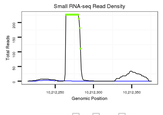
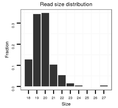
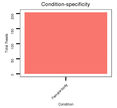
ID	Coordinate	Confidence	Class	Genome Locus
CG4901_in2	chr2L:10211264-10212326 +	Known Ortholog	mirtron	intron

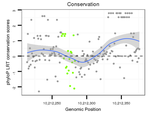
Name: dme-mirtron-CG4901_intron2

Predicted structure









Show Alternate Folds

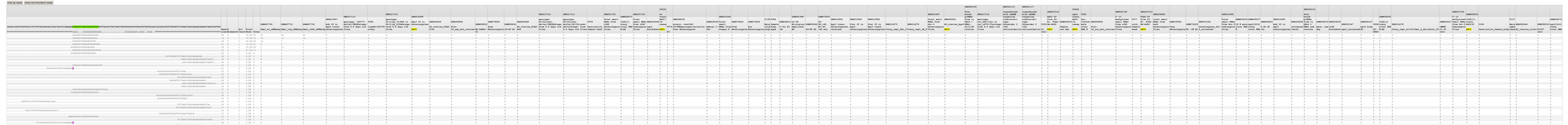
FlyBase annotation

mirn(CG4901-aj),CDS(CG4901-aj),CDS(CG4901-ak)

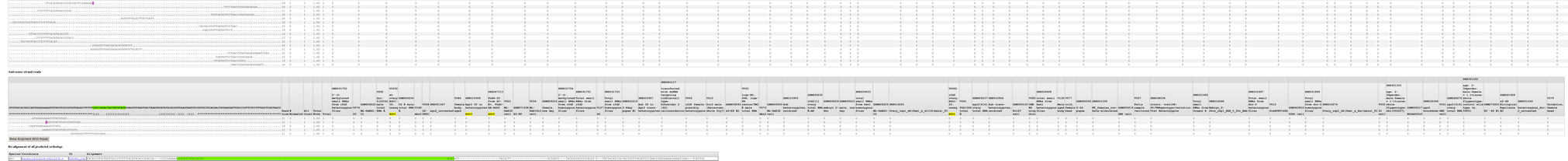
No Repeats/Low complexity found

Sense Strand Reads

Hide 3p reads | show mid mismatch reads



Anti-sense strand reads



Show Alignment With Reads

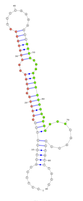
Re-alignment of all predicted orthologs

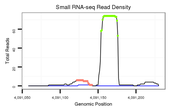
Generated 09/06/2019 at 07:01 PM

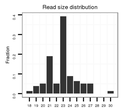
ID	Coordinate	Confidence	Class	Genomic Locus
sblock97631	**chr3L:4091108-4091180 +**	**Known Ortholog**	**three_prime_UTR**	**3pUTR**

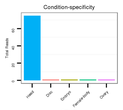
Legend: Mature Star Hairpin arm Mature/Star

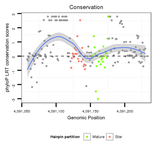
Predicted structure











Show Alternative Folds

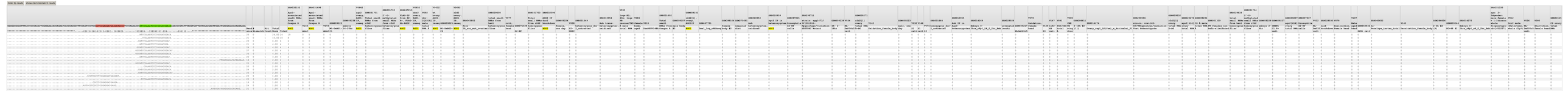
Flybase annotation

three_prime_UTR:FGS4989-u5,three_prime_UTR:FGS4989-u5,three_prime_UTR:FGS4989-u5

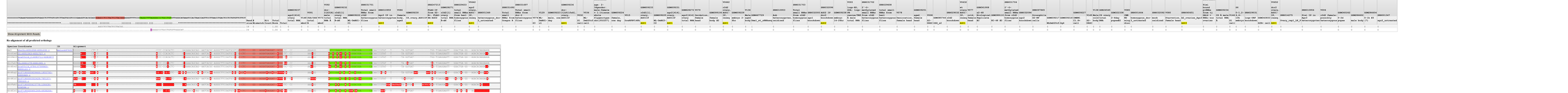
No Repeatmbr element found

Sense Small Reads

Hide Sp reads | Show mid mismatch reads



Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

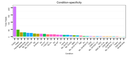
Generated 2019-09-23 at 0:07 AM

Sample	Date	Analyst	Comments

Genus: 1797 (in Mycobacteriaceae) | Species: Tuberculosis complex | Variant: Lineage 4 (Euro-American) | Serotype:

Ref: NC_000962.3 | Coverage: 1000x | Quality: 20 | Mapper: bwa-mem | Caller: freebayes

Total Reads: 1,000,000



Filter parameters

min length: 18

max length: 30

min read count: 10

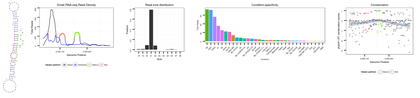
Total Reads: 1,000,000

Show 10 entries Show/hide columns

Sample	Total reads	Mapped reads	Unmapped reads	Mapped %	Sense reads	Antisense reads	Sense %	Antisense %	Unique sRNAs	Sense sRNAs	Antisense sRNAs	Mean length	Median length	Mode length	Mean coverage	Max coverage	Total bases	Sense bases	Antisense bases	Genome coverage %	Sense coverage %	Antisense coverage %	Mean RPM	Max RPM	Total RPM	Sense RPM	Antisense RPM	Mean RPKM	Max RPKM	Total RPKM	Sense RPKM	Antisense RPKM	Mean TPM	Max TPM	Total TPM	Sense TPM	Antisense TPM	Mean CPM	Max CPM	Total CPM	Sense CPM	Antisense CPM	Mean RPB	Max RPB	Total RPB	Sense RPB	Antisense RPB	Mean RPKB	Max RPKB	Total RPKB	Sense RPKB	Antisense RPKB	Mean TPB	Max TPB	Total TPB	Sense TPB	Antisense TPB	Mean CPB	Max CPB	Total CPB	Sense CPB	Antisense CPB
[redacted]	1,000,000	1,000,000	0	100.0	1,000,000	0	100.0	0.0	1	1	0	18.0	18.0	18.0	1000.0	1000.0	18,000,000	18,000,000	0	100.0	100.0	0.0	1000000.0	1000000.0	1000000.0	1000000

ID	Name	Description	Date	Drawing Scale
dna_152_chr15_:76546884-76562736	**Genome**	**Coordinates**	**Size**	**Genome Scale**
15:76546884-76562736	Homo sapiens (hg38)	15:76546884-76562736	15,853 bp	Click to Set Genome Scale in Preferences

Problems in 0 tracks



Alignments

Alignment Filter: Show all alignments

Alignment Color: Strand (+/-) | Strand (read1/read2) | Insert size | Insert size (FR/RF/TandemSV) | Insert size (Illumina/Nanopore/PacBio) | Insert size (Illumina/Nanopore/PacBio/Hi-C) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped/Hard-clipped) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped/Hard-clipped/Mapping quality) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped/Hard-clipped/Mapping quality/Sample) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped/Hard-clipped/Mapping quality/Sample/Group) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped/Hard-clipped/Mapping quality/Sample/Group/Read name) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped/Hard-clipped/Mapping quality/Sample/Group/Read name/Base quality) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped/Hard-clipped/Mapping quality/Sample/Group/Read name/Base quality/Primary alignment) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped/Hard-clipped/Mapping quality/Sample/Group/Read name/Base quality/Primary alignment/Mapped in proper pair) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped/Hard-clipped/Mapping quality/Sample/Group/Read name/Base quality/Primary alignment/Mapped in proper pair/Supplementary alignment) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped/Hard-clipped/Mapping quality/Sample/Group/Read name/Base quality/Primary alignment/Mapped in proper pair/Supplementary alignment/Secondary alignment) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped/Hard-clipped/Mapping quality/Sample/Group/Read name/Base quality/Primary alignment/Mapped in proper pair/Supplementary alignment/Secondary alignment/Read paired) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped/Hard-clipped/Mapping quality/Sample/Group/Read name/Base quality/Primary alignment/Mapped in proper pair/Supplementary alignment/Secondary alignment/Read paired/Read mapped) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped/Hard-clipped/Mapping quality/Sample/Group/Read name/Base quality/Primary alignment/Mapped in proper pair/Supplementary alignment/Secondary alignment/Read paired/Read mapped/Mate mapped) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped/Hard-clipped/Mapping quality/Sample/Group/Read name/Base quality/Primary alignment/Mapped in proper pair/Supplementary alignment/Secondary alignment/Read paired/Read mapped/Mate mapped/First in pair) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped/Hard-clipped/Mapping quality/Sample/Group/Read name/Base quality/Primary alignment/Mapped in proper pair/Supplementary alignment/Secondary alignment/Read paired/Read mapped/Mate mapped/First in pair/Second in pair) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate Pair/Gap/Inversion/Duplicate/Translocation/Deletion/Insertion/Soft-clipped/Hard-clipped/Mapping quality/Sample/Group/Read name/Base quality/Primary alignment/Mapped in proper pair/Supplementary alignment/Secondary alignment/Read paired/Read mapped/Mate mapped/First in pair/Second in pair/Low quality) | Insert size (Illumina/Nanopore/PacBio/Hi-C/Mate 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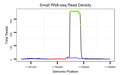
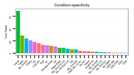
ID	Coordinates	Confidence	Class	Genome Score
block006243 / chr28:11750900-11750969 - Knowa Ortholog	chr28:11750900-11750969	Intergenic	Intergenic	Chim:-inf,0.00; Gibbon,Macaque,Lesser Bilby

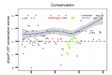
Legend: **Mature** **Hairpin** **Flanking region**

Predicted structure

Minimal MFE: -19.1







Show Alternative Forms

Picture annotation

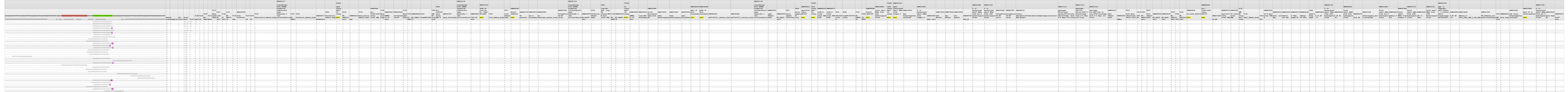
Strand: -

Top Repeatitiv Elements Found

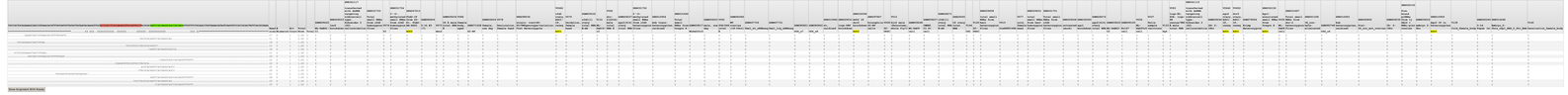
Name: Novel Bank

Show/Hide Alignment Details

Hide Ref Seq Show Mult Alignment Details



Add some virtual reads



Show Alignment With Reads

Mr alignment of all predicted miRNAs

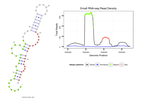
Generated 2019-03-01 at 17:17:-0700

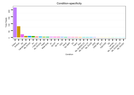
Sequence	Length	Circular	Digest	Created	Updated
TCATTA_Aal_Lib.ffb TCATCATT TCATAAB	7	false	md5:e8ffb7d7d7d7d7d7d7d7d7d7d7d7d7		

TCATTA_Aal_Lib.fffb TCATCATT TCATAAB | **Sequence Definition** | **Structure** | **Structure Tree** | **Structure Summary** | **Notes**

Q | **A** | **G** | **C** | **Other** | **Ambiguous** | **Gap** | **Total**

Circular sequence





Sequence

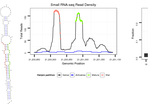
Primary sequence

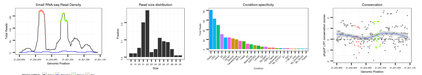
ATCATTCATCATTCATCATTC

ID	Location	Strand	Length	PhyloP score
chfam13.19992	**chr31:-21268899-21269163**	+	**Acacia Orthologs**	**Hsrw_grimo_1170**	**3p5TB**	Show LOCUS Genes Mouse Ensembl Mouse

Length **264** (**-21268899-21269163**)

Predicted structure:





Show Promoter/Terminator

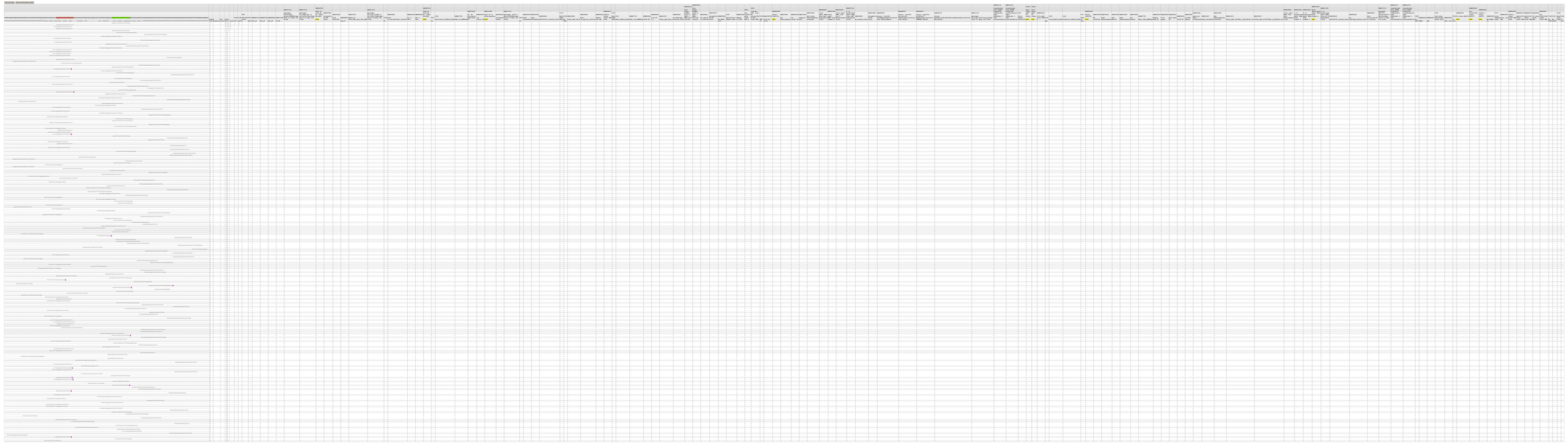
Flybase annotation

No Flybase annotation found in this locus. (chr31:-21267200-21271000 (dm6_grimo_CHR2:2257000-2261000))

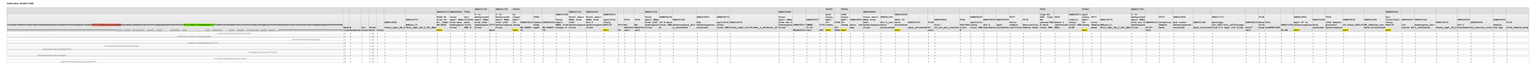
Nearby Genes (Ensembl v.104)

Gene Ortogroup Beads

Hide Ortogroup Beads Show Ortogroup Beads



Multi-locus ortogroup tracks



Show Ortogroup MSA Details

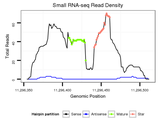
Per alignment of all genes in ortobeads:

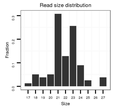
Generated MMseqs2 on Sep 12, 2021

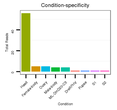
ID	Coordinate	Confidence	Class	Genome Locus
xlocus_chr2R:11296404-11296462 +	chr2R:11296404-11296462 +	**Known Orthologs**	**CDS**	**intron**

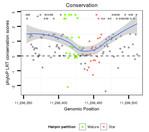
Legend: **Hairpin** **Mature** **Star** **Hairpin partner**

Predicted structure









Show Alternate Folds

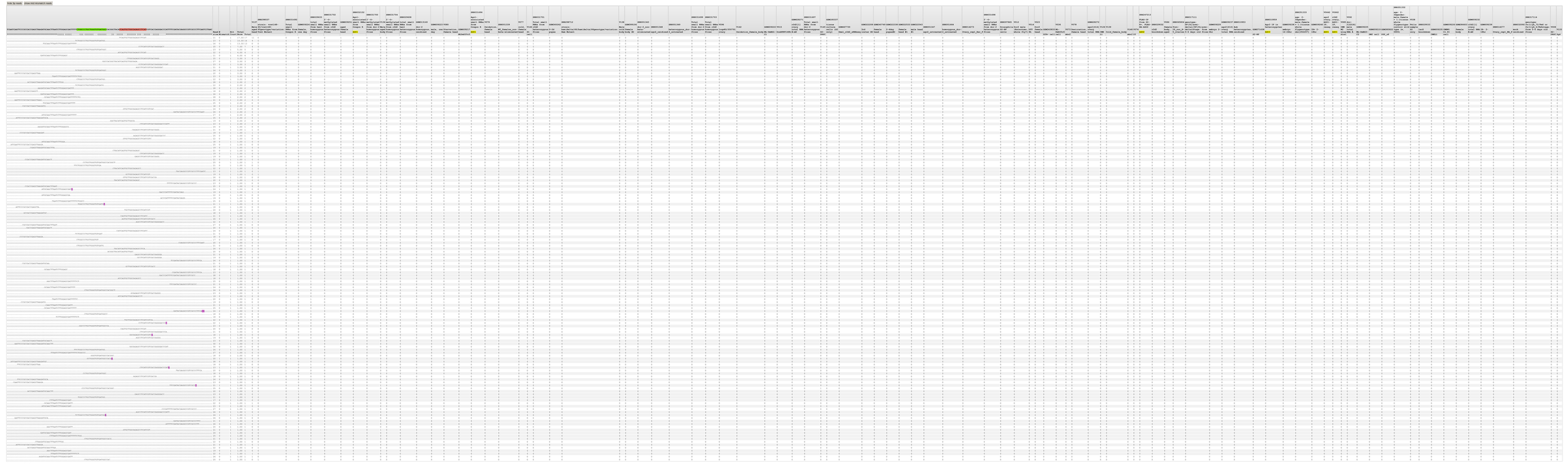
Flybase annotation

xenu(ZAP70-sq:CTR:24bs-ch1) fxc_pmo_CTR:24bs-ef

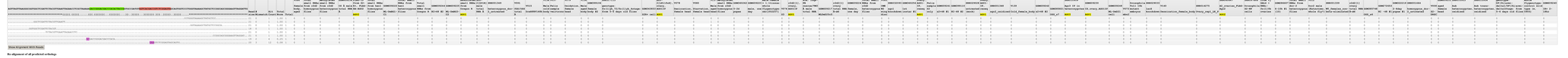
No Repeatds elements found

Some Stranded Reads

Hide 3p reads | show mul-mismatch reads



Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

Generated 09/09/2022 at 01:24 AM

Sequence
ATGCGAT
ATGCGAT
ATGCGAT

Sample	Reference	Genome	Date

Mem: 187.4G/1.21T(0.1%) Swap: 1.0G/8.0G Load avg: 1.00

Type	Name	Version	Description
Tool	Minimap2	2.24-r1122	Pairwise mapping and sequence alignment

Analysis Summary

Read Pileup Depth Density
Mean: 1.0
Median: 1.0
Mode: 1.0
Mode Count: 1.0
Mode Percentage: 100.0%
Mode Frequency: 1.0
Mode Rank: 1.0
Mode Rank Percentile: 100.0%
Mode Percentile: 100.0%
Mode Z-Score: 0.0
Mode Deviation: 0.0
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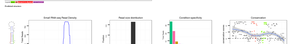
Mode Deviation

Test Name	Environment	Tester	Start Date/Time

Allstate FTPS Jan 31, 2 Thd Sept 2 Thd OCT2 - Session Finishing Time: jeudi, 2 Oct 2025 12:36:16

