCATCACACTTAACGCTT--TGTGCACC-GT---------ACATTTT----------C |
| droSec2 | scaffold_5:1224940-1225143 + | dse_1854 | ATCCC----------AGTT--ACG----CACAGCTAGAA--GAGATAAGTCAA----CAG----------ATTGGATTTGCGTCGATCGGCT----------TGATCT-GCC--TAACTGCTGTCTTGCAGGG-CT--GTAGGC---TTCGGTCCAAA---ATTT-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGAAA-TGATGCAA-GATGACAG---GCCC---AGTCCATAACACTTAACGCTT--TGTGCACC-GT---------ACAATTC---------- |
| droSim2 | 2L:2946882-2947085 + | dsi_32463 | ATCCC----------AGTT--ACG----CACAGCTAGAA--GAGATAAGTCAA----CAG----------ATTGGATTTGCGTCGATCGGCT----------TGATCT-GCC--TAACTGCTGTCTTGCAGGG-CT--GTAGGC---TTCGGTCCAAA---ATTT-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGAAA-TGATGCAA-GATGACAG---GCCC---AGTCCATAACACTTAACGCTT--TGTGCACC-GT---------ACAATTC---------- |
| dm3 | chr2L:3067697-3067900 + | dme_436 | ATCCC----------AGTT--ACG----CACAGCTAGAA--GAGATAAGTTAA----CAG----------ATTGGATTTGCGTCGATCGGAT----------TGATCT-GCC--TAACTGCTGTCTTGCAGGG-CT--GTAGGC---TTCGGTCCAAA---ATTA-AGTCTACAGTCGTCTGCGATTCCG-GGCAGTTGAAA-TGATGCAA-GATGACAG---GCTC---AGTCCATAACACTTAACGCTT--TGTGCACC-GT---------ACAATTT----------- |
| droEug1 | scf7180000409554:3024270-3024474 - | | ATCCC----------AGTT--ACG----CACAGCTAAAA--GAGATAACTCAA----CAG----------GTCGGATTGGCAGCGGATCGGAT----------TGATCT-GAT--TAACTGCTGTCTTGCAGCG-CT--GTAGAG---TGTGGTCCAAA---ATTT-AGTCTATAGTCGCTGCGATTCTG-GGCAGTTGTAA-TGATAAAAAGATGAGAG---GCCC---AAACCATCACACTTAACGCTT--TGTGCACC-AT---------ACAGATT---------- |
| droBia1 | scf7180000302188:2121990-2122199 + | | AACCC----------AGTT--ACG----CACAGCTAGAG--GAGATAAGTAAA----CAG----------ATCGG--ATTGGACTGGAGTGGATCGGAT----------TGCATCG-GCC--TAACTGCTGTCTTGCAGGG-CG--GTAGAG---TTTGGTCCAAA---ATTT-AGTCTACGGTCGCTGCGATTCCG-GGCAGTTGAAA-TGATGCAA-GAGGAGAG---ATC---AGTCCATACACTTAACGCTT--TGTGCACC-GT---------ACAGTTC----------C |
| droTak1 | scf7180000415438:753081-753236 - | | ATCCC----------AGTT--CCG----CACAG------ ----------GATGGATCGGAT----------GGCATCT-GCC--TAACTGCTGTCTTGCAGGG-CG--GTGGAG---TTTGGTCCAAA---ATTT-AGTCTATGGTCGCTGCGATTCCG-GGCAGTTGAAA-TGATGCGA-AATGAGAG---ACCC---A--------ACCTAACGCTT--TGTGCACC-- ---------- ------ |
| droEle1 | scf7180000491046:1758532-1758736 + | | ATCCC----------AGTT--ACG----CACAGTAGAA--GAGATAAGTCAA----CGG----------ATCGGATTGGCAGTGGATCGGAT----------TGCGTCT-GCC--TAACTGCCGTCTTGCAGCA-CT--GTAGTG---TTTGGTCCAAA---ATTT-AGTCTACACCGCTGCGATTCTG-GGCAGTTGAAA-TGATGCAAAGATGAGAG---GCCC---AGACCATCACACTTAACGCTT--TGTGCACC-GT---------ACAGTTC---------- |
| droRho1 | scf7180000780028:158211-158414 + | | ATCCC----------AGTT--ACG----CACAGCTAGAG--GAGATAAGTCAA----CGG----------ATCGGATTGGCAATGGATTGGAT----------TGGATCT-GCC--TAACTGCCGTCTTGCAGCG-CT--GTATTG---TTTGGTCCAAA---ATTT-AGTCTATAGTCGCTACGATTCTG-GGCAGTTGAAA-TGATGCAA-GAGGAGAG---GCCC---AATCCATCACACTTAACGCTT--TGTGCACC-GT---------ACAGTTC---------- |
| droFic1 | scf7180000453924:1051713-1051928 + | | ACCCC----------AGTT--ACG----CACAGCTAGAA--GAGATAAGG----------ATCGGATTGGCGTGGATCGGAT---------CGCCTGGGATCT-GCC--TAACTGCCGTCTTGCAGCG-CG--GTAGAG---TTTGGTCCAAA---ATTT-AGCCTACGCCGCTACGATTCCG-GGCAGTTGAAA-TGATGCAC-GATGCGAGTG-CGCCC---AACCCTCACACTTAACGCTT--TGTGCACC-GT---------ACAGTTCAGTAGTTCAGTAC |
| droKik1 | scf7180000302246:274508-274654 + | | ATCCC----------AGTT--ACG----CCCAGC-----  ----------GATCGGATCGGAT----------GCGTCT-GCC--TAACTGCTGTCTTGCAGCGCGT--GTGGAG---TGTGGTCCAAA---TTTA-AGTCTACAGTCGCTGCGATTCCG-GGCAGTTGAGTT-GGCC--GA-TGC----------  --TGGATCGCACTTAACGCTTCGTGTGCACC-GCAGA----GAAGAGTTC---------- |
| droAna3 | scaffold_12916:9588076-9588247 - | dan_4042 | ATCCC----------AGTTAAACG----CACAGCTTGAA--GGG----------GAACCGTT----------T--ATCT-CCCAATTAACTGCTGTCTTGCAGAGTGT--GTGGAG---GTTGGTCCAAA---TTT-TGTCTACACCACTGCGATTCCG-GGCAGTTGAAACTGATT--AA-TACGGAC--TCCCCAAAAACACATCACATCT-GCGCTT--TGTGCACC-GC---------AG----- |
| droBip1 | scf7180000396580:1442837-1443009 + | | ATCCC----------AGTTAAACG----CACAGCTTGAA--GGG----------GATCACCA----------T--TTCT-CCCAATTAACTGCCGTCTTGCAGCGTGT--GTGGAG---GTTGGTCCAAA---TTT-TGTCTACACCGCTGCGATTCCGCGGCAGTTGCAACTGAAACGA-TACGGAT--TCCTCA--AATACATCACATCT-GCGCTT--TGTGCACC-GC---------AG----- |
| dp5 | Unknown_singleton_3046:18-207 + | dps_31 | ---CC----------AGTT--ACG----CACAGCAACAA--AAGATAAAACTAATCTCG----------GATCGGATC-------T----TCCTTAAACGTT--TAACTGCCGTCTTGCAGCGCGT--GTGGAGG--ATAGGTCCAAA---ATTTCAGTCTACAACGCTGCGATTCCG-GGCAGTTGAGTT-CGAT----  ---CGGAT---CCACC--TTTAAATCACACTTAAGCTA--TGTGCAGA-GA-------GTACAGT-- |
| droPer2 | scaffold_1:8612775-8612986 - | dpe_229 | ATATCAGTAATCCAAGAATTAACGATT--ACG----CACAGCAACAA--AAGATAAAACTAATCTCG----------GATCGGATC-------T----TCCTTAAACGTT--TAACTGCCGTCTTGCAGCGCGT--GTGGAGG--ATAGGTCCAAA---ATTTCAGTCTACAACGCTGCGATTCCG-GGCAGTTGAGTT-CGAT----  ---CGGAT---CCACC--TTTAAATCACACTTAAGCTA--TGTGCAGA-GA-------GTACAGT-- |
| droWil2 | scf2_1100000004945:407265-407435 + | dwi_5419 | ATCAC----------AGTA--ACG----CACAGTTAAATACATGATATATCCT---CCA----------------------AAATGTGAATTAGATATAAGTTAT-ATCCAGTGATCG-ATTT--TAATTGCCGTCTTGCAGGGTGTTTGTAAAGAATCCAGGTCCAAATTT-AAAT-TCGTTATAATCATCTGCGATTCTG-GGCAATTGAATT-GA-CA--- ---------- ---------- ----CAGTT-G---------- ------ |
| droVir3 | scaffold_12963:14467459-14467611 - | dvi_24646 | ATTTTAACATGTCCAAC-------AGTT--TAG----CAAG------- ----------CTATGTAATG--TAACTGCCGTCTTGGAGCGCGT--GTGGATA-CAAAGGTCCAAA---ATTT-ATCCACACGATGTGCGATTCTG-GGCAGTTGA-- -------- ---------- ------TTTTACTAAATTGTT--TATGCAGATGTAAACATGGG-AG----- |
| droMoj3 | scaffold_6500:15423874-15424047 - | dmo_3155 | ATTTC----------AGTT--TCG----AA--TCGCAA--CACATT----------CCCACAACCAACGATTTTGGACGGTAGACAACACAGAGCACGC----------GGGATCTGTCTT--TAACTGCCGTCTTGCAGCTCGT--GTGGATGCCCAGGTCCAATT---AAGT-ATCCACACGTGCTGCGATTCCG-GGCAGTTGACGCGGA-GCAA-CACGA---------- ---------- -------- -- ------- |
| droGri2 | scaffold_15252:2029205-2029382 + | dgr_469 | ATTTG----------AATC--ACTAATTTACAATTCGAA--TAGAGGAATCAT---CATAATTTGTATATCAATCTATATAATCT----------TACA-ATGAT--TAACTGCCGTCTTGCCGGGCGT--GTGGGGA-CCCAGGTCCAAACAAAAGT-TGCCACATGTTGCGCATTCTG-AGCAGTTAAA- -------- ----------GTC--AGTT--------TA--ACTT--CATTCAG- -- ---------- ------- |

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| | PASS/FAIL |
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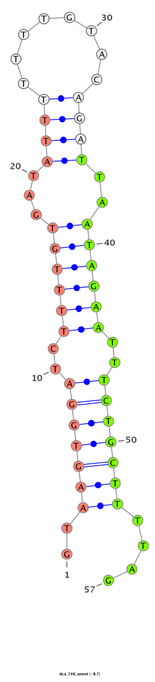
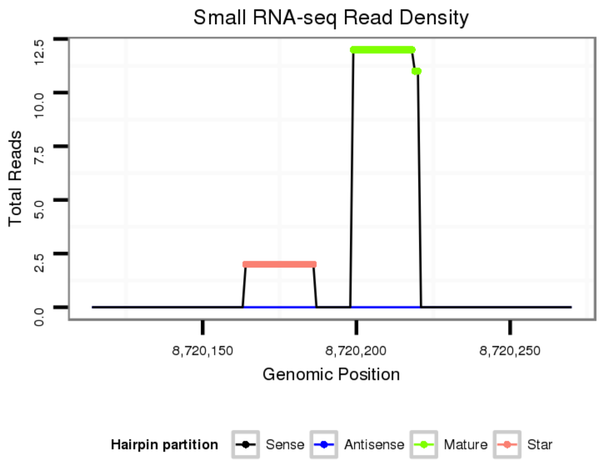
| crit.loop | 0 |
| crit.mor | 0 |
| crit.half | 0 |
| crit.total | 0 |
| crit.pairing | 1 |
| crit.top3 | 1 |
| crit.ptop3 | 1 |
| crit.uri | 0 |
| crit.back | 0 |
| rescue.total | 1 |
| rescue.dominant | 1 |
| rescue.known | 0 |
| rescue.confident | 2 |
| rescue.candidate | 10 |

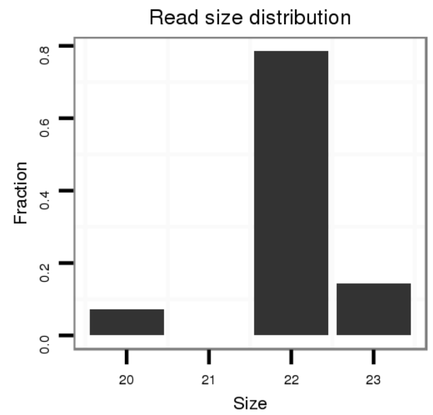
| ID: | Coordinate: | Confidence: | Class: | Genomic Locale: | |
|---|---|---|---|---|---|
| **dya_740** | **3L:8720164-8720220 +** | **candidate** | **Mirtron** | **intron** | [View on UCSC Genome Browser {Cornell Mirror}] |

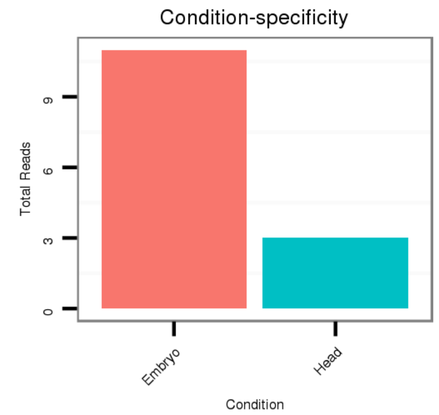
Legend: mature star **mismatch in alignment** mismatch in read

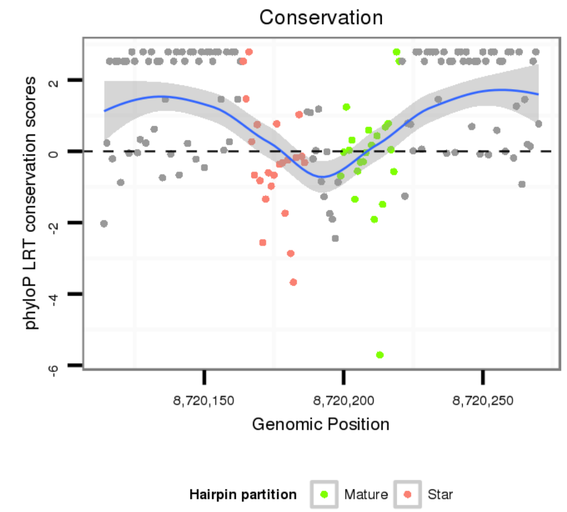
**Predicted structure**






Show Alternate Folds

**Flybase annnotation**

intron [Dyak\GE21661-in]; CDS [Dyak\GE21661-cds]; CDS [Dyak\GE21661-cds]

No Repeatable elements found

**Sense Strand Reads**

hide 3p reads | show mid mismatch reads

```
TAGAGGGGCCACCTTGGAGGCTTTCCTTACCAAAGTGATGTTTCTAAATGGTAAGTGGATCTTTTGTGATATTTTTTGTACAGATTAATAGAATTTCTGCTTTTAGCTAATATTCAAATTGTTGGCATGAGTGCCACAATAGGAAACCTCAGCGAA
**************************************************..(((((((..((((((...((((........))))..))))))..)))))))....**************************************************
```

| Read size | # Mismatch | Hit Count | Total Norm | Total | M056 embryo | M026 head | V046 embryo | V058 head |
|---|---|---|---|---|---|---|---|---|
| 22 | 0 | 1 | 11.00 | 11 | 7 | 2 | 2 | 0 |
| 23 | 0 | 1 | 2.00 | 2 | 2 | 0 | 0 | 0 |
| 20 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 |

**Anti-sense strand reads**

```
ATCTCCCCGGTGGAACCTCCGAAAGGAATGGTTTCACTACAAAGATTTACCATTCACCTAGAAAACACTATAAAAAAACATGTCTAATTATCTTAAAGACGAAAATCGATTATAAGTTTAACAACCGTACTCACGGTGTTATCCTTTGGAGTCGCTT
**************************************************..(((((((..((((((...((((........))))..))))))..)))))))....**************************************************
```

| Read size | # Mismatch | Hit Count | Total Norm | Total | V058 head |
|---|---|---|---|---|---|

Show Alignment With Reads

**Re-alignment of all predicted orthologs**

| Species | Coordinate | ID | Alignment |
|---|---|---|---|
| droYak3 | 3L:8720114-8720270 + | dya_740 | TAGAGGGGCCACCTTGGAGGCTTTCCTTACCAAAGTGATGTTTCTAAATGGTAAGTGGAT------CTTTTGTG---ATA----------TTTTTTTGTACAGA---------T-TAATAGAATTT---------CT-GCTTTTAGCTAATATTCAAATTGTTGGCATGAGTGCCACAATAGGAAACCTCAGCGAA |
| droEre2 | scaffold_4784:3232507-3232666 - | | TAGAGGTGCCACCTTGGAGGCTTTCCTTACCAAAGTGATGTTTCTAAATGGTAAGTGGAT------ACCTTGTG----T----------ACTTTTTGTATTTA-----TGGCA-TAAAGCAATTT--------TTGATTTTTAGCCAATATTCAAATTGTTGGCATGAGTGCCACAATAGGAAACCTTAGCGAA |
| droSec2 | scaffold_0:419542-419698 + | | GAGAGGGGCCACCTTGGAAGCTTTCCTTACCAAAGTGATGTTTCTAAATGGTAAGTGCAT------ATTTTATG---GT----------ACTTTTTGTACAGA---------T-TAATGGAATTT--------TTGTTTTCTAGCCAATATTCAAATTGTTGGCATGAGTGCCACAATAGGAAACCTCAGCGAA |
| droSim2 | 3L:7941948-7942104 + | | GAGAGGGGCCACCTTGGAAGCTTTCCTTACCAAAGTGATGTTTCTAAATGGTAAGTAGAT------ATTTAGTG---GT----------ACTTTTTGTACAGA---------T-TAATGGAATTT--------TTGCTTTCTAGCCAATATTCAAATTGTTGGCATGAGTGCCACAATAGGAAACCTCAGCGAA |
| dm3 | chr3L:8132195-8132351 + | dme_474 | TAGAGGGGCCACCTTGGAGGCTTTCCTTACCAAAGTGATGTTTCTAAATGGTAAGTGGAT------ATTTTGTG---GT----------ACTTTTTGTACAGA---------T-TAATGGAATTT--------TTGTTTTCTAGCCAATATTCAAATTGTTGGCATGAGTGCCACAATAGGAAATCTCAGCGAA |
| droEug1 | scf7180000409524:509659-509812 - | | TAGAGGGGTACCTTGGAGGCATTTCTCACCAAGGTGATGTTTTTGAATGGTAAATAATTTA---TTTTCTG---CTA----------ACTTTTTGAGTAA---------C-TA-----TCTT---------CT-GGTTTTAGCAAGCATTCAAATTGTGGGCATGAGTGCGACGATAGGAAATCTCAGCGAA |
| droBia1 | scf7180000302428:1119246-1119403 - | | CAGAGGAGCCACATTGGAGGCATTCCTCACAAAGGTGATGTTTTTGAATGGTAAATAATCT-G---TTCTCCA---GAA----------ACTTTATTGAATGA---------T-TTTTAAGATTT--------AT-GTTTTCAGCCAATATACAAATTGTGGGCATGAGTGCCACGATAGGAAATCTTAGCGAA |
| droTak1 | scf7180000415862:204640-204796 + | | CAGAGGAGCCACGGTAGAGGCATTCCTAACCAAGGTGATGTTTTTGAATGGTAAATATATG-G---TTTTCTT---CTC----------CCTTTTTGAATGAA---------C-TA-TAGAATAG--------AT-CATTTCAGCCAACATTCAAATTGTGGGAATGAGTGCCACGATAGGAAATCTCAGCGAA |
| droEle1 | scf7180000491249:6106567-6106724 - | | CAGAGGAGCCACCTTGGAGGCTTTCCTCACAAAGGTGATGTTTTTGAATGGTAAGTGCTCG-A---TTTTCTC---TTA----------AATTTCTTAGTTAA---------T-CAATAGATTT--------TC-ATACCCAGCCAGCATTCAAATTGTGGGCATGAGTGCCACGATAGGAAACCTTAGTGAA |
| droRho1 | scf7180000777746:906-1062 + | | TAGAGGAGCCACCTTGGAGGCTTTCCTCACAAAGGTGATGTTTTTGAATGGTAAGTGAGCC-A---TTTTCTG---GTA----------ACTTGCTAAAACGG---------T-TAATA-AGTTT--------CC-TTTTTCAGCCGGGCATTCAAATTGTGGGCATGAGCGCAACGATAGGAAATCTCAGTGAA |
| droFic1 | scf7180000454065:454250-454406 + | | CAGAGGGCCACCTTGGAGGCATTTCTTACAAAAGTTATGTTTTTAAATGGTAAGTGGGTT-A---GTTTTTT---ACA----------ACGTTTTTGATGCA---------T-TAA-GCACCGG---------CT-GCTTTCAGCCAACATACAAATTGTGGGCATGAGTGCCACAATAGGAAACCTAACGAA |
| droKik1 | scf7180000302274:487830-487990 + | | ACGGGGAGCCACCTTGGAGGCTTTCTAACCAAGGTGATGTTTCTGAATGGCAAGTAAACA-ACACCTTGCACG---ATA---A----------CCTTCTTGTTATAG--------CT-T--TAG-ATTT--------TT-CCTTGCAGCAAATATTCAAATTGTGGAATGAGTGCCACGATAGGCAATCTCAGTGAA |
| droAna3 | scaffold_13337:13515179-13515336 - | | AAGGGGAGGAACCTTGGAGGCTTTCTCACCAAAGTAATGTTTTTGAATGGTAATTTCTCA-A---AATATTT---C-----------------------------------ACTTTTTC----T-ACTTTTATTATTTGGTGTATT-TTTTTTAGCCAACATACAAATTGTGGGTATGAGTGCCACGATTGGAAATCTAAGCGAA |
| droBip1 | scf7180000396589:538963-539119 + | | TAGGGGAGGAACCTTGGAAGCTTTCTCACCAAGGTGATGTTTTTGAATGGTAAGATCTCA-A---ATGTATC---CCA----------CGTTTC----T-AATGTTATTATTTGGTCTATT-TGTTTCAGCCAACATACAAATTGTGGGCATGAGTGCCACAATTGGAAATCTAAGCGAA |
| dp5 | XR_group3a:1172485-1172646 + | | ACGGGGTGCCACCTTGAGGGCTTTCTCACCAAAGTAATGTTTTTGAATGGTAGGTGGCAT-G--G-GTTTATGAGCCGT----------AATTTATGTACAAGCTTCC----T-ACTG-GACTT---------T--TCCTTAGCAAATATTCAAATTGTGGGCATGAGTGCAACGATAGGAAACCTAAGCGAC |
| droPer2 | scaffold_23:1192946-1193107 + | | ACGGGGTGCCACCCTTGAGGGCTTTCTCACCAAAGTAATGTTTTTGAATGGTAGGTGGCAT-G--G-GTTTATGAGCCGT----------AATTTATGTACAAGCTTCC----T-ACTG-GACTT---------T--TCCTTAGCAAATATTCAAATTGTGGGCATGAGTGCAACGATAGGAAACCTAAGCGAG |
| droWil2 | scf2_1100000004540:105639-105799 + | | TAGGGGTGCCACCTTGGAGGCTTTCTCACCAAAGTAATGTTTCTGAATGGTATGTGCTGG-A---GTTTTCT---TCA--TTGAAATA----------TGTTTTGGA-----------TTGAA-ATTTCTT---------TT-ATTTTTAGCTGGCATCCAAATAGTGGGCATGAGTGCAACGATAGGTAATCTATCTGAG |
| droVir3 | scaffold_13049:7780920-7781078 + | | CCGGGGCGGTACATTGGAGGCTTTTCTGACCAAGGTCATGTTTTTGAATGGTATCTATAT------ACTGCCAT---A----C----------ACTCC-TTCACAGG-T------GCTAACTGTTC----CATC-TC-CATTTAAGCCAACATTCAAATTGTGGGCATGAGCGCCACCATTGGAAATCTGAATGAA |
| droMoj3 | scaffold_6680:11429465-11429632 + | | ACGGGGTGGGACACTAGAGGCTTTCCTAACCAAGGTCATGTTCTTGAAAGGTATTCACAT------GTTTACCC-ACA----TAGATAAA----------TAATTCAAG-T------ACGAATTGTACTACTTTGTT-GC-GATTTTAGCGAACATTCAAATTGTAGGCATGAGCGCCACGATTGGCAATCTGAATGAA |
| droGri2 | scaffold_15110:6833804-6833970 + | | ACGTGGGGCCACTTTGGAGGGCTTCCTCACCAAGGTTATGTTTCTAAATGGTAAATGCAT------ATTGCAAA----AATGTATATGAATATTTTATATATGTATAATTATGTTACTTGTTG------------T-----------------TACAGCCAACATTCAAATTGTGGGCATGAGCGCCACGATAGGCAATTTGAATGAA |