Legend: Passed Failed Canceled

Results summary



Results summary

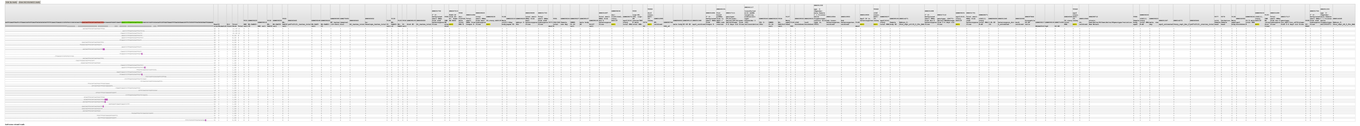
Failure summary

Test case: 1:0:0:0:0:0:0:0

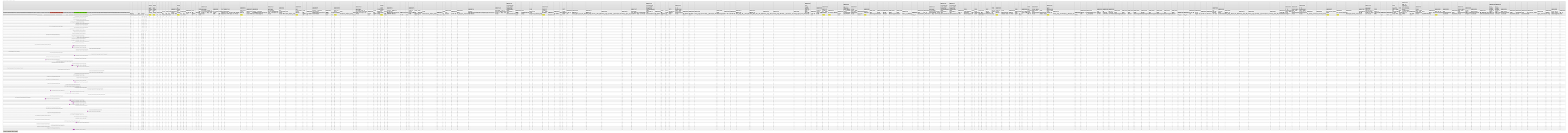
Test case: 1:0:0:0:0:0:0:0

Failing Repeat Group

Filter: Show all | Show failed | Show failed leaf



Filter: Show all | Show failed



Failure summary

Failure summary

Test case: 1:0:0:0:0:0:0:0

Test case: 1:0:0:0:0:0:0:0

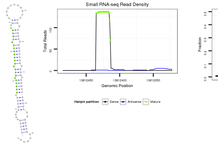
Failing Repeat Group

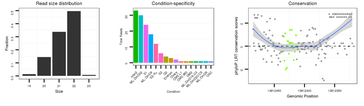
Filter: Show all | Show failed | Show failed leaf

ID	Coordinates	Confidence	Class	Genome Locus
dme_323	**chr2L:13812372-13812435 +**	**candidate**	**Canonical miRNA**	**intiumne_to_intron**

Legend: 5'arm 3'arm Terminal loop Mature

Predicted structure





Show Alternate Folds

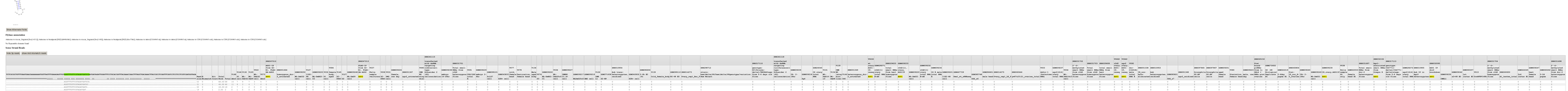
Flybase annotation

Adalsene to ovoid_Tagteb[Dm2-V7.1]; Adenosine to Neuloprid [DEL:BN0186]; Adenosine to ovoid_Tagteb[Dm2-V6]; Adenosine to Neuloprid [DEL:Dm1786]; Adenosine to ninra [CG10690-xd]; Adenosine to CTP [CG10690-xd]; Adenosine to CTP [CG10690-xb]; Adenosine to CTP [CG10690-xa];

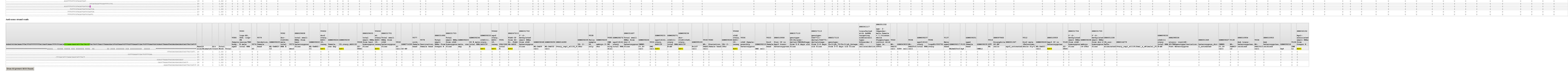
No Drosophila ncRNA Hairpin

Score Strand Reads

Hide Zp reads Show mid-mismatch reads



Antisense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

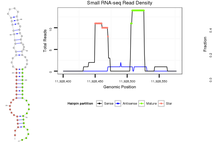
Generated 2026-05-07 at 11:17 AM

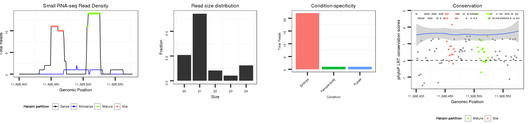
ID	Coordinate	Confidence	Class	Genome Locale
hyn_ins	**chr3L:11928450-11928527 +**	**Known Ortholog**	**mirtron**	**anthurne_to_intron**

View on UCSC Genome Browser (Cornell Mirror)

Length: 77 nt | Strand: + | Genome: anthurne

Predicted structure





Show Alternate Folds

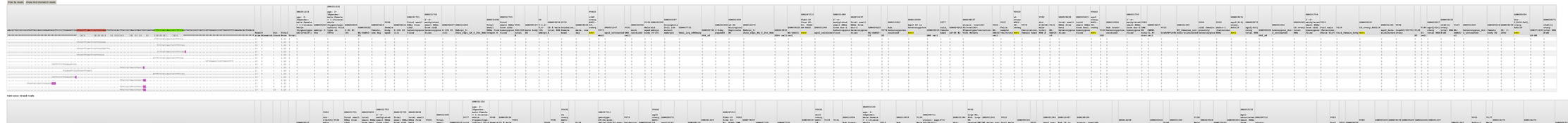
Flybase annotation

Anthurne to intro (CG40017-nd, intro:2kp:4kj, fbtr:_pma_3.TR, [5ss:ccl], CDS:[5ss:ccl], CDS:[5ss:ccl], intro:[5ss:ccl], CDS:[5ss:ccl])

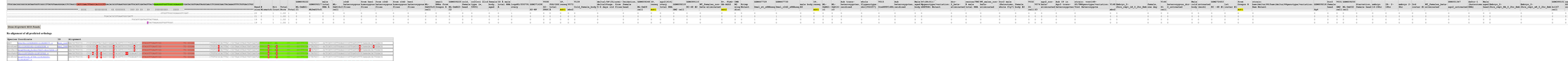
No Reportable chimeric fusel

Sense Strand Reads

Hide 36 reads | show mid-mismatch reads

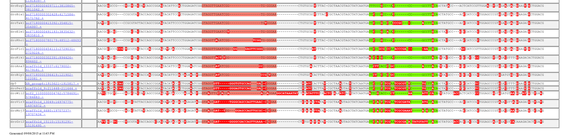


Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

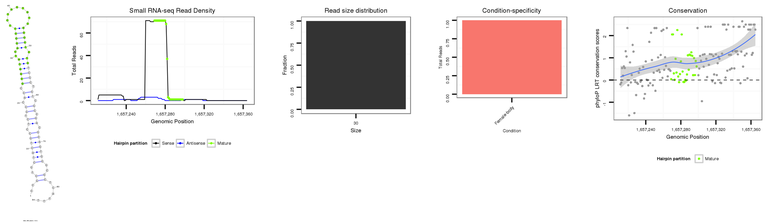


Generated 2026-06-01 at 12:43 PM

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dme_280	**chr3R:1657261-1657314 +**	**candidate**	**Canonical miRNA**	**3pUTR**	(View on UCSC Genome Browser (Control Mirror))

Legend: exons; pre; mature-3p; pre-loop; mature-5p; miRNA-Seq

Predicted structure



Show Alternate Folds

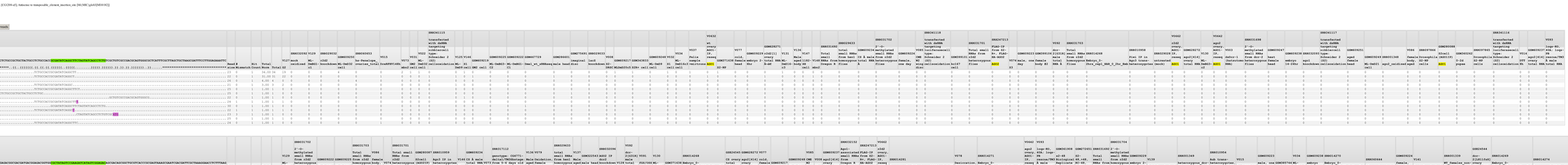
FlyBase annotation

flare_prime_3TR [pAch1-v1]; flare_prime_3TR [CG2336-uf]; Anticoron to transposable_element_insertion_site [MCMC:pAch[MI00182]]

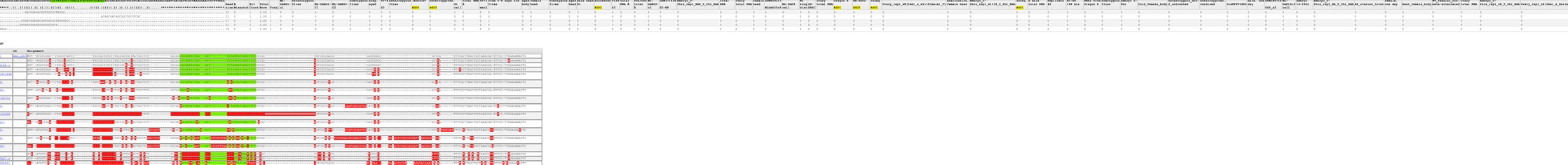
No Repeatable elements found

Sense Strand Reads

Hide 3p reads | Show mid mismatch reads



Anti-sense strand reads



Show Alignment With Reads

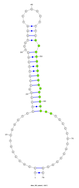
Re-alignment of all predicted orthologs

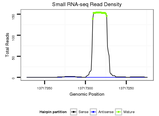
Species Coordinate
ID
Alignment
Dm3
dme_280
dsi3_chr3:1657261-1657314:+
dsim3_chr3:1657261-1657314:+
dsec3_chr3:1657261-1657314:+
dmel6_chr3R:1657261-1657314:+
dere6_scaffold_4770:1621650-1621583
dyak6_scaffold_2:1657261-1657314
dpse3_scaffold_15245:1:1657261-1657314:+
dpse3_scaffold_15245:1:1657261-1657314:+
dpse3_scaffold_15245:1:1657261-1657314:+

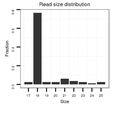
ID	Coordinate	Confidence	Class	Genomic Locus	
dme_282	**chr2L:13717274-13717322 -**	**candidate**	**Canonical miRNA**	**5pUTR**	[View on UCSC Genome Browser (Cons&Chains)]

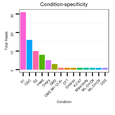
Score: **[illegible]** **Genome Coverage: [illegible]**

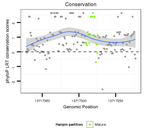
Predicted structure











Show Alignments Panel

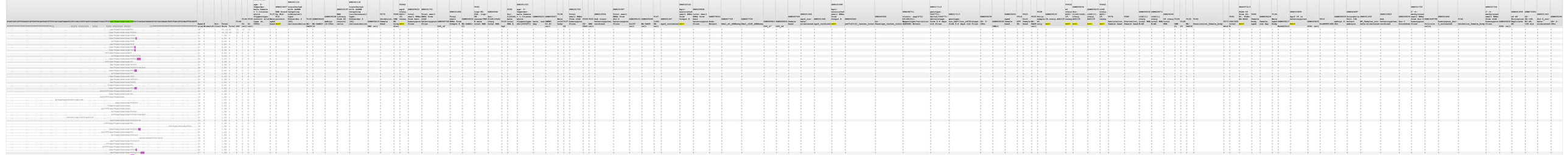
FASTA annotation

>mapquable_chrom_insertion_site [P-Cons(0.9)PAN3] (Ex_gene_1378 [CG31014-rf], boulapur [INCLE.B39196.hl], baltoraca to mapquable_chrom_insertion_site [P [BEEC.B.9522.1], mapquable_chrom_insertion_site [P [GEN.GE.0996.1], mapquable_chrom_insertion_site [P [ceb.CG2.0.0.[illegible]], boulapur [INCLE.B39196.hl], baltoraca to mapquable_chrom_insertion_site [P [ceb.N.P.CG2.0.0.[illegible]], boulapur [INCLE.B39196.hl], mapquable_chrom_insertion_site [P [GEN.GE.0996], boulapur [INCLE.B39196.hl], mapquable_chrom_insertion_site [P [GEN.GE.0997]]

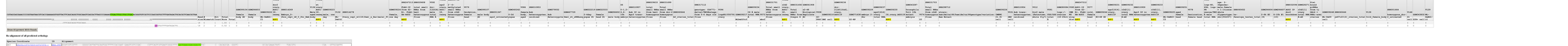
>>> Alignments viewer load

Sense Strand Reads

Side By Reads | show mid mismatch reads



Antisense strand reads



Show Alignment With Reads

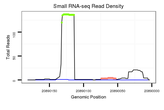
Re-alignment of all predicted orthologs

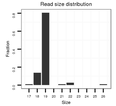
Created 2024/8/2023 at 6:29 AM

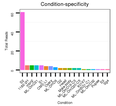
ID	Coordinate	Confidence	Class	Genome Locale	
dme_246	**chr21:20890053-20890132 -**	**candidate**	**Canonical miRNA**	**intron**	View on UCSC Genome Browser (GeneLMBrowser)

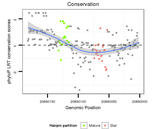
Legend: **Mature** **Star** **Terminal loop** **Miscellaneous**

Predicted structure









Show Alternate Folds

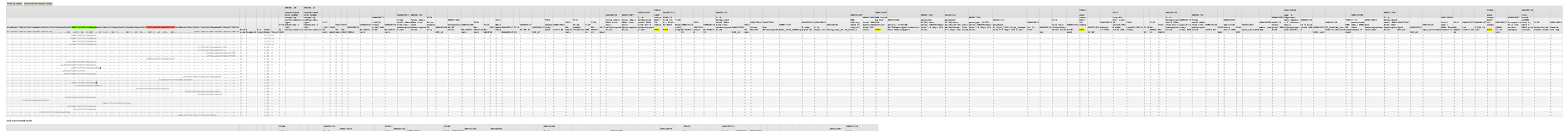
Flybase annotation

intron [CG7776-xg] intron [ch-xg] intron [ch-xg]

No Repeats stream found

Some Sized Reads

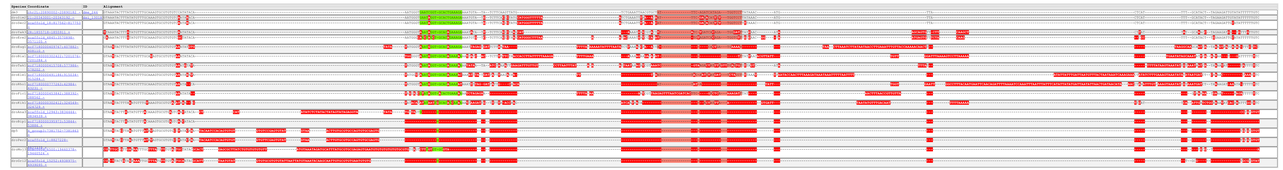
Hide 2p reads show mid-mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted evidenga

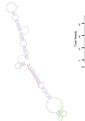


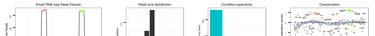
Generated 2020/06/23 at 01:08 AM

ID	Description	Collection	Date	Curate Score
ckbca.1189fx1 / chr X:49142286-49144411	Kazera-Ortiz-Bag_Serine_tetRnrna_tm_tetrna	Kazera-Ortiz-Bag_tetRnrna_tm_tetrna	2020-10-05	Kazera Bacon 10.0482798410

Curate **accept** 2020-10-05 Kazera Bacon

Predicted structure





Show 20 more tracks

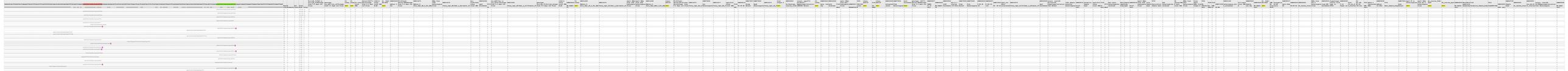
Flybase annotation

- Tc-Serine-tRNA-tetracycline-TGA (X:49138416-49138511, tetracycline in stem (Kgp:1.00,Cgl:0.00,Ce:0.00,Dm:0.00), tetracycline in stem (Kgp:1.00,Cgl:0.00,Ce:0.00,Dm:0.00), tetracycline in stem (Kgp:1.00,Cgl:0.00,Ce:0.00,Dm:0.00), tetracycline in stem (Kgp:1.00,Cgl:0.00,Ce:0.00,Dm:0.00))
- No flybase annotation found

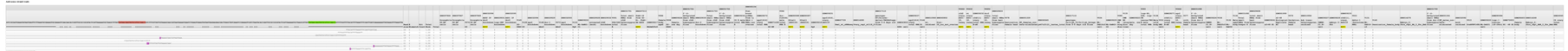
Genome	Coordinates
dm6	chrX:19767001-19767101, chrX:19767201-19767301
dm3	chrX:19767001-19767101, chrX:19767201-19767301

Trace Visual Mode

Hide Ins bases Show Insertion Counts

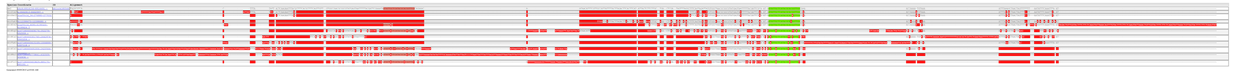


Left-over small reads



Show alignment to other

Multiplexed alignment of all genome orthologs



Nucleotide frequency (every 100)

ID	Coordinates	Confidence	Class	Genome Locus
dme_380 | chr2R:5852281-5852379 -	**candidate**	**Canonical miRNA**	**MyTH**	Show on GEM. Genome Browser. (Loaded Bibtrack)

Legend: Mature Loop Star Mature Star, alternative

Predicted structure:

-30.90 kcal/ mol

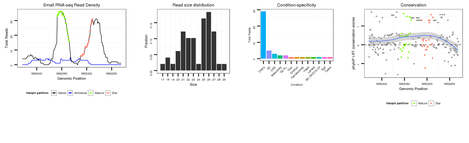
Show Structure Data

Flybase annotation

Fly_genes: CR32243-RA (-)

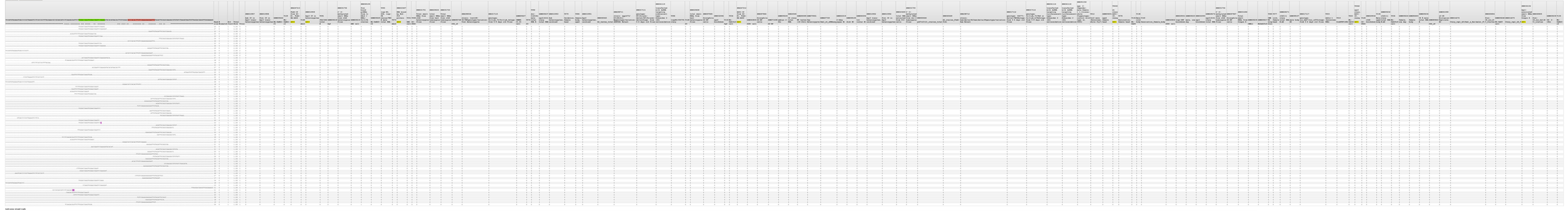
Tx: Exons(dm) (Intron Hunt)

Tracks Overall Reads

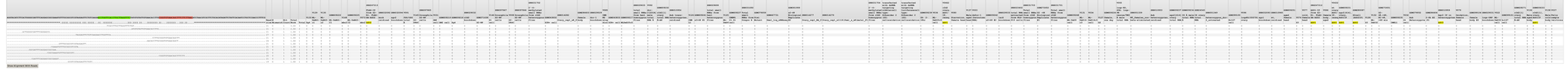


Show Overlap Data

Hide Tx reads Show NGS MismatchTracks



Anti-sense overall reads



Show Alignment With Reads

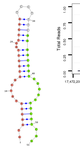
Re-alignment of all predicted orthologs

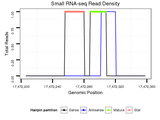
Generated MAFFIX(v7.at 7.1) - MD

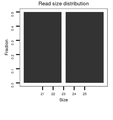
ID	Coordinate	Confidence	Class	Genome Locale
CG30222_in4	**chr2R:17472256-17472308** +	**Known Ortholog**	**miRNA**	**intron**

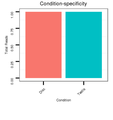
Genome: GGG GA CTCCCCCCCCCCCCCCCCC AGGCCCCCCC

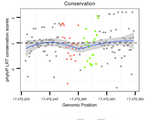
Predicted structure











Show Alternate Folds

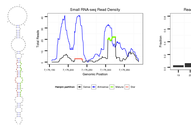
Flybase annotation

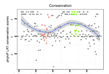
mirna:CG30222-4d, mirna:CG30222-5d, CR8:JX206222-1d, CR8:JX206222-2d, CR8:JX206222-3d, CR8:JX206222-4d, CR8:JX206222-5d, CR8:JX206222-6d, CR8:JX206222-7d, CR8:JX206222-8d, CR8:JX206222-9d, CR8:JX206222-10d, CR8:JX206222-11d, CR8:JX206222-12d, CR8:JX206222-13d, CR8:JX206222-14d, CR8:JX206222-15d, CR8:JX206222-16d, CR8:JX206222-17d, CR8:JX206222-18d, CR8:JX206222-19d, CR8:JX206222-20d, CR8:JX206222-21d, CR8:JX206222-22d, CR8:JX206222-23d, CR8:JX206222-24d, CR8:JX206222-25d, CR8:JX206222-26d, CR8:JX206222-27d, CR8:JX206222-28d, CR8:JX206222-29d, CR8:JX206222-30d, CR8:JX206222-31d, CR8:JX206222-32d, CR8:JX206222-33d, CR8:JX206222-34d, CR8:JX206222-35d, CR8:JX206222-36d, CR8:JX206222-37d, CR8:JX206222-38d, CR8:JX206222-39d, CR8:JX206222-40d,