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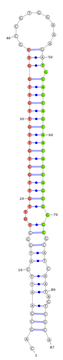
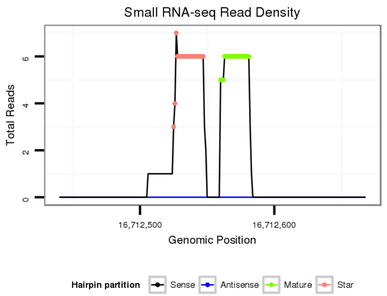
| crit.pairing | 1 |
| crit.top3 | 1 |
| crit.tptop3 | 1 |
| crit.uri | 0 |
| crit.back | 1 |
| rescue.total | 1 |
| rescue.dominant | 1 |
| rescue.known | 0 |
| rescue.confident | 0 |
| rescue.candidate | 2 |

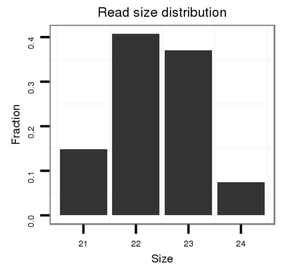
| ID: | Coordinate: | Confidence: | Class: | Genomic Locale: | |
|---|---|---|---|---|---|
| **dya_1790** | **2L:16712490-16712618 +** | **candidate-rescued** | **Canonical miRNA** | **5pUTR** | [View on UCSC Genome Browser [Cornell Mirror]] |

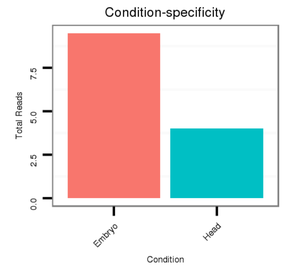
Legend: mature star mismatch in alignment mismatch in read

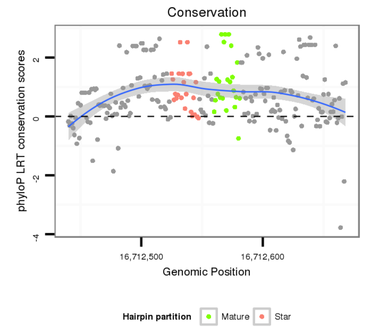
**Predicted structure**






Show Alternate Folds

**Flybase annnotation**

utr5 [utr5_plus_3417]

**Repeatable elements**

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

**Sense Strand Reads**

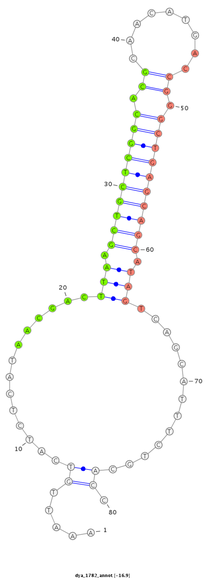
hide 3p reads  show mid mismatch reads

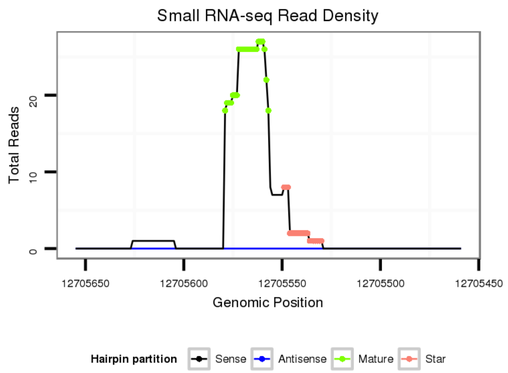
```
                                                
```

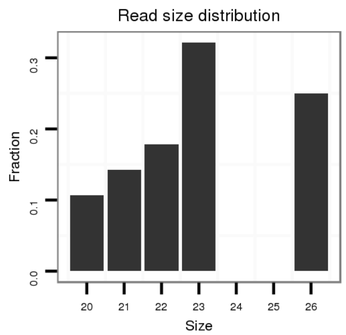
| ID: | Coordinate: | Confidence: | Class: | Genomic Locale: | |
|---|---|---|---|---|---|
| **dya_1782** | **3R:12705509-12705605 -** | **candidate-rescued** | **Canonical miRNA** | **intergenic** | [View on UCSC Genome Browser {Cornell Mirror}] |

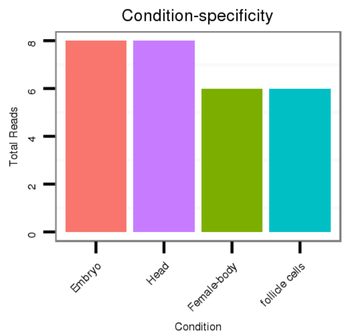
Legend: mature star mismatch in alignment mismatch in read

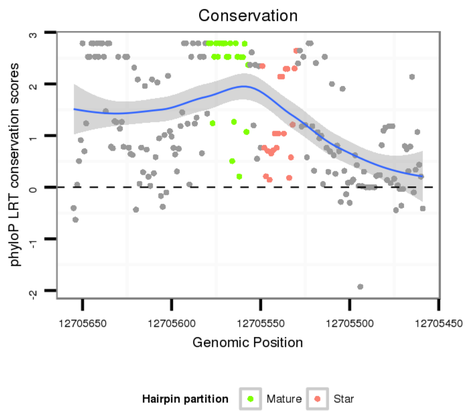
**Predicted structure**






Show Alternate Folds

**Flybase annnotation**

intergenic

No Repeatable elements found

**Sense Strand Reads**

hide 3p reads  show mid mismatch reads

```
TCCCAAACGGAAGTGTTGATATGGCCGCAGCTCAGTCGCAGTCGCAGCTCAGTCGGTATAGAAATTGTCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGGCTGAGCAGCATAGTCAGCATTTCTGCACCTCCCAGAATCCAGCCCATCCTCAGTCGGTCTTCCACCACTGTTGCCACCCACTTTT
*****************************************************.....((.............(((.(((((((((.((.........).)))))))))).)))).............)).*****************************************************
```

| Read size | # Mismatch | Hit Count | Total Norm | Total | M026 head | M056 embryo | M043 female body | GSM1528802 follicle cells | V058 head | V120 male body | V046 embryo | V052 head |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 23 | 0 | 1 | 9.00 | 9 | 3 | 5 | 0 | 0 | 0 | 0 | 1 | 0 |
| 26 | 0 | 1 | 6.00 | 6 | 0 | 0 | 0 | 6 | 0 | 0 | 0 | 0 |
| 22 | 0 | 1 | 4.00 | 4 | 3 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | 1 | 4.00 | 4 | 0 | 0 | 3 | 0 | 1 | 0 | 0 | 0 |
| 23 | 1 | 1 | 3.00 | 3 | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 26 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 24 | 1 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 21 | 1 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

**Anti-sense strand reads**

```
AGGGTTTGCCTTCACAACTATACCGGCGTCGAGTCAGCGTCAGCGTCGAGTCAGCCATATCTTTAACAGTAGAGTATTGCTGAATTCGACGAGCCGTGCGTTGTACTGGCCCGACTCGTCGTATCAGTCGTAAAGACGTGGAGGGTCTTAGGTCGGGTAGGAGTCAGCCAGAAGGTGGTGACAACGGTGGGTGAAAA
*****************************************************.....((.............(((.((((((((((.((.........)).)))))))))).)))).............)).*****************************************************
```

| Read size | # Mismatch | Hit Count | Total Norm | Total | V058 head |
|---|---|---|---|---|---|

Show Alignment With Reads

**Re-alignment of all predicted orthologs**

| Species | Coordinate | ID | Alignment |
|---|---|---|---|
| droYak3 | 3R:12705459-12705655 - | dya_1782 | T--CCC-AAACGGAAGTGTTGATATGGC--CGCAGCT-CAGTCGCAGTCGCA----------G----------CTC----------AGTCGGTATAGAAATTG-----TCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG----CTGAGCAGCATAGTCAGCATTTCTGC---ACCT--CCCAGAATCCA-------G---------CCCATCCTC----------AGTCGGTCTTCCACCACTGTTG-CCACCCACTTT |
| droEre2 | scaffold_4770:13232498-13232696 + | der_1512 | T--CCC-AAACGGAAGTGTTGATATGGC--CGCAGCT-CAGTCGCAGTCGCA-----GTCGCAG----------CTC----------AGTCGGTATAGAAATTG-----TCATCTCATAACGACTTAAGCTGCTCGCACGCAACATGACCGGG----CTGAGCAGCATAGTCAGCATTTCTGC---ACCT--CCCAGAATCCA-------G---------CCCATCCGCGA-T--------------CTTCCACCACTATTG-CCACCCACTTTT |
| droSec2 | scaffold_0:13567275-13567468 + | dse_131 | T--TCCC-AAACGGAAGTGTTGATATGGC--CGCAGCT-CAGTCGCAGTCGCA----------G----------CTC----------AGTCGGTATAGAAATTG-----TCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG----CTGAGCAGCTTAGTCATCATTTCTGC---ACCT--CCCAGAATCCA-------G---------CCCATCCTCG--TTAGCGAACA-------------CACTATTG-CCACCCACTTTT |
| droSim2 | 3r:12738956-12739149 + | dsi_32436 | A--CCCC-AAACGGAAGTGTTGATATGGC--CGCAGCT-CAGTCGCAGTCGCA----------G----------CTC----------AGTCGGTATAGAAATTG-----TCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG----CTGAGCAGCATAGTCAGCATTTCTGC---ACCT--CCCAGAATCCA-------G---------CCCATCCTCG--TTAGCGAACA-------------CACTATTG-CCACCCACTTTT |
| dm3 | chr3R:8419602-8419793 - | dme_234 | T--CCC-AAACGGAAGTGTTGATATGGC--CGCAGCT-CAGTCACAGTCCA----------G----------CTC----------AGTCGGTATAGAAATTG-----TCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG----CTGAGCAGCATAGTCAGCATTTCTGC---ACCT--CCCAGAATCCA-------G---------CCCATCCTCC--TCAGCAA--------------ACACTATTG-CCACCCACTTTT |
| droEug1 | scf7180000409615:635445-635629 - | | TATTCC-AAACGGAAGTGTTGATATGGC--CGCAGCT-CAGTCGCAGTCGCA----------G----------CTC----------AGTCGGTATAGAAATTG-----TCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACTGGG----CTGAGCAGCATAGTCAGCATTTCTGC---ACCT--CCCAGAATCCG-------T---------TTCACGCTGCTTTTT-------------------ATA-CAACCCACTTGT |
| droBia1 | scf7180000302402:97564-97761 - | | C--TCCC-GAGCGGAAGTGTTGATATGGC--CGCAGCT-CAGTCGCAGTCGCG-----GTCGCAG----------CTCAG------TCGC--------A--A------TTCAGCGGTATAGAAATTG-----TCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG----CTGAGCAGCATAGTCAGCATTTCTGC---ACCT--CCCAGCATCCA-------G---------CACACGCGC--TGGGC-----------------------CCACCCACTTTC |
| droTak1 | scf7180000415366:130675-130864 + | | C--TCCC-AAACGGAAGTGTTGATATGGC--CGCAGCT-CAGTCGCAGTCGCA----------G----------CTCAG------TCGC--------A--A------TTCAGTCGGTATAGAAATTG-----TCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG----CTGAGCAGCATAGTCAGCATTTCTGC---ACCT--CCCAGAATCCA-------G---------CTCACGCGC-C----------------------TTT-CCACCCACTTTT |
| droEle1 | scf7180000490994:97235-97427 - | | T--GCCC-AAACGGAAGTGTTGATATGGC--CGCAGCT-CTGTCGCAG-GTCA-----GTCGCAG----------CTCAG------CCGC--------A--A------GTGAGTCGGTATAGAAATTG-----TCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG----CTGAGCAGCATAGTCAGCATTTCAGC---ACCT--CCCAGAATCGGGGCATATAG---------CCCACCG--------------------------------CCCCGTTTT |
| droRho1 | scf7180000777772:6583-6773 - | | T--TTC-AAAGGGAAGTGTTGATATGGC--CGCAGCT-CAGCCGCAGTCGCA----------G----------CTCAG------TCGC--------A--A------GTGAGTCGGTATAGAAATGG-----TCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG----CTGAGCAGCATAGTCAGCATTTCTGC---ACCT--CCCAGAATCCA-------GAAACCAGCACCCA-----------------------G-CCACCCGTTTT |
| droFic1 | scf7180000453812:694063-694255 + | | T--TCCC-AAACGGAAGTGTTGATCTACC--CGCAGCT-CAGTCGCAGTCGCA----------G----------CTCAG------TCGC--------A--G------ATCAGTCGGTATAGAAATGG-----TCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGAG----CTGAGCAGCATAGTCAGCATTTCTGC---ACCT--CCCAGAATCCA-------G---------CCAGGCACGCACTT-AC----------------------A-CACCCACTTCA |
| droKik1 | scf7180000302256:649519-649716 + | | C--TCT-AAACGGAAGTGTTGGTATTGC--CGCAGCT-CAGCCGCTGTCGCAGCT-CAGT----------------------------------CACTGAGAG----GCCGAGGCGCTGAGTCC-GCTCTGCGGTACAGAAATTG-----TCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGACCGGG----CTGAGCAGCATAGTCAGCATTTCTGC---AGTT--CCCAGAAGGCA-------G---------------------------------CCACCCACTTTT |
| droAna3 | scaffold_12911:3351170-3351291 - | | -------AACGGAAGTGTTGATATGGC--CGCAGGC-TGG----------------------------CTG----------GGGCGGTGTAGGAATTG-----TCATCTCACAACGACTTAAGCTGCTCGGCACGCAACATGAC-----------TGAGCAGCGTAGTCAGCATTTCTGC---ACCT--CC---------------------------------------------------------------------------- |
| droBip1 | scf7180000396640:216821-216945 - | | -------AACGGAAGTGTTGATATGGC--CGCAGGC-TGG----------------------------CTC----------AGCGGGTGTAGGAATTG-----TCATCTCATAACGACTTAAGCTGCTCGGCACGCAACATGAC-----------TGAGCAGCGTAGTCAGCATTTCTGC---ACCT--CCCAG------------------------------------------------------------------------ |
| dp5 | 2:2527942-2528073 - | | -------AACGGAAGTGTTGATACTGCCCGCGGCT-CAGTCACAGTCGCA-----GTCGCAG----------CTC----------AGCCTTTCTCTGT-GGCATAGAAATGG-----TCATCCCATAACGACTTAAGCTCCTCGGCA-----------------------CAGTCAGCATTTCTGCGAGTAGAT--------------------------CC |
| droPer2 | scaffold_7:2696941-2697072 - | | -------AACGGAAGTGTTGATACTGCCCGCGGCT-CAGCCACAGTCACA-----GTAGCAG----------CTC----------AGCCTTTCTCTGT-GGCACAGAAATGG-----TCATCCCATAACGACTTAAGCTCTCA-----------------------GCACAGTCAGCATTTCTGCGAGTAGAT--------------------------CC |
| droWil2 | scf2_1100000004943:2230151-2230327 - | | -------AACGGAAGTGTTGATATTGC--CCTTGCT-C------------------------CTC----------AGCGGGTCATCCTGTCATCCATAACGACTTAAGCTGTCCAGCACGCGCTGACTAACCTCAGCGTGAGCAGCATAGTCAGCAATTCTGCAGGAGCATCTGATATAAGACA-------T---------CACACATCC----------------------CCACCACCTCACGCACAACCCCCCTT |
| droVir3 | scaffold_12855:538332-538473 + | | C--GACAAAGCGGAAGTGTTGATATTGT--CGCAGCT-CAGCCCGGCAGGC----------A----------CTTAGG----CTGC--------C--A------CTGCCGCGCCTGCTGAAACTG-----TTGTCCCATAAAGACTTAAGCTGCTCGCACGCACGCG--------------TCAGCGATTGCGG-----------------------TTG-C--TCCCGTTTA |
| droMoj3 | scaffold_6540:12428193-12428380 - | | -------AACGGAAGTGTTGATATTGC--CGCAGCTCAGCG-TGGCGGCG----------A----------CTGCGACTGCGACTGAGGCA----------GAGCGCCCGTTCAAACTG-----TTGTCCCATAACGACTTAAGCTGTCCAGCACGCAGCGTCAGCGAT-----TCCCGCTGCTCTGC----CTTTTGTGC---GCCT--GG---GGGCCA-------G---------ACTTCAAGTCACAGCAC----------------------A-CGCACACTCTG |
| droGri2 | scaffold_14906:1656718-1656910 + | | -------AACGGAAGTGTTGATATTGC--CGCAGCT-TAGTGC----TGGCAGCGACAGTAGCGGAGGTGGAGATGGAGACGGAGGTGGAGGCGGAGAGGGTGACTGAGACTGAGGCA----------GCCAGAGTGTGAAATTGA----GTTGTCCCATAACGACTTAAGCTGCTCAGCACGCAGCG--------------TCAGCGATTGC--------------------------CACCGCGCTTCT-CCGCCCTATTTT |

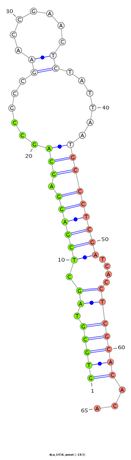
Generated: 09/08/2015 at 07:44 PM

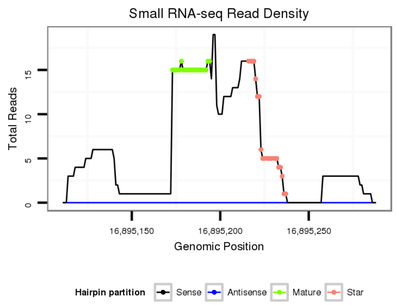
| | PASS/FAIL |
|---|---|
| crit.star | 0 |
| crit.loop | 0 |
| crit.mor | 0 |
| crit.half | 0 |
| crit.total | 0 |
| crit.pairing | 1 |
| crit.top3 | 1 |
| crit.tptop3 | 1 |
| crit.uri | 0 |
| crit.back | 1 |
| rescue.total | 1 |
| rescue.dominant | 1 |
| rescue.known | 0 |
| rescue.confident | 1 |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

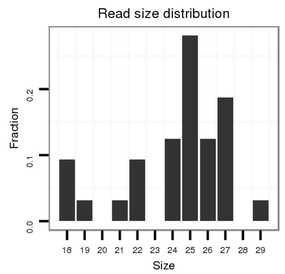
| ID: | Coordinate: | Confidence: | Class: | Genomic Locale: | |
|---|---|---|---|---|---|
| **dya_1456** | **X:16895161-16895238 +** | **candidate-rescued** | **Mirtron** | **intron** | [View on UCSC Genome Browser [Cornell Mirror]] |

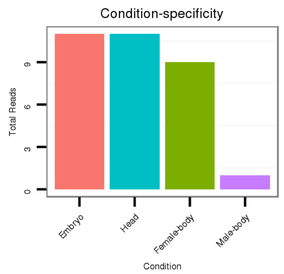
Legend: mature star mismatch in alignment mismatch in read

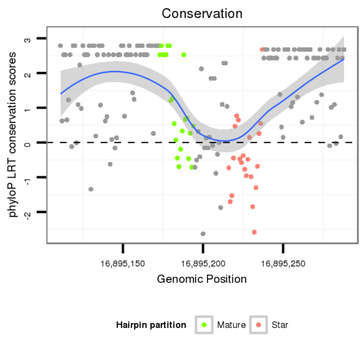
**Predicted structure**






Show Alternate Folds

**Flybase annnotation**

intron [Dyak\GE17723-in]; CDS [Dyak\GE17723-cds]; CDS [Dyak\GE17723-cds]; utr3 [utr3_plus_8558]

No Repeatable elements found

**Sense Strand Reads**

hide 3p reads  show mid mismatch reads

```
AGCCGCCAAACTCGACGGTCATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACAAAGTGCGTAGCTCGAGGAGCAGCCGCCGAACCGAACTCTATTAATGCCCTCGATCACCTCGCACACAGATCCCTCCAACCTTTCCGTGTAAGATCAAACCCGAACCGAACACGCAGCA
*********************************************************(((((.(((.(((((((.(((.....((.......)).....))))))))))....))))))).**********************************************
```

| Read size | # Mismatch | Hit Count | Total Norm | Total | M043 female body | M056 embryo | M026 head | V058 head | V120 male body | V046 embryo |
|---|---|---|---|---|---|---|---|---|---|---|
| 25 | 0 | 1 | 8.00 | 8 | 4 | 3 | 0 | 0 | 0 | 1 |
| 27 | 0 | 1 | 4.00 | 4 | 0 | 0 | 4 | 0 | 0 | 0 |
| 26 | 0 | 1 | 2.00 | 2 | 1 | 0 | 1 | 0 | 0 | 0 |
| 22 | 0 | 1 | 2.00 | 2 | 0 | 1 | 0 | 0 | 1 | 0 |
| 27 | 0 | 1 | 2.00 | 2 | 1 | 1 | 0 | 0 | 0 | 0 |
| 24 | 0 | 1 | 2.00 | 2 | 0 | 2 | 0 | 0 | 0 | 0 |
| 18 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| 23 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| 23 | 1 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 21 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 22 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| 26 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| 18 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| 26 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| 27 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| 19 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| 18 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |

**Anti-sense strand reads**

```
TCGGCGGTTTGAGCTGCCAGTAGGTGTGCTGTGGACCGTTACGTCACGTTCACGCATTGTTTCACGCATCGAGCTCCTCGTCGGCGGCTTGGCTTGAGATAATTACGGGAGCTAGTGGAGCGTGTGTCTAGGGAGGTTGGAAAGGCACATTCTAGTTTGGGCTTGGCTTGTGCGTCGT
*****************************************************(((((.(((.(((((((.(((.....((.......)).....))))))))))....))))))).**********************************************
```

| Read size | # Mismatch | Hit Count | Total Norm | Total | V058 head | M043 female body |
|---|---|---|---|---|---|---|

Show Alignment With Reads

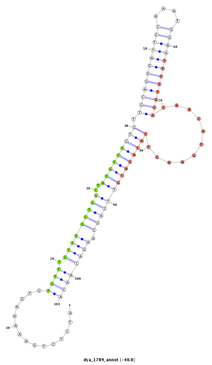
**Re-alignment of all predicted orthologs**

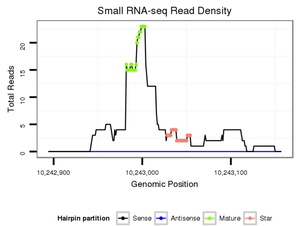
| Species | Coordinate | ID | Alignment |
|---|---|---|---|
| droYak3 | X:16895111-16895288 + | dya_1456 | AGCCGCCAAACTCGACGGTCATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------G-AGGAGCAGC----------GC--CGA--------ACCGAACTC----------TATTAATGC--C----------C---------TC--G----------A---TC---ACC----------TCG----------CA--CACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAACCCGAACCGAACACGCAGCA |
| droEre2 | scaffold_4690:8587854-8588031 + | der_401 | AGCCGCCAAACTCGACGGTATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------G-GGAGCACA----------GC--CGA--------ACCGAACTC----------TATTAATGC--C----------C---------TC--G----------A---TC---CCC----------TCG----------CA--CACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAACCCGAACCGAACACGCAGCA |
| droSec2 | scaffold_8:576711-576895 + | | AGCCGCCAAATCGACGGTCATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGAA----------G-GGAGCA--------------TGGAGCACC--GC--CGA--------ACCGAACTC----------TAGTAATGA--A----------A---TC---ACC----------TCG----------CA--CACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAGCCCGAACCGAACACGCAGCA |
| droSim2 | ks:17364855-17365039 + | dsi_32460 | AGCCGCCAAATCGACGGTCATCCACACGACACCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGAA----------G-GGAGCA--------------TGGAGCACC--GC--CGA--------ACCGAACTC----------TAGTAATGA--A----------A---TC---ACC----------TCG----------CA--CACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAGCCCGAACCGAACACGCAGCA |
| dm3 | chrX:18267185-18267369 + | dme_425 | AGCCGCCCAACTCGACGGTCATCCACACGAGCCCTGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGAA----------G-GGAGCA--------------CGGAGCACC--GC--CGA--------ACCGAACTC----------TAGTAATGA--A----------A---TC---ACC----------TCG----------CA--CACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAGCCCGAACCGAACACGCAGCA |
| droEug1 | scf1800000409528:449294-449472 + | | AGCCGCCAAACTCGACGGTATCCACACGACACCTATCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------A-GGAGCACC----------CAG--CTA--------TTATAACTG----------TATTAATAT--C----------C---------TC--G----------A---TG---ACC----------A---TGA----------AA--TACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAACCCGAACCGACCACGCACA |
| droBia1 | scf1800000302432:991025-991196 - | | AGCCGCCGAACTTACGGTATCCACACGACGCCGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------A-GGAGCACC----------GC--CGA--------C-CAAAACTC----------CATAATGC---C----------C---------C--G----------A---TG---ACC----------CCG----------CA--ACAGATCCCTCCATCCTTTCC---GTGCAAGATCAAGCCCGAACCGAACACGCAGCA |
| droTak1 | scf1800000415395:271880-272072 + | | AGCCGCCGAACTCGACGGTATCCACACGACACCGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------A-GGAGCACC----------CA--CGA--------C-CAGAACTC----------TGAATGT--C----------C---------TC--G----------T---AC-T--TA----------G---AT-TGCCTCCAACTTACCACA--CACAGATCCCTCCAACCTTTCC---GTGCAAGATCAAACCCGAACCGACCACGCAGCA |
| droEle1 | scf1800000491006:507673-507853 + | | AGCCGCCGAACTCGACGGTATCCACACGACACCGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------G-AGGAGCACC----------CA--CGA--------C-CAGAACTG----------TATTAATGA--T----------TGTC---------TC--G----------A---TG---ACC----------TGC----------A--AACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAACCCGAACCGACCACGCAGCA |
| droRho1 | scf1800000779985:1003450-1003621 + | | AGCCGCCGAACTCGACGGTATCCACACGACACCGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------A-AGGAGCCC----------CA--CGA--------C-CAGAACTG----------TAGTAATG---T----------C---------T--G----------A---TG---ACC----------TCG----------C--CACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAACCCGAACCGACCACGCAGCA |
| droFic1 | scf1800000453829:1364555-1364749 - | | AGCCGCCGAACTCGACGGTCATCCACACGACACCGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------G-GGGAGCGCT----------TAAT--CGA---GTTGAGCAGAATA----------TAGTAATGC--C----------C---------TC--G----------T---TT---CTT----------G----TA-ACCTCCGAT---CCGT--AACAGATCCCTCCAACCTTTCC---GTGTAAGATCAAACCCGAACCGACCACGCAGCA |
| droKik1 | scf1800000302696:1335662-1335841 + | | AGCCGCCGAACTCGACGGTCATACACACGACCTCGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTC----------A-GGAGCGCC----------CC--T--T--------T-------T----------AAGTTGGAGCCGAACGAGTAACCAA--T----------T---------T--T----------T---T--T---------TCGAATT----------TC--CGAAGATCCCTCCAACCTTTCGAAGTGTAAATCAAACCAGACCGAACACGCAGCA |
| droAna3 | scaffold_13248:931379-931586 - | | AGCCGCCGAAACTCGACGGTCATACACACGACCTCGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTCC----------A-AAGAGCCT----------TCT--CGA--------ATTT-----CATTAATTA--A----------TTATAATTATAATTATAATTTTAATAATTATT--TG--G----------A---AA---CCC----------TGC----------TTTATATAGTTATGATCCCTCCAAACTTTCC---GTGTAAGATCAAACCCGAACCGAACACGCAGCA |
| droBip1 | scf1800000395920:35111-35313 + | | AACCGCCGAATTTACGGTCATCACACGACCTCGGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTCCCCTTAG-----A-GAGAAAGCTTTCAAATAAAAACATTATATATC--TATT-AAA--------TATAATTTA----------TATAATTA--T----------T---------T--T----------T---CT---ATT----------TCA----------AT--TATTGATCCCTCCAAATTTTCC---GTGTAAGATCAAACCCGAACCGAACACGCAGCA |
| dp5 | XL_group3a:228604-228785 + | | AGCCAGCGAACTCGACGGTATCCACACGACACCGAAGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTG----------G-AAA---CTTTG----------AACGGGGCCAGCAGCCTC--------TAC----TAATCTTCA----------T---------T--T----------T---A-TTCCA----------T---CCATATCACAGATCCCTCCAACCTTTCC---AGTAAGATCAAACCCGAACCGAACACGCAGCA |
| droPer2 | scaffold_39:508452-508633 - | | AGCCAGCGAACTCGACGGTATCCACACGACACCGAAGCAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCTG----------G-AAA---CTTTG----------AACGGGGCCAGCAGCCTC--------TAC----TAATCTTCA----------T---------T--T----------T---A-TTCCA----------T---CCAATACACAGATCCCTCCAACCTTTCC---AGTAAGATCAAACCCGAACCGAACACGCAGCA |
| droWil2 | scf2_1100000004515:1509862-1510103 + | | AACCGCCGAATCGACGGTATCCACACACACCTCGGCAATGCAGTGCAAGTGCGTAAGTATCAATGCGTATGTAT----------G-ATCTGTA--T----------TCGT-----CAT--CG--T----------T--------T--T----------CTTTGATAATCCTGAATTCACAAACTGTTCCTCCCTACACAAAAGTTGTATCCCA-TTCCATGCTAAATCTTGTTTTCCATTTCTTTTATT----GC--CACAGATCCCTCCAACTTTCA---AGTAAGATCAAACCCGAACCGAATACACAGCA |
| droVir3 | scaffold_12970:3051811-3051881 + | | AGCCGCCGAATCGACGGTCATCCATACGACCATCGAATGCAGTGCAAGTGCGTAACA---AAGTGCGTAGCT----------T-T--------T----------T---T--T----------T--------T--T----------T---T--T---------T---T--T---T---T---

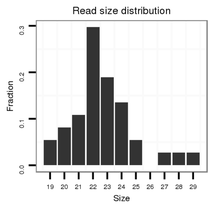
| ID: | Coordinate: | Confidence: | Class: | Genomic Locale: | |
|---|---|---|---|---|---|
| **dya_1789** | **3R:10242944-10243107 +** | **candidate-rescued** | **Canonical miRNA** | **intron** | [View on UCSC Genome Browser (Cornell Mirror)] |

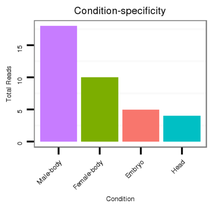
Legend: mature star sub-match in alignment mismatch in read

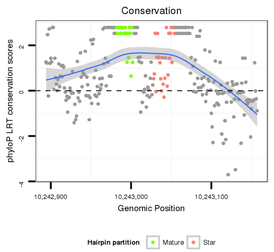
**Predicted structure**




Show Alternate Folds

**Flybase annotation**

intron [Dyak/GE26033-in]; utr5 [utr5_plus_10181]

No Repeatable elements found

**Sense Strand Reads**

hide 3p reads  show mid mismatch reads

```
ACCCAGTGATTAGTGATATTAACAGCTTACCATTCCCCCATCCCAATGGACGCCATATCTGGACCAGCATGAGATCTCTGAAAAAGTGTGTTTGTTTGCTGGCTACGTCTGTGTTGCAGGGATTCCAAATGGAATTCCCTGCACAACATGAACTCACAGATGTTCAGCAAGACAACACGTCAAAAAATTCAACAGGAGATTCAAGATTGGAGCTGCTGAAGTGATCTACCAACTACCCAAAAACCATCGAAAGTGTTGAAATAAT
**********************************************************************************************************************************************************************************************************************************************
```

| Read size | # Mismatch | Hit Count | Total Norm | Total | V120 male body | M043 female body | M056 embryo | V058 head | GSM1528802 follicle cells | M026 head | V052 head |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 22 | 0 | 1 | 7.00 | 7 | 0 | 4 | 1 | 2 | 0 | 0 | 0 |
| 23 | 0 | 1 | 2.00 | 2 | 2 | 0 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | 1 | 2.00 | 2 | 2 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | 1 | 2.00 | 2 | 0 | 1 | 0 | 0 | 0 | 0 | 1 |
| 24 | 0 | 1 | 2.00 | 2 | 0 | 2 | 0 | 0 | 0 | 0 | 0 |
| 27 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 25 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 23 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 29 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 27 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 25 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 20 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |

**Anti-sense strand reads**

```
TGGGTCACTAATCACTATAATTGTCGAATGGTAAGGGGGTAGGGTTACCTGCGGTATAGACCTGGTCGTACTCTAGAGACTTTTTCACACAAACAAACGACCGATGCAGACACAACGTCCTAAGGTTTACCTAAGAGTGTCTACAAGCTCTGTTGTGCAGTTTTTTTAGTTGTCCTCTAAGTTCTAACCTCGACGACTTCACTAGATGGTTGATGGCTTTTTGGTAGCTTTCACAACTTTATTA
**********************************************************************************************************************************************************************************************************************************************
```

| Read size | # Mismatch | Hit Count | Total Norm | Total | V120 male body | M043 female body | V058 head | V052 head | M056 embryo | M026 head | V046 embryo |
|---|---|---|---|---|---|---|---|---|---|---|---|

Show Alignment With Reads

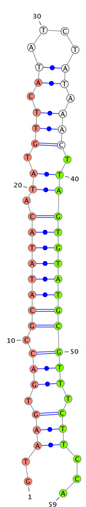
**Re-alignment of all predicted orthologs**

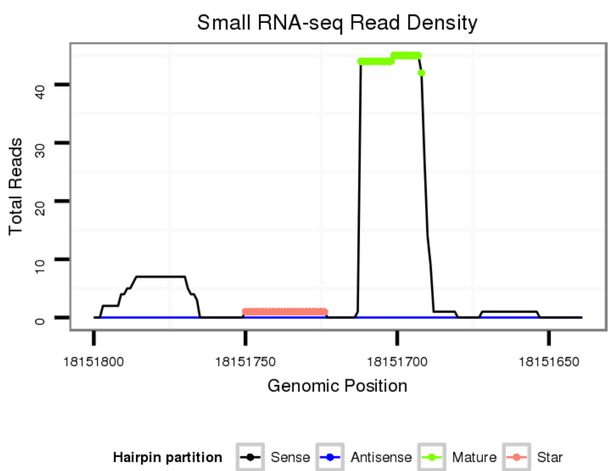
| Species | Coordinate | ID | Alignment |
|---|---|---|---|
| droYak3 | 3R:10242894-10243157 + | dya_1789 | AC----------CCAGTGATTA---GTGAT---------ATTA---ACAGCTTA-CCATTCCC-C-CATCCCCAATGGACGC-CA--TA--------TCT----------GGACCAGCATGAGATCTCTGAAA-AAGTGTTTGTTTGCTGG-CTACGTCTGTGTTGCAGGGAT----------TCCAAA----------TGGA-APTCCTGCACAA-CA-TGAACTCACAGATGTTCAGCAAGACAACACGTCAAAAAATCAACAGGA-GATTCAAG-AT----TGGAGCTGCTGAAGTG----ATCTACCAACTA--------CCCAAAAACC---ATCGAAAGTGTTGAAAT----------AAT |
| droEre2 | scaffold_4770:15603059-15603322 - | dere_1519 | AC----------CCAGTGATTA---GTGAT---------ATTA---ACAGCTTA-CCATTCCC-C-CATCCCCAATGGACGC-CA--TA--------TCT----------GGACCAGCATGAGATCTCTGAAA-AAGTGTTTGTTTGCTGG-CTACGTCTGTGTTGCAGGGC----------TCCAAA----------TGGA-TPTCCTGCACAA-CA-TGAACTCACAGATGTTCAGCAAGACAACACGTCAAAAATATCAACAGGA-GATTCAAG-AT----TGGAGCTGCTGAAGTG----AT-TA-TA-TA--------A-G-GAAACC---ATCGAAAGTGTTGAAAT----------AAT |
| droSec1 | scaffold_211572871:1572933 - | dsec_143 | AC----------CCAGTGATTA---GTGAT---------ATTA---ACAGCTTA-CCATTCC-T-CATCCCAATGGACGC-CA--TA--------TCT----------GGACCAGCATGAGATCTCTGAAA-AAGTGTTTGTTTGCTGG-CTACGTCTGTGTTGCAGGGA----------TCCAAA----------TGGA-TPTCCTGCACAA-CA-TGAACTCACAGATGTTCAGCAAGACAACACGTCAAAAATATCAACAGGA-GATTCAAG-AT----ATAGCTGCTGAAGTG----AT-TAACTA--------A-TAAAAACC---ATCGAAAGTGTTGAAAT----------AAT |
| droSim2 | 3R:14862027-14862286 + | dsim_12453 | AC----------CCAGTGATTA---GTGAT---------ATTA---ACAGCTTA-CCATTCC-T-CATCCCAATGGACGC-CA--TA--------TCT----------GGACCAGCATGAGATCTCTGAAA-AAGTGTTTGTTTGCTGG-CTACGTCTGTGGGGA----------TCCAAA----------TGGA-TPTCCTGCACAA-CA-TGAACTCACAGATGTTCAGCAAGACAACACGTCAAAAAATCAACAGGA-GATTCAAG-AT----ATAGCTGCTGAAGTG----AT-TAACTA--------A-TAAAAACC---ATCGAAAGTGTTGAAAT----------AAT |
| dsim3 | chr3L:6211124-6211383 + | dsim_164 | AC----------CCAGTGATTA---GTGAT---------ATTA---ACAGCTTA-CCATTCC-T-CATCCCAATGGACGC-TCCGA--TA--------TCT----------GGACCAGCATGAGATCTCTGAAA-AAGTGTTTGTTTGCTGG-CTACGTCTGTGTTGCAGGGA----------TCCAAA----------TGGA-TPTCCTGCACAA-CA-TGAACTCACAGATGTTCAGCAAGACAACACGTCAAAAAATCAACAGGA-GATTCAAG-AT----ATAGCTGCTGAAGTG----ATT-TAACTA--------ATCAAAAAGC---ATCGAAAGTGTTGAAAT----------AAT |
| droEug1 | scf7180000409692:688174:688473 + | deug_1 | AC----------CCAGTGATTA---GTGAT---------ATTA---ACAGCTTA-AATAGTGCAATGGACGC-CA--TA--------TCT----------GGACCAGCATGAGATCTCTGAAA-AAGTGTTTGTTTGCTGG-CTACGTCTGTGTTGCAGGTA----------TCCAAA----------TGGA-TPTCCTGCACAA-CA-TTTGGCAACTGGCATGTGTTCAGCAAGACAACACTGCCAAAAAATCAACAGGA-GATTCAAG-AT----TGGAGCTGCTGAAGTG----AAC-TA-G-G----------ACTTTTCAT----------AT |
| droBia1 | scf7180000302402:8304835:8305076 + | dbia_1 | AC----------CCAGTGATTA---GTGAT---------ATTT---ACAGCTTA-A-TAAAA--T-T--TCATGGATAA-TT--TA--------TCT----------GGACCAGCATGAGATCTCTGAAA-AAGTGTTTGTTTGCTGG-CTACGTCTGTGTTTGTAGGTA----------TCCAAA----------TGGA-TPTCCTGCACAA-TT-TGCAATGCAACAGATGTTCAGCAAGACAACACGTCAAAAATATCAACAGGA-GATTCAAG-AT----TGAGCTGCTGAAGTG----AAC-TA-G-G----------ATTCAAAAGTGTTGAAAT----------AT |
| droTak1 | scf7180000415380:1425398:1425656 - | dtak_1 | AC----------CCAGTGATTA---GTGAT---------ATTT---ACAGCTTA-A-TAAAA--T-T--TCATGGATAA-TT--TA--------TCT----------GGACCAGCATGAGATCTCTGAAA-AAGTGTTTGTTTGCTGG-CTACGTCTGTGTTTGTAGGAT----------TCCAAA----------TGGA-TPTCCTGCACAA-TT-TGGCAATGCAACAGATGTTCAGCAAGACAACACGTCAAAAAATCAACAGGA-GATTCAAG-AT----TAGCTGCTGAAGTG----AT-TACCAATGCAAAAGTGTTGAAAT----------AT |
| droEle1 | scf7180000490995:524297-524615 - | dele_1 | AC----------CCAGTGATTA-TTGGATGTTA---GTGAT---------A-TT---ACAGCTTA-AAG-AAAA--T-T--TCAATGGATAA-TT--TA--------TCT----------GGACCAGCATGAGATCTCTGAAA-AAGTGTTTGTTTGCTGG-CTACGTCTGTGTTTGTAGGAT----------TCCAAA----------TGGA-TPTCCTGCACAA-TT-TGCAACTCACAGATGTTCAGCAAGACAACACGTCAAAAAATCAACAGGA-GATTCAAG-AT----TGAGCTGCTGAAGTG----AAC-TA-G-G----------ATTCAAAAGTGTTGAAAT----------AT |
| droRho1 | scf7180000377158:35290:35522 - | drho_1 | AC----------CCAGTGATTA---GTGAT---------A-TT---ACAGCTTA-AAG-AAAA--T-T--TCAATGGATAA-TT--TA--------TCT----------GGACCAGCATGAGATCTCTGAAA-AAGTGTTTGTTTGCTGG-CTACGTCTGTGTTTGTAGAT----------GATCTCTGAAA-AAGTGTTTGTTTGCTGG-CTACGTCTGTGTTTGTAGAAA----------TCCAAA----------TGGA-TPTCCTGCACAA-TT-TGCAACTCACAGATGTTCAGCAAGACAACACGTCAAAAAATCAACAGGA-GATTCAAG-AT----TGAGCTGCTGAAGTG----AAC-TA-G-G----------ATTCAAAACTA--------ATCAAAAGC---ATCGAAAGTGTTGAAAT----------AT |
| droFic1 | scf7180000453800:2293559-2293824 - | dfic_1 | AC----------CCAGTGATTA---GTGAT---------ATTT---ACAGCTTA-AGGG-AAAAAA-GCCAATGGAAACTT--TA--------TCT----------GGACCAGCATGAGATCTCTGAAA-AAGTGTTTGTTTGCTGG-CTACGTCTGTGTTTGTAGGAT----------TCCAAA----------TGGA-TPTCCTGGGCCTTAGCAACTCACAGATGTTCAGCAAGACAACACGTCAAAAAATCAACAGGA-GATTCAAG-AT----TAGGCTGCTGAAGTG----AT-AAACTA--------A-TAAAACC---ATCGAAAGTGTTGAAAT----------AT |
| droKik1 | scf7180000302475:1404883-1405154 + | dkik_1 | AC----------CCAGTGATTA---GTGAT---------ATTT---ACAGCTTA-AGG-AAAA--T-T--TCAATGGATAA-TT--TA--------TCT----------GCACCAGCATGAGATCTCTGAAA-AAGTGTTTGTTTGCTGG-CTACGTCTGTGTTTGTAGCAT----------GATCTCTGAAA-AAGTGTTTGTTTGCTGG-CTACGTCTGTGTTTGTAGCAGA----------TCAGCAAGACAACACGTCAAAAATATCAACAGGA-GATTCAAG-AT----TAGCTGCTGAAGTG----AAC-TA-G-G----------ATTCAAAACTA--------A-TAAAACC---ATCGAAAGTGTTGAAAT----------AT |
| droAna3 | scaffold_13340:938906-939168 - | dan_4036 | A-----------------------------TGATT---G-GAT---------CTTCGCG---------AAA---------AAAAAAA-AGACA--CAGCA---------TCTGATCTGGATCTGGAACTGAATCTGGATCAGCATGAGATCTCTGAAGAAGTGTTTGTTTGCTGG-CTACGTCTGTGTTTGTAGCAGA----------GTCCTCTTCCTCCTCC

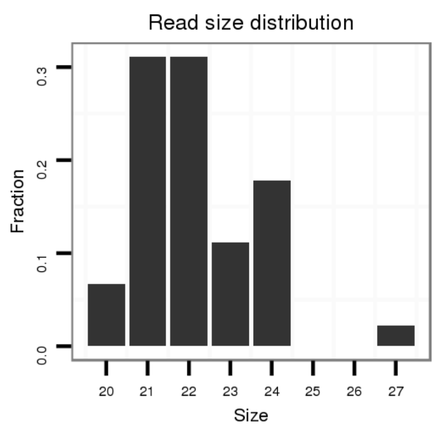
| ID: | Coordinate: | Confidence: | Class: | Genomic Locale: | |
|---|---|---|---|---|---|
| **dya_140** | **2R:18151689-18151750 -** | **candidate-rescued** | **Mirtron** | **intron** | [View on UCSC Genome Browser {Cornell Mirror}] |

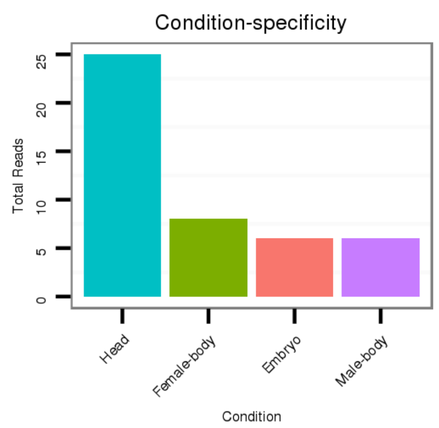
Legend: mature star mismatch in alignment mismatch in read

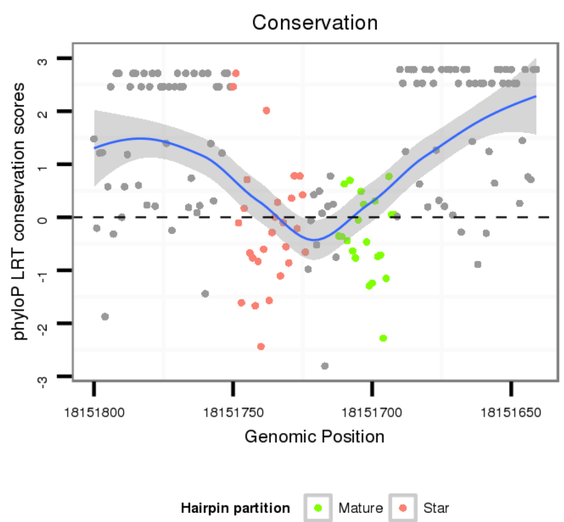
**Predicted structure**






Show Alternate Folds

**Flybase annnotation**

intron [Dyak\GE11660-in]; CDS [Dyak\GE11660-cds]; CDS [Dyak\GE11660-cds]; utr3 [utr3_plus_2684]

No Repeatable elements found

**Sense Strand Reads**

hide 3p reads | show mid mismatch reads

| TTGGTCGAATTGCCAAGGAGGACTGGTCGGAGGACATACTAAATGCCAAGGTAAGTGACCGCATATACATATGTTCATATCTATAAACTTAGTGTATGCGTTTCTTCCATAGCAATGCGTTTGCAACAACACAATGTCTGGAGCCATGTGACGATTTATAAA<br>**********..(((.(((.(((((((((.((.(((.((....)).))).)))))))))))).)))...********** | Read size | # Mismatch | Hit Count | Total Norm | Total | V058 head | M043 female body | V120 male body | V052 head | M056 embryo | V046 embryo |
|---|---|---|---|---|---|---|---|---|---|---|---|
| .....TTAGTGTATGCGTTTCTTCCA..... | 21 | 0 | 1 | 14.00 | 14 | 10 | 3 | 0 | 0 | 1 | 0 |
| .....TTAGTGTATGCGTTTCTTCCAT..... | 22 | 0 | 1 | 13.00 | 13 | 3 | 3 | 2 | 2 | 2 | 1 |
| .....TTAGTGTATGCGTTTCTTCCATAG..... | 24 | 0 | 1 | 8.00 | 8 | 3 | 0 | 3 | 1 | 0 | 1 |
| .....TTAGTGTATGCGTTTCTTCCATA..... | 23 | 0 | 1 | 5.00 | 5 | 1 | 0 | 0 | 3 | 0 | 1 |
| .....TTAGTGTATGCGTTTCTTCC..... | 20 | 0 | 1 | 3.00 | 3 | 0 | 0 | 1 | 2 | 0 | 0 |
| .....TTGCCAAGGAGGACTGGTCGGAGGAC..... | 26 | 0 | 1 | 2.00 | 2 | 0 | 0 | 2 | 0 | 0 | 0 |
| ...GTCGAATTGCCAAGGAGGACTGGTCGGA..... | 28 | 0 | 1 | 2.00 | 2 | 0 | 0 | 1 | 0 | 1 | 0 |
| .....GTTTCTTCCATAGCAATGCGT..... | 21 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| .....AAGGAGGACTGGTCGGAG..... | 18 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....CTTAGTGTATGCGTTTCTTCCA..... | 22 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....GCCAAGGAGGACTGGTCGGAGGA..... | 23 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| .....ACACAATGTCTGGAGCCAT..... | 19 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....GTAAGTGACCGCATATACATATGTTCA..... | 27 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....CAAGGAGGACTGGTCGGAGGAC..... | 22 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .TGGTCGAATTGCCAAGGAGGACC..... | 23 | 1 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| .....CTGGTCGGAGGACATACTAAATGCCAAGC..... | 29 | 1 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |

**Anti-sense strand reads**

| AACCAGCTTAACGGTTCCTCCTGACCAGCCTCCTGTATGATTTACGGTTCCATTCACTGGCGTATATGTATACAAGTATAGATATTTGAATCACATACGCAAAGAAGGTATCGTTACGCAAACGTTGTTGTGTTACAGACCTCGGTACACTGCTAAATATTT<br>**********..(((.(((.(((((((((.((.(((.((....)).))).)))))))))))).)))...********** | Read size | # Mismatch | Hit Count | Total Norm | Total | V120 male body |
|---|---|---|---|---|---|---|

Show Alignment With Reads

**Re-alignment of all predicted orthologs**

| Species | Coordinate | ID | Alignment |
|---|---|---|---|
| droYak3 | 2R:18151641-18151800 - | dya_140 | TTGGTCGAATTGCCAAGGAGGACTGGTCGGAGGACATACTAAATGCCAAGGTAAGTGA---CCGC-A-TATACA--TA----------T----------GTTCAT-------ATCTA----------TAA----------ACTTAGTGT---ATGCG-TTT---------CTTCCATAGCAATGCGTTTGCAACAACACAATGTCTGGAGCCATGTGACGATTTATA |
| droEre2 | scaffold_4845:12533575-12533732 - | | TTGGTCGAATCGCCAAGGAAGACTGGTCGGAGGACATACTAAATGCCAAGGTAACTGA---GCTG-A-GGTATACATAA----------G----------T-------ATTTA----------TAA----------ACTAAGTTC---ATGTG-TTT---------CTCCATAGCAATGCGTTTGCAACAACACAATGTCTGGAGCCATGTGACGATTTATA |
| droSec2 | scaffold_1:10817661-10817817 + | | TTGGTCGAATTGCCAAGGAGGACTGGTCGGAGGACATACTAAATGCCAAGGTGAGTAA---GCCG-A-GATAAACAAA----------TT----------TGAA----------ACAAAGTTCACCAAGTG-ATC---------CGCCCATAGCAATGCGTTTGCAACAACACAATGTCTGGAGCCATGTGACGATTTATA |
| droSim2 | 2r:13968979-13969135 + | dsi_19943 | TTGGTCGAATTGCCAAGGAGGACTGGTCGGAGGACATACTAAATGCCAAGGTGAGTGA---GCCG-A-GATAAACAAA----------TT----------TGAA----------ACAAAGTTCATCAAGTG-ATC---------CGCCCATAGCAATGCGTTTGCAACAACACAATGTCTGGAGCCATGTGACGATTTATA |
| dm3 | chr2R:13316399-13316555 + | dme_426 | TTGGTCGAATTGCCAAGGAGGACTGGTCGGAGGACATACTAAATGCCAAGGTGAGTGA---GCCG-A-GATAAACATCA----------TT----------TAAA----------ACTAAGTTCATCATGTG-TTC---------CGCCCATAGCAATGCGTTTGCAACAACACAATGTCTGGAGCCATGTGACGATTTATA |
| droEug1 | scf7180000409672:1794874-1795027 - | | TAGGAGGCATTGCCAAGGAGGACTGGTCGGAGGACGTATTGAATGCCAAGGTGAGTGA---ACCA-A-AATATA---T----------TC----------TTAA----------ATTATGTAAATCATGTTTACT---------TGTTTATAGCAATGCGTTTGCAACAACACCATGTCTGGGGCCATGTGACGTTTTATA |
| droBia1 | scf7180000301754:5568296-5568449 + | | TGGGCAGGATTGCCAAGGAGGACTGGTCGGAGGACATACTCAATGCCAAGGTGCGTA---TTTG-A-GGTACA--TAC----------TC----------TGCA----------GTTCAGTACGTCATGAC-AAC---------TCCTTATAGCAATGCGTTTGCGCACAACACCATGTCCGGGGCCATGTGACGTTTTATA |
| droTak1 | scf7180000415138:444578-444652 - | | A----------...----.-.------..--.----------.----------.----------.---.----------.--------CTTCATGTA-AACCTCTA----TCTTTATAGCAATGCGTTTGCAACAACACCATGTCCGGGGCCATGTGACGTTTTATA |
| droEle1 | scf7180000491214:983885-984038 - | | TGGGTCGAATTGCCAAGGAGGACTGGTCGGAGGACATACTTAATGCCAAGGTGCGTGG---TTGT-A-TAAATA---C----------AC----------AAAA----------ATCAGATTCATCATTTATATT---------CCCTTACAGCAATGCGTTTGCAACAACACCATGTCGGGAGCCATGTGACGTTTTATA |
| droRho1 | scf7180000776786:29239-29394 + | | TGGGTCGCATTAGCAAGGAGGACTGGTCGGAGGACATACTCAATGCCAAGGTGGGTAG---GCCT-A-GATATATCGAA----------T----------T-------ATTTA----------T--TCA----------ACTTAATT-----TGAT-ACC---------TCTTCGCAGCAATGCGTTTGCAACAACACGATGTCTGGAGCCATGTGACGTTTTATA |
| droFic1 | scf7180000453948:2127734-2127888 - | | TGGGAAGAATTGCCAAGGAGGACTGGTCGGAGGACATACTAACACGCCAAGGTGGGTGG---AA---.-.------..--.----------TTTGTAGCATTC---CGA--------ATCCAAGC----------.---.----------ACAAAGTT---AT----TC---CT----TTTTTACAGCAATGTGTTTGCAATAACACAATGTCGGGGCCATGTGACGTTTTATA |
| droKik1 | scf7180000302411:420143-420304 + | | TGGGAGGCATTGCCAAAGAAGACTGGTCGGAGGATATACTCAACGCCAAGGTAACTGG---GT---.-AATATTCATCA----------.-------ATGC---CAAGATTTAGG-GCT-AAC----------.---.----------AAAAAGGT-------TA-TTC---------CGCTTACAGAAATGCGTCTGGCACAACACCATGTCGGGAGCCATGTGACGTTTCATA |
| droAna3 | scaffold_13266:8811023-8811174 + | | TGGACCGCATATCCAAGGAGGATTGGTCTGAGGACATTCTAAATGCCAAGGTTTGTTAGGAGATG-A-AATAAACAACAAAAACA-------.----------.-----.-------.-----.----------.---.----------.CTAA-----CAT-TT-CTT---------TTCAAACAGCAATGTGTTTGCAATAACACAATGACTGGATCCATGTGACGTTTCATA |
| droBip1 | scf7180000395994:25902-26055 - | | TGGACCGCATTGCCAAGGAGGATTGGTCGGAGGACATTCTCAATGCCAAGGTTTGTTCAAAGATG-A-AATAATCGATA----------.----------.-----.-------.-----.----------AAA----------ACTAATTAT--ATTGT-GTT---------CCCAAACAGCAATGCGTTTGCAACAATACAATGTCTGGATCCATGTGACGTTTCATA |
| dp5 | 3:4779174-4779334 + | | TGGGTCGTATTGCCAAGGAGGATGGTCGGAGGATATTCTAAATGCCAAGGTGAGTGT---AT---.-T------..--.----------.----------.-----.-------.-----CTCAAGGTTTATTCT---CCACTTGATTGGTTCTAAAA---------.---ATGCT-CTC---------TTGTTATAGCAATGCGTGTGCAACAATACCATGTCTGGAGCTATGTGACGTTTTCTA |
| droPer2 | scaffold_2:4973142-4973302 + | | TGGGTCGTATTGCCAAGGAGGATGGTCGGAGGATATTCTAAATGCCAAGGTGAGTGT---AT---.-T------..--.----------.----------.-----.-------.-----CTCAAGGTTTATTCT---CCACTTGATTGGTTCTAAAA---------.---ATGCT-CTC---------TTGTTATAGCAATGCGTGTGCAACAATACCATGTCTGGAGCTATGTGACGTTTTCTA |
| droWil2 | scf2_1100000004963:1636374-1636541 - | | TCACCCGCATAGCCAAAGAGGATTGGACCGGAGGATGTGTTCAACGCCAAGGTAAGCGA---ATGA-A-AGG---GTTAAAAACG-------T----------.---TTCCTTTGT--TTTTC----------TAT----------TATTAATTT---GTTTT-CTT---------CTCTCTTAGCAATGCGTTTGTCAAAATACCATGTCCGGAGGTATGTGACGTTTTTA |
| droVir3 | scaffold_12875:12855287-12855438 - | dvi_6567 | TTGGGGGCATCGCCAAGGAGGACTGGTCTGAGGATATCTCTAATGCCAAGGTACGTGC---A---.-GCTCAACAAAA---ACACGGCAGTTT----------.-----.-------.-----TTAA----------TTTAA-----.-.------.-TTCC-------CTTTTGCAGCAATGCGTCTGCAACAACACCATGTCCGGTGCCATGTGACGCCTTTTTA |
| droMoj3 | scaffold_6496:20116982-20117136 - | | TTGGCCGCATTGCCAAGGAAGACTGGTCCGAGGACATTTTAAATGCCAAGGTATGTACA--GCTGCA-CAATTT---.-----TA-------T----------GATCTG-------CTCT-----------.---.----------ATTCCA---.-CTCCA-TTC---------CATTTATAGCAATGCGTCTGCAACAACACTATGTCTGGCGCCATGTGACGCTTTTTA |
| droGri2 | scaffold_14413:547-707 + | | TGGGAGGCATTGCCAAGGAGGATTGGTCCGAGGATATTCTAAATGCTAAGGTATAATC---.-----.-.------.-GAAA----------TTTTTGAAATGC---CACAATCGAGT-----.----------GTA----------ATAAA-----.-.------.-TTCTCTTTTTGAATTTGCAGCAATGCGTCTGCAACAATACCATGTCCGGTGCCATGTGACGCTTTTTA |

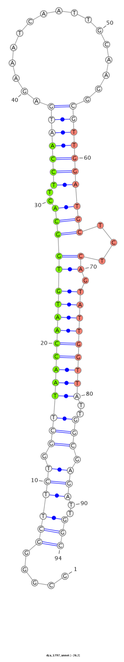
Generated: 09/08/2015 at 07:02 PM

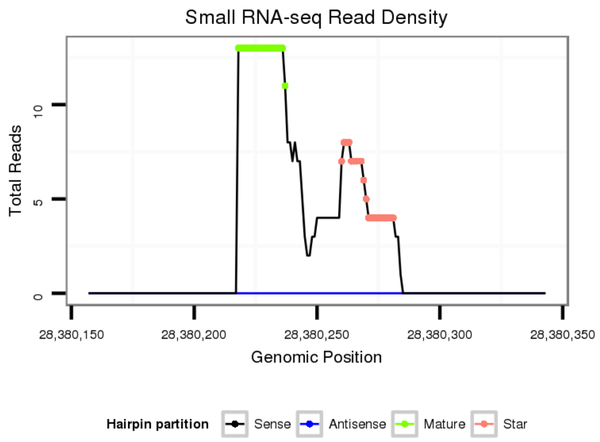
| | PASS/FAIL |
|---|---|
| crit.star | 0 |
| crit.loop | 0 |
| crit.mor | 0 |
| crit.half | 0 |
| crit.total | 1 |
| crit.pairing | 1 |
| crit.top3 | 1 |
| crit.tptop3 | 1 |
| crit.uri | 0 |
| crit.back | 1 |
| rescue.total | 1 |
| rescue.dominant | 1 |
| rescue.known | 0 |
| rescue.confident | 0 |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

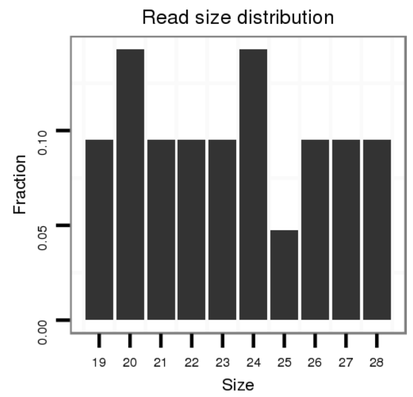
| ID: | Coordinate: | Confidence: | Class: | Genomic Locale: | |
|---|---|---|---|---|---|
| **dya_1797** | **3R:28380207-28380293 +** | **candidate-rescued** | **Canonical miRNA** | **5pUTR** | [View on UCSC Genome Browser {Cornell Mirror}] |

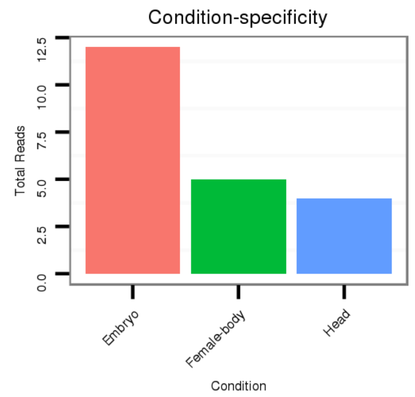
Legend: mature star mismatch in alignment mismatch in read

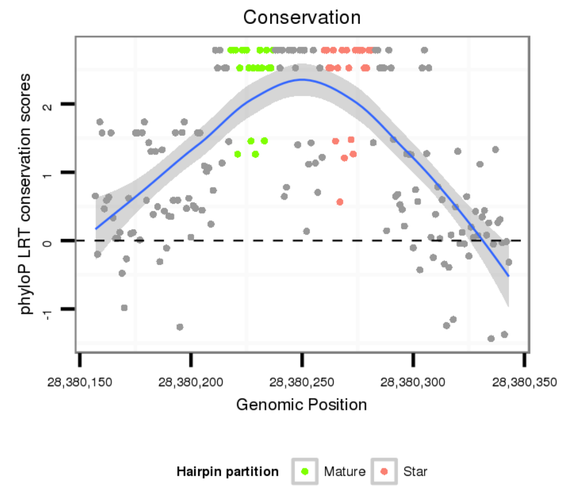
**Predicted structure**






Show Alternate Folds

**Flybase annnotation**

utr5 [utr5_plus_l2954]

No Repeatable elements found

**Sense Strand Reads**

hide 3p reads  show mid mismatch reads

| GTAGCAACGTTTGTAATCCGCGAAAGTGCAGTCGCAGAATTTTCCGGCGGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACCAGACCGTTCCGATTAGTCCGAATTAAACCC | Read size | # Mismatch | Hit Count | Total Norm | Total | M056 embryo | M026 head | M043 female body | V046 embryo | V058 head | GSM1528802 follicle cells |
|---|---|---|---|---|---|---|---|---|---|---|---|
| **********.....((((((.((((((((((((((((..(((((((.....))))))))))...)).)))))))))..))).))).))))********** | | | | | | | | | | | |
| .....TAACCAATGTGGCACTTCCA..... | 20 | 0 | 1 | 3.00 | 3 | 1 | 0 | 1 | 1 | 0 | 0 |
| .....TAACCAATGTGGCACTTCCAATGAGAAA..... | 28 | 0 | 1 | 2.00 | 2 | 1 | 0 | 1 | 0 | 0 | 0 |
| .....TAACCAATGTGGCACTTCCAATGAGA..... | 26 | 0 | 1 | 2.00 | 2 | 1 | 0 | 1 | 0 | 0 | 0 |
| .....TAACCAATGTGGCACTTCC..... | 19 | 0 | 1 | 2.00 | 2 | 2 | 0 | 0 | 0 | 0 | 0 |
| .....TAACCAATGTGGCACTTCCAATGAGAA..... | 27 | 0 | 1 | 2.00 | 2 | 1 | 0 | 1 | 0 | 0 | 0 |
| .....TTGGATGCTCTCAGTATTGGTT..... | 23 | 1 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....AATTGCAAGGCGTTGGATGCT..... | 21 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....TAACCAATGTGGCACTTCCAATGA..... | 24 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| .....TAACCAATGTGGCACTTCCAAT..... | 22 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....TTGGATGCTCTCAGTATTGGTG..... | 22 | 1 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....TTGGATGCTCTCAGTATTGGTTAT..... | 24 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....TGGATGCTCTCAGTATTGGTTAT..... | 23 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| .....TTGCAAGGCGTTGGATGCTCT..... | 21 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....TTGGATGCTCTCAGTATTGGTTATT..... | 25 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 1 | 0 | 0 |
| .....AGAAATCAATTGCAAGGCGTTGG..... | 23 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....TTGGATGCTCTCAGTATTGGTT..... | 22 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....TCAATTGCAAGGCGTTGGATGCTC..... | 24 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |

**Anti-sense strand reads**

| CATCGTTGCAAACATTAGGCGCTTTCACGTCAGCGTCTTAAAAGGCCGCCCCGAAGACCGAATTGGTTACACCGTGAAGGTTACTCTTTAGTTAACGTTCCGCAACCTACGAGAGTCATAACCAATAACCGCTCTAACCGGGGCCCTGTCGTAATGGTCTGGCAAGGCTAATCAGGCTTAATTTGGG | Read size | # Mismatch | Hit Count | Total Norm | Total | V058 head | V052 head | V120 male body |
|---|---|---|---|---|---|---|---|---|
| **********.....((((((.((((((((((((((((..(((((((.....))))))))))...)).)))))))))..))).))).))))********** | | | | | | | | |

Show Alignment With Reads

**Re-alignment of all predicted orthologs**

| Species | Coordinate | ID | Alignment |
|---|---|---|---|
| droYak3 | 3R:28380157-28380343 + | dya_1797 | G-TAGCAACG----------TT-TGTAATCC------GCGAAAGTGC----------AG------TCGCAGAA---TTT------TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTACCAG------AC----------CGTTCCGATTAGTCCGAATTAAACCC |
| droEre2 | scaffold_4820:530478-530664 - | der_1522 | G-TAGCAACG----------TG-TACAATCC------GCGAAAGTGC----------AG------TCGCAGAA---TTT------TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGCCAGCATAAGTAG------AC----------AGTTCCGATCAGTCCGCAGTAAACCC |
| droSec2 | scaffold_2807:1085-1271 + | dse_1845 | G-TAGCAACG----------TT-TACAATCC------GCGAAAGTGC----------CG------TCGCAGAA---TTT------TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTAGTAG------AC----------AGTTCCGATCAGTCCGCAGTAAACCC |
| droSim2 | 3r:26724016-26724202 + | dsi_32457 | G-TAGCAACG----------TT-TACAATCC------GCGAAAGTGC----------AG------TCGCAGAA---TTT------TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTAGTAG------AC----------AGTTCCGATCAGTCCGCAGTAAACCC |
| dm3 | chr3R:27444043-27444229 + | dme_422 | G-TAGCATCG----------TT-TACAATCC------GCGAAAGTGC----------AG------TCGCAGAA---TTT------TCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGGGACAGCATTAGTAG------AC----------AGTTCCGATCAGTCCGCAGTAAACCC |
| droEug1 | scf7180000409488:463421-463601 - | | G-TAGCAACG----------T-TACAAATC------GCGAAAGTGC----------------------AGAA---TTT------TCCGGCC-GGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGAGACAGCATTTGTAA------GC----------AGTTTCGTTCAGTCCGAGTTAAAACT |
| droBia1 | scf7180000302035:101882-102083 + | | G-AGCAACG----------TT-T-TGAATC------GCGAAAGTGC----------AGTCGGCGTAGCAGAC---TTTC-CTCCTCCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCTGTATTGGTTATTGGCGAGATTGGCCCCGAGCCAGCGTCAGTAGGTCTAGGC----------AGTTCCGATCAGTCCGAGTTAAACCC |
| droTak1 | scf7180000415712:510640-510848 + | | G-CAGCAACGTTT-TCCACTTCCATTTCCCGACC------GCGAAAGTGC----------------------AGAA---TTTCCCTTTTCCCGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGTTTGGCCCCGAGCCAGCATAAGTATATCTAGAT----------CCG--CGTTCCGATCAGTCCGAGTTAAACCC |
| droEle1 | scf7180000491194:1479823-1480036 + | | ATTAGCAACG----------TT-TGTAAATC------GCGAAAGTGC----------T--CGGAGTGTCAGAC---TTT------TTTGGCG-GGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGACGTTGGATGCTCTCAGTATTGGTTATTGGCAAGATTGGCCCCGAGACAGCAGTATTCT----AGGCACTTGGATACCAAT--CCAAT--AGTTCCGATCAGTCCGACTTTAATAC |
| droRho1 | scf7180000779322:264797-265012 - | | G-TAGCAACG----------TT-TGTAAATC------GAGAAAGTGCTTGGGGACGCGGTCGCAG------TCGCAGAC---TTT------TCCGGCG-GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATAGGCCCCTAGCCAGCAATATTAG------GCACTGG--------TACCCAT--AGTTCCGATCAGTCCGAATTAAACCC |
| droFic1 | scf7180000454114:125762-125960 + | | G-TAGCAACA----------GT-AAAAAATC------GCGAAAGTGC----------AG------TCGAAGAG---TTT------ACCGGCG--GGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGGCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGAGCCAGCGGTAATTGG------GCACTAG--------ACCCTAT--AGTTCCGATCAGTCCGAATTTGAACC |
| droKik1 | scf7180000302810:681809-682011 + | | A-CAGAGAGAAAA-AACACAACCGT-A-AGAATCGCGAGTGGGAAAGAGT--G----------G------ACGCGGTG---TA------TCCGGCGCGGGCTTCTGGCTTAACCAATGTGGCACTTCCAATGAGCAATCAATTGCAAGTCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCCAGCCAGCAATAGTTG------T-----------TGTTCCGCTTAGTCCGAGT--AATTT |
| droAna3 | scaffold_12911:3664262-3664461 - | dan_200 | G-AAGCAACAAACCATCCGTACCGG-AAGAATC------GCGAT----C----------AG------TGCAGAAAAGTTA------TACGGCG-GGCGATTCTGGCCTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGTCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGAGACAACTGTTGTCC------AC----------C----------CAGTCTAGTCCGTTCTAGTTTGAGTC |
| droBip1 | scf7180000396640:523306-523505 - | | G-AAGCAAGAATTCATCGAAACCGG-AAGATTC------GCGAT----C----------AG------TGCAGAAAAGTTA------TACGGCG-GGCGACTCTGGCCTAACCAATGTGGCACTTCCAATGAGAAATCAATTGCAAGTCGTTGGATGCTCTCAGTATTGGTTATTGGCGAGATTGGCCCCGAGCCAACAGTTGTCT------AC----------CC----------AGTCTAGTCCATT-GTAGGTTGCCCC |
| dp5 | 2:16675561-16675698 - | dps_3828 | G-------------------------------------------------------------GGGTCTCTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTTGGACGTTCTCAGTATTGGTTATTGGCAAGAAGAGCCCACAGCAGCTATAAGAG------TT----------ACA--------ATTGTAAAGAT------AGATTAGCGCT |
| droPer2 | scaffold_0:3721652-3721789 + | dpe_2482 | G-------------------------------------------------------------GGGTCTCTGGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTACAAGTCGTTGGACGTTCTCAGTATTGGTTATTGGCAAGAAGAGCCCACAGCAGCTATAAGAG------TT----------ACA--------ATTGTAAAGAT------AGATTAGCGCT |
| droWil2 | scf2_1100000004902:9400240-9400386 + | dwi_5416 | G-------------------------------------------------------------CTTCTAGCTTAATCAATGCGACACTTCCAATGAGCAATCCATTCGAAATCGTTGGATGATATCAGTATTGGTTATTGGCGAGAAGCATCTAAAAGCAGCTTTAAGTT------AA----------CAAACAATTAGATTGTTA--AGCATTATAAGTTAAGACA |
| droVir3 | scaffold_13047:9559456-9559595 - | dvi_24635 | G-------------------------------------------------------------GGTTTTCTAGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTCGAAATCGTTGGATGTTCTCAGTATTGGTTATTGGCCAGAAGAACCCAAACACAGCTATAAGAA------AC----------CAAA--------AATAA---AATAAACAACAAAGACA |
| droMoj3 | scaffold_6540:7667644-7667784 - | dmo_270 | G-------------------------------------------------------------AGTTTTCTAGCTTAACCAATGTGGCACCTCCAATGAAAAATCAATTCGAAATCGTTGGATGTTCTCAATATTGGTTATTGGCCAGAAGAGGTCAAACACAGCTATAAGAA------AC----------GAAA--------CGATCA---AATATATGATATAAACTC |
| droGri2 | scaffold_14906:2448950-2449065 - | dgr_463 | G-------------------------------------------------------------GGTTTTCTAGCTTAACCAATGTGGCACTTCCAATGAAAAATCAATTTGCAATCGTTGGATGTTCTCAGTATTGGTTATTGGCCAGATGAATCCAAACACAGCAATA----------------------------------------ATTAAACC |