ID	Coordinates	Confidence	Class	Genomic Locus
chlamAA0249 chr28:7175230-7175335	+ Reverse Orientation	unclassified_no_ESS	unclassified_no_ESS	UNA-ncLCR (Genome Browser, Ensembl Ortholog)

Length: 106 bp | 25.5% GC | 0.0% Ambiguous

Predicted structure





Show Genomic Context

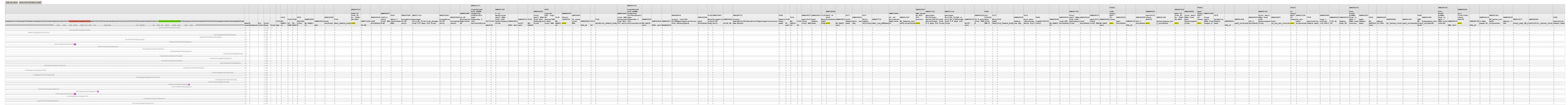
Flanking genomic

Reference: chr28:7175130-7175235 (+), Distance: 0 to 100 bp (100 nt)

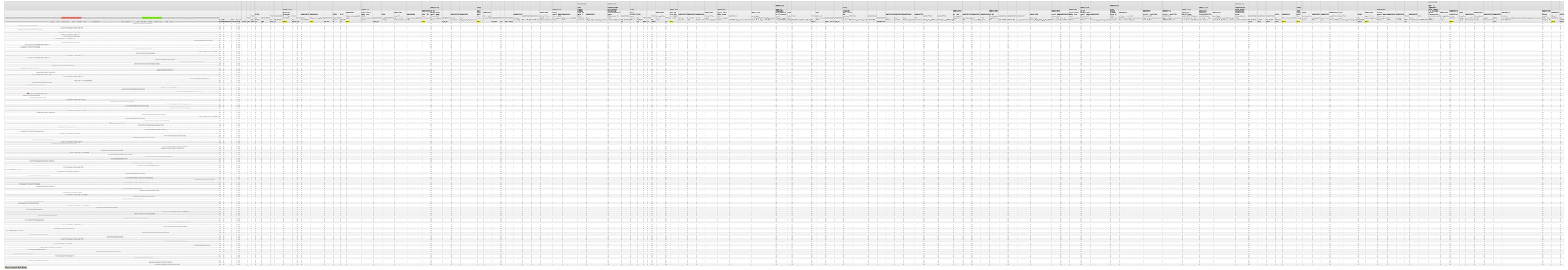
TTA TCACCATC CCACCA TCGAT

Homo Sensed Reads

Hide Tip Details | Show Hide ACCAMOTIF Hunter

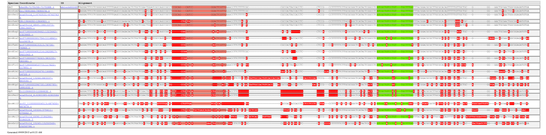


Sub-cover-detail reads



Show Alignment With Reads

Bp alignment of all predicted orthologs

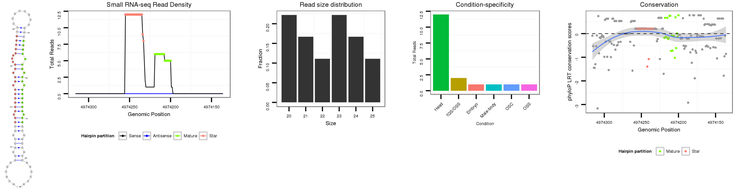


Generated 2026-05-04 at 07:12 PM

ID:	Coordinate:	Confidence:	Class:	Genome Locale:
sblock79863	**chr3L:4974186-4974266 -**	**Known Orthologs**	**intron**	**intron**
				[View on UCSC Genome Browser (Cactus43Mels)]

Legend: miRNA Sp Mismatch in alignment Mismatch in loop

Predicted structure



Show Alternate Folds

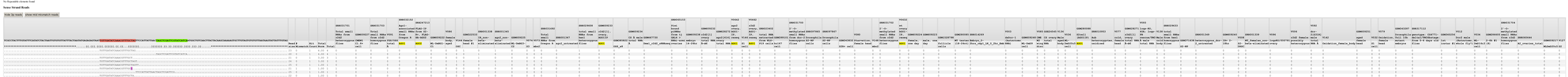
Flybase annotation

intron:[Con:0], intron:[Con:0]

No Repeatable elements found

Sense Strand Reads

Hide 3p reads Show mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

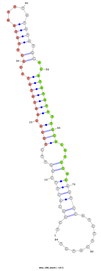
Re-alignment of all predicted orthologs

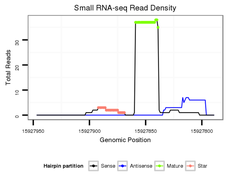
ID	Created	Updated	Size	Sample Seqs
**ddsu|43178	rfa-TL|NZ0986-N21135**	Kaarre-Orfanlig	1	1	1

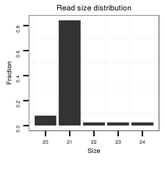
ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
dme_188	**chr2L:15927839-15927897 -**	**candidate**	**Canonical miRNA**	**intron**	[View on UCSC Genome Browser (Core18 Mirror)]

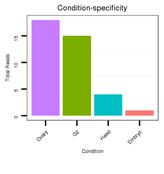
Legend: **mature** **star** sub-match in ally one or **mismatch in seed**

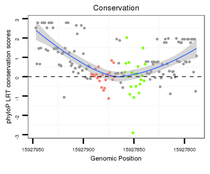
Predicted structure











Show Alternate Folds

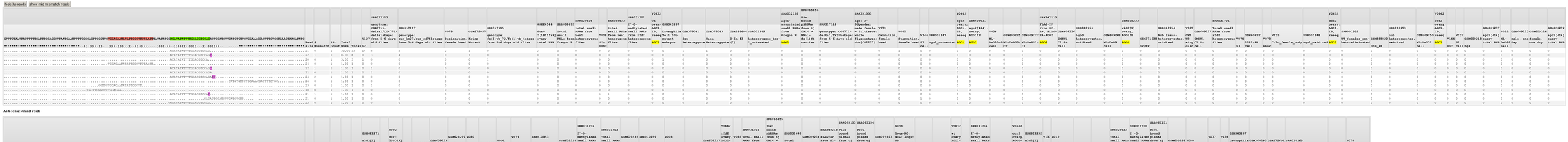
Flybase annotation

intron [beat-lb-in]

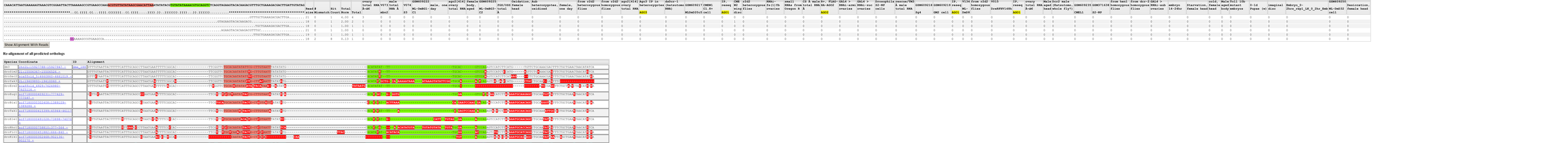
No Repeatable elements found

Sense Strand Reads

hide 3p reads show mid mismatch reads



Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

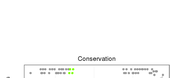
Generated: 09/09/2025 at 01:39 AM

	PASSPAL
orfs.star	0
orfs.loop	0
orfs.exp	0
orfs.mid	0
orfs.3p	0
orfs.5p	0
orfs.hairpin	0
orfs.flank	0
orfs.mature	0
orfs.star	0
mature.loop	0
mature.exp	0
mature.mid	0
mature.3p	0
mature.5p	0
mature.hairpin	0
mature.flank	0
mature.mature	0
mature.star	0
mature.conflicts	0
mature.candidate	0

ID:	Coordinate:	Confidence:	Class:	Genome Locale:	
Eaat2_in6	**chr21:738436-738507 -**	**Known Ortholog**	**intron**	**intron**	View on UCSC Genome Browser (ConSeMbase)

Legend: exon CDS intron 5'-UTR 3'-UTR

Predicted structure



Show Alternate Folds

Flybase annotation

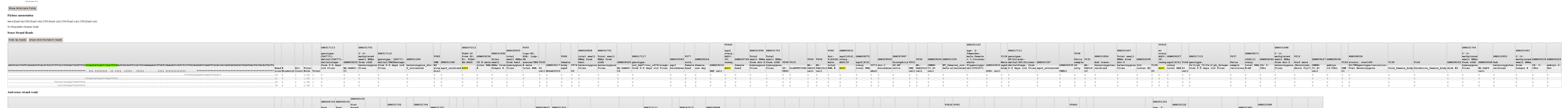
intron [Eaat2-in] CDS [Eaat2-cds] CDS [Eaat2-cds] CDS [Eaat2-cds] CDS [Eaat2-cds]

No Repeatds element found

Sense Strand Reads

Node 3p reads Show red mismatch reads

Anti-sense strand reads



Show alignment With Reads

Re-alignment of all predicted orthologs

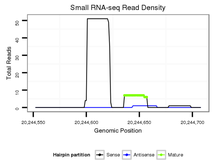
Generated 2019-09-27 at 14:54:54

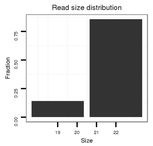
UCSC Genome Bioinformatics
UCSC Genome Browser
UCSC Table Browser
UCSC Genome Browser Gateway
UCSC Genome Browser Downloads
UCSC Genome Browser Mirrors
UCSC Genome Browser Blat
UCSC Genome Browser In Silico PCR
UCSC Genome Browser Table Schema
UCSC Genome Browser Frequently Asked Questions
UCSC Genome Browser Help
UCSC Genome Browser Genome Browser Gateway
UCSC Genome Browser Genome Browser Help
UCSC Genome Browser Genome Browser Mirrors
UCSC Genome Browser Genome Browser Downloads
UCSC Genome Browser Genome Browser Table Schema
UCSC Genome Browser Genome Browser Frequently Asked Questions
UCSC Genome Browser Genome Browser Help

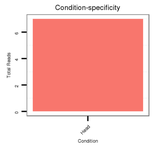
ID:	Coordinate:	Confidence:	Class:	Genome Locale:	
dme_198	**chr3L:20244602-20244658 +**	**candidate**	**Canonical miRNA**	**intron**	View on UCSC Genome Browser [Cons8.Mmu47]

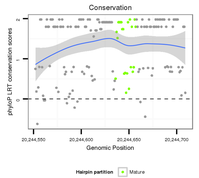
Legend: Mature Star Mismatch in alignment Mismatch in star

Predicted structure









Show Alternate Folds

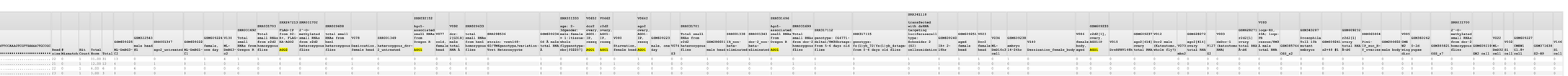
Flybase annotation

intron:[chr3L:-in]; intron:[chr3L:-in]; intron:[chr3L:-in]

No Repeatable elements found

Sense Strand Reads

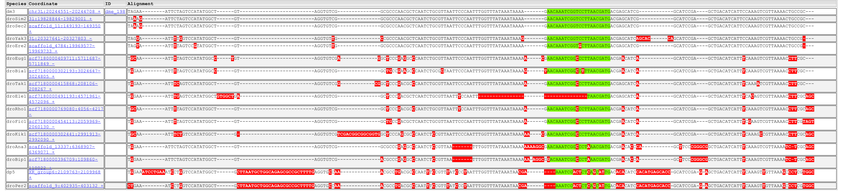
Hide 3p reads | Show mid-mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs



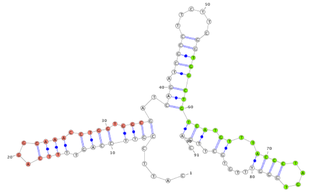
Generated 09/09/2015 @11:41AM

ch-star	0
ch-total	0
ch-mature	0
ch-passing	0
ch-mismatch	0
ch-hairpin	0
ch-miRNA	0
ch-hairpin	0
ch-miRNA	0
mean-hairpin	0
mean-miRNA	0
mean-confident	0
mean-candidate	0

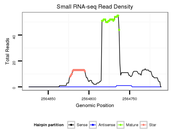
ID	Coordinate	Confidence	Class	Genomic Locale	
sblock2092	**chr21:-2564761-2564824 -**	**Known Ortholog**	**CDS**	**CDS**	View on UCSC Genome Browser (GenoBlMatch)

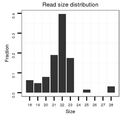
Layout: Sense Antisense Mature Star

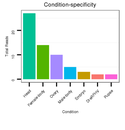
Predicted structure

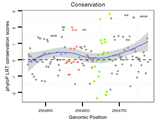


sblock2092_annot [−26.4]









Show Alternate Folds

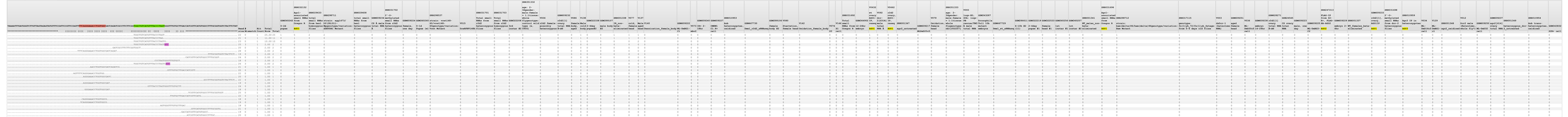
Flybase annotation

CDS:(CG9964-xk1:five_prime_UTR:[Cg(c9964-xf)]

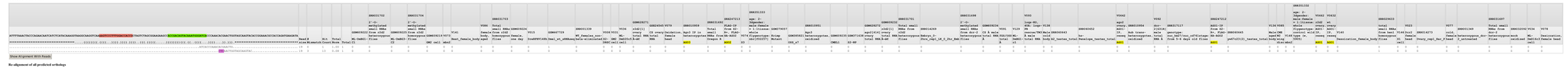
No Repeatable element found

Sense Strand Reads

Hide 3p reads show mid mismatch reads

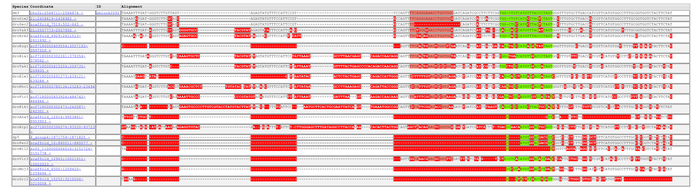


Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

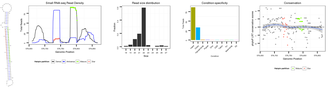


Generated 09/09/2023 at 01:42 AM

ID	Length	Frameshifts	Stop	Stop codon
chrom:1:1347[illegible]/-/ac:NM:Ins:CTA:TAG:CTA:0:0	1	Insertion:NM:Ins	Intergenic	Intergenic_no_stop_codon

Chr: chr1:[illegible]
Strand: Minus (-)

Protein sequence



Show Nucleotide View

Phase consistency
Phase consistency
Phase consistency
Phase consistency

Legend

Read - with Insertion Mutation	Read - with Deletion Mutation
Read - with Substitution Mutation	Read - with Ambiguous Mutation
Read - with Inversion Mutation	Read - with Inversion Mutation
Read - with Inversion Mutation	Read - with Inversion Mutation

Hide Alignment

Add Alignment Add Alignment Group

Alignment Group Group

Add Alignment Group Add Alignment Group

Alignment Group Group

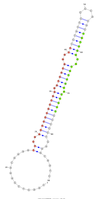
Alignment Group Group

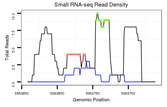
Alignment Group

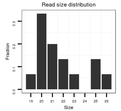
ID	Coordinate	Confidence	Class	Genome Locale	
sblock177975	**chrX:5963712-5963792 -**	**Known Ortholog**	**three_prime_UTR**	**3pUTR**	[View on UCSC Genome Browser (GoldEliMore)](#)

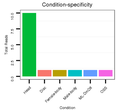
Legend: Stem Loop Terminal Loop Mature Star

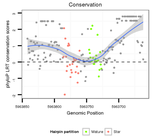
Predicted structure











Show Alternate Fonts

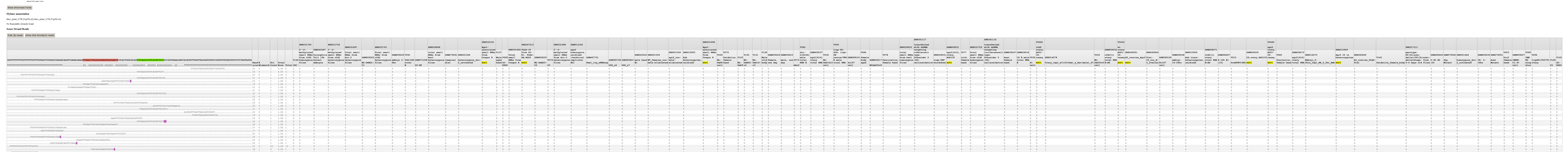
FASTmer annotation

three_prime_UTR:[Tp53Gv2] three_prime_UTR:[Tp53Gv2]

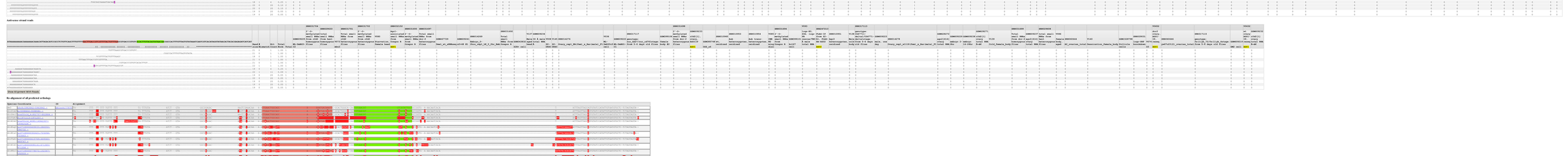
No Repeatitis elements found

Sense Strand Reads

Hide 3p reads show red mismatch reads



Left-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

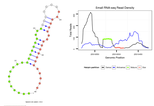
Generated 2025-05-21 at 12:04 -0400

Project	Locus	Condition	Cells	Sample name
Tgmut1_2_1kd	chr 19: 2151447 to 2151612	Scramble-Untreated	1	Scramble_kd_Sgf 150

Total: **1** Sgf 150 **100.00%** (**1 cells/sample**)

Sgf 150 **100.00%** (**1 cells/sample**)

Primer Locus



Show/Hide Alignment

Show/Hide Alignment

Alignment Legend

Alignment Legend

Alignment Legend

ID

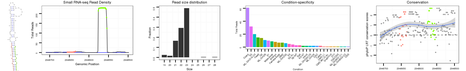
cb0ce3c90e7:cbc28:2940540:29d8660 - Kaeros Ortholog

Coordinates: Strand: Strand Length

Name: **Kaeros Ortholog** Strand: **Strand**

Show Alignment Ruler

Predicted structure



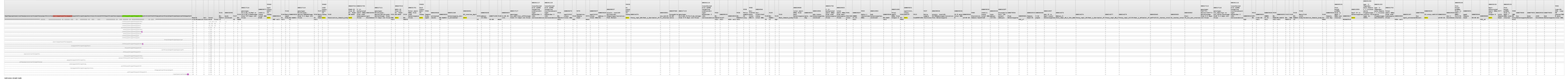
Show Structure Forms

Fold-back annotation

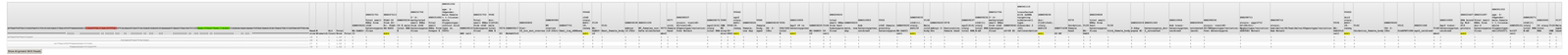
Mirnp:ppp01-42

No Repeats across Loop

Inner Visual Blast

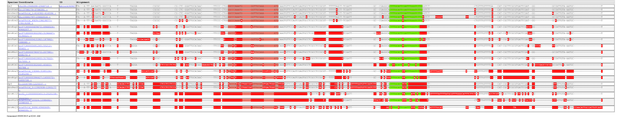


Full-cover strand traits



Show Organism MSA Results

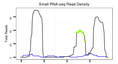
Ma alignment of all predicted orthologs

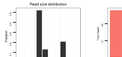


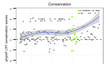
ID	Coordinates	Confidence	Class	Genome Locus
Mus-el_lncl_chr3R:23763060-23763152	Known OrthDeg	ncRNAs	intron	Ensembl Search