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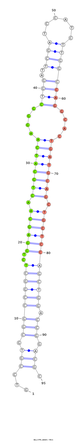
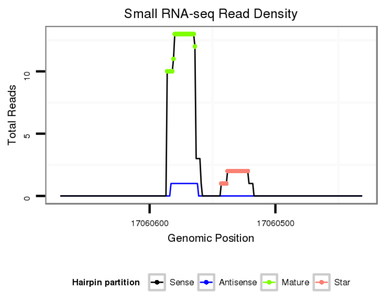
| | PASS/FAIL |
|---|---|
| crit.star | 1 |
| crit.loop | 0 |
| crit.mor | 0 |
| crit.half | 0 |
| crit.total | 0 |
| crit.pairing | 1 |
| crit.top3 | 1 |
| crit.tptop3 | 1 |
| crit.uri | 0 |
| crit.back | 1 |
| rescue.total | 1 |
| rescue.dominant | 1 |
| rescue.known | 0 |
| rescue.confident | 7 |
| rescue.candidate | 5 |

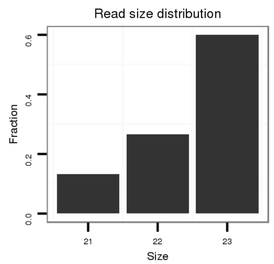
| ID: | Coordinate: | Confidence: | Class: | Genomic Locale: | |
|---|---|---|---|---|---|
| **dya_1791** | **3L:17060481-17060621 -** | **candidate-rescued** | **Canonical miRNA** | **antisense_to_3pUTR** | [View on UCSC Genome Browser [Cornell Mirror]] |

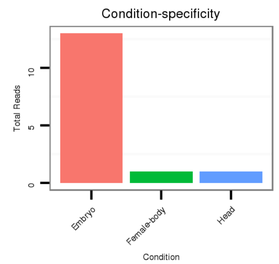
Legend: mature star mismatch in alignment mismatch in read

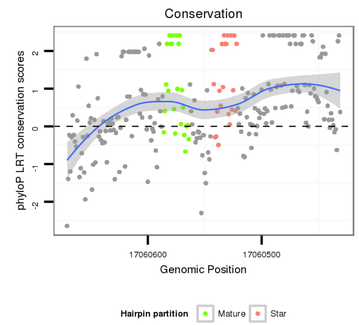
**Predicted structure**






Show Alternate Folds

**Flybase annnotation**

Antisense to utr3 [utr3_minus_5980]

No Repeatable elements found

**Sense Strand Reads**

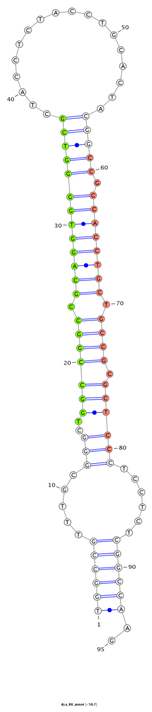
hide 3p reads  show mid mismatch reads

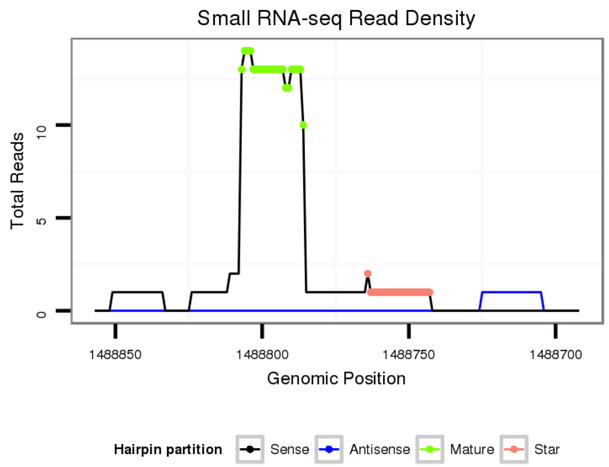
```
                                                
```

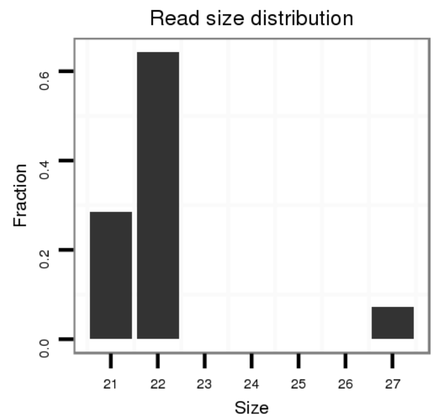
| ID: | Coordinate: | Confidence: | Class: | Genomic Locale: | |
|---|---|---|---|---|---|
| **dya_80** | **3R:1488742-1488807 -** | **candidate-rescued** | **Canonical miRNA** | **CDS** | [View on UCSC Genome Browser {Cornell Mirror}] |

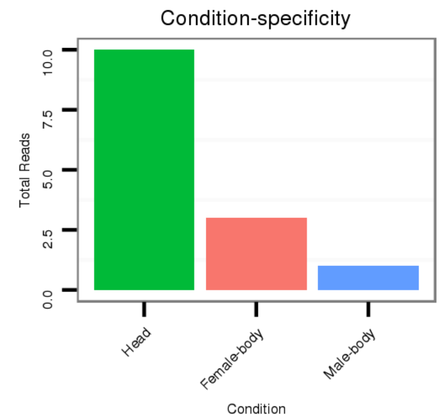
Legend: mature star mismatch in alignment mismatch in read

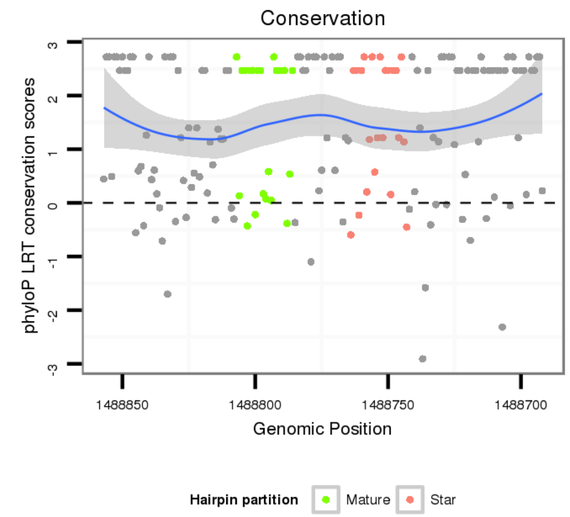
**Predicted structure**






Show Alternate Folds

**Flybase annnotation**

CDS [Dyak\GE25296-cds]

No Repeatable elements found

**Sense Strand Reads**

hide 3p reads show mid mismatch reads

| CAACATGTGGTTCGCAATTTCTGTGTTCGCCATTTTGGCCGTTTGCGGGCTGGCCGGCCGCAGGTGGGGTCGCTACCTCTACCTGCACTACGGCCGCCACCTGCTGCCGCGCTCCCTCCTCTCGGCCAAGAACCGCGCCCCCACGCCCCCCCTCTCGCCCACCAAG<br>**********(((((.....(((..(((((((.(((((((((((((.....)))))).)))))))).)))).)))))).....)))))).. | Read size | # Mismatch | Hit Count | Total Norm | Total | V058 head | V052 head | M043 female body | M056 embryo | V120 male body |
|---|---|---|---|---|---|---|---|---|---|---|
| .....TGGCCGGCCGCAGGTGGGGTCG..... | 22 | 0 | 1 | 8.00 | 8 | 3 | 4 | 1 | 0 | 0 |
| .....TGGCCGGCCGCAGGTGGGGTC..... | 21 | 0 | 1 | 3.00 | 3 | 2 | 1 | 0 | 0 | 0 |
| .....TGGCCGGCCGCAGGTGGGGTCT..... | 22 | 1 | 1 | 2.00 | 2 | 1 | 1 | 0 | 0 | 0 |
| .....TTTGGCCGTTTGCGGGCTGGC..... | 21 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 1 | 0 |
| .....GGTCGCTACCTCTACCTGCACTACGGC..... | 27 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 |
| .....TGGCCGGCCGCAGGTGGGGTCGT..... | 23 | 1 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 |
| .....CCGCCACCTGCTGCCGCGCTCC..... | 22 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 1 |
| .....GGCCGGCCGCAGGTGGGGTCG..... | 21 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 |
| .....GTGGTTCGCAATTTCTGT..... | 18 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 |
| .....GGGCTGGCCGGCCGCAGGT..... | 19 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 1 | 0 |
| .....CACCTGCTGCCGCGCTCGT..... | 19 | 2 | 20 | 0.05 | 1 | 1 | 0 | 0 | 0 | 0 |

**Anti-sense strand reads**

| GTTGTACACCAAGCGTTAAAGACACAAGCGGTAAAACCGGCAAACGCCCGACCGGCCGGCGTCCACCCCAGCGATGGAGATGGACGTGATGCCGGCGGTGGACGACGGCGCGAGGGAGGAGAGCCGGTTCTTGGCGCGGGGGTGCGGGGGGGAGAGCGGGTGGTTC<br>**********(((((.....(((..(((((((.(((((((((((((.....)))))).)))))))).)))).)))))).....)))))).. | Read size | # Mismatch | Hit Count | Total Norm | Total | M043 female body | M026 head | V058 head |
|---|---|---|---|---|---|---|---|---|
| .....GGCGCGGGGGTGCGGGGGGGA..... | 21 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 |

Show Alignment With Reads

**Re-alignment of all predicted orthologs**

| Species | Coordinate | ID | Alignment |
|---|---|---|---|
| droYak3 | 3R:1488692-1488857 - | dya_80 | CAACATGTGGTTCGCAATTTCTGTGTTCGCCATTTTGGCCGTTTGCG---GGCTGGCCGGCCGCAGGTGGGGTCGCTACCTCTACCTGCACTACGGCCGCCACCTGCTGCCGCGCTCCCTCCTCTCGGCCAAGAACCGCGCCCCCACGCCCCCCCTCTCGCCCACCAAG |
| droEre2 | scaffold_4770:1383614-1383779 - | der_85 | CAACATGTGGTTCGCAATTTCTGTGTTCGCCATTTTGGCCGTTTGCG---GGCTGGCCGGCCGCAGGTGGGGCCGCTACCTCTACCTGCACTACGGCCGCCACCTGCTGCCGCGCTCCCTCCTCTCGGCCAAGAACCGCGCGCCCACTCCCCCACTCTCGCCCACCAAG |
| droSec2 | scaffold_6:1229707-1229872 - | | CAACATGTGGTTCGCCATTTCTCTGTTCGCCATCTTGGCCGTTTGCG---GGCTGGCCGGCGCGCAGGTGGGGTCGCTACCTCTACCTGCACTACGGCCGCCACCTGCTGCCGCGCTCCCTCCTCTCGGCCAAGAACCGCGCGCCCACGCCCCCTCTCTCGCCCACCAAG |
| droSim2 | 3r:1012835-1013000 - | | CAACATGTGGTTCGCCATTTCTCTGTTCGCCATCTTGGCCGTTTGCG---GGCTGGCCGGCGCGCAGGTGGGGTCGCTACCTCTACCTGCACTACGGCCGCCACCTGCTGCCGCGCTCCCTCCTCTCGGCCAAGAACCGCGCGCCCACGCCCCCTCTCTCGCCCACCAAG |
| dm3 | chr3R:1108441-1108606 - | dme_384 | CAACATGTGGTTCGCCATTTCTCTGTTTGCCATCTTGGCCGTTTGCG---GGTTGGCCGGCCGCAGGTGGGGTCGCTACCTCTATCTGCACTACGGCCGCCACCTGCTGCCGCGCTCCCTCCTCTCGGCCAAGAACCGCGCGCCCACGCCCCCTCTCTCGCCCACCAAG |
| droEug1 | scf7180000409766:16869-17034 - | | CAACATGTGGTTTGCAATTTCCATTTTTGCCATTTTGGCCGTTTGCG---GATTGGCCGGTCGCAAGTGGGGCCGCTACCTCTACTTGCACTATGGCCGCCACCTGCTGCCCCGCTCCTTTCTAACGGCCAAGAACCGAGGTCCCACGCCCCCTCTTTCGCCCACCAAG |
| droBia1 | scf7180000302411:860218-860383 - | | CAACATGTGGTTCGCCATTTCCATTTTCGCCCTCCTGGCCGTGTGCG---GGCTGGCCGGCCGCCGGTGGGGTCGCTACCTCTACCTGCACTACGGCCGCCACCTGCTGCCCCGCTCCCTCCTGGCGGCCAAGAACCGCGCGCCCACGCCGCCCCTGTCGCCCACCAAG |
| droTak1 | scf7180000415789:282569-282734 + | | CAACATGTGGTTTGCCATTTCCATCTTTGCCATTTTGGCCGTTTGCG---GGCTGGCCGGTCGCAGGTGGGGTCGCTACCTCTACCTGCACTACGGCCGCCACCTGCTGCCCCGCTCCCTCCTGACGGTCAAGAACCGCGCGCCCACGCCCCCCCTCTCGCCCACCAAA |
| droEle1 | scf7180000491021:376339-376504 + | | CAACATGTGGTTTGTCATTTCCATTTTTGCCATTTTGGCTGTTTGCG---GGTTGGCCGGTCGCAGGTGGGGTCGCTACCTTTACCTGCACTATGGCCGCCACCTGCTGCCCCGCTCCCTGCTAGCGGTCAAAAACCGAGGTCCCACACCCCCACTTTCGCCCACCAAG |
| droFic1 | scf7180000453850:483104-483269 - | | CAACATGTGGTTCGCCATTTCAGTCTTCGCCCTTTTGGCCGTTTGCG---GGCTGGCCGGTCGCCGGTGGGGTCGCTACCTCTACCTGCACTACGGCCGCCACCTGCTGCCCCGCTCCCTGCTCGCCGCCAAGAACCGCGCCCCCACCCCGCCCCTCTCGCCCACCAAG |
| droKik1 | scf7180000302461:523333-523498 - | | CAACATGTGGTTCGTGATTTCCGTCTTCGCCATTTTGGCGGTCTGCG---GCCTAGCAGGTCGCGCGTGGGGTCGCTACCTTTACCTGCATTATGGCGCCACCTGCTGCCCCGCTCAATGCTTACAGCCAAGAACCGAGCGCCCACGCCCCCGCTCTCGCCCACCAAG |
| droAna3 | scaffold_13340:23291617-23291782 - | | CAACATGTGGTTCGTGATTTCCGTATTCGCCCTTGTGGCCCTTTTCG---GCCTGGCAGAGAGTCGTTGGGGCAGATACCTCTACCTGCACTACGGTGCTCATCTGCTGCCCCGCTCTCTGCTAGCCGCCAAAAACCGGTCCCCACGCCCCCACTCTCGCCCACCAAG |
| droBip1 | scf7180000396395:295439-295604 - | | CAACATGTGGTTCGTGATTTCCGTATTCGCCCTTGTGGCCCTTTTTG---GGCTGGCGGAGCGTCGTGGGGCAGGTACCTGTACCTGCACTACGGCCGCCACCTGCTGCCCCGCTCCATGCTGACCGCCAAGAACCGGTCCCCACGCCCCCCCTCTCGCCCACCAAG |
| dp5 | 2:21677107-21677272 + | | CAACATGTGGTTTGTGGTCGTACTCTTCGCTGTGGCCGCCGTGTGCG---GCCTGGCCGGTCGAAAGTGGGGCCGCTACCTGTACCTGCACTATGGCGCGCATCTGCTGCCGCGCTCTCTGCTGGCAAACAAGAACCGTGCGCCCACGCCGCCCCTCTCGCCCACCAAA |
| droPer2 | scaffold_3:4461895-4462060 + | | CAACATGTGGTTTGTGGTCGTACTCTTCGCTGTGGCCGCCGTGTGCG---GCCTGGCCGGTCGAAAGTGGGGCCGCTACCTGTACCTGCACTATGGCGCGCATCTGCTGCCGCGCTCTCTGCTGGCAAACAAGAACCGTGCGCCCACGCCGCCCCTCTCGCCGACCAAA |
| droWil2 | scf2_1100000004943:12820461-12820629 + | | AAAAATGTGGTTCATACTCTTGTTTTTGTTGCTGTGGTGCCTGCGGTGCTTTGGCCGGCCGCAGAATGGGGCAGATACCTGTATTTACATTATATACGCGCATCTATTGCCACGTTCCATACAATCGGCCAAAAATCGTGCACCCACACCGCCTCTATGACCCACCAAG |
| droVir3 | scaffold_12855:7804371-7804535 + | | -AACATGTGGTTTGTTGTGGCACTTTTTGCAATTGTCGCCGTCTGCG---GCGTTGCAGGTCGAAATGGGGTCGATACCTCTACCTGCACTACGGCCGCCACTTGCTGCCACGCTCAATGCTCACGGCCAAGAATCGGTCCCCACGCCGCCGCTCTCGCCAACCAAA |
| droMoj3 | scaffold_6540:23024005-23024170 + | | CAAGATGTGGTTCATTCTGGGACTCTTTGCAATTGTCGCCGTTGCG---GCGTAGCCGGTCGCAAATGGGGCCGCTACCTGTACCTGCACTATGGCCGCCACTTTCTGCCACGCTCCATGCTGTCATCAAGAATCGGTCCCCACACCGCCGCTCTCGCCCACCAAA |
| droGri2 | scaffold_15074:4359079-4359244 + | | AAACATGTGGTTTGTTGTCGCACTGTTTTGCAATTGTCGCCGCCTGCG---GCGTTGCTGGTCGCAAATGGGGTCGTTACCTCTATCTGCACTATGGCGCGCACTTGCTACCACGCTCAATGCTCACGGCGAAAAATCGGTCACCGACGCCGCCGTCTCGCCTACCAAA |

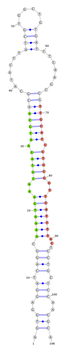
Generated: 09/08/2015 at 07:52 PM

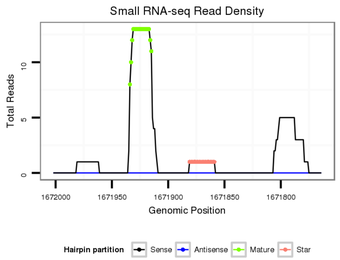
| | PASS/FAIL |
|---|---|
| crit.star | 0 |
| crit.loop | 0 |
| crit.mor | 0 |
| crit.half | 0 |
| crit.total | 0 |
| crit.pairing | 1 |
| crit.top3 | 1 |
| crit.tptop3 | 1 |
| crit.uri | 0 |
| crit.back | 1 |
| rescue.total | 1 |
| rescue.dominant | 1 |
| rescue.known | 0 |
| rescue.confident | 1 |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

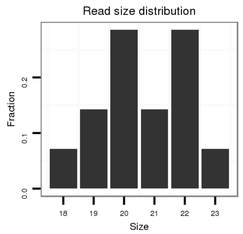
| ID: | Coordinate: | Confidence: | Class: | Genomic Locale: | |
|---|---|---|---|---|---|
| **dya_668** | **3L:1671814-1671952 -** | **candidate-rescued** | **Canonical miRNA** | **intron** | [View on UCSC Genome Browser [Cornell Mirror]] |

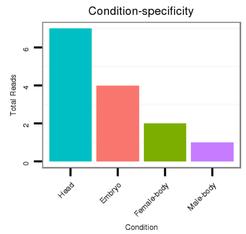
Legend: mature star mismatch in alignment mismatch in read

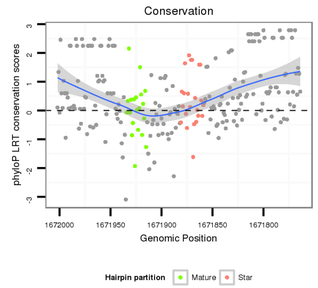
**Predicted structure**






Show Alternate Folds

**Flybase annnotation**

intron [Dyak/GE20925-in]; CDS [Dyak/GE20925-cds]; CDS [Dyak/GE20925-cds]

No Repeatable elements found

**Sense Strand Reads**

hide 3p reads | show mid mismatch reads

```
CACCACGTGTCCGGCGAATGCCAGTGTGCGCCTGGTTTCACGGGTCCCCTGTAAGTGGAGGATCAGGCAAAATGAAACGTAGAATGCAACGCATACTTATCGTGGCTGTGATTTCAAGCCGTTGCATCCTGCGGTTCATTTTACTCCTGCTCCAACGCAAAACCCATACTAATCCTCCGCTCCAACTAGATGCGATATGCGCTGTCCGGACGGGAAGCATGGCGCCCAGTGCCAACAGG
*************************************************.(((..(((.((((.((((((((..((((.(((((((.........((((......)))).......)))))))).))))))..))))))).))))..))))..))))..))))..*************************************************
```

| | Read size | # Mismatch | Hit Count | Total Norm | Total | M056 embryo | V058 head | M026 head | M043 female body | V120 male body | V052 head |
|---|---|---|---|---|---|---|---|---|---|---|---|
| .....AAAATGAAACGTAGAATGCA..... | 20 | 0 | 1 | 4.00 | 4 | 1 | 1 | 1 | 1 | 0 | 0 |
| .....ATGCGCTGTCCGGACGGGAA..... | 19 | 0 | 1 | 2.00 | 2 | 0 | 0 | 0 | 1 | 1 | 0 |
| .....CAAAATGAAACGTAGAATGCAA..... | 22 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....ATGAAACGTAGAATGCAACGCA..... | 22 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| .....AAATGAAACGTAGAATGCAACG..... | 22 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....CAAAATGAAACGTAGAATGCA..... | 21 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....GCGCTGTCCGGACGGGAAGCATGGC..... | 25 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| .....GCTGTCCGGACGGGAAGCATGGCGCCC..... | 27 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AATGAAACGTAGAATGCAACGC..... | 22 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AAAATGAAACGTAGAATG..... | 18 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....CTGTCCGGACGGGAAGCATGGC..... | 22 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |
| .....CAGTGTGCGCCTGGTTTCAC..... | 20 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 1 | 0 | 0 |
| .....AATGAAACGTAGAATGCAACG..... | 21 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| .....AAATGAAACGTAGAATGCA..... | 19 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 1 | 0 | 0 |
| .....TTGCATCCTGCGGTTCATTTTAC..... | 23 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....AAATGAAACGTAGAATGCAACG..... | 22 | 1 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| .....AAAATGAAACGTAGAATGC..... | 19 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |

**Anti-sense strand reads**

```
GTGGTGCACAGGCCGCTTACGGTCACACGCGGACCAAAGTGCCCAGGGGACATTCACCTCCTAGTCCGTTTTACTTTGCATCTTACGTTGCGTATGAATAGCACCGACACTAAAGTTCGGCAACGTAAGGTTGCGTTTTGGGTATGATTAGGAGGCGAGGTTGATCTACGCTATACGCGACAGGCCTGCCCTTCGTACCGCGGGTCACGGTTGTCC
*************************************************.(((..(((.((((.((((((((..((((.(((((((.........((((......)))).......)))))))).))))))..))))))).))))..))))..))))..))))..*************************************************
```

| | Read size | # Mismatch | Hit Count | Total Norm | Total | V058 head |
|---|---|---|---|---|---|---|

Show Alignment With Reads

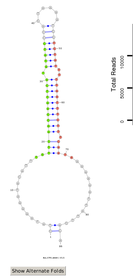
**Re-alignment of all predicted orthologs**

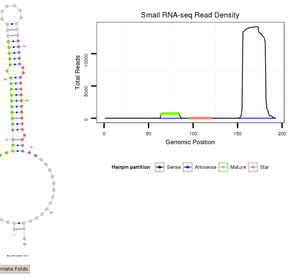
| Species | Coordinate | ID | Alignment |
|---|---|---|---|
| droYak3 | 3L:1671764-1672002 - | dya_668 | CACCACGTGTCCGGCGAATGCCAGTGTGCGCCTGGTTTCACGGGTCCCCTGTAAGTGGAG----------GAT-CA-GG--C----AAAAT-GAAACGTAGAATGCACG--------CA----------T--ACTTATCGTGGCTGTGATTTCAAGCCGTTGCATCCTGCGGTTCATTT----------TAATCCTGC----T----------CCAACGCAAAA-CCCATA-----CTAATCCTCCGCTC-----C-AACTAGATGCGATATGCGCTGTCCGGACGGGAAGC----------ATGGCGCCCAGTGCCAACAGG |
| droEre2 | scaffold_4784:1702664-1702939 - | der_1510 | CACCACGTGTCCGGCGAATGCCAGTGTGCGCCTGGTTCACGGGTCCCCTGTAAGTGGACGA----------A--C----G--AGCCTC-TTT--GGCGGCGTTAACTTCTGGCG----------GAGGAT-C-GG--C----AAAAT-GAAACGTAGAATGCAACG--------CA----------T--A-TTCGTGTCGCTATTT-AAGCCGTTGCATCCTGCGCTCATTT----------TAATCCTGC----T----------CCAACGCAAAA-CCCATA-----CTAATCCTCCGCTC-----C-AACTAGATGCGATATGCGCTGTCCGGACGGGAAC----------AGGGCGCCCAGTGCCAGGG |
| droSec2 | scaffold_21746138-17464154 - | dse_994 | CACCACGTGTCCGGCGAATGCCAGTGTGCGCCGGTTTCACGGGTCCCCTGTAAGTGACGG----------A--C----G--GGCGTC-TTT--GGCGGCACAAGCTTCTGGCC----------GAGGAT-TC-GGATT----AAAAT-GAAACGTAGAATGCAACG--------A----------T--A-TTCTCGTGGCTGTGATTTCAGCCCTTGCATCCTACGTTCATTT----------TGTCCTGC----T----------CCAACGCAAAA-CCCATA-----CTAATCTCCGCTC-----C-AACTAGATGCGATATGCGCTGTCCGGACGGGAAGC----------ATGGCGCCCAGTGCCAGGG |
| droSim2 | 3L:1629569-1629846 - | dsi_4243 | CACCACGTGTCCGGCGAATGCCAGTGTGCGCCGGTTTCACGGGTCCCCTGTAAGTGGCGG----------G--C----A--GGCGTC-TTT--GGCGGCCACAAGCTTCTGGCC----------GAGGAT-A-GGATT----AAAAT-GAAACGTAGAATGCAACG--------A----------T--A-TTCCCGTGGCTGTGATTTCAGCCCTTGCATCCTACGTTCATTT----------TGTCCTGC----T----------CCAACGCAAAA-CCCATA-----CTAATCTCCGCTC-----C-AACTAGATGCGATATGCGCTGTCCGGACGGGAAGC----------ATGGCGCCCAGTGCCAGGG |
| dmel | chr3L:11719696-1719972 - | dme_418 | CACCACGTGTCCGGCGAATGCCAGTGTGCGCCGGTTTCACGGGTCCCCTGTAAGTGGAGGA----------A--C----G--GGCGTC-TTT--GGCGGCACAAGCTTCTGGCC----------GAGGAT-CA-GG--C----AAAAT-GAAACGTAGAATGCAACG--------A----------T--A-TTCCCGTGGCTGTGATTTCAGCCCTTGCATCCTACGTTCATTT----------TGTCCTGC----T----------CCAACGCAAAA-CCCATA-----CTAATCTCCGCTC-----C-AACTAGATGCGATATGCGCTGTCCGGACGGGAAGC----------ATGGCGCCCAGTGCCAGGG |
| droEug1 | scf7180000407356:39346-39641 - | | CACCACGTGTCCGGCGAATGCCAGTGTGCGCCGGTTTCACGGTCCCCTGTAAGTGGAGGAA-A--C--TTGA----C----G--AGCCTC-TTG--GGCGGCATAACCCTATCGCG----------GAGGAT-CA-GG--C----AAAAT-GAAACGTAGAATGCATCG--------A----------T--A-TTCCCGTGGCTGTGATTTCAGCCCTTGCATCCTACGTTCATTT----------TGTCCTGC----T----------CAATTAGGTTATGCTCTTGAAA-A-ATA-----CTAATCCTCCGCTC-----C-AACTAGATGCGATATGCGCTGTCCGGACGGGAAC----------ATGGCGCCCAGTGCCAGGG |
| droBia1 | scf7180000302428:8410899-8411008 - | | ----------G--C----A--GGCGTC-TTT--GGCGGCATAACCCTATCGCG----------GAGGAT-CA-GG--C----AAAAT-GAAACGTAGAATGCATCG--------A----------T--A-TTCCCGTGGCTGTGATTTCAGCCCTTGCATCCTACGTTCATTT----------TGTCCTGC----T----------CCAACGCAAAA-CCCATA-----CTAATCCTCCGCTC-----C-AACTAGATGCGATATGCGCTGTCCGGACGGGAAC----------ATGGCGCCCAGTGCCAGGG |
| droTak1 | scf7180000415095:40441-40678 + | | GATGGGCCAAGGAACGTATGTCAATCCGGATGGGGGTGAATTGCAGGAGAG----------GATCTGCGAGGCGG----------ACAAGTACGG--G----------AATGCACTGG----C-AATGCGCTGCATGTGGATC--------A----------T--A-TGCACACGACTGTGC----------T--------T----------TTAACGGG--A-CGGGAAAGTGC----------T--------T----------ACTGCAGCATTGGCTGCAGCAGTGCCAGTGCACCAGGCCTGCACCTTCCTGCGGCTGGCGCACTGTGGCGATCA |
| droRe1 | scf7180000491249:3840772-3841003 + | | GATGGGCCAAGGATCCTGTATCTCAATCCGGATGGCGGCGGCGAATTGTAGGAG----------GAGGATTTGCGAGGCGG----------ACAAGTATGG--G----------AATTGCACTGG----C-AACGCGCTGCATGTGGATC--------A----------T--A-TGCACACGACTGTGC----------T--------T----------CCAACGGG--A-CGGGCAAATGC----------T--------T----------AATCAGCATTGGCTGCAGCAGTGCCAGTGCACAGACCCTGTACCTTCCTGCGGCTGGCGCACTGTGGCGATCA |
| droRho1 | scf7180000776850:217126-217435 + | | CACCACGTGTCCGGCGAATGCCAGTGTGCACCTGGTTTCACGGGTCCCTGTAAGTGGAGGAA-A--C--TAGA----C----G--AGTGTC-TTT--CGGTGACATCATCGAAATGGCA----------GAGGAT-CA-GG--C----AAAAT-GAAACGTAGAATGCATCG--------A----------T--A-TCAAGCAAGT------TAATTA-A-GGTTTGTT--------ATAC-T-AATTACTGCATCCTAGCATTGATTT----------TGTTTTCTGAGCTCTCCGATATGTTA-G-GAAAA-A-CGTA-----CTAATCCTCCGCTC-----C-AACTAGATGCGATGCGCTGTCCGGACGGGAAGC----------ATGGCGCCCAGTGCCAGGG |
| droPic1 | scf7180000454113:356473-356728 + | | CACCACGTGTCCGGCGAATGCCAGTGTGCGCCGGTTTCACGGGTCCCTGTAAGTGGAGGAA-A--C--TCGA----C--G--A--GGCGCC-TTT----------AGGATGTG-GG-T----G-AGCTGTGATGCATGTGGATGCTGAAACTGTGTG----------A----------T--A-TTGT--------TTTGCCCTGCGCATTTCAGCATTGATTT----------TGTTTTCCCCCTGGCGCTTTGCCAAGT----------GACGT---------T----------T----------AGCGAA-CCCGT-----CTAACTTAA-T-TAACGCCG-CAACTAGATGCGATGCGCTGTCCGGACGGGAAGC----------AGGGCGCCCAGTGCCAGGG |
| droKik1 | scf7180000302577:200384-200696 - | | CACCACGTGTCCGGCGAATGCCAGTGTGCGCCGGTTTCACGGGTCCCCTGTAAGTGGCAAA----------GAGG----------AGCTGCCTCTTGCCTCGGAGACATATCA----------TTTCGCCTTGAGCTG-T-G-A-C----A----------C-CTATGCATG-CACATTTTATTA-T-A--TT----------TA-CCTGGGATATTAGCATTGATTT----------TTCCTT---------T----------CACCA-CCGAA-CCCGT-----CTAATCCTCCGCTC-----C-AAATAGATGCGATGCGCTGTCCGGACGGGAAGC----------AGGGCGCCCAGTGCCAGGG |
| droAna3 | scaffold_13337:1119407-1119716 + | | CACCACGTGTCCGGCGAATGCCAGTGTGCGCCGGTTTCACGGGTCCCTGTAAGTGCCGA----------GAGGA----------GGATTC-TTT----CACGCAAAAGGGTCATGGCATA----GAGCCTAGGGGTATGGCATTGCCTGCTAGCTGTAGCTTCTTTATGCCCCGGGGCTGTATGCTTGATTTCCCTGCTA----------TAG-TTTGGCGATTAGGGTGATCGTTCTATGACCCCGGGGCTGTATGCTTGATTTCCCTGCTA----------A-G-G-G-AAT--G-GGA-----CTAATCCTCCGCTC-----C-AACTAGATGCGATGCGCTGTCCGGACGGGAAGC----------AGGGCGCCAGTGCCAGGG |
| droHip1 | scf7180000396371:1451505-1451819 + | | CACCACGTGTCCGGCGAATGCCAGTGTGCGCCGGTTTCACGGGTCCCCTGTAAGTGCCGA----------GAGGA----------GGATTCGTTTT-GACGCAAAAGGGAACATGGCATA----GAGCCTAGGGCTTATAGTGTGCGTGCGTGATGCTTTGCATTGATTACAAATGTGCGCTGTGCGCTGTGCGCT

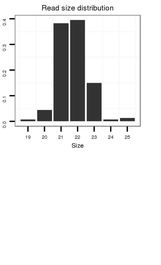
| ID: | Coordinate: | Confidence: | Class: | Genomic Locus: |
|---|---|---|---|---|
| **dya_1793** | **v2_chrUn_1311:45-143 +** | **candidate-rescued** | **Canonical miRNA** | **intergenic** |
| | | | | [View on UCSC Genome Browser (Comfil Mitmit)] |

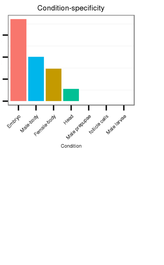
Legend: Loop Star Mature 5 arm in mature Mature 3 arm in mature

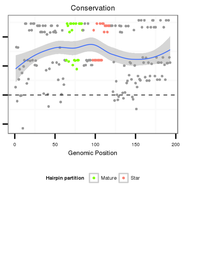
## Predicted structure






Show Alternate Folds

## Flybase annotation

dRNA:Dyak\FBrRNAAGE26302-RA]

## Repeatable elements

| Name | Class | Family | Strand |
|---|---|---|---|
| AT_rich | Low_complexity | Low_complexity | + |

**mature**

1. dya_1793 v2_chrUn_1311:45-143 +
2. v2_chrUn_2920:788-728 +
3. v2_chrUn_1929:235-293 +
4. v2_chrUn_4644:179-199 +
5. v2_chrUn_4933:1063-1023 +
6. v2_chrUn_2147:1-41 +
7. v2_chrUn_2347:62-94 +
8. v2_chrUn_5370:203-223 +
9. v2_chrUn_5306:4414-4361 +
10. v2_chrUn_5762:888-908 +
11. v2_chrUn_2944:2472-2492 +
12. v2_chrUn_2944:2472-2492 +
13. v2_chrUn_2613:7268-7288 +
14. v2_chrUn_2167:926-7846 +
15. v2_chrUn_2944:4355-4375 +
16. v2_chrUn_2763:2951-2911 +
17. v2_chrUn_4475:1-41 +
18. v2_chrUn_5370:1395-1435 +
19. v2_chrUn_3133:52-5242 +
20. v2_chrUn_924:1125-1143 +
21. v2_chrUn_2514:436-456 +
22. v2_chrUn_4130:1030-1030 +
23. v2_chrUn_5306:4414-4361 +
24. v2_chrUn_3472:129-149 +
25. v2_chrUn_3944:8-44 +
26. v2_chrUn_5746:1201-1241 +
27. v2_chrUn_3273:1669-1689 +

**star**

1. dya_1793 v2_chrUn_1311:97-119 +
2. v2_chrUn_2920:743-763 +
3. v2_chrUn_4230:975-997 +
4. v2_chrUn_1739:110-1132 +
5. v2_chrUn_1938:198-220 +
6. v2_chrUn_2147:1-41 +
7. v2_chrUn_4644:101-161 +
8. v2_chrUn_5347:954-978 +
9. v2_chrUn_5370:634-595 +
10. v2_chrUn_3294:4174-4396 +
11. v2_chrUn_3472:98-140 +
12. v2_chrUn_3472:98-140 +
13. v2_chrUn_2364:9-31 +
14. v2_chrUn_4164:187-1189 +
15. v2_chrUn_0614:6856-6898 +
16. v2_chrUn_0615:581-533 +
17. v2_chrUn_2:1-41 +
18. v2_chrUn_5370:1396-1436 +
19. v2_chrUn_3:6:2924-3946 +
20. v2_chrUn_4:87:4873-4893 +
21. v2_chrUn_4933:868-890 +
22. v2_chrUn_2990:90-130 +
23. v2_chrUn_5347:954-978 (5746:1243-1270) +
24. v2_chrUn_3543:2504-2556 +
25. v2_chrUn_6:26:1323-1324 +
26. v2_chrUn_3524:411-421 +

## Sense Strand Reads

Hide 3p reads  Show mid mismatch reads

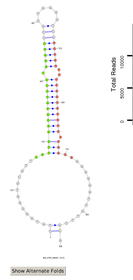
```
TACATAAGTCCTTATGAGAACTAAGACATTTCCCAGCATTTATTTTAGGTATAAAAATACATTTATTGAAGGAATTGATATATCCAGTAAAATCGTATTTTTAATTTCTTTCAATTAAAAAATTATTGACATATATAGAAATAAATTATAAACTCTAAGCGTGATCACTCGGCTCATGGCTCGATG
```

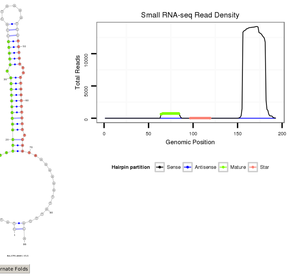
| Read # | Size | Mismatch | Hit Count | Total Norm | Total | V120 male body | V120 female body | M043 follicle cells | M043 female body | V058 head | M026 head | M056 embryo | V052 head | V046 embryo | SRR1275484 Male pregonads | SRR1275485 Male larvae | SRR1275486 Male pregonads |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | GSM1528802 | | | | | | | | | | | |
| 26 | 0 | | 20 | 7843.75 | 156875 | 120737 | 13571 | 4323 | 7163 | 6650 | 1335 | 2956 | 134 | 7 | 4 | 0 | 0 |
| 21 | 0 | | 20 | 1203.60 | 24072 | 12503 | 4326 | 2979 | 1618 | 595 | 1388 | 415 | 46 | 2 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 723.45 | 14469 | 9 | 9311 | | 313 | 2801 | 441 | 275 | 1291 | 28 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 7352.94 | 12797 | 1832 | 952 | | 327 | 473 | 546 | 152 | 164 | 9 | 1 | 1 | 0 |
| 25 | 0 | | 20 | 511.95 | 10221 | 3068 | 4608 | | 831 | 415 | 516 | 536 | 153 | 89 | 3 | 2 | 0 |
| 25 | 0 | | 20 | 464.26 | 8886 | 583 | 7839 | | 0 | 0 | 424 | 40 | 0 | 46 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 251.35 | 5027 | 2080 | 0 | | 1350 | 360 | 12 | 0 | 66 | 1158 | 0 | 1 | 0 |
| 20 | 0 | | 20 | 240.90 | 4858 | 1000 | 0 | | 213 | 157 | 1474 | 38 | 2102 | 2 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 204.45 | 4093 | 0 | 4084 | | 0 | 0 | 0 | 0 | 0 | 0 | 4 | 0 | 0 |
| 30 | 0 | | 20 | 179.49 | 3590 | 1576 | 0 | | 895 | 249 | 229 | 0 | 0 | 0 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 159.89 | 2878 | 2372 | 265 | | 33 | 29 | 159 | 3 | 6 | 1 | 5 | 0 | 0 |
| 23 | 0 | | 20 | 149.05 | 2981 | 1284 | 972 | | 370 | 207 | 8 | 0 | 90 | 45 | 1 | 1 | 1 |
| 24 | 0 | | 20 | 135.70 | 2714 | 704 | 1642 | | 232 | 104 | 19 | 45 | 45 | 14 | 0 | 2 | 1 |
| 21 | 0 | | 20 | 125.35 | 2507 | 497 | 485 | | 927 | 306 | 20 | 115 | 147 | 6 | 4 | 0 | 0 |
| 18 | 0 | | 20 | 121.72 | 2191 | 1256 | 494 | | 127 | 45 | 120 | 128 | 19 | 2 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 121.00 | 2420 | 409 | 1194 | | 649 | 26 | 25 | 94 | 17 | 4 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 90.40 | 1892 | 99 | 5 | | 293 | 23 | 12 | 1293 | 2 | 258 | 3 | 0 | 0 |
| 26 | 1 | | 20 | 91.55 | 1831 | 155 | 1 | | 2 | 15 | 1228 | 424 | 4 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 76.05 | 1521 | 0 | 272 | | 583 | 407 | 16 | 27 | 0 | 16 | 0 | 0 | 0 |
| 25 | 0 | | 20 | 71.70 | 1434 | 414 | 370 | | 311 | 35 | 46 | 31 | 24 | 3 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 18.98 | 1279 | 1223 | 6 | | 0 | 40 | 10 | 0 | 0 | 0 | 0 | 0 | 0 |
| 17 | 0 | | 20 | 66.45 | 1333 | 0 | 1195 | | 0 | 136 | 0 | 0 | 0 | 0 | 2 | 0 | 0 |
| 20 | 0 | | 20 | 65.76 | 1314 | 56 | 101 | | 441 | 0 | 202 | 134 | 369 | 13 | 0 | 0 | 0 |
| 25 | 0 | | 20 | 63.80 | 1276 | 6 | 1252 | | 11 | 0 | 0 | 4 | 3 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 57.50 | 1035 | 16 | 744 | | 43 | 128 | 13 | 50 | 39 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 50.47 | 912 | 268 | 313 | | 98 | 27 | 59 | 130 | 6 | 11 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 48.46 | 972 | 513 | 157 | | 87 | 55 | 53 | 70 | 32 | 5 | 2 | 0 | 0 |
| 28 | 0 | | 20 | 48.45 | 969 | 7 | 936 | | 0 | 0 | 10 | 17 | 1 | 0 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 35.95 | 719 | 158 | 327 | | 51 | 52 | 19 | 85 | 103 | 29 | 1 | 0 | 0 |
| 22 | 0 | | 20 | 34.15 | 683 | 157 | 0 | | 206 | 83 | 0 | 97 | 24 | 115 | 0 | 1 | 0 |
| 30 | 0 | | 20 | 18.32 | 681 | 12 | 589 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 29.00 | 580 | 3 | 577 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 31 | 0 | | 20 | 28.00 | 560 | 0 | 560 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 26.45 | 529 | 142 | 0 | | 183 | 0 | 29 | 0 | 11 | 162 | 1 | 1 | 0 |
| 23 | 0 | | 20 | 23.45 | 469 | 195 | 159 | | 44 | 30 | 14 | 15 | 11 | 1 | 0 | 0 | 0 |
| 29 | 0 | | 18 | 22.61 | 407 | 228 | 137 | | 1 | 0 | 21 | 20 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 21.80 | 436 | 49 | 132 | | 216 | 5 | 26 | 4 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 18.60 | 372 | 19 | 353 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 17 | 0 | | 20 | 17.70 | 354 | 154 | 1 | | 64 | 50 | 4 | 41 | 15 | 0 | 0 | 0 | 0 |
| 17 | 0 | | 20 | 16.55 | 331 | 0 | 331 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 16.44 | 296 | 103 | 46 | | 46 | 16 | 10 | 47 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 16.40 | 328 | 2 | 297 | | 20 | 1 | 0 | 6 | 1 | 1 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 16.39 | 295 | 0 | 295 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 15.50 | 310 | 112 | 0 | | 60 | 15 | 0 | 123 | 0 | 0 | 0 | 0 | 0 |
| 25 | 0 | | 20 | 15.35 | 307 | 43 | 247 | | 15 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 15.05 | 301 | 25 | 144 | | 43 | 14 | 0 | 60 | 5 | 4 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 14.80 | 267 | 45 | 181 | | 24 | 4 | 0 | 8 | 0 | 5 | 0 | 0 | 0 |
| 27 | 0 | | 18 | 14.78 | 266 | 97 | 92 | | 34 | 5 | 16 | 31 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 14.45 | 289 | 5 | 284 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 14.25 | 285 | 8 | 36 | | 42 | 36 | 9 | 112 | 13 | 2 | 0 | 0 | 0 |
| 27 | 0 | | 20 | 13.80 | 276 | 18 | 258 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | | 18 | 13.12 | 263 | 247 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 13.70 | 274 | 18 | 92 | | 79 | 18 | 1 | 61 | 4 | 1 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 13.35 | 267 | 8 | 244 | | 11 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 |
| 26 | 1 | | 20 | 12.30 | 246 | 19 | 1 | | 0 | 7 | 237 | 0 | 2 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 10.30 | 206 | 56 | 0 | | 148 | 28 | 0 | 22 | 2 | 0 | 0 | 1 | 0 |
| 20 | 0 | | 20 | 10.25 | 265 | 78 | 0 | | 57 | 0 | 3 | 61 | 3 | 63 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 10.21 | 249 | 4 | 40 | | 51 | 42 | 17 | 39 | 13 | 33 | 0 | 0 | 0 |
| 15 | 0 | | 20 | 10.05 | 261 | 0 | 261 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 10.00 | 254 | 54 | 0 | | 45 | 36 | 13 | 73 | 0 | 22 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 12.75 | 255 | 40 | 51 | | 23 | 29 | 11 | 87 | 9 | 5 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 12.23 | 245 | 41 | 0 | | 110 | 38 | 0 | 26 | 21 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 12.20 | 244 | 101 | 0 | | 0 | 8 | 0 | 71 | 3 | 61 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 11.85 | 237 | 70 | 0 | | 59 | 42 | 0 | 0 | 21 | 45 | 0 | 0 | 0 |
| 27 | 0 | | 20 | 11.80 | 236 | 6 | 203 | | 10 | 1 | 7 | 9 | 0 | 0 | 0 | 0 | 0 |
| 27 | 0 | | 18 | 11.47 | 210 | 46 | 0 | | 0 | 1 | 109 | 54 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 18 | 11.56 | 208 | 103 | 35 | | 25 | 23 | 2 | 8 | 11 | 1 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 11.35 | 231 | 45 | 32 | | 38 | 15 | 0 | 69 | 17 | 0 | 0 | 1 | 0 |
| 21 | 0 | | 20 | 11.35 | 227 | 15 | 0 | | 49 | 27 | 0 | 17 | 15 | 64 | 0 | 0 | 0 |
| 19 | 0 | | 17 | 11.28 | 192 | 23 | 153 | | 3 | 2 | 9 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 18 | 11.22 | 202 | 5 | 180 | | 6 | 3 | 1 | 6 | 1 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 10.55 | 211 | 78 | 0 | | 52 | 30 | 0 | 38 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 10.00 | 180 | 80 | 34 | | 30 | 0 | 7 | 29 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 9.85 | 197 | 35 | 0 | | 48 | 28 | 16 | 36 | 11 | 3 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 9.80 | 196 | 45 | 19 | | 23 | 22 | 6 | 61 | 14 | 6 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 9.28 | 167 | 115 | 9 | | 22 | 8 | 3 | 1 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 8.75 | 175 | 19 | 57 | | 61 | 4 | 2 | 23 | 3 | 6 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 8.25 | 165 | 5 | 25 | | 60 | 9 | 4 | 58 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 8.25 | 165 | 0 | 0 | | 133 | 0 | 0 | 32 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 8.22 | 148 | 22 | 9 | | 76 | 20 | 0 | 10 | 0 | 10 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 8.15 | 163 | 4 | 15 | | 79 | 24 | 2 | 11 | 23 | 3 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 8.05 | 161 | 3 | 132 | | 2 | 2 | 5 | 1 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 7.60 | 152 | 0 | 0 | | 139 | 0 | 0 | 11 | 0 | 2 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 7.40 | 152 | 19 | 21 | | 90 | 14 | 0 | 4 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 7.55 | 151 | 56 | 0 | | 41 | 30 | 1 | 2 | 15 | 6 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 7.35 | 147 | 147 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 7.25 | 145 | 2 | 143 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 7.10 | 142 | 33 | 0 | | 54 | 37 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 18 | 7.06 | 127 | 29 | 95 | | 0 | 0 | 1 | 2 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 6.35 | 127 | 15 | 0 | | 12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 6.35 | 127 | 15 | 0 | | 11 | 2 | 79 | 16 | 0 | 3 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 6.25 | 125 | 2 | 0 | | 54 | 9 | 1 | 55 | 4 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 19 | 6.14 | 117 | 58 | 21 | | 20 | 12 | 2 | 3 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 6.10 | 122 | 42 | 18 | | 34 | 0 | 0 | 9 | 13 | 6 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 6.10 | 122 | 0 | 30 | | 29 | 18 | 24 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 19 | 6.05 | 115 | 25 | 35 | | 24 | 15 | 0 | 10 | 4 | 2 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 5.95 | 119 | 3 | 99 | | 12 | 1 | 1 | 3 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 5.95 | 119 | 27 | 47 | | 8 | 8 | 9 | 13 | 4 | 3 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 5.90 | 118 | 0 | 0 | | 66 | 0 | 5 | 0 | 0 | 18 | 0 | 0 | 0 |
| 27 | 0 | | 17 | 5.88 | 100 | 57 | 10 | | 13 | 1 | 10 | 9 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 5.85 | 117 | 0 | 117 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 5.80 | 116 | 40 | 20 | | 17 | 22 | 0 | 3 | 11 | 3 | 0 | 0 | 0 |
| 27 | 0 | | 20 | 5.80 | 116 | 8 | 0 | | 53 | 4 | 0 | 50 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 5.80 | 116 | 45 | 27 | | 21 | 7 | 1 | 10 | 4 | 1 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 5.80 | 116 | 4 | 82 | | 3 | 2 | 4 | 2 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 5.75 | 115 | 4 | 78 | | 14 | 3 | 4 | 12 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 18 | 5.78 | 104 | 6 | 92 | | 0 | 2 | 0 | 0 | 4 | 0 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 5.60 | 112 | 2 | 38 | | 46 | 18 | 0 | 2 | 4 | 2 | 0 | 0 | 0 |
| 21 | 0 | | 18 | 5.78 | 104 | 6 | 82 | | 3 | 2 | 4 | 2 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 5.45 | 109 | 0 | 56 | | 11 | 12 | 4 | 20 | 4 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 5.45 | 109 | 15 | 20 | | 45 | 3 | 0 | 5 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 5.40 | 108 | 41 | 0 | | 25 | 25 | 0 | 3 | 8 | 6 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.35 | 107 | 28 | 0 | | 35 | 17 | 0 | 13 | 12 | 2 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.35 | 107 | 0 | 0 | | 88 | 2 | 0 | 17 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 18 | 5.28 | 95 | 12 | 0 | | 35 | 17 | 4 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 18 | 5.28 | 95 | 3 | 0 | | 21 | 43 | 4 | 13 | 10 | 1 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.25 | 105 | 0 | 105 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.15 | 103 | 48 | 0 | | 13 | 15 | 0 | 9 | 8 | 10 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.05 | 101 | 12 | 0 | | 39 | 6 | 0 | 42 | 0 | 2 | 0 | 0 | 0 |
| 16 | 0 | | 20 | 5.05 | 101 | 0 | 101 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.95 | 99 | 5 | 89 | | 4 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.95 | 99 | 28 | 37 | | 12 | 9 | 3 | 6 | 4 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 4.84 | 92 | 92 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 4.80 | 96 | 8 | 10 | | 56 | 13 | 1 | 3 | 4 | 1 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 4.65 | 93 | 4 | 47 | | 7 | 0 | 13 | 2 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 4.60 | 92 | 4 | 83 | | 0 | 1 | 2 | 2 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 4.60 | 92 | 0 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 4.50 | 90 | 40 | 16 | | 12 | 12 | 0 | 4 | 6 | 2 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 4.50 | 90 | 2 | 3 | | 52 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 4.40 | 88 | 10 | 0 | | 52 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.35 | 87 | 20 | 0 | | 32 | 21 | 0 | 5 | 8 | 1 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.35 | 87 | 4 | 47 | | 24 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 4.30 | 86 | 20 | 0 | | 49 | 0 | 1 | 13 | 3 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 4.25 | 76 | 29 | 16 | | 13 | 5 | 3 | 8 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 4.20 | 84 | 19 | 18 | | 26 | 0 | 1 | 9 | 11 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 4.05 | 81 | 0 | 0 | | 21 | 18 | 0 | 14 | 0 | 28 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 4.05 | 81 | 2 | 24 | | 24 | 2 | 6 | 21 | 1 | 1 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 4.00 | 80 | 3 | 12 | | 39 | 4 | 0 | 11 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.00 | 80 | 26 | 0 | | 11 | 17 | 0 | 5 | 11 | 10 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.95 | 79 | 7 | 45 | | 22 | 0 | 1 | 1 | 2 | 1 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.95 | 79 | 7 | 45 | | 22 | 0 | 1 | 1 | 2 | 1 | 0 | 0 | 0 |
| 21 | 0 | | 18 | 3.94 | 71 | 15 | 43 | | 7 | 2 | 3 | 1 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 3.85 | 77 | 1 | 0 | | 27 | 5 | 9 | 31 | 3 | 1 | 0 | 0 | 0 |
| 31 | 0 | | 20 | 3.75 | 75 | 0 | 75 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 3.70 | 74 | 1 | 3 | | 37 | 20 | 2 | 4 | 7 | 0 | 0 | 0 | 0 |
| 18 | 0 | | 18 | 3.47 | 66 | 1 | 50 | | 4 | 3 | 4 | 2 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.45 | 73 | 3 | 66 | | 3 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.45 | 73 | 1 | 4 | | 32 | 3 | 5 | 27 | 0 | 3 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.45 | 73 | 15 | 0 | | 32 | 10 | 0 | 5 | 8 | 3 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 3.45 | 73 | 2 | 49 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 3.45 | 73 | 0 | 43 | | 11 | 3 | 1 | 13 | 0 | 1 | 0 | 1 | 0 |
| 29 | 0 | | 20 | 3.40 | 72 | 0 | 0 | | 25 | 5 | 22 | 24 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 17 | 3.59 | 61 | 48 | 0 | | 9 | 1 | 2 | 1 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 3.50 | 63 | 0 | 63 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | | 18 | 3.50 | 63 | 60 | 3 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 16 | 0 | | 20 | 3.45 | 69 | 0 | 65 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 3.40 | 68 | 52 | 0 | | 8 | 1 | 0 | 7 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.35 | 67 | 0 | 0 | | 21 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 28 | 1 | | 20 | 3.30 | 66 | 6 | 0 | | 54 | 0 | 0 | 4 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 19 | 3.16 | 60 | 41 | 2 | | 2 | 2 | 2 | 2 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 3.15 | 63 | 15 | 13 | | 8 | 13 | 0 | 10 | 0 | 4 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.05 | 61 | 9 | 24 | | 14 | 0 | 4 | 0 | 0 | 0 | 0 | 1 | 0 |
| 18 | 0 | | 20 | 3.05 | 61 | 0 | 53 | | 0 | 7 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.00 | 60 | 0 | 57 | | 0 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.00 | 60 | 0 | 0 | | 57 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.00 | 60 | 2 | 0 | | 57 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 23 | 0 | | 18 | 2.94 | 53 | 4 | 22 | | 18 | 2 | 1 | 5 | 1 | 1 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 2.85 | 57 | 0 | 0 | | 17 | 0 | 0 | 0 | 0 | 40 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.80 | 56 | 0 | 0 | | 23 | 0 | 0 | 13 | 0 | 20 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 2.85 | 57 | 1 | 52 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 2.82 | 48 | 38 | 12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 2.80 | 56 | 4 | 18 | | 26 | 2 | 0 | 2 | 0 | 2 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 2.75 | 55 | 3 | 40 | | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 2.70 | 54 | 1 | 14 | 0 | 0 | 16 | 4 | 12 | 7 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.70 | 54 | 0 | 0 | 0 | 37 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 2.70 | 54 | 0 | 0 | 0 | 48 | 0 | 0 | 4 | 0 | 2 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 2.65 | 53 | 51 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 2.65 | 53 | 2 | 0 | 18 | 0 | 0 | 27 | 1 | 5 | 0 | 0 | 0 | 0 |
| 25 | 0 | | 18 | 2.68 | 47 | 23 | 11 | 9 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 27 | 0 | | 20 | 2.60 | 52 | 0 | 43 | 0 | 9 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.60 | 52 | 0 | 0 | 0 | 4 | 8 | 0 | 28 | 0 | 12 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 2.60 | 52 | 26 | 9 | 12 | 2 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| 32 | 0 | | 20 | 2.55 | 51 | 7 | 25 | 14 | 0 | 0 | 0 | 0 | 0 | 5 | 0 | 0 | 0 |
| 32 | 0 | | 20 | 2.55 | 51 | 0 | 51 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 2.55 | 51 | 16 | 9 | 20 | 3 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 2.55 | 51 | 0 | 0 | 50 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 2.50 | 50 | 1 | 16 | 27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.45 | 49 | 22 | 11 | 2 | 4 | 0 | 1 | 7 | 2 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 2.45 | 49 | 41 | 0 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 2.40 | 48 | 7 | 0 | 23 | 0 | 11 | 3 | 3 | 1 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.40 | 48 | 13 | 0 | 0 | 16 | 0 | 13 | 6 | 0 | 0 | 0 | 0 | 0 |
| 31 | 0 | | 20 | 2.40 | 48 | 0 | 48 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.40 | 48 | 0 | 0 | 17 | 3 | 0 | 12 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 2.40 | 48 | 0 | 0 | 29 | 2 | 0 | 16 | 0 | 1 | 0 | 0 | 0 | 0 |
| 25 | 0 | | 20 | 2.35 | 47 | 2 | 32 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 