Strand: + Score: 60.00 Length: 93 Structure: (((((.((((.((((.....)))).)))).))))) ncRNA-Seq

Predicted structure







Show Alignment Help

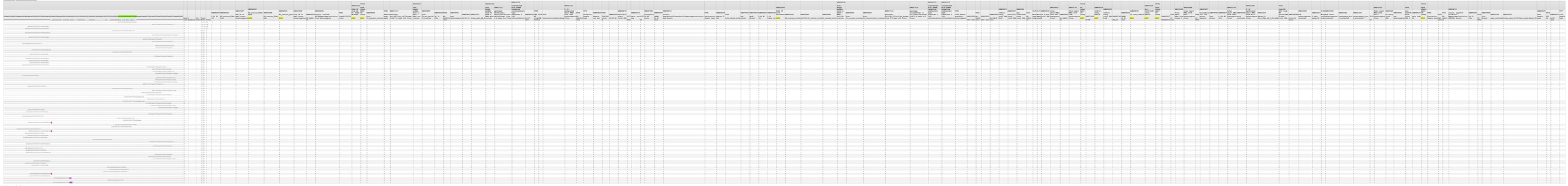
Filters: annotations

Min Filter: 0 Max Filter: 60 Hide: 0 Only: 0 Min Mm: 0 Max Mm: 0

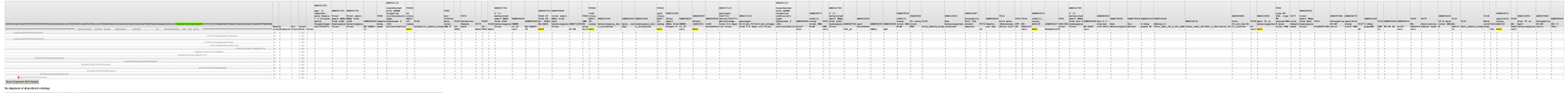
Hide Ambiguous Alignments: Off

Sam Sorted Reads

Hide Sq reads show NH/HI/AS/MD reads

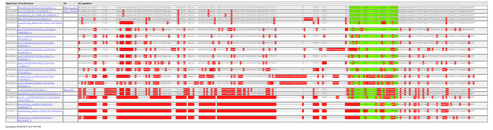


Left-over read reads



Show Alignment With Reads

Re-alignment of all predicted ncRNAs



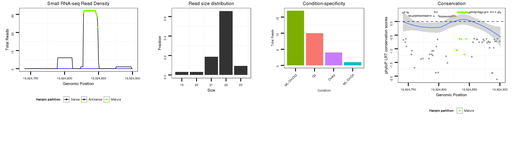
Alignment MAFFIX2 v7.475 by FFT-NS

ID	Coordinates	Confidence	Class	Genome Locale
dme_251	chrX:19924791-19924850 +	candidate	Canonical miRNA	metazoa_to_betrem

[View on UCSC Genome Browser (GenomeMine)]

Legend: **Stem** **5p** **Terminal Loop** **3p** **Flanking Seq**

Predicted structure



Show Alignments Fields

Fields: samseqtree

hexdpcnt:2|bc7%:0|MM:7|NM:0|, hexdpcnt:2|bc7%:0|MM:7|NM:0|, hetscore:nc:nm:c:2|nc:0|, hetdpcnt:nc:nm:c:2|nc:0|

No 16-position cluster hexdpcnt

Sense Strand Reads

Hide Sp reads Show mm mismatch reads

Read ID	Strand	Sense	Antisense	Mature	Total	Sense %	Antisense %	Mature %	Dominant	Sense Alignment	Antisense Alignment	Mature Alignment
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

Antisense strand reads

Read ID	Strand	Sense	Antisense	Mature	Total	Sense %	Antisense %	Mature %	Dominant	Sense Alignment	Antisense Alignment	Mature Alignment
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

Show Alignment With Repeats

Re-alignment of all predicted orthologs

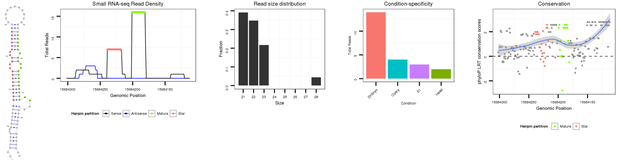
Species	Coordinates	LD	Alignment
[illegible]	[illegible]	[illegible]	[illegible]

Genome Alignment of chr19:1234

ID	Coordinate	Confidence	Class	Genomic Locus
shdock48703	**chr2R:15684162-15684252 -**	**Known Ortholog**	**intergenic**	**intergenic**

Legend: **Mature** **Hairpin Arm** **Star** **Miscleavage**

Predicted structure



Show Alternate Folds

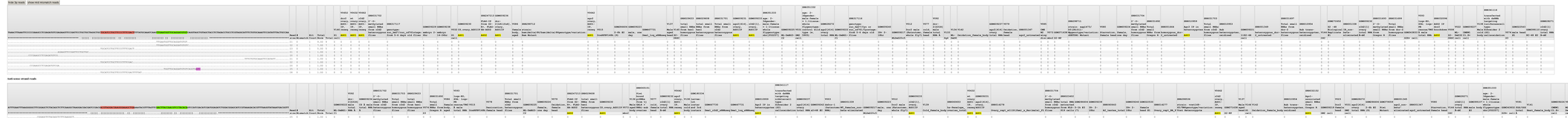
Flybase annotation

intergenic

No Repeatmk elements found

Same Strand Reads

Hide by reads | show mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

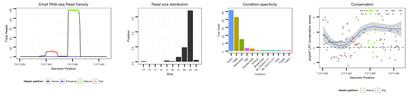
Generated 2022/8/22 8:12:22 AM

ID	Coordinate	Strand	Conflict	Novelty Score
dme_147	**chr3L:7017301-7017365**	+	**conditions 1 canonical mRNA**	**intron**

View on UCSC Genome Browser (Ensembl Mirror)

Length: 65 bp

Predicted structure



Show Advanced Plots

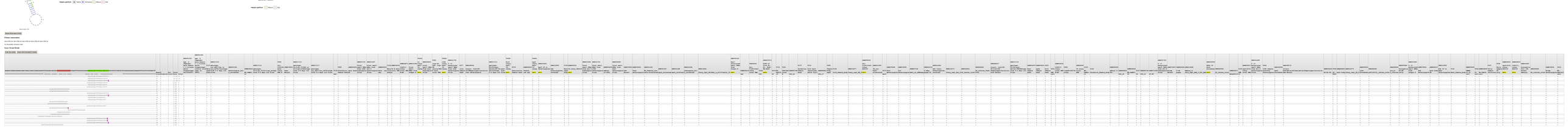
Fitness annotation

dme-v1-r6: dme-v1-r6: dme-v1-r6: dme-v1-r6: dme-v1-r6: dme-v1-r6: dme-v1-r6

79 Drosophila sequence hits

Tissue Small RNA

Hide Tissues | Show Individual Samples



Sub-tree ribosil rsnh

Show Alignment With Notes

Rv alignment of all predicted orthologs

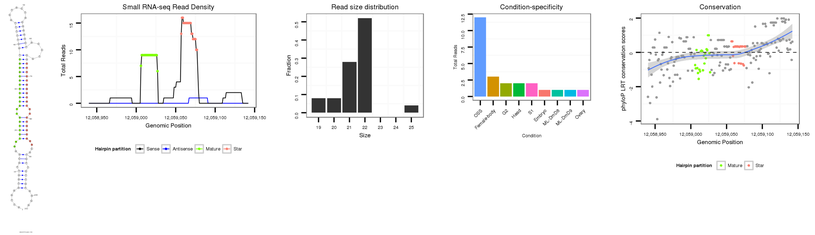
Conservation: 23/23 (100.0%) conserved

Consensus: ACGTACGTACGT

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:	
sblock147574	**chr3R:12058990-12059092 +**	**Known Ortholog**	**intron**	**intron**	(View on UCSC Genome Browser (Cornell Mirror))

Legend: Sense Sense Antisense Antisense mismatch to sense mismatch to antisense

Predicted structure



Show Alternate Folds

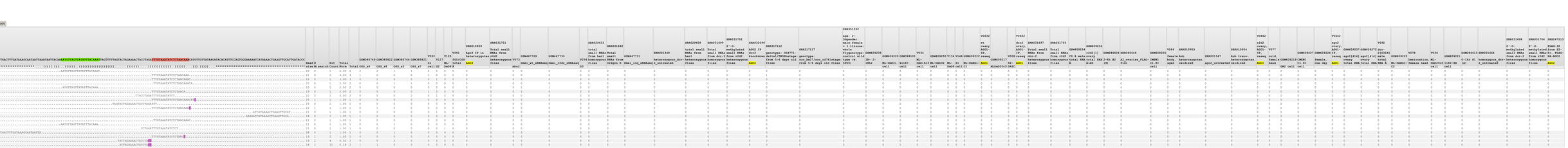
Flybase annotation

intron [here-in]

No Repeatable elements found

Sense Strand Reads

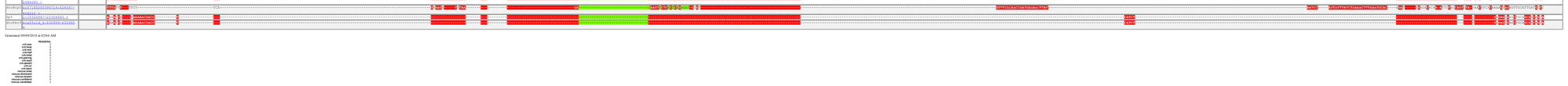
Hide 3p reads | Show mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

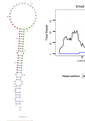


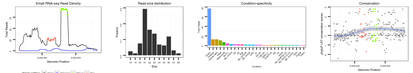
Generated 09/09/2015 at 02:04 AM

ID	Location	Length	Strand	Score (cm)
dme_396_ubrX:2805582-2805514 +	condition 2	68	+	2	2.9

Genome: dm6 (Drosophila melanogaster)

Predicted structure:





Show secondary map

Flanks annotation

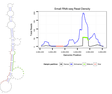
5' flank: CTCGCGCGCGCGCTCTTCTTCT

ID	1	Name	Alignment_1	Sites	1000
Partitions	1	Patterns	1000	Max. Gap	0.00%

Alignment_1 (DNA, 1000 sites, 1000 patterns, gappyness = 0.00%) = Dataset_Amphibia_Vertebrata_18_18S18S_Sanchez_et_al.fasta

Type: DNA | Gappyness: 0.00% | Gappyness

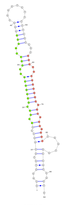
Alignment Summary

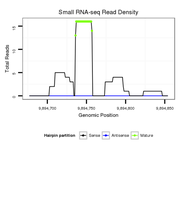


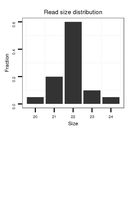
ID:	Coordinate:	Confidence:	Clan:	Genomic Locale:
sblock102079	**chr3L:9894727-9894804 +**	**Known Ortholog**	**CDS**	**intron**
				[View on UCSC Genome Browser (Grand Mean)]

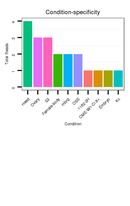
Legend: [illegible] [illegible] [illegible]

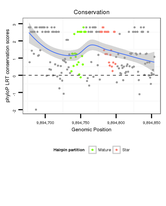
Predicted structure











Show Alternate Folds

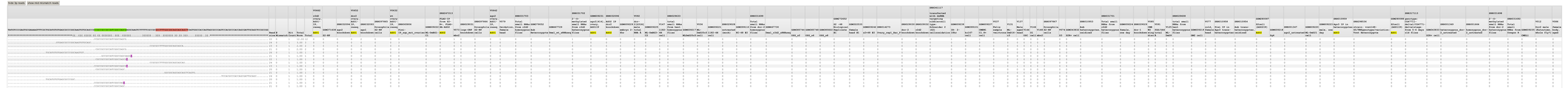
Flybase annotation

intro [mel] -tE CDS [mel] -c6j intro [mel] -tG intro [mel] -tI

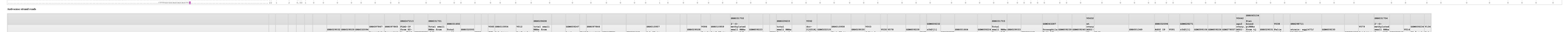
No Repeatmk elements found

Sense Strand Reads

Hide 3p reads show mid mismatch reads



Anti-sense strand reads



Show Alignment With Reads

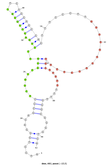
Re-alignment of all predicted orthologs

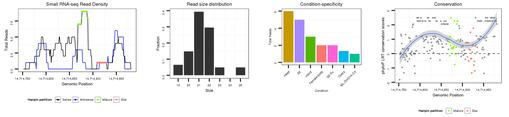
Generated 09/09/2025 at 12:21:32

ID	Coordinate	Confidence	Class	Genome Length
dme_403	**chr2R:14714802-14714931 +**	**candidate**	**Canonical miRNA**	**metazoa_to_intron**

Flags: **[Low]** **[Ambiguous]** **[Intronic]** **[Conserved]**

Predicted structure





Show Alternate Forms

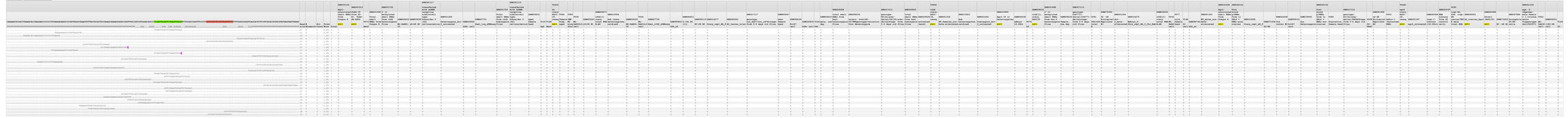
Flybase annotation

Indicates in dmel (CG0000 id)

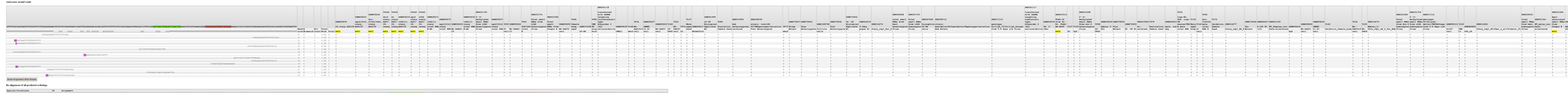
No Reporter Gene Trap

Sense Strand Reads

Scale Tip Colors Show Not mismatch reads



Antisense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

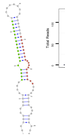
Generated 2026-05-25 at 04:04 GMT

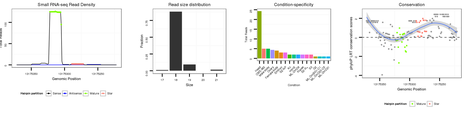
Genome
dmel
dsim
dsec
dyak
dere
dana
dpse
dpse
dwil
dvir
dmoj
dgri
dmel
dsim
dsec
dyak
dere
dana
dpse
dpse
dwil
dvir
dmoj
dgri

ID	Coordinates	Coordinates	Class	Genome Locale
dme_295 : chrX:13175272-13175322 -	**coordinates**	**Canonical miRNA**	**intron**	Open in UCSC Genome Browser (Local/Mirror)

Legend: Mature Star Terminal loop Alternative 3' Alternative 5'

Predicted structure:





Show Alternative Paths

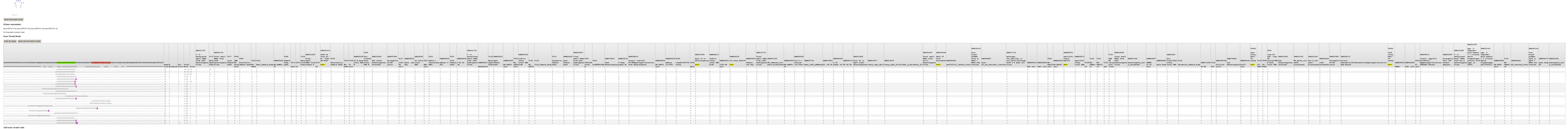
Flybase annotation

intron(13174.0 bp) intron(1074.0 bp) intron(2074.0 bp) intron(2074.0 bp)

In Repeats Antisense Small

Nearby Virtual Reads

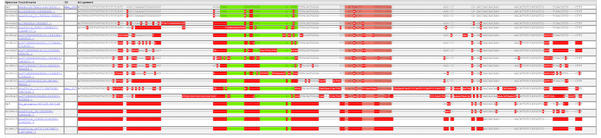
Hide Up reads Show 100 Downstream reads



Anti-sense overall reads

Show 20 genes 50 kb Reads

Nt alignment of all predicted miRnAg:

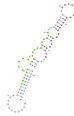


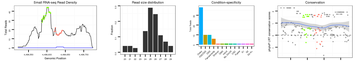
Consensus MFE/Total pairs cons

ID	Creation	Updated	Title	Source Code
dme_413_v1c136.0496771.e496675	1 months 2 days ago	1 months 2 days ago	Drosophila melanogaster (Fruit fly)	Dmel v6.56 (Ensembl Metazoa, Ensembl Genomes)

dme_413_v1c136.0496771.e496675 + (modified, Canonical model, 3p) : 18

Predicted structure





Show/Hide Hairpin Data

Primary sequence

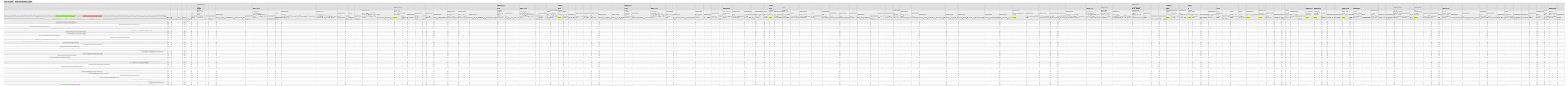
CTC GTC TTG TAC GTA GTA GTA GTA TTG TCA GTC

Secondary structure (dot-bracket)

.((((.((((.((((.((((.)))).)))).)))).)))).

Total Mirna Reads

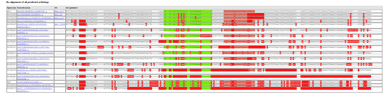
Hide Tab Details Show Mirna Reads Table



Hide Mirna Genome Loci

Show Alignment Table Hide

Multiple Alignment (Click on a column to view details)

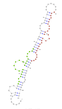


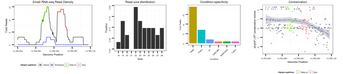
Generated 2022-08-22 at 23:01:00

ID	Name	Description	Date	Source Code
rdsaxk7YN	**rbc CB.1.4 7b4950-LC7f5b2**	Scanvo Orthodoxy Jarvus	2 hrs	https://colab.research.google.com/drive/1-xJ-Ed7Ldq-Bm-ec-yJ-ZqMXbbqqqq

Seq: 1,000,000 | 1,000,000 | 1,000,000 | 1,000,000

Predicted structure:





Show/hide Sequence Table

Primary assemblies

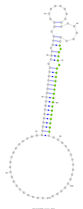
CB.1.4 7b4950 rc4 ARCHIVE-ID: 1 | 1 | 1 |

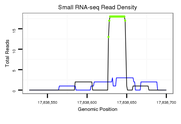
ID:	Coordinate:	Confidence:	Class:	Genome Locale:
sblock1151945	**chr3R:17838577-17838650 +**	**Known Ortholog**	**intergenic**	3pUTR

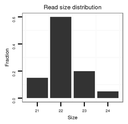
Click on UCSC Genome Browser (Control/Menu)

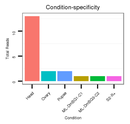
Legend: Sense Antisense Mature Hairpin Arm

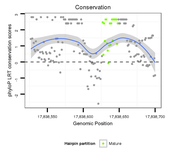
Predicted structure











Show Alternate Folds

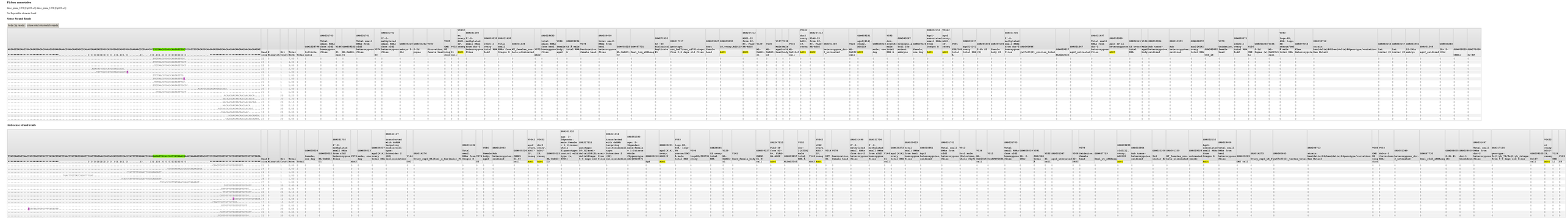
Flybase annotation

flux_peak_578 [FlyBrid v2] flux_peak_578 [FlyBrid v2]

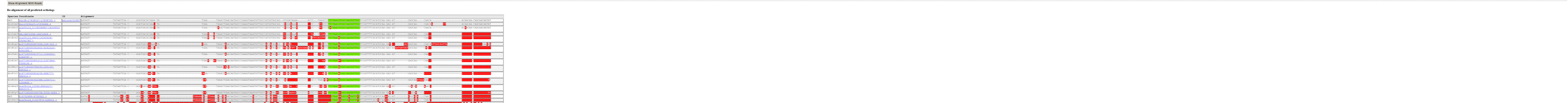
No Repeatable elements found

Sense Strand Reads

Hide Sp reads | Show mid mismatch reads



Anti-sense strand reads



Show Alignment With Reads

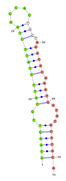
Re-alignment of all predicted orthologs

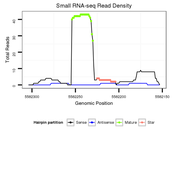
Generated 09/09/2019 at 02:53 AM

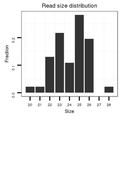
ID	Coordinate	Confidence	Class	Genomic Locale
CG3160_in3	**chrX:5582203-5582254 -**	**Known Ortholog**	**miRNA**	**intron**

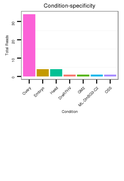
Layer: DNA RNA Predicted structure Conservation

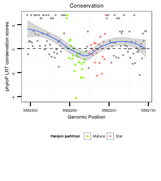
Predicted structure











Show Alternate Folds

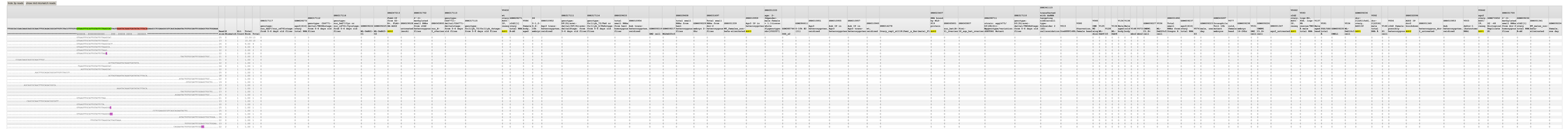
Flybase annotation

mus(2)32400-aj CDS (FlyBase-ade) CDS [CG3160-ade]

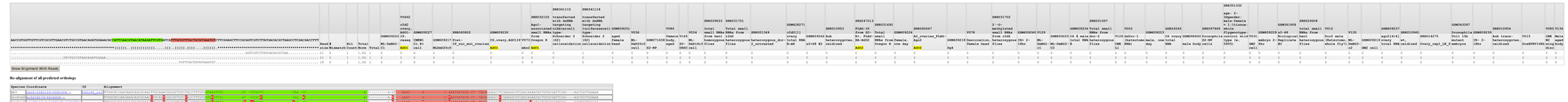
No Repeatmk elements found

Sense Strand Reads

Hide Sp reads | Show red mismatch reads

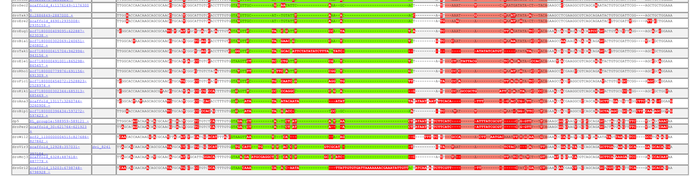


Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

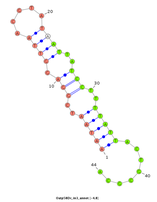


Generated 09/05/2022 at 07:04 PM

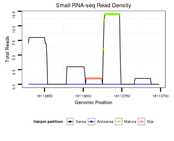
ID	Coordinate	Confidence	Class	Genomic Locale	
Oatp58Dc_in3	**chr2R:18113752-18113821 -**	**Known Ortholog**	**miRNA**	**intron**	View on UCSC Genome Browser (Grmh37/Mm10)

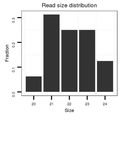
Legend: Exon miRNA Mature Star Hairpin arm

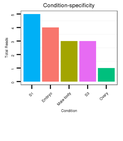
Predicted structure

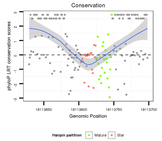


Oatp58Dc_in3_mature(-5.6)









Show Alternate Fields

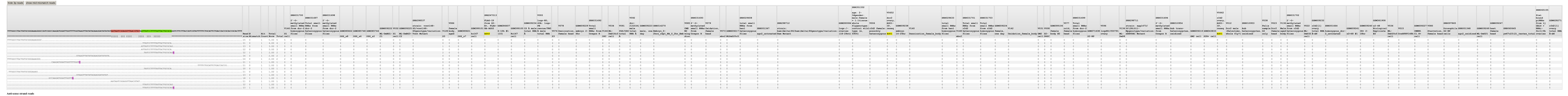
Flybase annotation

intron(FlyatMiRs, sg) CDS (DmgMDs v.ch) CDS (DmgMDs v.ch)

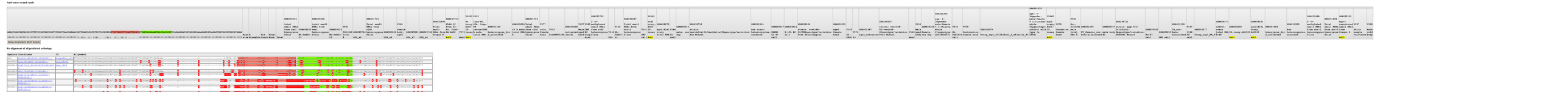
No Repeatible elements found

Sense Strand Reads

Hide Sp reads | Show mid mismatch reads

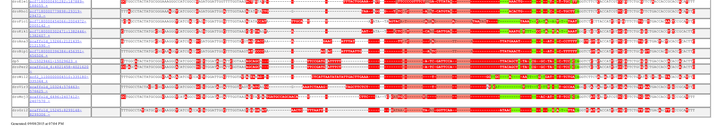


Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

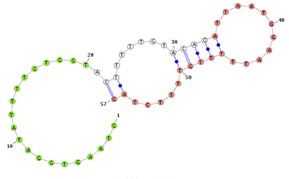


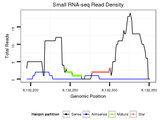
Generated 09/08/2015 at 07:04 PM

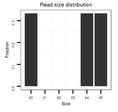
ID	Coordinate	Confidence	Class	Genome Guide
dme_388	**chr3L:8132245-8132301 +**	**candidate**	**MiRNA**	**intron**

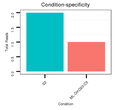
Legend: **miRNA** **Passenger strand** **Alternative**

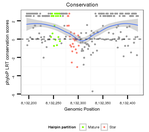
Predicted structure











Show Alternate Folds

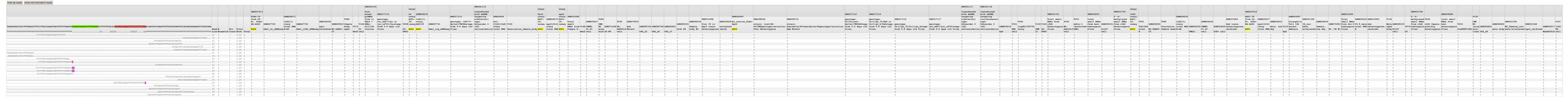
Flybase annotation

bradipoda:2015,gab:10.1042,novo_fragment:[ssa:91]:-8:.[]; intra:[ssa:91:-8]; CDS:[ssa:91:+:.]; CDS:[ssa:91:+:.]

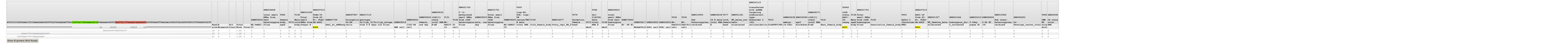
No Repeatmask elements found

Same Strand Reads

Hide 3p reads | show red mismatch reads

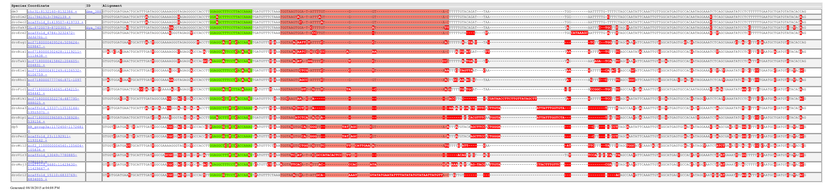


Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthology



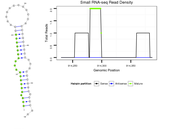
Generated 09/30/2021 at 04:05 PM

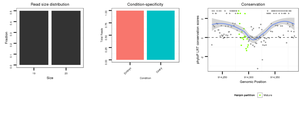
ID	Candidate	Confidence	Class	Strand Guide
GRch38|C_in1|chr21:9142280-9143377 +	Known OrfStalling	intron	intron	

View on UCSC Genome Browser (Local Mirror)

Legend: Stem 5p Terminal Loop Stem 3p Mismatch

Predicted structure:





Show Alternative Folds

Fasta sequence

>GRch38|C_in1|chr21:9142280-9143377 +|Hs|GTF|ENSF00-00|CTF|ENSF00-00|CTF|ENSF00-00|

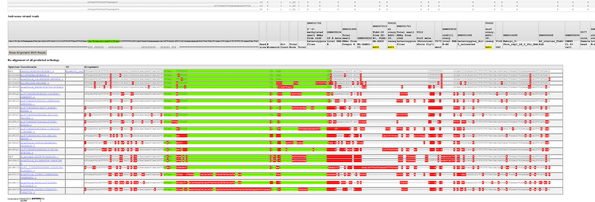
Nets Grand Reads

Nets Reads Show/Hide Intronic/Exonic reads

Sub-nets Grand reads

Show Alignment With Reads

Bp alignment of all predicted orthologs



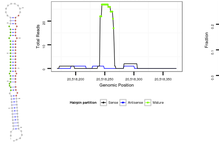
Variant Frequency **position** 0

0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0

ID	Coordinates	Confidence	Class	Genome Locus
sblock1.54733	**chr18:20518218-20518323 +**	**Known Orthologs**	**intron**	**intron**

Legend: **miRNA** **sno** **Protein Coding** **Pseudogene**

Predicted structure



Show Alternate Fields

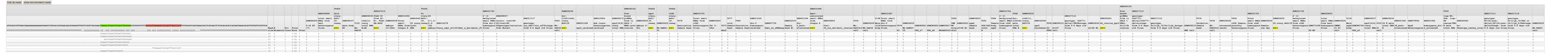
Flybase annotation

dm3:Chr 4R: 1 Mbrs:[20-40]

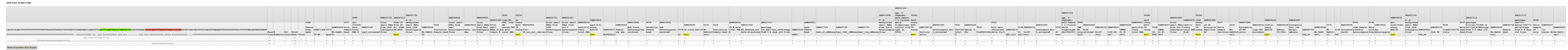
To Hyperlink chrom Scale

Score Strand Reads

Hide Sp reads Show Hid mismatch reads



Antisense strand reads



Show Alignment With Reads

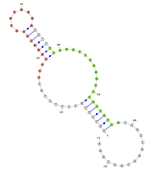
Re-alignment of all predicted orthologs

Generated 2020-Oct-21 at 07:18 AM

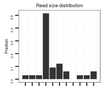
ID	Coordinate	Confidence	Tags
dme_379	chr2R:4791662-4791747 +	Candidate	Unknown	[View on GEM Genome Browser (Cactus/FlyBase)]

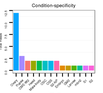
Legend: Genes CDS Exons & Introns miRNA/hairpin

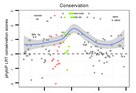
Predicted structure



dme_379_sense1 | 10.0[]



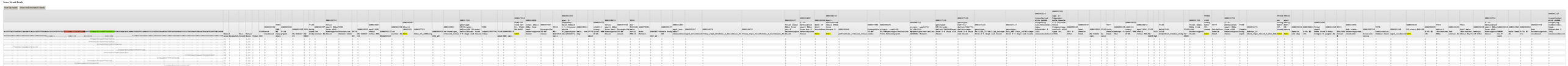




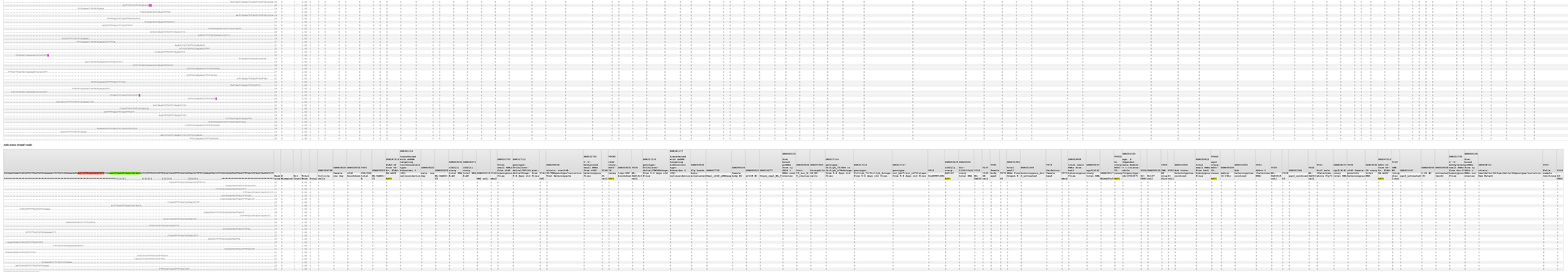
Show Alternate Folds

Sense Strand Reads

Hide Sp Indels Show read mismatch/indels

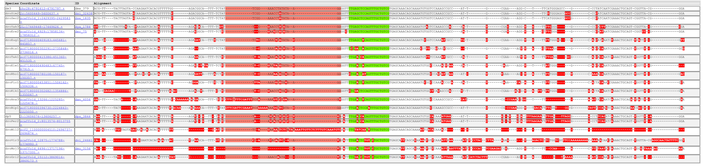


Antisense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

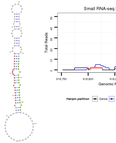


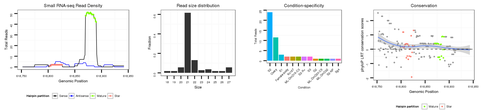
Generated 06-Feb-2017 at 05:11 PM

ID	Candidate	Confidence	Class	Genome Locus
dme_258 ; chr2R:618882-618892 +	**candidate**	**Canonical miRNA**	**intergenic**	chr2L:6-22,500; Genome Browser; JBrowse(Chrom)

Legend: Stem 5' Terminal loop 3' Terminal loop Mature/Star

Predicted structure:





Show Alignment Profile

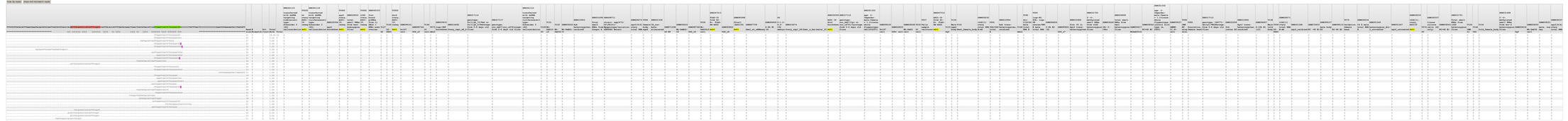
Fisher association

a:0;b:2;c:0;d:11;-Log

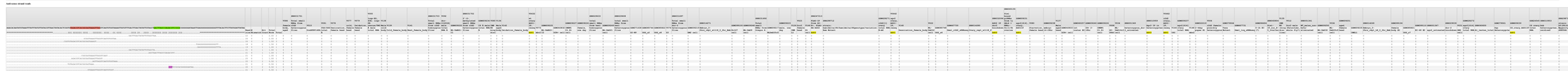
Yu Bayesian Score:Inad

Sense Strand Reads

Hide Top Hairpin Show read strand in reads

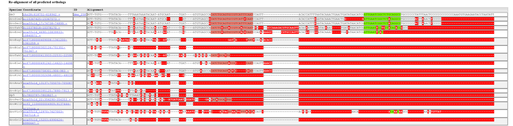


Antisense strand reads



Show All Aligned MIR Reads

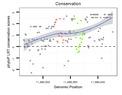
Re-alignment of all predicted miRnAgs


Species Coordinate
ID
MIR Genes
Homo sapiens
Mus musculus
Rattus norvegicus
Bos taurus
Canis lupus familiaris
Gallus gallus
Xenopus tropicalis
Danio rerio
Drosophila melanogaster
Drosophila simulans
Drosophila sechellia
Drosophila yakuba
Drosophila erecta
Drosophila ananassae
Drosophila pseudoobscura
Drosophila persimilis
Drosophila willistoni
Drosophila mojavensis
Drosophila virilis
Drosophila grimshawi
Anopheles gambiae
Apis mellifera
Caenorhabditis elegans
Caenorhabditis briggsae
Caenorhabditis remanei
Caenorhabditis brenneri
Caenorhabditis japonica
Pristionchus pacificus
Ciona intestinalis
Ciona savignyi
Saccharomyces cerevisiae
Saccharomyces paradoxus
Saccharomyces mikatae
Saccharomyces bayanus
Saccharomyces kudriavzevii
Saccharomyces castellii
Saccharomyces kluyveri
Saccharomyces cerevisiae
Candida albicans
Candida glabrata
Candida tropicalis
Candida parapsilosis
Candida dubliniensis
Candida guilliermondii
Candida lusitaniae
Candida pelliculosa
Candida tenuis
Candida sake
Candida bacillisporus
Candida zeylanoides
Candida orthopsilosis
Candida cladogenus

ID	Coordinate	Confidence	Class	Genome Locus
chbuck103084	**chr31:11689515-11689577**	**+ Known Ortholog**	**antisense_to_5p/3R**	**antisense_to_intron**

Legend: **Exon** **Intron** **Primary miRNA** **MIMIMIMIMIM**

Predicted structure:



Show Windows Folds

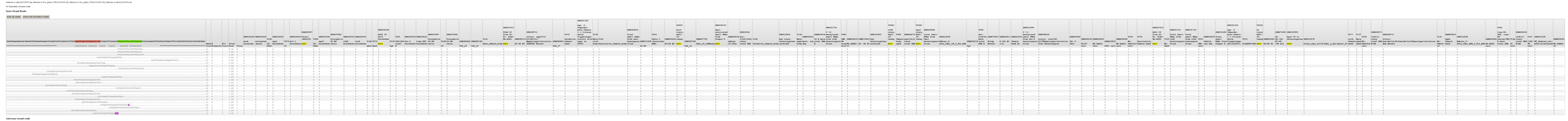
Fields: annotation

Valexon is Mem(2/3/4/5/6), Valintron is Fin_plus_UTR,E1/3/4/5/6,E2), Valexon is Fin_plus_UTR,E1/3/4/5/6), Valexon is Mem(2/3/4/5/6)

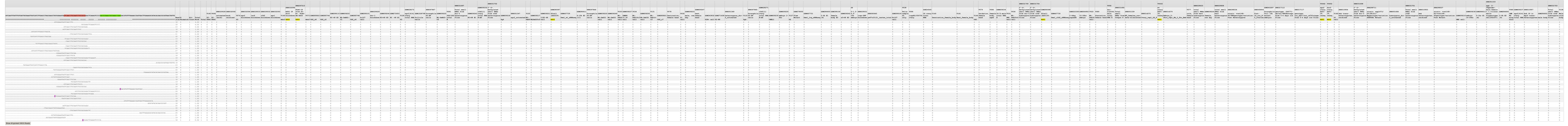
To Expandin column Read

Name Sread Reads

Hide Sp reads | Show NO PRIMARY reads



Anti-sense sread reads



Show Expanded With Reads

No alignment of all predicted orthologs

Generated 2022-03-17 at 21:14:

ID	Coordinate	Confidence	Class	Genome Locus
CGR233_lock	**chr28:10836685-10836738** – Known Ortholog	mirtron	intron	chr28:10135,Gallus Brown (GalGBR1001)

Legend: **Hairpin** **Mature** **Star** **Alternative Mature**

Predicted structure:

Show Processing Info

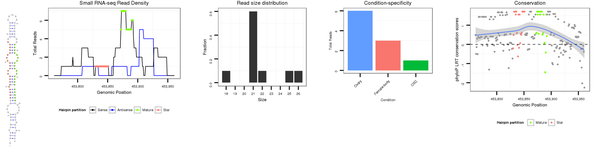
Flank annotation:

CGR233_lock chr28:10836685-10836738|chr28:10811-10873|+|0|0|0

ID	Coordinate	Confidence	Class	Genomic Locus
sblock192886	**chrX:453811-453911 +**	**Known Ortholog**	**Intron**	**Intron**