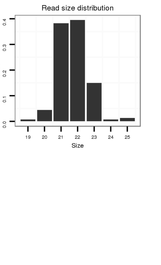
| ID: | Coordinate: | Confidence: | Class: | Genomic Locus: |
|---|---|---|---|---|
| **dya_1793** | **v2_chrUn_1311:45-143 +** | **candidate-rescued** | **Canonical miRNA** | **intergenic** |
| | | | | [View on UCSC Genome Browser (Comfil Mitmit)] |

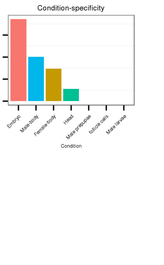
Legend: Loop Star Mature 5 arm in mature Mature 3 arm in mature

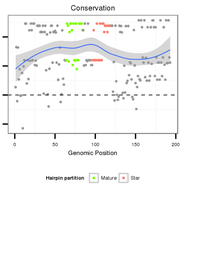
## Predicted structure






Show Alternate Folds

## Flybase annotation

dRNA:Dyak\FBrRNAAGE26302-RA]

## Repeatable elements

| Name | Class | Family | Strand |
|---|---|---|---|
| AT_rich | Low_complexity | Low_complexity | + |

**mature**

1. dya_1793 v2_chrUn_1311:45-143 +
2. v2_chrUn_2920:788-728 +
3. v2_chrUn_1929:235-293 +
4. v2_chrUn_4644:179-199 +
5. v2_chrUn_4933:1063-1023 +
6. v2_chrUn_2147:1-41 +
7. v2_chrUn_2347:62-94 +
8. v2_chrUn_5370:203-223 +
9. v2_chrUn_5306:4414-4361 +
10. v2_chrUn_5762:888-908 +
11. v2_chrUn_2944:2472-2492 +
12. v2_chrUn_2944:2472-2492 +
13. v2_chrUn_2613:7268-7288 +
14. v2_chrUn_2167:926-7846 +
15. v2_chrUn_2944:4355-4375 +
16. v2_chrUn_2763:2951-2911 +
17. v2_chrUn_4475:1-41 +
18. v2_chrUn_5370:1395-1435 +
19. v2_chrUn_3133:52-5242 +
20. v2_chrUn_924:1125-1143 +
21. v2_chrUn_2514:436-456 +
22. v2_chrUn_4130:1030-1030 +
23. v2_chrUn_5306:4414-4361 +
24. v2_chrUn_3472:129-149 +
25. v2_chrUn_3944:8-44 +
26. v2_chrUn_5746:1201-1241 +
27. v2_chrUn_3273:1669-1689 +

**star**

1. dya_1793 v2_chrUn_1311:97-119 +
2. v2_chrUn_2920:743-763 +
3. v2_chrUn_4230:975-997 +
4. v2_chrUn_1739:110-1132 +
5. v2_chrUn_1938:198-220 +
6. v2_chrUn_2147:1-41 +
7. v2_chrUn_4644:101-161 +
8. v2_chrUn_5347:954-978 +
9. v2_chrUn_5370:634-595 +
10. v2_chrUn_3294:4174-4396 +
11. v2_chrUn_3472:98-140 +
12. v2_chrUn_3472:98-140 +
13. v2_chrUn_2364:9-31 +
14. v2_chrUn_4164:187-1189 +
15. v2_chrUn_0614:6856-6898 +
16. v2_chrUn_0615:581-533 +
17. v2_chrUn_2:1-41 +
18. v2_chrUn_5370:1396-1436 +
19. v2_chrUn_3:6:2924-3946 +
20. v2_chrUn_4:87:4873-4893 +
21. v2_chrUn_4933:868-890 +
22. v2_chrUn_2990:90-130 +
23. v2_chrUn_5347:954-978 (5746:1243-1270) +
24. v2_chrUn_3543:2504-2556 +
25. v2_chrUn_6:26:1323-1324 +
26. v2_chrUn_3524:411-421 +

## Sense Strand Reads

Hide 3p reads  Show mid mismatch reads

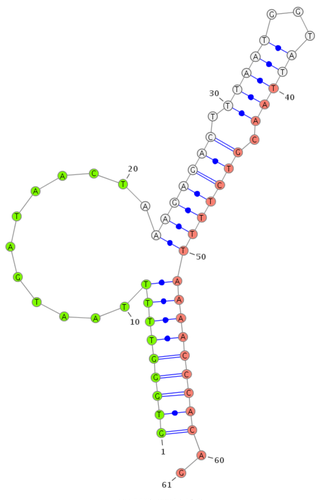
```
TACATAAGTCCTTATGAGAACTAAGACATTTCCCAGCATTTATTTTAGGTATAAAAATACATTTATTGAAGGAATTGATATATCCAGTAAAATCGTATTTTTAATTTCTTTCAATTAAAAAATTATTGACATATATAGAAATAAATTATAAACTCTAAGCGTGATCACTCGGCTCATGGCTCGATG
```