Score: **[illegible]** **[illegible]** **[illegible]**

Predicted structure



Show Alternate Folds

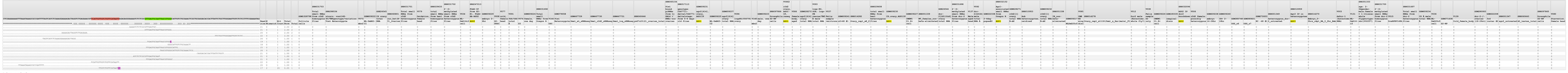
Fold-seq annotation

bioalpaca [Zfp175:ENSCZG76813]: mfold [-hgid=4]; mfold [-hgid=6]; bioalpaca [Zfp175:ENSCZG76813]

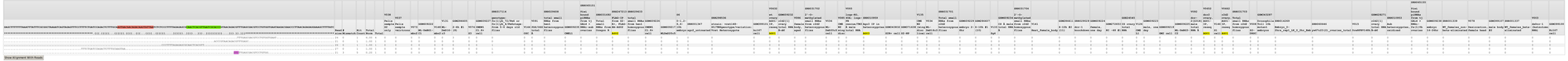
No Rnaseqdb clusters found

Score Ordered Reads

Side Ip reads | Show mid mismatch reads

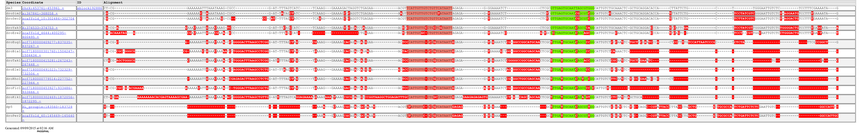


Antisense strand reads



Show Alignment With Reads

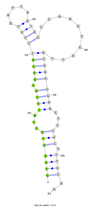
Re-alignment of all predicted orthologs

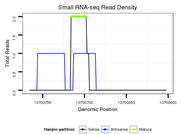

Species Coordinate
ID
Alignment
Consensus:CTCTCTC

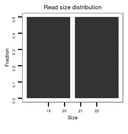
ID:	Coordinate:	Confidence:	Class:	Genome Locale:	
Lip1_in2	**chr2L:10700652-10700716 -**	**Known Orthologs**	**miRNA**	**intron**	Chr2 (v6 UCSC Genome Browser (Comel/Mimo))

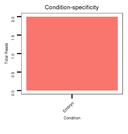
Legend: Genes Exons Known miRNA Novel miRNA

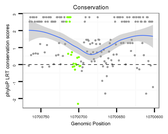
Predicted structure











Show Alternate Folds

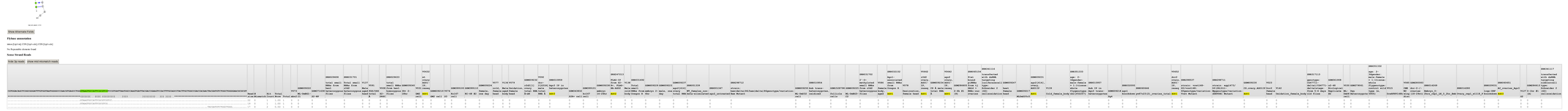
Flybase annotation

seq=[gb=dq] CDS [gb=dq] CDS [gb=dq]

No Repeatds chosen fond

Sense Strand Reads

Hide 3p reads | Show mid mismatch reads



Anti-sense strand reads

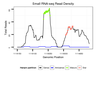
Show Alignment With Reads

Re-alignment of all predicted orthologs

ID	Accession	Length	Mean	Total Length
dme_392	**chr X:11147967-11175208**	**Conditions**	**Counts of mRNA 5' ends**	

Show/hide Conditions/Counts

Predicted structure



dme_392 (size = 2244)

Show/hide Input Data

Fetched assemblies

Fetched Small RNA-seq Read Density: 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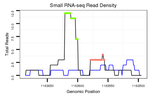
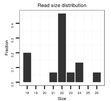
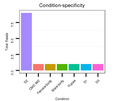
ID	Coordinates	Confidence	Size	Genome Locus
xblock1267	**chr21:-:1163545-1163636**	**Known Orthologs**	**intron**	**intron**

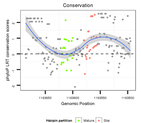
Legend: Gene **Exon** **Intron** **Conserved Intron** **Alignment Gap**

Predicted structure









Show Alternate Folds

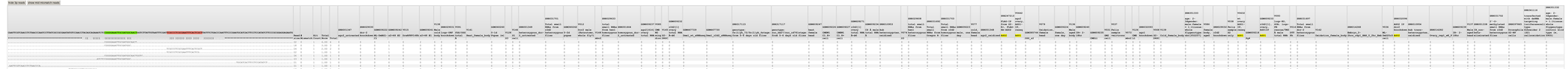
Fichier annotation

mmu11:21900-42; fru_pima_1.0:JC0040-of2; fru_pima_1.0:JC0040-of2

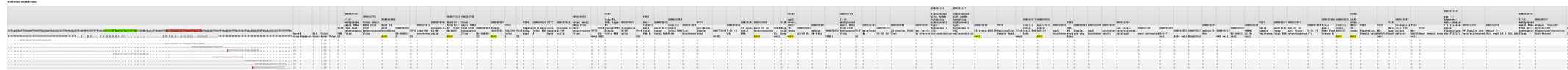
Vr Repeatdb stream found

Some Strand Reads

Scale 2p reads show red mismatch reads



Anti-sense strand reads



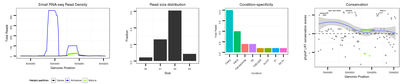
Show Alignment With Reads

Re-alignment of all predicted orthologs

ID	Coordinate	Strand	Type	Genome Length
dmo-mir-2283-as chr38:9343246-9343321 -	**Known OrthoDB**	**antisense_to_intron**	**antisense_to_intron**	23cc-ch12.fa (Genome Browser Extended Bases)

Score: [illegible]

Predicted structure



Show/Hide Hairpin Plot

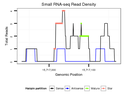
FASTA annotation

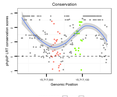
>hairpin|dmo-mir-2283-as|chr38:9343246-9343321|+|Known OrthoDB|+|+|+

ID	Coordinate	Confidence	Class	Subclass Locus
dme_394	chr3R:15716981-15717119 +	condition-specific	canonical miRNA	intron

Genome: dm6 dm3 mm10 mm9 hg38 hg19 panTro4 rheMac8 rnor6 rnor5 danRer10 danRer7 sacCer3 sacCer2 ce11 ce10 dm6 dm3 mm10 mm9 hg38 hg19 panTro4 rheMac8 rnor6 rnor5 danRer10 danRer7 sacCer3 sacCer2 ce11 ce10

Predicted structure:





Show Informative Reads

Filter: mismatches:

nm=2:3:4:7:11 up:nm=2:3:4:7:11 up:nm=2:3:4:7:11 up:

ID	Coordinate	Confidence	Size	Genome Locus
dme_385 | chr3L:3545656-3545783 +	**candidate**	**Canonical miRNA**	**intron**	

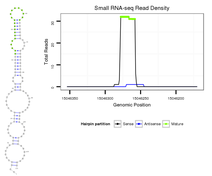
View on UCSC Genome Browser (Grandi Mirror)

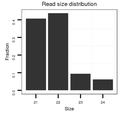
Target: **GGG** in **CCCC

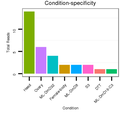
ID	Coordinate	Confidence	Class	Genomic Locale	
dme_420	**chr3R:15046220-15046304 -**	**candidate**	**Canonical miRNA**	**intron**	View on UCSC Genome Browser (Local Mirror)

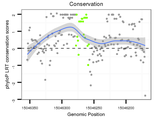
Legend: Stem 5p Terminal loop 3p Mature Alternative Mature

Predicted structure









Show Alternative Folds

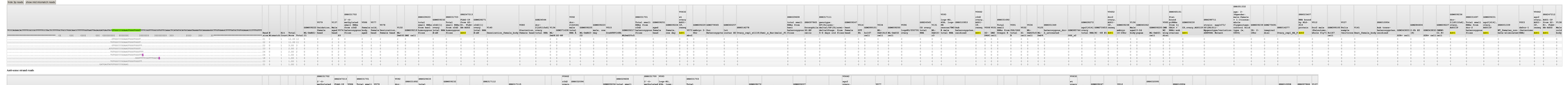
Flybase annotation

sequence_variant:2928192_snvs:3-dt-ni

No Repeatitle elements found

Sense Strand Reads

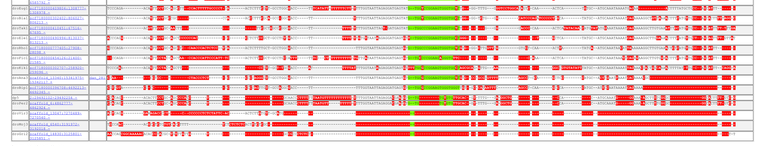
Hide Sp reads | show red mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs



Generated 09/09/2024 at 02:51 AM

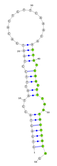
ID	Confidence	Strand	Type	Genome Coord
dbtech216052:chr21:12421082-12421990	**Known OrfStalling**	Sense	Intron	Intron at Chr: Genome Reference: (Ensembl/Mammal)

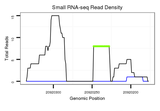
Length: 909 bp (CTCTCTC

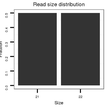
ID	Coordinate	Confidence	Chrs.	Genome Locus
Mtp_ia3	chr21:20920227-20920285 -	known Ortholog	mirtron	intron

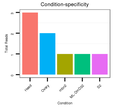
Legend: **miRNA** **Passenger strand** **Loop sequence**

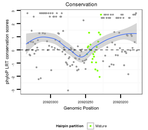
Predicted structure











Show Alternate Folds

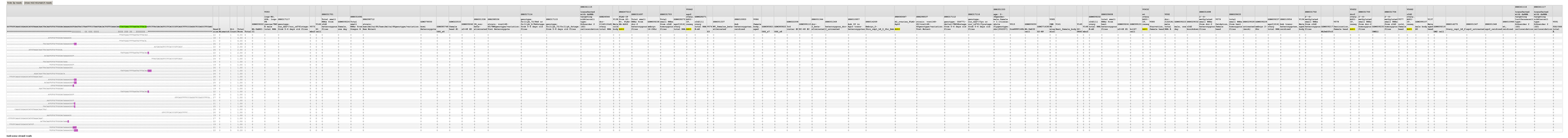
Flybase annotation

mirn:Dme-mir-279:Dme-mir-279:Dme-mir-8:

No Repeatmasker elements found

Some Stranded Reads

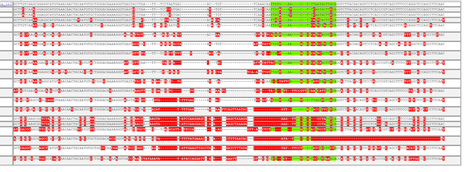
Sort by reads | show mid-mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs

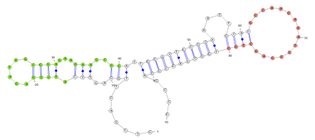

Species Consensus
25
Alignment
Dmel
Dsim
Dsec
Dmel
Dyak
Dere
Dyak
Dere
Dpse
Dpse
Dpse

ID	Coordinate	Confidence	Class	Genomic Locus
dme_401	**chr2L:4955590-4955715 +**	**candidate**	**Canonical miRNA**	**CDS**

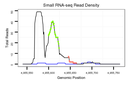
View on UCSC Genome Browser (Local Mirror)

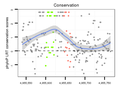
Legend: Stem 5p Terminal Loop Stem 3p Mature 5p Mature 3p

Predicted structure:



dme_401_annot [-35.7]





Show Structure Folds

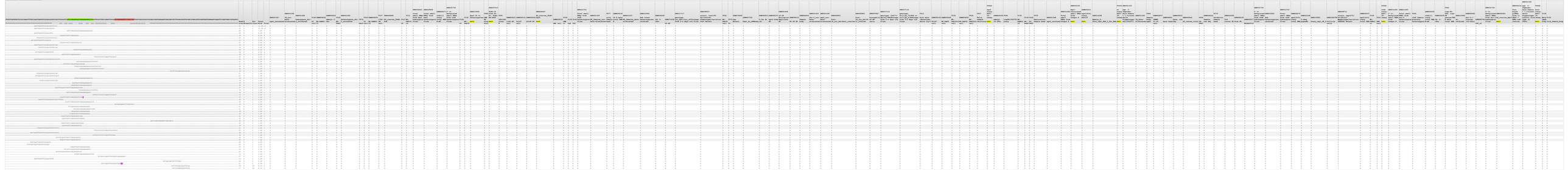
FlyTabs annotation

CDS:Manual:dme_401_pre_CTR:Manual:yes, Intron:no transposable_element_region:no, pp:[0.00,1.00]:+:0:Stem:[0]0:0:0:0:0:0:

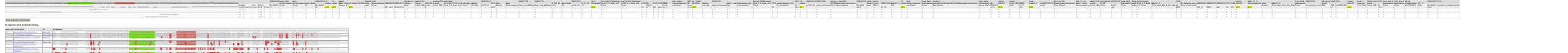
No Repeatmask overlap found

Some Small Reads

Hide 5p reads Show 3p/ star/ mature reads



Antisense strand reads:



Show Alignment With Reads

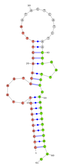
Re-alignment of all predicted orthologs:

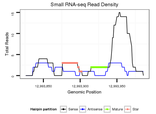
Generated 2026-02-27 at 22:22 +00

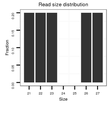
ID	Coordinate	Confidence	Class	Genome Guide
CG30456_in5	chr2R:12993876-12993936 +	Known Ortholog	miRNA	Intron

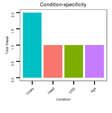
Score: 0.000 (0.000 / 0.000) [0.000/0.000]

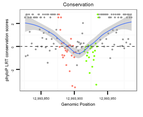
Predicted structure











Show Alternate Folds

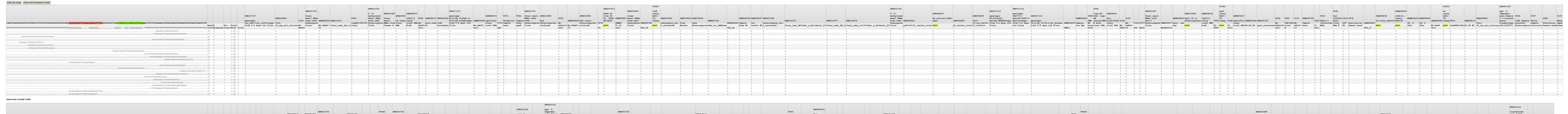
Flybase annotation

mus(2)30406-aj,CR[CR30406-aj],CR[CR30406-aj],CR[CR30406-aj],CR[CR30406-aj],CR[CR30406-aj],CR[CR30406-aj],CR[CR30406-aj]

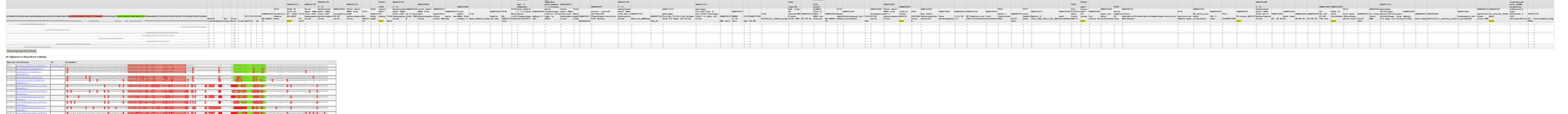
No Repeatmi elements found

Sense Strand Reads

Scale by reads | show mid mismatch reads

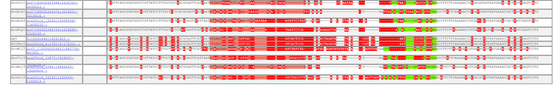


Antisense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

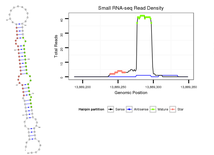


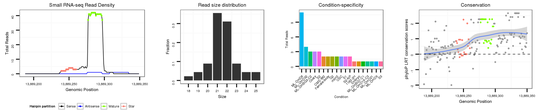
Created 2026/05/3 at 7:56 PM

ID	Coordinate	Candidates	Class	Genome Locale
dme_250	chr3R:13889238-13889299 +	candidate	Canonical miRNA	intergenic

View: **DNA** **RNA** **Predicted structure** **Alignment**

Predicted structure





Show Alternate Forms

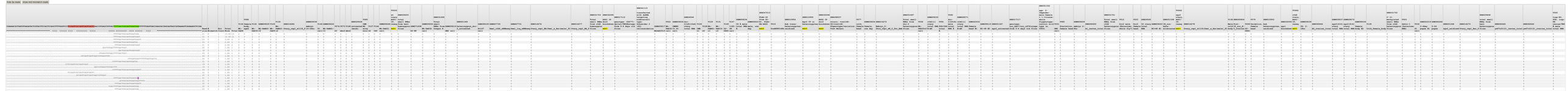
Flybase annotation

intergenic

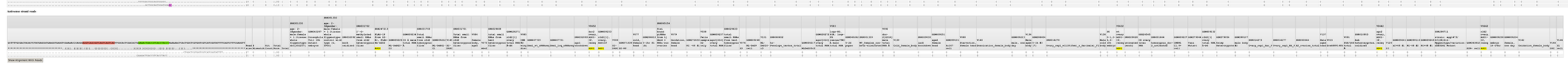
No Repeatmasker elements found

Sense Strand Reads

Hide Sp Valid Show mid-strength reads

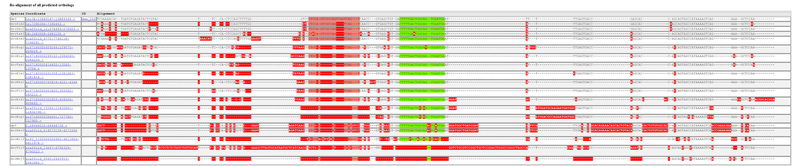


Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs



Generated 2009-09-27 at 12:21 AM

ID	Coordinate	Confidence	Class	Genome Locus
dmel_400	**chr3R:23407899-23407135 -**	**candidate**	**Canonical miRNA**	**intron**

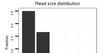
Flank: **dmel** **CTTCGCCGCCGC

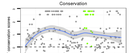
ID	Coordinate	Confidence	Class	Genome Locus
block92371	**chr2L:6973236-6973348 (-)**	**Known Orthologs**	**Intra_prime_UTR**	**5pUTR**

View on UCSC Genome Browser (GenBD/Mirror)

Legend: **Stem** **Loop** **Mismatch** **Bulge** **Hairpin Loop**

Predicted structure





Show Alignments Profile

Flybase annotation

chr2L:7qa6cc5:dUTP:152,192:fwrc_intra_UTR:2pf:4(1 fwrc_intra_UTR:2pf:4(1

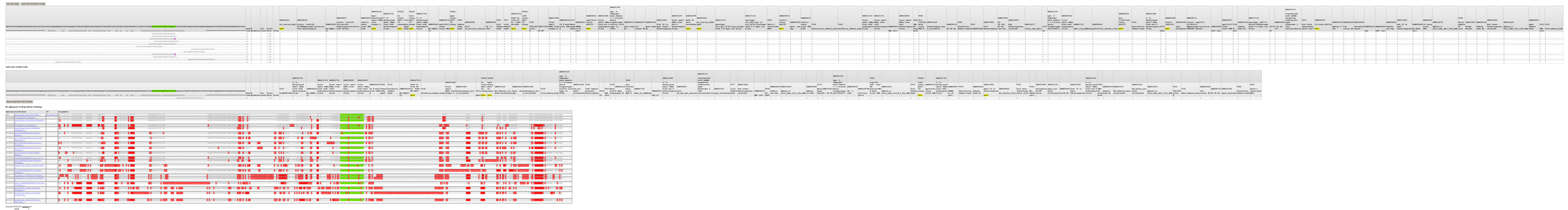
Small RNA-seq Read Stack

Hide Sp Stack | Show mid mismatch reads

Anti-sense strand reads

Show Alignments With Reads

Re-alignment of all predicted orthologs

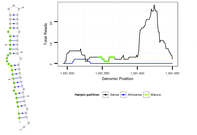


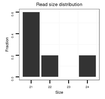
ID	Coordinate	Confidence	Class	Genome Locus
CG7861_in5	chr2R:19315461-19316002 +	Known Ortholog	miRNA	Dmel

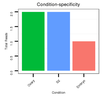
[View on UCSC Genome Browser (GenomeBrowse)]

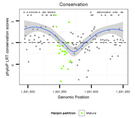
Legend: Stem Terminal Loop Mature

Predicted structure:









Show Alternate Folds

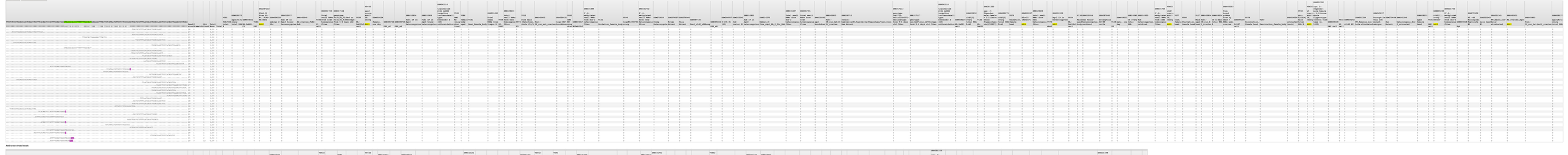
Flybase annotation

intron [Flies.org] CDS [Flies.org] CDS [Flies.org]

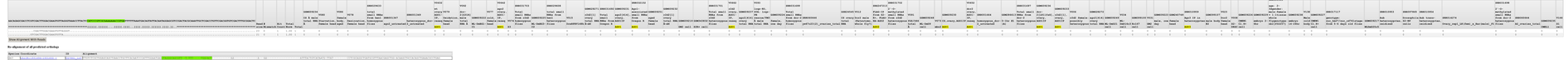
5x Expandable Genome Scale

Some Strand Reads

Hide Sp reads Show mid-mismatch reads



Antisense strand reads



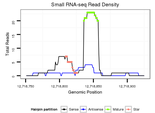
Show Alignment With Reads

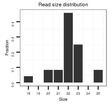
Re-alignment of all predicted orthologs

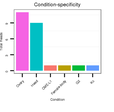
Generated 2019-04-23 at 7:04 PM

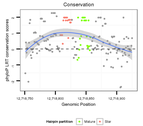
ID	Coordinate	Confidence	Class	Genome Locus
dme_411	**chr2R:12718801-12718875 +**	**candidate**	**Canonical miRNA**	**intergenic**
Legend: DICER DROSHA 5'-Arm 3'-Arm PAIRED/SINGLE				

Predicted structure









Show Alternate Folds

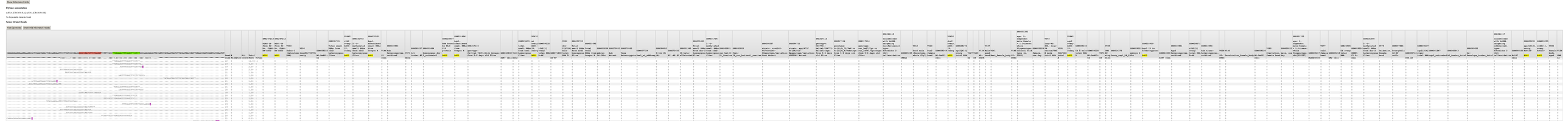
Flybase annotation

mRNA:FBGN0014242,mRNA:CR31630-RE

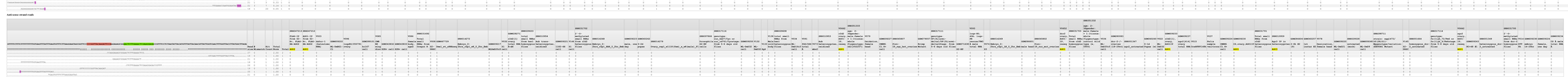
No Repeatmasker elements found

Sense Strand Reads

Sort by reads | Show red mismatch reads

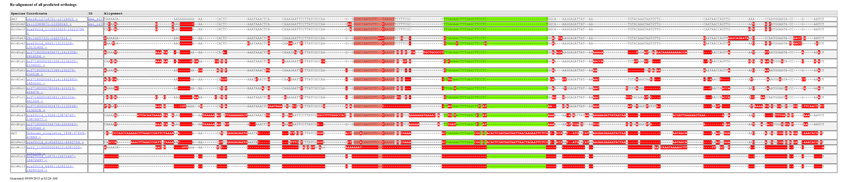


Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

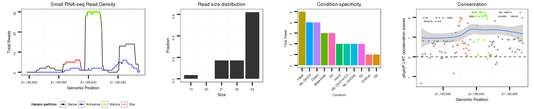


Generated 09/09/2025 at 02:24 AM

ID	Coordinate	Confidence	Class	Genome Locale
dme_259	**chr3L:21195567-21195619 +**	**candidate**	**Canonical snRNA**	**antisense_to_intron**	[View on UCSC Genome Browser (GeneID/dme)]

Length: 53 nt | GC: 43.4% | Structure: 36.2% paired

Predicted structure:



Show Alternate Folds

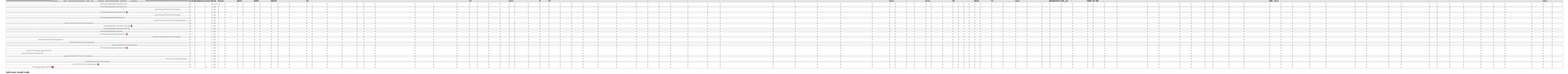
Flybase annotation

intersects intron(2L(37976:-),3L(-),3R(-),4(-),X(17570:-)), intersects 5-prime(2L(37976:-),3L(-),3R(-),4(-),X(17570:-))

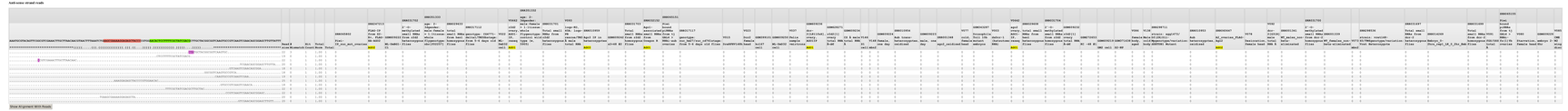
No Repeatmasker elements found

Sense Strand Reads

Hide 36 reads | Show 454 mismatch reads

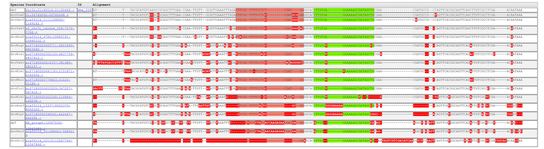


Anti-sense strand reads



Show Alignment With Frame

Re-alignment of all predicted orthologs



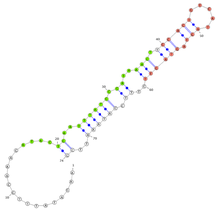
Generated 2026-03-25 at 02:28 AM

ID:	Coordinate:	Confidence:	Class:	Genomic Locale:
sblock181387	**chrX:9538471-9538856 -**	**Known Ortholog**	**intron**	**intron**

[View on UCSC Genome Browser (GenomeMotif)]

Legend: exon ss Annotated Unannotated mismatch/error

Predicted structure



sblock181387, score: [-6.9]

Show Alternate Folds

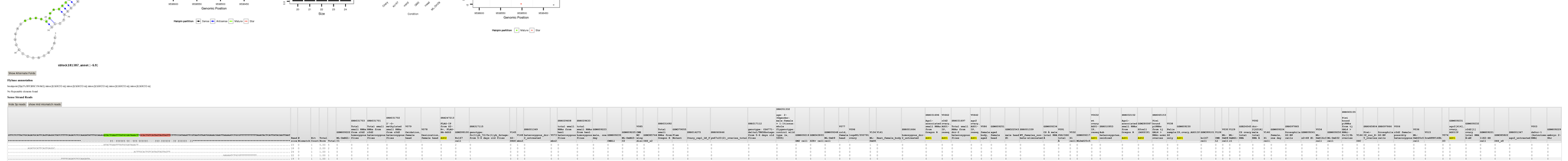
Flybase annotation

Sequence: [Sq:7:X:9538471:9538856:N:N] intron:[CG8023-xd], intron:[CG8023-xd], intron:[CG8023-xd], intron:[CG8023-xd], intron:[CG8023-xd], intron:[CG8023-xd]

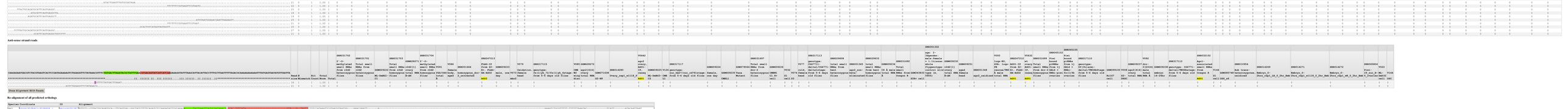
No Repeatmk elements found

Some Strand Reads

Hide 3p reads | show mid mismatch reads

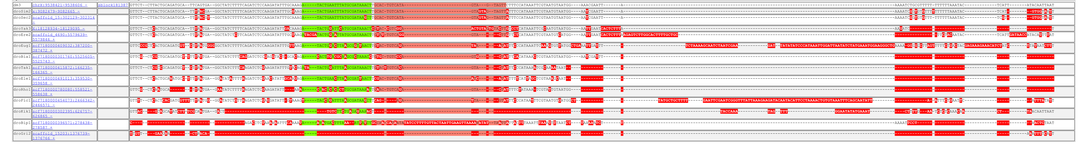


Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs



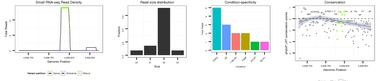
Generated 09/09/2015 at 01:27 AM

ID	Creation date	Confidence	Size	Genome locus
Mtuk9986d9	**chr2R:4836721-4838822 +**	**Known Orthologs**	**interspecie**	**interspecie**

Edit on UCSC Genome Browser (GoldMine)

Length: **2101 nt** (**0.0 % of 100 nt minimum**)

Predicted structure:



Show Genome Frame

Flybase annotation

0 exp. Dopamineless (1)

1 Dopamine Gained Gain

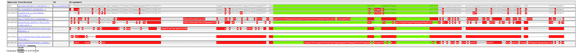
Gain Gained Mutations

Gain by exons Show 20 bp Gained Gain

Gain color of dead mods

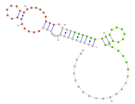
Show Expanded MFA Probes

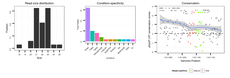
Ru alignment of pri-pre-mir-2a/2b/p


Species Sequences
Ru alignment
Dmel
Dsim
Dsec
Dmel
Dyak
Dere
Dpse
Dpse
Dpse

ID	Length	Condition	Flag	Genome coverage
cdbrna8.3(ITS)_cbr76_1164112-1164122PR	11	**Reverse Orientation**	**cdbrna8_ca_1164_cdbrna8_ca_Sp1750**	1164112-1164122 (Reverse Orientation)

Sequence: **CCCCCCCCCCC**





cdbrna8.3(ITS)_cbr76_1164112-1164122PR

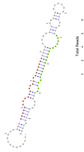
Sequence: **CCCCCCCCCCC**

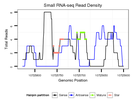
Flanking sequence:
TTTT

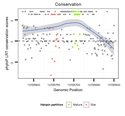
ID	Coordinates	Confidence	Class	Genome Locus
dme_393 / chr3R:10725658-10725778 +	**cand0dme**	**Canonical miRNA**	**CDS**	Flybase(FlyBase) Genome Browser (GrameDbMirror)

Legend: Mature Star Terminal loop Conserved

Predicted structure:







Show Alignment Fields

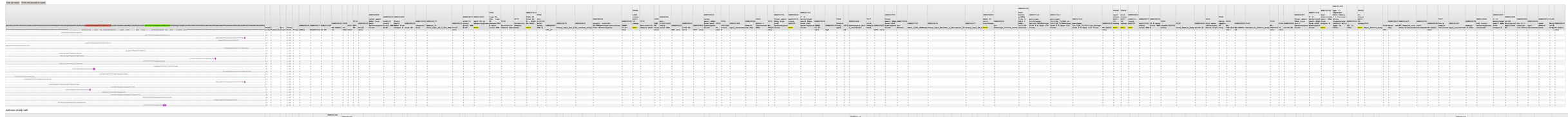
Fields annotation:

CIGAR,MD,Q,A,AS,

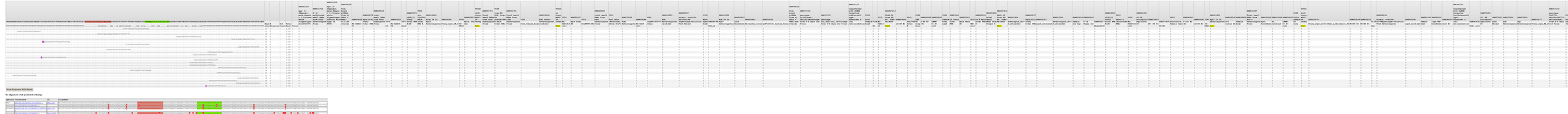
To Assembly Genome Itself

Some Strand Reads

Scale: by Reads Group by Strand & reads

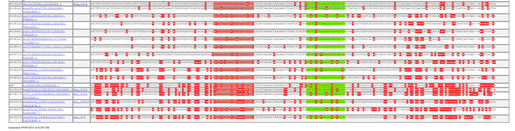


Anti-sense strand reads



Show Alignment With Reads

By alignment of all predicted orthologs:



Generated 2018-07-23 at 22:42:-0[0]

ID	Coordinate	Confidence	Class	Genome Locus
CG4294_in1	chr2R:18492684-18492767 -	Known Ortholog	miRNA	[View on UCSC Genome Browser (GenomEMotif)]

Score: 1000 Strand: - Length: 83 Annotation:

Predicted structure

Show Alternate Folds

Flybase annotation

mus(CG294-mL):CTR,[CG4294-mL],CTR,[CG4294-mL],CTR,[CG4294-mL],CTR,[CG4294-mL]

No Repeats Genes found

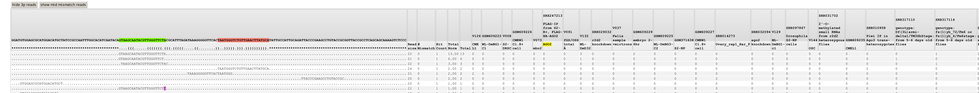
Sense Strand Reads

Scale: by reads | show mid mismatch reads

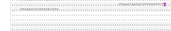
Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs



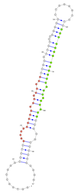
Conserved PRMS:[0:0 gt 0:2]a 0:4

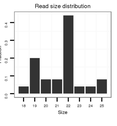

dmel
dsim
dsec
dyak
dere
dpse
dpse
dpse

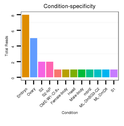
ID	Coordinate	Confidence	Class	Genome Locale
sblock53072	**chr2R:20896404-20896491 -**	**Known Ortholog**	**intron**	**intron**

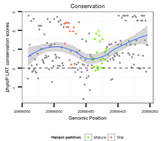
Layout: Stem Loop Mature Star Mismatch

Predicted structure









Show Alternate Folds

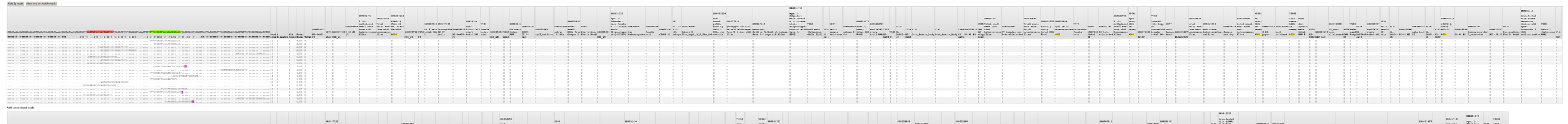
Flybase annotation

intron[2p:o]

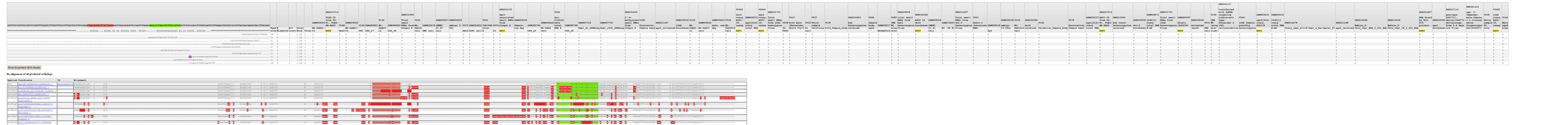
No Repeatable elements found

Sense Strand Reads

hide 3p reads show red mismatch reads

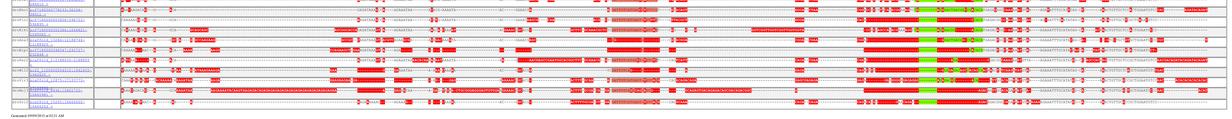


Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs



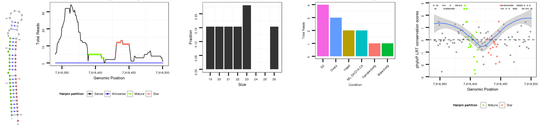
Generated 09/09/2022 at 02:21 AM

ID	Coordinates	Coordinate	Strand	Genome Locus
pdc5_int8 : chr2R:7918390-7918451	+	**Known Orthologs**	**mirtron**	**intron**

View on UCSC Genome Browser (Local Mirror)

Legend: **Stem** **5p** **Terminal Loop** **3p** **Flanking Seq**

Predicted structure



Show Alternate Fields

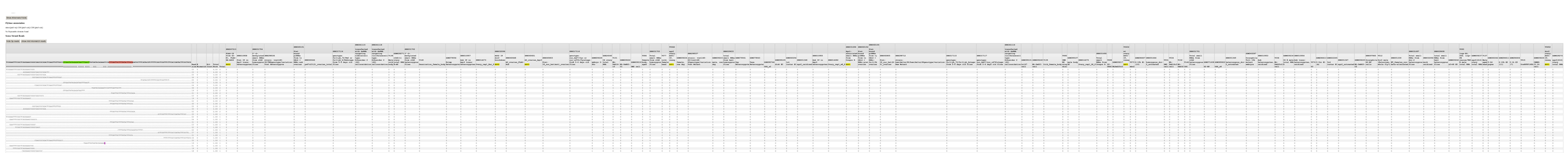
Flybase annotation

intron(pdc:-q),CTR(pdc:+-kb),CTR(pdc:+-kb)

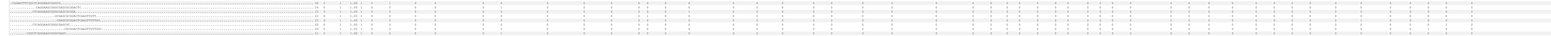
No Ensembl ncRNA hit

Sense Strand Reads

Hide 3p reads | Show read mismatch reads

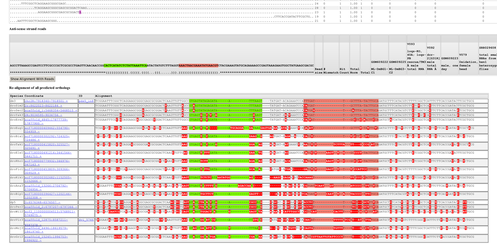


Antisense strand reads



Show Mismatch Mirt Reads

Re-alignment of all predicted orthologs

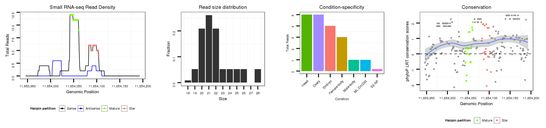


Generated 2019-05-21 at 7:04 PM

ID	Coordinate	Strand	Class	Genomic Locus
dme_389	chrX:11653996-11654143 +	+	candidate	Canonical miRNA	intron	Chr6:44236 Genome Browser (UcscBlat)[1]

Score: 8.00 (Structure: 0.00, Expression: 8.00)

Predicted structure



Show Alternate Form

Fhlene annotation

Seqlength:[Sp]76,SP:[0]0.79,NG[]; mirco:[n-a]; bioalignd:[Sp]76,SP:[0]0.79,NG[]

No Expansion (stem0 0 bad)

Sense Strand Reads

Sense Strand Reads

Show Sense Strand Reads

Antisense strand reads

Antisense Strand Reads

Show Antisense Strand Reads

Re-alignment of all predicted orthologs

Re-alignment of all predicted orthologs

Show Alignment With Reads

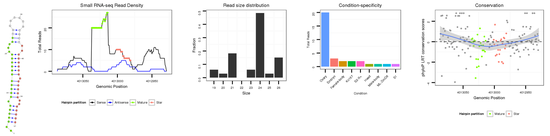
Generated 2020/07/07 at 07:31:48

ID	Coordinate	Confidence	Class	Variable Locus
collin_in2	**chr2R:4012979-4013037 -**	**Known Ortholog**	**intron**	**intron**

View on UCSC Genome Browser (Cached Mirror)

Legend: Spliced Read Coverage Mismatch

Predicted structure:



Show Alternate Folds

Fisher assemblies

(((((((((.((((((((((.(((((((((.(((((((((.(

ID	Coordinate	Collection	Class	Possible Scaffold
Pka-C2_ice1	chr38:26521587-26521648	Known Orthologs	intron	intron

Length: 62 bp | 0.0 RNA-seq Reads | 0.0 RNA-seq Junctions

Predicted structure:

Show Alternate Folds

FASTA for annotation

>Pka-C2_ice1|chr38:26521587-26521648|Pka-C2-ice1|-|TR-|Pka-C2-ice1|-|TR-|Pka-C2-ice1|-|Pka-C2-ice1|-|

>1x Expandable Jackpack Fold

Some Small Reads

Hide No Hairpin | Show NO-PROMISCUOUS Hairpin

Half-sister Jackpack Folds

Show Expanded With Reads

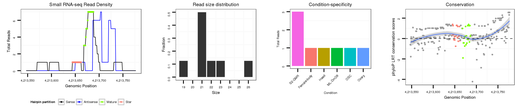
No alignment of all predicted scaffolds

Generated 2022-06-21 at 17:00 -0700

ID	Coordinate	Strand	Class	Genome Length
dme_404	chr3L:14213597-14213727	+	candidate	Canonical miRNA	intron	130

Legend: Stem 5p 3p Terminal Loop Mismatch

Predicted structure:



Show Alternate Forms

Python annotation

dme-404:chr3L:

Strand: +

Genomic Hairpin Seq:

Sense Strand Reads

Hide 5p reads | Show mid-mismatch reads

Antisense strand reads

Show Alignment With Reads

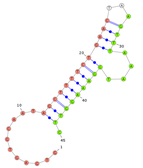
Re-alignment of all predicted orthologs

Generated 2026-05-22 at 22:12:48

ID	Coordinate	Confidence	Class	Genome Locale
Fatp_ia4	chr2L:10512870-10512934 -	Known Ortholog	miRNA	hsa

Score: 0.000 Strand: + Length: 65 Structure: ((((((((((.....)))))))))).....