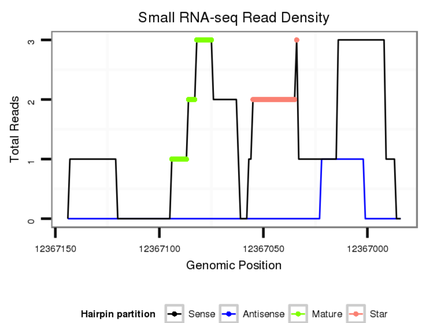
| Read # | Size | Mismatch | Hit Count | Total Norm | Total | V120 male body | V120 female body | M043 follicle cells | M043 female body | V058 head | M026 head | M056 embryo | V052 head | V046 embryo | SRR1275484 Male pregonads | SRR1275485 Male larvae | SRR1275486 Male pregonads |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | GSM1528802 | | | | | | | | | | | |
| 26 | 0 | | 20 | 7843.75 | 156875 | 120737 | 13571 | 4323 | 7163 | 6650 | 1335 | 2956 | 134 | 7 | 4 | 0 | 0 |
| 21 | 0 | | 20 | 1203.60 | 24072 | 12503 | 4326 | 2979 | 1618 | 595 | 1388 | 415 | 46 | 2 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 723.45 | 14469 | 9 | 9311 | | 313 | 2801 | 441 | 275 | 1291 | 28 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 7352.94 | 12797 | 1832 | 952 | | 327 | 473 | 546 | 152 | 164 | 9 | 1 | 1 | 0 |
| 25 | 0 | | 20 | 511.95 | 10221 | 3068 | 4608 | | 831 | 415 | 516 | 536 | 153 | 89 | 3 | 2 | 0 |
| 25 | 0 | | 20 | 464.26 | 8886 | 583 | 7839 | | 0 | 0 | 424 | 40 | 0 | 46 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 251.35 | 5027 | 2080 | 0 | | 1350 | 360 | 12 | 0 | 66 | 1158 | 0 | 1 | 0 |
| 20 | 0 | | 20 | 240.90 | 4858 | 1000 | 0 | | 213 | 157 | 1474 | 38 | 2102 | 2 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 204.45 | 4093 | 0 | 4084 | | 0 | 0 | 0 | 0 | 0 | 0 | 4 | 0 | 0 |
| 30 | 0 | | 20 | 179.49 | 3590 | 1576 | 0 | | 895 | 249 | 229 | 0 | 0 | 0 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 159.89 | 2878 | 2372 | 265 | | 33 | 29 | 159 | 3 | 6 | 1 | 5 | 0 | 0 |
| 23 | 0 | | 20 | 149.05 | 2981 | 1284 | 972 | | 370 | 207 | 8 | 0 | 90 | 45 | 1 | 1 | 1 |
| 24 | 0 | | 20 | 135.70 | 2714 | 704 | 1642 | | 232 | 104 | 19 | 45 | 45 | 14 | 0 | 2 | 1 |
| 21 | 0 | | 20 | 125.35 | 2507 | 497 | 485 | | 927 | 306 | 20 | 115 | 147 | 6 | 4 | 0 | 0 |
| 18 | 0 | | 20 | 121.72 | 2191 | 1256 | 494 | | 127 | 45 | 120 | 128 | 19 | 2 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 121.00 | 2420 | 409 | 1194 | | 649 | 26 | 25 | 94 | 17 | 4 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 90.40 | 1892 | 99 | 5 | | 293 | 23 | 12 | 1293 | 2 | 258 | 3 | 0 | 0 |
| 26 | 1 | | 20 | 91.55 | 1831 | 155 | 1 | | 2 | 15 | 1228 | 424 | 4 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 76.05 | 1521 | 0 | 272 | | 583 | 407 | 16 | 27 | 0 | 16 | 0 | 0 | 0 |
| 25 | 0 | | 20 | 71.70 | 1434 | 414 | 370 | | 311 | 35 | 46 | 31 | 24 | 3 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 18.98 | 1279 | 1223 | 6 | | 0 | 40 | 10 | 0 | 0 | 0 | 0 | 0 | 0 |
| 17 | 0 | | 20 | 66.45 | 1333 | 0 | 1195 | | 0 | 136 | 0 | 0 | 0 | 0 | 2 | 0 | 0 |
| 20 | 0 | | 20 | 65.76 | 1314 | 56 | 101 | | 441 | 0 | 202 | 134 | 369 | 13 | 0 | 0 | 0 |
| 25 | 0 | | 20 | 63.80 | 1276 | 6 | 1252 | | 11 | 0 | 0 | 4 | 3 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 57.50 | 1035 | 16 | 744 | | 43 | 128 | 13 | 50 | 39 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 50.47 | 912 | 268 | 313 | | 98 | 27 | 59 | 130 | 6 | 11 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 48.46 | 972 | 513 | 157 | | 87 | 55 | 53 | 70 | 32 | 5 | 2 | 0 | 0 |
| 28 | 0 | | 20 | 48.45 | 969 | 7 | 936 | | 0 | 0 | 10 | 17 | 1 | 0 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 35.95 | 719 | 158 | 327 | | 51 | 52 | 19 | 85 | 103 | 29 | 1 | 0 | 0 |
| 22 | 0 | | 20 | 34.15 | 683 | 157 | 0 | | 206 | 83 | 0 | 97 | 24 | 115 | 0 | 1 | 0 |
| 30 | 0 | | 20 | 18.32 | 681 | 12 | 589 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 29.00 | 580 | 3 | 577 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 31 | 0 | | 20 | 28.00 | 560 | 0 | 560 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 26.45 | 529 | 142 | 0 | | 183 | 0 | 29 | 0 | 11 | 162 | 1 | 1 | 0 |
| 23 | 0 | | 20 | 23.45 | 469 | 195 | 159 | | 44 | 30 | 14 | 15 | 11 | 1 | 0 | 0 | 0 |
| 29 | 0 | | 18 | 22.61 | 407 | 228 | 137 | | 1 | 0 | 21 | 20 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 21.80 | 436 | 49 | 132 | | 216 | 5 | 26 | 4 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 18.60 | 372 | 19 | 353 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 17 | 0 | | 20 | 17.70 | 354 | 154 | 1 | | 64 | 50 | 4 | 41 | 15 | 0 | 0 | 0 | 0 |
| 17 | 0 | | 20 | 16.55 | 331 | 0 | 331 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 16.44 | 296 | 103 | 46 | | 46 | 16 | 10 | 47 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 16.40 | 328 | 2 | 297 | | 20 | 1 | 0 | 6 | 1 | 1 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 16.39 | 295 | 0 | 295 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 15.50 | 310 | 112 | 0 | | 60 | 15 | 0 | 123 | 0 | 0 | 0 | 0 | 0 |
| 25 | 0 | | 20 | 15.35 | 307 | 43 | 247 | | 15 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 15.05 | 301 | 25 | 144 | | 43 | 14 | 0 | 60 | 5 | 4 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 14.80 | 267 | 45 | 181 | | 24 | 4 | 0 | 8 | 0 | 5 | 0 | 0 | 0 |
| 27 | 0 | | 18 | 14.78 | 266 | 97 | 92 | | 34 | 5 | 16 | 31 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 14.45 | 289 | 5 | 284 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 14.25 | 285 | 8 | 36 | | 42 | 36 | 9 | 112 | 13 | 2 | 0 | 0 | 0 |
| 27 | 0 | | 20 | 13.80 | 276 | 18 | 258 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | | 18 | 13.12 | 263 | 247 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 13.70 | 274 | 18 | 92 | | 79 | 18 | 1 | 61 | 4 | 1 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 13.35 | 267 | 8 | 244 | | 11 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 |
| 26 | 1 | | 20 | 12.30 | 246 | 19 | 1 | | 0 | 7 | 237 | 0 | 2 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 10.30 | 206 | 56 | 0 | | 148 | 28 | 0 | 22 | 2 | 0 | 0 | 1 | 0 |
| 20 | 0 | | 20 | 10.25 | 265 | 78 | 0 | | 57 | 0 | 3 | 61 | 3 | 63 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 10.21 | 249 | 4 | 40 | | 51 | 42 | 17 | 39 | 13 | 33 | 0 | 0 | 0 |
| 15 | 0 | | 20 | 10.05 | 261 | 0 | 261 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 10.00 | 254 | 54 | 0 | | 45 | 36 | 13 | 73 | 0 | 22 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 12.75 | 255 | 40 | 51 | | 23 | 29 | 11 | 87 | 9 | 5 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 12.23 | 245 | 41 | 0 | | 110 | 38 | 0 | 26 | 21 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 12.20 | 244 | 101 | 0 | | 0 | 8 | 0 | 71 | 3 | 61 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 11.85 | 237 | 70 | 0 | | 59 | 42 | 0 | 0 | 21 | 45 | 0 | 0 | 0 |
| 27 | 0 | | 20 | 11.80 | 236 | 6 | 203 | | 10 | 1 | 7 | 9 | 0 | 0 | 0 | 0 | 0 |
| 27 | 0 | | 18 | 11.47 | 210 | 46 | 0 | | 0 | 1 | 109 | 54 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 18 | 11.56 | 208 | 103 | 35 | | 25 | 23 | 2 | 8 | 11 | 1 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 11.35 | 231 | 45 | 32 | | 38 | 15 | 0 | 69 | 17 | 0 | 0 | 1 | 0 |
| 21 | 0 | | 20 | 11.35 | 227 | 15 | 0 | | 49 | 27 | 0 | 17 | 15 | 64 | 0 | 0 | 0 |
| 19 | 0 | | 17 | 11.28 | 192 | 23 | 153 | | 3 | 2 | 9 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 18 | 11.22 | 202 | 5 | 180 | | 6 | 3 | 1 | 6 | 1 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 10.55 | 211 | 78 | 0 | | 52 | 30 | 0 | 38 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 10.00 | 180 | 80 | 34 | | 30 | 0 | 7 | 29 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 9.85 | 197 | 35 | 0 | | 48 | 28 | 16 | 36 | 11 | 3 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 9.80 | 196 | 45 | 19 | | 23 | 22 | 6 | 61 | 14 | 6 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 9.28 | 167 | 115 | 9 | | 22 | 8 | 3 | 1 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 8.75 | 175 | 19 | 57 | | 61 | 4 | 2 | 23 | 3 | 6 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 8.25 | 165 | 5 | 25 | | 60 | 9 | 4 | 58 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 8.25 | 165 | 0 | 0 | | 133 | 0 | 0 | 32 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 8.22 | 148 | 22 | 9 | | 76 | 20 | 0 | 10 | 0 | 10 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 8.15 | 163 | 4 | 15 | | 79 | 24 | 2 | 11 | 23 | 3 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 8.05 | 161 | 3 | 132 | | 2 | 2 | 5 | 1 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 7.60 | 152 | 0 | 0 | | 139 | 0 | 0 | 11 | 0 | 2 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 7.40 | 152 | 19 | 21 | | 90 | 14 | 0 | 4 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 7.55 | 151 | 56 | 0 | | 41 | 30 | 1 | 2 | 15 | 6 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 7.35 | 147 | 147 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 7.25 | 145 | 2 | 143 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 7.10 | 142 | 33 | 0 | | 54 | 37 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 18 | 7.06 | 127 | 29 | 95 | | 0 | 0 | 1 | 2 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 6.35 | 127 | 15 | 0 | | 12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 6.35 | 127 | 15 | 0 | | 11 | 2 | 79 | 16 | 0 | 3 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 6.25 | 125 | 2 | 0 | | 54 | 9 | 1 | 55 | 4 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 19 | 6.14 | 117 | 58 | 21 | | 20 | 12 | 2 | 3 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 6.10 | 122 | 42 | 18 | | 34 | 0 | 0 | 9 | 13 | 6 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 6.10 | 122 | 0 | 30 | | 29 | 18 | 24 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 19 | 6.05 | 115 | 25 | 35 | | 24 | 15 | 0 | 10 | 4 | 2 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 5.95 | 119 | 3 | 99 | | 12 | 1 | 1 | 3 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 5.95 | 119 | 27 | 47 | | 8 | 8 | 9 | 13 | 4 | 3 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 5.90 | 118 | 0 | 0 | | 66 | 0 | 5 | 0 | 0 | 18 | 0 | 0 | 0 |
| 27 | 0 | | 17 | 5.88 | 100 | 57 | 10 | | 13 | 1 | 10 | 9 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 5.85 | 117 | 0 | 117 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 5.80 | 116 | 40 | 20 | | 17 | 22 | 0 | 3 | 11 | 3 | 0 | 0 | 0 |
| 27 | 0 | | 20 | 5.80 | 116 | 8 | 0 | | 53 | 4 | 0 | 50 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 5.80 | 116 | 45 | 27 | | 21 | 7 | 1 | 10 | 4 | 1 | 0 | 0 | 0 |
| 30 | 0 | | 20 | 5.80 | 116 | 4 | 82 | | 3 | 2 | 4 | 2 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 5.75 | 115 | 4 | 78 | | 14 | 3 | 4 | 12 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 18 | 5.78 | 104 | 6 | 92 | | 0 | 2 | 0 | 0 | 4 | 0 | 0 | 0 | 0 |
| 18 | 0 | | 20 | 5.60 | 112 | 2 | 38 | | 46 | 18 | 0 | 2 | 4 | 2 | 0 | 0 | 0 |
| 21 | 0 | | 18 | 5.78 | 104 | 6 | 82 | | 3 | 2 | 4 | 2 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 5.45 | 109 | 0 | 56 | | 11 | 12 | 4 | 20 | 4 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 5.45 | 109 | 15 | 20 | | 45 | 3 | 0 | 5 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 5.40 | 108 | 41 | 0 | | 25 | 25 | 0 | 3 | 8 | 6 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.35 | 107 | 28 | 0 | | 35 | 17 | 0 | 13 | 12 | 2 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.35 | 107 | 0 | 0 | | 88 | 2 | 0 | 17 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 18 | 5.28 | 95 | 12 | 0 | | 35 | 17 | 4 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 18 | 5.28 | 95 | 3 | 0 | | 21 | 43 | 4 | 13 | 10 | 1 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.25 | 105 | 0 | 105 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.15 | 103 | 48 | 0 | | 13 | 15 | 0 | 9 | 8 | 10 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 5.05 | 101 | 12 | 0 | | 39 | 6 | 0 | 42 | 0 | 2 | 0 | 0 | 0 |
| 16 | 0 | | 20 | 5.05 | 101 | 0 | 101 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.95 | 99 | 5 | 89 | | 4 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.95 | 99 | 28 | 37 | | 12 | 9 | 3 | 6 | 4 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 4.84 | 92 | 92 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 4.80 | 96 | 8 | 10 | | 56 | 13 | 1 | 3 | 4 | 1 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 4.65 | 93 | 4 | 47 | | 7 | 0 | 13 | 2 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 4.60 | 92 | 4 | 83 | | 0 | 1 | 2 | 2 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 4.60 | 92 | 0 | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 4.50 | 90 | 40 | 16 | | 12 | 12 | 0 | 4 | 6 | 2 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 4.50 | 90 | 2 | 3 | | 52 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 4.40 | 88 | 10 | 0 | | 52 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.35 | 87 | 20 | 0 | | 32 | 21 | 0 | 5 | 8 | 1 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.35 | 87 | 4 | 47 | | 24 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 4.30 | 86 | 20 | 0 | | 49 | 0 | 1 | 13 | 3 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 4.25 | 76 | 29 | 16 | | 13 | 5 | 3 | 8 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 4.20 | 84 | 19 | 18 | | 26 | 0 | 1 | 9 | 11 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 4.05 | 81 | 0 | 0 | | 21 | 18 | 0 | 14 | 0 | 28 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 4.05 | 81 | 2 | 24 | | 24 | 2 | 6 | 21 | 1 | 1 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 4.00 | 80 | 3 | 12 | | 39 | 4 | 0 | 11 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 4.00 | 80 | 26 | 0 | | 11 | 17 | 0 | 5 | 11 | 10 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.95 | 79 | 7 | 45 | | 22 | 0 | 1 | 1 | 2 | 1 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.95 | 79 | 7 | 45 | | 22 | 0 | 1 | 1 | 2 | 1 | 0 | 0 | 0 |
| 21 | 0 | | 18 | 3.94 | 71 | 15 | 43 | | 7 | 2 | 3 | 1 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 3.85 | 77 | 1 | 0 | | 27 | 5 | 9 | 31 | 3 | 1 | 0 | 0 | 0 |
| 31 | 0 | | 20 | 3.75 | 75 | 0 | 75 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 3.70 | 74 | 1 | 3 | | 37 | 20 | 2 | 4 | 7 | 0 | 0 | 0 | 0 |
| 18 | 0 | | 18 | 3.47 | 66 | 1 | 50 | | 4 | 3 | 4 | 2 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.45 | 73 | 3 | 66 | | 3 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.45 | 73 | 1 | 4 | | 32 | 3 | 5 | 27 | 0 | 3 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 3.45 | 73 | 15 | 0 | | 32 | 10 | 0 | 5 | 8 | 3 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 3.45 | 73 | 2 | 49 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 3.45 | 73 | 0 | 43 | | 11 | 3 | 1 | 13 | 0 | 1 | 0 | 1 | 0 |
| 29 | 0 | | 20 | 3.40 | 72 | 0 | 0 | | 25 | 5 | 22 | 24 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 17 | 3.59 | 61 | 48 | 0 | | 9 | 1 | 2 | 1 | 0 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 18 | 3.50 | 63 | 0 | 63 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 30 | 0 | | 18 | 3.50 | 63 | 60 | 3 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 16 | 0 | | 20 | 3.45 | 69 | 0 | 65 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 3.40 | 68 | 52 | 0 | | 8 | 1 | 0 | 7 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.35 | 67 | 0 | 0 | | 21 | 2 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 28 | 1 | | 20 | 3.30 | 66 | 6 | 0 | | 54 | 0 | 0 | 4 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 19 | 3.16 | 60 | 41 | 2 | | 2 | 2 | 2 | 2 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 3.15 | 63 | 15 | 13 | | 8 | 13 | 0 | 10 | 0 | 4 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.05 | 61 | 9 | 24 | | 14 | 0 | 4 | 0 | 0 | 0 | 0 | 1 | 0 |
| 18 | 0 | | 20 | 3.05 | 61 | 0 | 53 | | 0 | 7 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.00 | 60 | 0 | 57 | | 0 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.00 | 60 | 0 | 0 | | 57 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 3.00 | 60 | 2 | 0 | | 57 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 23 | 0 | | 18 | 2.94 | 53 | 4 | 22 | | 18 | 2 | 1 | 5 | 1 | 1 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 2.85 | 57 | 0 | 0 | | 17 | 0 | 0 | 0 | 0 | 40 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.80 | 56 | 0 | 0 | | 23 | 0 | 0 | 13 | 0 | 20 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 2.85 | 57 | 1 | 52 | 0 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 2.82 | 48 | 38 | 12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 2.80 | 56 | 4 | 18 | | 26 | 2 | 0 | 2 | 0 | 2 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 2.75 | 55 | 3 | 40 | | 3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 26 | 0 | | 20 | 2.70 | 54 | 1 | 14 | 0 | 0 | 16 | 4 | 12 | 7 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.70 | 54 | 0 | 0 | 0 | 37 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 2.70 | 54 | 0 | 0 | 0 | 48 | 0 | 0 | 4 | 0 | 2 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 2.65 | 53 | 51 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 2.65 | 53 | 2 | 0 | 18 | 0 | 0 | 27 | 1 | 5 | 0 | 0 | 0 | 0 |
| 25 | 0 | | 18 | 2.68 | 47 | 23 | 11 | 9 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 27 | 0 | | 20 | 2.60 | 52 | 0 | 43 | 0 | 9 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.60 | 52 | 0 | 0 | 0 | 4 | 8 | 0 | 28 | 0 | 12 | 0 | 0 | 0 |
| 24 | 0 | | 20 | 2.60 | 52 | 26 | 9 | 12 | 2 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| 32 | 0 | | 20 | 2.55 | 51 | 7 | 25 | 14 | 0 | 0 | 0 | 0 | 0 | 5 | 0 | 0 | 0 |
| 32 | 0 | | 20 | 2.55 | 51 | 0 | 51 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 22 | 0 | | 20 | 2.55 | 51 | 16 | 9 | 20 | 3 | 0 | 0 | 3 | 0 | 0 | 0 | 0 | 0 |
| 29 | 0 | | 20 | 2.55 | 51 | 0 | 0 | 50 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 23 | 0 | | 20 | 2.50 | 50 | 1 | 16 | 27 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.45 | 49 | 22 | 11 | 2 | 4 | 0 | 1 | 7 | 2 | 0 | 0 | 0 | 0 |
| 28 | 0 | | 20 | 2.45 | 49 | 41 | 0 | 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 19 | 0 | | 20 | 2.40 | 48 | 7 | 0 | 23 | 0 | 11 | 3 | 3 | 1 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.40 | 48 | 13 | 0 | 0 | 16 | 0 | 13 | 6 | 0 | 0 | 0 | 0 | 0 |
| 31 | 0 | | 20 | 2.40 | 48 | 0 | 48 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 20 | 0 | | 20 | 2.40 | 48 | 0 | 0 | 17 | 3 | 0 | 12 | 0 | 0 | 0 | 0 | 0 | 0 |
| 21 | 0 | | 20 | 2.40 | 48 | 0 | 0 | 29 | 2 | 0 | 16 | 0 | 1 | 0 | 0 | 0 | 0 |
| 25 | 0 | | 20 | 2.35 | 47 | 2 | 32 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 

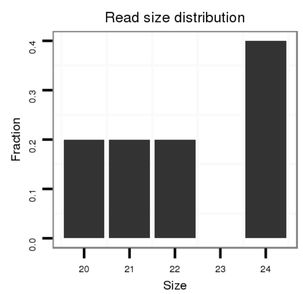
| ID: | Coordinate: | Confidence: | Class: | Genomic Locale: | |
|---|---|---|---|---|---|
| **dya_1408** | **X:12367034-12367094 -** | **candidate-rescued** | **5p_tailed_mirtron** | **intron** | [View on UCSC Genome Browser [Cornell Mirror]] |

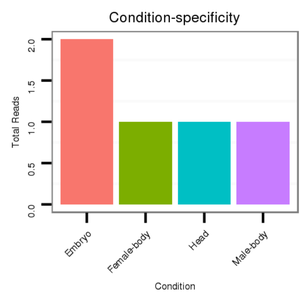
Legend: mature star mismatch in alignment mismatch in read

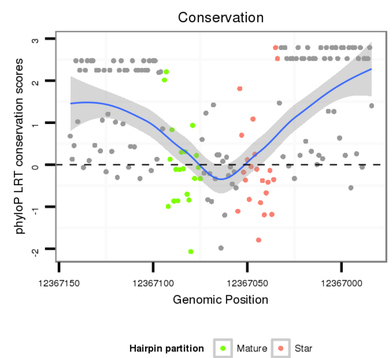
**Predicted structure**




Show Alternate Folds

**Flybase annnotation**

intron [Dyak\GE15814-in]; CDS [Dyak\GE15814-cds]; CDS [Dyak\GE15814-cds]

No Repeatable elements found

**Sense Strand Reads**

hide 3p reads  show mid mismatch reads

```
AGCTGGACCACAAACCCAGGACCACTCACCCACTGGCCCAGCACATTCAGGTGGGTTTTAATGATAACTAAAGAGACTTTAATGGTATTAACGTCTTTTAAAACCCACAGATCACCCGTGACCGCACTGGATTGCAGCAGAGCATCCTGAAGGTCCCCAA
```

| | Read size | # Mismatch | Hit Count | Total Norm | Total | M043 female body | M056 embryo | V120 male body | V058 head | M026 head | V046 embryo |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ********** | | | | | | | | | | | |
| .....AACGTCTTTTAAAACCCACAGT..... | 22 | 1 | 1 | 17.00 | 17 | 8 | 6 | 1 | 2 | 0 | 0 |
| .....AACGTCTTTTAAAACCCACAGC..... | 22 | 1 | 1 | 2.00 | 2 | 0 | 2 | 0 | 0 | 0 | 0 |
| .....GATTGCAGCAGAGCATCCTGAAG..... | 23 | 0 | 1 | 2.00 | 2 | 1 | 0 | 1 | 0 | 0 | 0 |
| .....GTGGTTTTTAATGATAACT..... | 20 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| .....GATTGCAGCAGAGCATCCTGAAGGTCCC... | 28 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....TAACGTCTTTTAAAACCCACAG..... | 22 | 0 | 1 | 1.00 | 1 | 0 | 1 | 0 | 0 | 0 | 0 |
| .....GATCACCCGTGACCGCACTG..... | 20 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....TGATAACTAAAGAGACTTTAA..... | 21 | 0 | 1 | 1.00 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| .....ATTAACGTCTTTTAAAACCCACAG..... | 24 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .GCTGGACCACAAACCCAGGACCA..... | 23 | 0 | 1 | 1.00 | 1 | 1 | 0 | 0 | 0 | 0 | 0 |
| .....TTAATGATAACTAAAGAGACTTTA..... | 24 | 0 | 1 | 1.00 | 1 | 0 | 0 | 0 | 0 | 1 | 0 |

**Anti-sense strand reads**

```
TCGACCTGGTGTTTGGGTCCTGGTGAGTGGGTGACCGGGTCGTGTAAGTCCACCCAAAAATTACTATTGATTTCTCTGAAATTACCATAATTGCAGAAAATTTTGGGTGTCTAGTGGGCACTGGCGTGACCTAACGTCGTCTCGTAGGACTTCCAGGGGTT
```

| | Read size | # Mismatch | Hit Count | Total Norm | Total | M043 female body | M056 embryo |
|---|---|---|---|---|---|---|---|
| ********** | | | | | | | |
| .....GGCGTGACCTAACGTCGTCTC..... | 21 | 0 | 1 | 1.00 | 1 | 1 | 0 |

Show Alignment With Reads

**Re-alignment of all predicted orthologs**

| Species | Coordinate | ID | Alignment |
|---|---|---|---|
| droYak3 | X:12366984-12367144 - | dya_1408 | AGCTGGACCACAAACCCAGGACCACTCACCCACTGGCCCAGCACATTCAGGTGGGTTT----------TTA----------ATG-------ATAACTAAAGAGACTTTA-------AT----G---GTA----------TTAA----------GT----C-TT-T-T----------AAAACCCACAGATCACCCGTGACCGCACTGGATTGCAGCAGAGCATCCTGAAGGTCCCCAA |
| droEre2 | scaffold_4690:6167968-6168128 - | der_385 | AGCTGGACCACAACCCCAGGACCACTCACCCACTGGCCCAGCACATTCAGGTGGGTTT----------TTA----------ATG-------GTAACTTAAAGAGACTTA-------GT----G---GTA----------TTAA----------C----------GT----C-TT-T-T----------GAAATCCACAGATCACCCGTGACCGCACTGGATTGCAGCAGAGCATCCTGAAGGTCCCCAA |
| droSec2 | scaffold_34:308804-308971 + | | AGCTGGACCACAACCCCAGGCCCACTCACCCACTGGCCCAGCACATTCAGTGGGTTA----------TTA----------TTG-------ATAACTTAAGGAACTTAA-------AT----G---GTA----------TTAA----------C----------GTTTTGGTTTT-TGC----------TTAACCCACAGCTCACCCGTGACCGCACCGGATTGCAGCAGAGCATCCTGAAGGTGCCCAA |
| droSim2 | x:8494583-8494744 + | | AGCTGGACCACAACCCCAGGCCCACTCACCCACTGGCCCAGCACATTCAGTGGGTTA----------TTA----------TTG-------ATAACTTAAGGAACTTAA-------AT----G---GTA----------TTAA----------C----------GT----C-TT-TGC----------TTAACCCACAGCTCACCCGTGACCGCACTGGATTGCAGCAGAGCATCCTGAAGGTGCCCAA |
| dm3 | chrX:8946372-8946532 + | | AGCTGGACCACAACCCCAGCCAGCCACTCACCCACTGGCCCAGCACATTCAGTGGGTTA----------TTA----------TTG-----C-TTAACTTAAGAGACTTA-------CT----G---GTA----------TAAA----------T----------GT----C-TT-TGT----------TTAATCCACAGATCACCCGTGACCGCACTGGCTTGCAGCAGAGCATCCTGAAGGTGCCCAA |
| droEug1 | scf7180000408176:387398-387562 + | | AGCTGGACCACAACCCCAGGACCACTCACCCACTGGCCCAGCATATTCAGGTGGTCC----------T----------CTG--ATAC---TTTTTTTAACTTAA-------CTCC---G---AAT----------TCAACGT----------CA----TT--TT-T-T----------CACTCCCATAGATACCCGTGACCGCACTGGATTGCAGCAGAGCATCCTGAAGGTGCCCAA |
| droBia1 | scf7180000301760:2677784-2677975 + | | AGCTGGACCACAACCCCAGGACCACCCCACTGGCCCAGCACATTCAGGTGGGTTTGGATTACCCATTAGAAATATTATTTTCTGTCTTAGCCATTTGTAAATCATTCCAAAACGA-----------AATTGT------AA----G----T----------GCAA----------T----C----C-----------TCCTTCCAGATCACCCGTGACCGCACTGGATTGCAGCAGAGCATCCTGAAGGTGCCCAA |
| droTak1 | scf7180000415169:971778-971883 - | | TT----------TA----------ATG-----CTTTTGTAAATAATTTT-------AA----G----T----------GCAATAT----------C----------T----C-AT-T----------AAATCCCACAGATCACCCGTGACCGCACTGGATTGCAGCAGAGCATCCTGAAGGTGCCCAA |
| droEle1 | scf7180000491006:2458450-2458516 + | | T----------G----------TTT----------TTT----------G----G----T----------GGAATCCCAGATCACCCGTGACCGCACCGGATTGCAGCAGAGCATCCTGAAGGTGCCCAA |
| droRho1 | scf7180000779841:469277-469523 + | | AGCTGGACCACAACCCCAGGACCACTCACCCACTGGCCAGCACATTCAGGTGAGCAA----------CATTCCAAACCGA-----------AACATT------AG----G----T--GTTCAACTTGATTTAAGTTATTTTAGTTTTTCATTTTGATACAAATATCTATCTTCCGAAATACTCTTTTTATATTTTATTTGCTATTTAAACATTCC----------TA----TC-T-AT-T----------GGAACCCCAGATCACCCGTGATCGCACCGGATGCAGCAGAGCATCCTGAAGGTGCCCAA |
| droFic1 | scf7180000453829:917158-917319 + | | AGCTGGACCACAACCCCAGGACCACTCACCCACTGGCCCAGCACATTCAGGTGAGTTTGAA----------T----------CTAC----------T----G----T----GTTGTACAA----------CCTTAATTATATTAAAAGAAAAG-----GTTGTACAA----------AT--AT-T----------TG--ATTCCAGATCACCCGTGACCGCACTGGATGCAGCAGAGCATCCTTAAAGTGCCCAA |
| droKik1 | scf7180000302698:123344-123496 - | | AGCTGGACCACAACCCCAGGACCACTCACCCACTGGCCCAGCATATTCAGGTAAGGAA----------T-G----------AG---CTT----------CTTTG------AT----G----GCT----------TTAA----------CTAATTTA----------T----C----C----C----------TCTTCCTTAAGATCACCCGTGACCGCACTGGCTCAGCAGAGCATCCTGAAGGTGCCCAA |
| droAna3 | scaffold_13047:768181-768280 + | | AACTGGACCACAACCCCAGGACCACCACCCACTGGCCCAGCACATC----------T----------C----C----C----C----------CAGATCACCCGGACCCAACTGGCCTGCAACAGAGCATCCTGAAGGTGCCCAA |
| droBip1 | scf7180000396431:551930-552029 + | | AACTGGACCACAACCCCAGGACCACCACCCACTGGCCCAGCACATTC----------T----------C----C----C----C----------AGATCACCCGGACCCAACTGGCCTGCAACAGAGCATCCTGAAGGTGCCCAA |
| dp5 | XL_group1e:8225794-8225850 + | | ----------T----------C----C----C----C----------GGCATCTAGATCACCGCGGATCGCACTGGCCTGCAGCAGAGCATCCTGAAGGTCCCCAA |
| droPer2 | scaffold_13:341752-341808 - | | ----------T----------C----C----C----C----------GGCATCTAGATCACCGCGGATCGCACTGGCCTGCAGCAGAGCATCCTGAAGGTCCCCAA |
| droWil2 | scf2_1100000004963:636680-636850 - | | AGCTTAGACAGAAACCCG-CACCAGACACCCCTTGGCCAGCATATCAGGTAAGTTTCG----------A GCGAAATGCCC---TGT----------GTTTTCGTCTGTAAGCTAAC--T----------CATTGATT----CCTAAT----------T----C-T-T----------CTCTTTAAGATCACCGCGGATCGCACTGGCCTGCAGCAAAGTATCTCAAAGTGCCCAC |
| droVir3 | scaffold_12970:2686230-2686390 - | | AGCTGGACCATAACCCGG-CACAACACACCCCTGGCCAGGATATCAGGTCAGATGCA----------T----------C----C----C----C----------CCAACTTTA----TCAAAACAACA----ATTATACAA----------T----C-T-T----CAGTTATAACT--TTTTCCAGATCACAGCGGATCGCACCGGCCTGCAGCAGAGCATCTCAAGGTGCCCAA |
| droMoj3 | scaffold_6473:3421281-3421454 - | | AGCTGGACCACAACCCCG-CACTACACACCCCTTGGCCCAGCACATCAGGTAACCAAG----------AAAGAAATATTATTGTGT---------AAATATATATGTATATTGAA--A----------CAACCAT----------T----------TA----TT--TA-T-AT-T----------CACTCTGTCTAGATAACCGCGGATCGCACTGGCCTGCAGCAGAGCATCCTGAAGGTGCCCAA |
| droGri2 | scaffold_15081:1106607-1106768 + | | AATTGGACCACAACCCCG-CACTACACACCCCTGGCAGCACATTCAGGTGTAAGCAT----------A CA--------ATATTATTTATTGA-----------TGCAATC----C----T----------GATGATTGA----------ACTGT----CAT-CCT----------A----AACAGATTACACGCGGATCGCACTGGATTACAGCAGAGTATCCTGAAGGTGCCCAA |

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