Predicted structure



Fatp_ia4_seed | -6.40

Show Alternate Fields

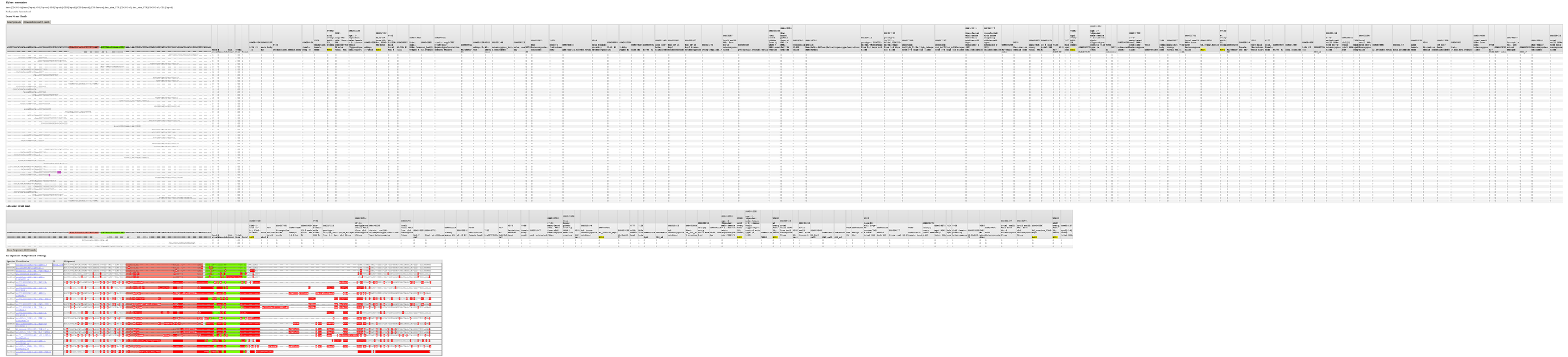
Flybase annotation

seed:FAS001:sl;seq:Fatp:sl;CDS:Fatp:sub;CDS:Fatp:sub;CDS:Fatp:sub;CDS:Fatp:sub;CDS:Fatp:sub;dna_pma_CTR:JZAN01:sl;dna_pma_CTR:JZAN01:sl;CDS:Fatp:sub

No Repeatmk elements found

Same Strand Reads

Sort by reads | show red mismatch reads



Anti-sense strand reads

Show Alignment With Reads

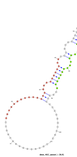
Re-alignment of all predicted orthologs

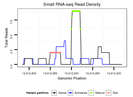
Generated 09/08/2025 at 07:07 PM

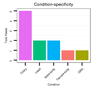
ID	Condition	Confidence	Class	Genome Locus
dme_402 (chr2R:19612834-19612969 +	**candidate**	**Canonical miRNA**	**intron**	chr2R:19612834-19612969

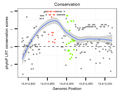
Legend: Mature Star Terminal loop Flanking sequence

Predicted structure:









Show Structure Profile

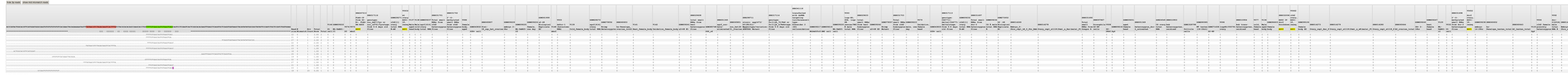
Flybase annotation

dme:CR44184-RA(+)(Exon)

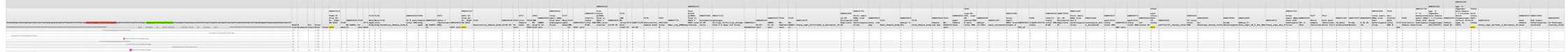
No Ensembl Genes found

Nanos Versus Brain

Hide Sp reads | Show 500 mismatch reads

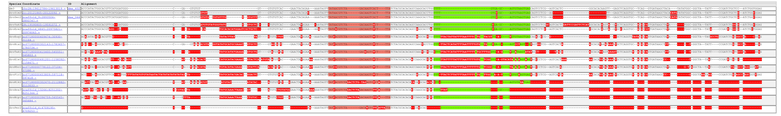


Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted miRnAcgs

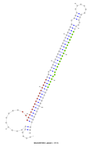


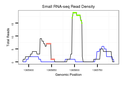
ID	Coordinate	Confidence	Class	Genome Locus
block665662	**chr28:1365763-1365863**	**Known Orthologs**	**intron**	**intron**

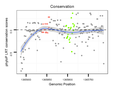
View on UCSC Genome Browser (Central Mirror)

Legend: Stem Hairpin Loop Internal Loop Bulge Multiloop

Predicted structure







Show Structure Data

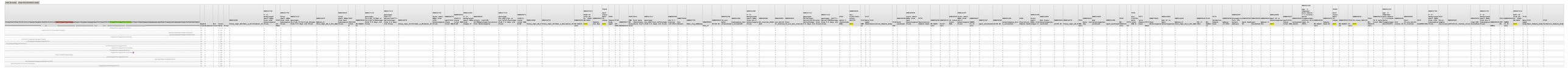
Fetus annotation

mm10:chr28:0 nt

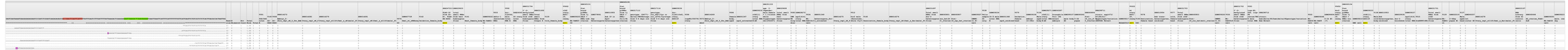
No Ensembl Ortholog found

Some Small Reads

Hide Ns reads Show NM mismatch reads

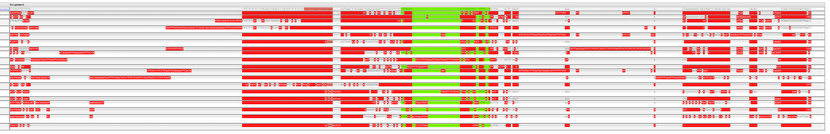


Indicator detail table



Show Ensembl BED Bands

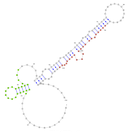
Rn alignment of all predicted orthologs



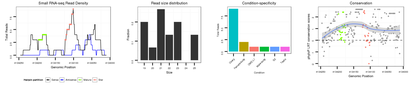
ID	Condition	Condition - Class	Genome Locus
**dme_412	chr3L:4134060-4134196 -**	**condition 1	canonical miRNA	intron**	chr3L:4134,060-4134,196 (-) Genome Browser (Ensembl) (Mirbase)

Strand: **(-)** Structure: **hairpin** Type: **canonical miRNA**

Predicted structure



dme_412_pred (-, 0.0, 0)



Show Alternative Folds

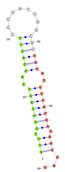
FlyBase annotations

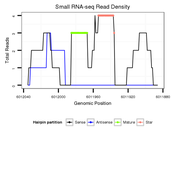
Info: Dsuzu-Shared-Mat1-05-(+), Dsuzu-Shared-Mat1-05-(-), Dsuzu-Shared-Mat1-05-1-(+), Dsuzu-Shared-Mat1-05-1-(-), Dsuzu-Shared-Mat1-05-2-(+), Dsuzu-Shared-Mat1-05-2-(-), Dsuzu-Shared-Mat1-05-3-(+), Dsuzu-Shared-Mat1-05-3-(-), Dsuzu-Shared-Mat1-05-4-(+), Dsuzu-Shared-Mat1-05-4-(-), Dsuzu-Shared-Mat1-05-5-(+), Dsuzu-Shared-Mat1-05-5-(-), Dsuzu-Shared-Mat1-05-6-(+), Dsuzu-Shared-Mat1-05-6-(-), Dsuzu-Shared-Mat1-05-7-(+), Dsuzu-Shared-Mat1-05-7-(-), Dsuzu-Shared-Mat1-05-8-(+), Dsuzu-Shared-Mat1-05-8-(-), Dsuzu-Shared-Mat1-05-9-(+), Dsuzu-Shared-Mat1-05-9-(-), Dsuzu-Shared-Mat1-05-10-(+), Dsuzu-Shared-Mat1-05-10-(-), Dsuzu-Shared-Mat1-05-11-(+), Dsuzu-Shared-Mat1-05-11-(-), Dsuzu-Shared-Mat1-05-12-(+), Dsuzu-Shared-Mat1-05-12-(-), Dsuzu-Shared-Mat1-05-13-(+), Dsuzu-Shared-Mat1-05-13-(-), Dsuzu-Shared-Mat1-05-14-(+), Dsuzu-Shared-Mat1-05-14-(-), Dsuzu-Shared-Mat1-05-15-(+), Dsuzu-Shared-Mat1-05-15-(-), Dsuzu-Shared-Mat1-05-16-(+), Dsuzu-Shared-Mat1-05-16-(-), Dsuzu-Shared-Mat1-05-17-(+), Dsuzu-Shared-Mat1-05-17-(-), Dsuzu-Shared-Mat1-05-18-(+), Dsuzu-Shared-Mat1-05-18-(-), Dsuzu-Shared-Mat1-05-19-(+), Dsuzu-Shared-Mat1-05-19-(-), Dsuzu-Shared-Mat1-05-20-(+), Dsuzu-Shared-Mat1-05-20-(-),

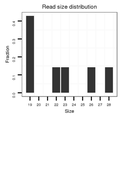
ID	Coordinate	Confidence	Class	Genomic Locale
dme_428	**chr21:6011936-6011985 -**	**candidate**	**MiRNA**	**intron**

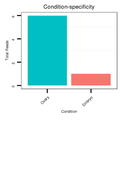
Legend: Exon Intron Flanking Sequence Mature Arm

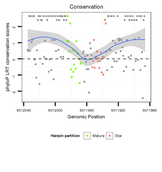
Predicted structure











Show Alternate Folds

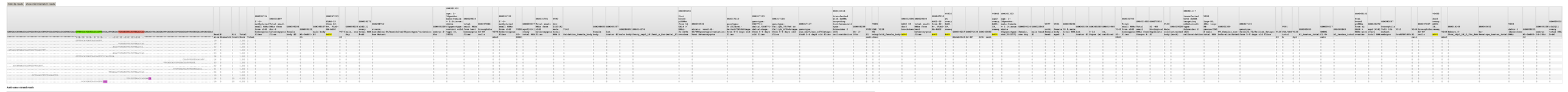
Flybase annotation

mess:CG9894-mL:for_pma_CTR:[CG9894-uf]; CG9:[CG9894-uh]; CG9:[CG9894-ub]; mess:[CG9894-uf]; for_pma_CTR:[CG9894-uf]

No Reputable cDroom load

Sense Strand Reads

Hide 2p reads | show red mismatch reads



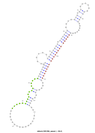
Anti-sense strand reads

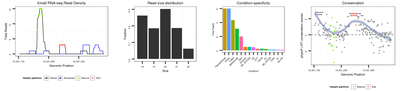
Show Alignment With Reads

Re-alignment of all predicted orthologs

ID	Coordinate	Reference	Strand	Genome Locus
chbo4:299286 / chrX:164711153-164713333	**Xaseen Orthologs**	**intergenic**	**intergenic**	Show on UCSC Genome Browser (Linear View)

Predicted structure





Show Alignment Details

FASTA sequences

>chbo4:299286-299486(+) /chr:chbo4:299286-299486(+) /chr:chbo4:299286-299486(+) /chr:chbo4:299286-299486(+) /chr:chbo4:299286-299486(+) /chr:chbo4:299286-299486(+) /chr:chbo4:299286-299486(+)

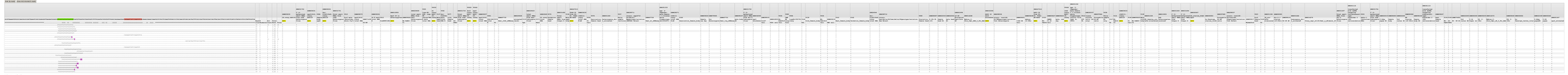
TCTGAGGTC CCCGAC CCGAG TCCGG

Alignment

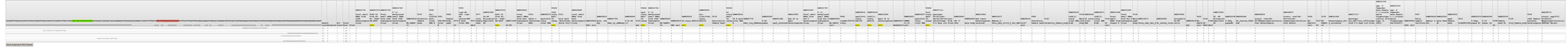
Species	
chbo4:299286-299486(+)	
chr:chbo4:299286-299486(+)	
chr:chbo4:299286-299486(+)	
chr:chbo4:299286-299486(+)	
chr:chbo4:299286-299486(+)	
chr:chbo4:299286-299486(+)	
chr:chbo4:299286-299486(+)	

Notes Viewed Reads

Hide Reads Show Mismatch Reads

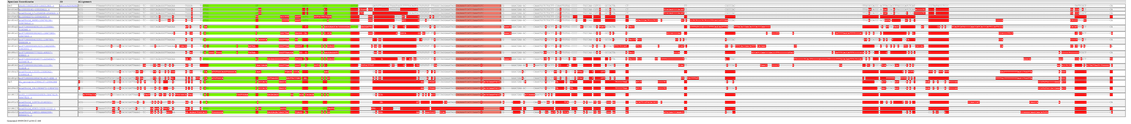


Soft-clipped viewed reads



Show All Ignored MGR Reads

Re-alignment of all predicted orthologs

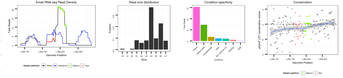


Generated 2026-03-12 12:01:07 GMT

ID	Locus	Strand	Length	Type	Genome Coords
chRanA70(**70**)	chr28::1252139-1252239	+	Human Orthology	Intron	Chrom:70-70 Strand:Minus Locus:Intron

Length: 101 bp

Predicted structure:



Data Sources Used

Primary assemblies:

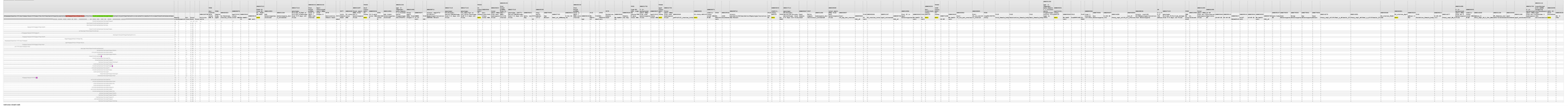
Human: hg38 (GRCh38.p14) Mouse: mm39 (GRCm39.p35) Rat: mRatBN7.2 (GCA_015227675.2)

All Mapped Genomes in Cluster

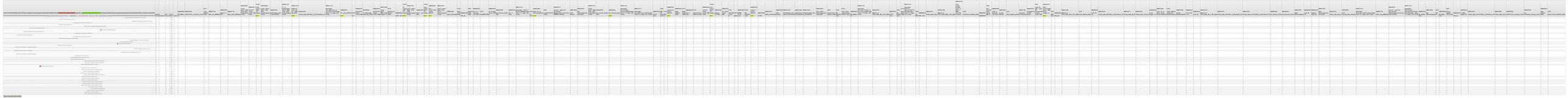
Species	Size
Human (hg38 (GRCh38.p14))	
Mouse (mm39 (GRCm39.p35))	
Rat (mRatBN7.2 (GCA_015227675.2))	
Macaque (rheMac10 (GCA_000772875.2))	
Dog (canFam3.1 (GCA_000002285.2))	
Human (hg38 (GRCh38.p14))	
Mouse (mm39 (GRCm39.p35))	
Rat (mRatBN7.2 (GCA_015227675.2))	
Macaque (rheMac10 (GCA_000772875.2))	
Dog (canFam3.1 (GCA_000002285.2))	

Human Small Blocks

Hide Alignment Details Show Alignment Details



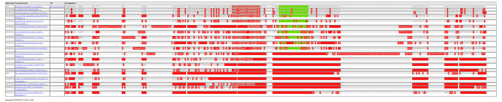
Individual Small Gaps



Multiple Alignment Of Orthologs

Hide Alignment Of Orthologs

Rn: Alignment of all gap-stripped orthologs

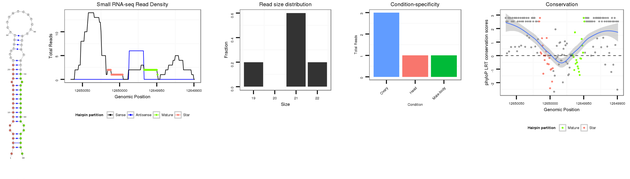


Expand HOMINIDAE (Hs, Mf) (+ 100)

ID	Coordinate	Confidence	Class	Genome Locus
unc-104_in6	**chr2R:12649949-12650016 -**	**Known Ortholog**	**mirtron**	**hairpin**

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

Predicted structure



Show Alternate Folds

Flybase annotation

mirror(unc-104-xj):CDS:[unc-104-xj],CDS:[unc-104-xj],CDS:[unc-104-xj],CDS:[unc-104-xj],CDS:[unc-104-xj],CDS:[unc-104-xj],CDS:[unc-104-xj]

No flyanadit clusters found

Some Strand Reads

Strip 3p reads | show mid mismatch reads

| Seq | Mismatch | Count | Score | Total | C1 | | |

ID	CONFIDENCE	Strand	Conditions	Genome	Genome Size
dme_383	1	+	Condition 1	Canonical mel64v1	Intergenic

Show 10 | 25 | 50 | 100 | 250 | 500 | 1000 | 2500 | 5000 | 10000 | 25000 | 50000 | 100000 | 250000 | 500000 | 1000000 | 2500000 | 5000000 | 10000000 | 25000000 | 50000000 | 100000000 | 250000000 | 500000000 | 1000000000 | 2500000000 | 5000000000 | 10000000000 | 25000000000 | 50000000000 | 100000000000 | 250000000000 | 500000000000 | 1000000000000 | 2500000000000 | 5000000000000 | 10000000000000 | 25000000000000 | 50000000000000 | 100000000000000 | 250000000000000 | 500000000000000 | 1000000000000000 | 2500000000000000 | 5000000000000000 | 10000000000000000 | 25000000000000000 | 50000000000000000 | 100000000000000000 | 250000000000000000 | 500000000000000000 | 1000000000000000000 | 2500000000000000000 | 5000000000000000000 | 10000000000000000000 | 25000000000000000000 | 50000000000000000000 | 100000000000000000000 | 250000000000000000000 | 500000000000000000000 | 1000000000000000000000 | 2500000000000000000000 | 5000000000000000000000 | 10000000000000000000000 | 25000000000000000000000 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ID	Confidence	Confidence	Size	Global Score
Mmu5a31478_chr2RHLcr1621869-1621978 +	**Known Orthologs**	**Interrupted**	**Interrupted**	0.0

Show ACCESS Global Review (Local Filter)

Predicted structure

Show Alignment

Flanking alignments

Flanking Alignment

No flanking alignments found

Alignment Quality

Hairpin position Genes Intronic Intergenic

View Visual Box

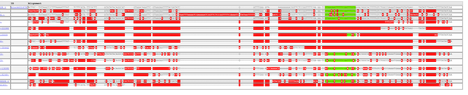
Show Visual

Show Visual (Alignment Viewer)

Add Genes Overall Table

Show Alignment MSA Review

Pre-alignment of all genomes in ortholog:



Show Alignment MSA Review