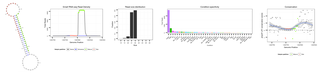
Job	Date	Time	Duration	Sites
1	2025-08-25	08:00:00	00:00:00	1

ONLY 25.00% CONFIRMS, SAMPTOR - Control Cassette with Clip-On

Tip: 0 Cassette: 1 Clip-On: 1 Sites: 1 Duration: 00:00:00



DESCRIPTION

Cycle Time Line Plot

Cycle Time Histogram

Cycle Time Capability

Cycle Time Control Chart

Cycle Time Control Chart - Cycle Time, Limits, and Violations

Test Results

Cycle Time Control Chart

| | | |

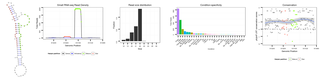
Filter: Gene | Variant | Sample | Region | Coverage | Quality | Mapping | Chr | Pos | Ref | Alt | Type | Length | Depth | Genotype | Allele Freq | Strand Bias | Mapping Qual | Base Qual | Gene Name | Impact | Consequence | Protein Change | Exon | Intron | Distance | Upstream | Downstream | Region Type | Regulatory | Motif | Conservation | Population | Clinvar | Cosmic | Tumor Freq | Normal Freq | Somatic Status | Quality Score | Filter | Comments | Phase | Haplotype | Allele Depth | Genotype Quality | Read Depth | Mapping Quality | Base Quality | Strand Bias | Allele Frequency | Confidence | Annotation | Transcript | Exon Number | Intron Number | Distance to Gene | Upstream Gene | Downstream Gene | Regulatory Region | Motif Name | Motif Position | Conservation Score | Population Freq | Clinvar Id | Cosmic Id | Tumor Frequency | Normal Frequency

Sample ID: 2025-11-17-10-00-00-00000-00000-00000-0-0-0

Date	Time	Location	Operator
2026-01-27	00:00	Unknown	Unknown

Depth	Hole Size	Casing	Weight
0 - 1000	26"	20"	94.0 lb/ft
1000 - 2000	17½"	13⅜"	68.0 lb/ft
2000 - 3000	12¼"	9⅝"	47.0 lb/ft
3000 - 4000	8½"	7"	29.0 lb/ft

Product Legend



Well Information

Well Name: Well Name
Well Type: Well Type
Drilling Contractor: Drilling Contractor
Rig Name: Rig Name
Rig Type: Rig Type
Rig Floor Elevation: Rig Floor Elevation
Rig Floor Elevation Type: Rig Floor Elevation Type
Water Depth: Water Depth
Water Depth Type: Water Depth Type
Total Depth: Total Depth
Total Depth Type: Total Depth Type

Well Data

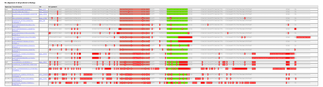
Well Data	Well Data Description

Well Data	Well Data Description	Value	Unit	Date	Time	Comment

Well Data Log

Well Data Log	Well Data Log Description	Well Data Log Type	Well Data Log Value	Unit	Date	Time	Comment

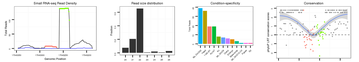
Well Data Log Image



id	coordinate	strand	length	score
dme_341	**chr2R:17843237-17843297**	+ (sense)	Metrios	**Intron**

chr2R:17843237-17843297

Predicted structure



Show Genome Viewer

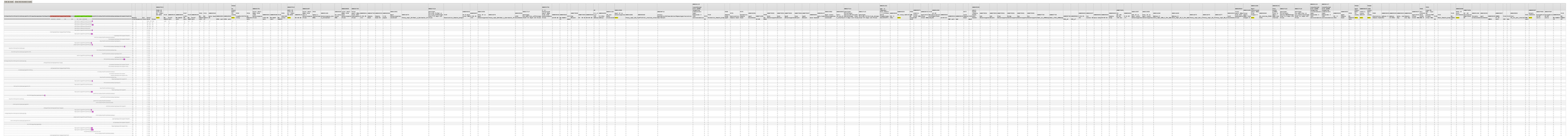
Alignment

Alignment with up 250 bp (chr2R:17843147-17843297) and 250 bp (chr2R:17843297-17843347)

10 Top-scoring hairpin loci

Table Simple Reads

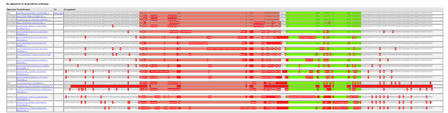
Filter Table Show Hide Hierarchy Clusters



Soft-masked Genome Reads

Genome Browser (Multiz)

Hit alignment of all predicted orthologs

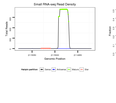


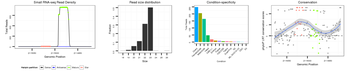
Genome-wide distribution of this locus

ID	NAME	CONFIG	RUN	GRAPH GUIDE
dna_114_chr31:21149750-21150230	**condition_Canonical mRNA_intron**			Schema for "Alignment Summary Graphs"

Total: 1

Predicted structure:





Show Analysis Notes

Primer assessment

Primer pair 1

No primer pair assessment

Solo Small Reads

Hide Small Reads Show Small Reads in Image

| Seq | Start | End | Strand | Length | Count | Genome | Gene | Gene Type | Gene Strand | Gene Start | Gene End | Gene Length | Gene Alignment Start | Gene Alignment End | Gene Alignment Length | Gene Alignment Coverage | Gene Alignment Identity | Gene Alignment Gaps | Gene Alignment Mismatches | Gene Alignment Score | Gene Alignment Mapq | Gene Alignment Flags | Gene Alignment Cigar | Gene Alignment Tags | Gene Alignment Mate Name | Gene Alignment Mate Start | Gene Alignment Mate Strand | Gene Alignment Mate Gene | Gene Alignment Mate Gene Type | Gene Alignment Mate Gene Strand | Gene Alignment Mate Gene Start | Gene Alignment Mate Gene End | Gene Alignment Mate Gene Length | Gene Alignment Mate Gene Alignment Start | Gene Alignment Mate Gene Alignment End | Gene Alignment Mate Gene Alignment Length | Gene Alignment Mate Gene Alignment Coverage | Gene Alignment Mate Gene Alignment Identity | Gene Alignment Mate Gene Alignment Gaps | Gene Alignment Mate Gene Alignment Mismatches | Gene 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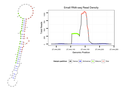
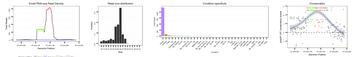
ID	Name	Updated	Size	Description
27	dme_miR_iab-8b_27-hairMiR_27-hairSTS	2 months ago	1 variant, 2 covered arms	Apr 19

Type: **ncRNA** Subtype: **miRNA** Genome: **dme**

Predicted Structure





Sequence

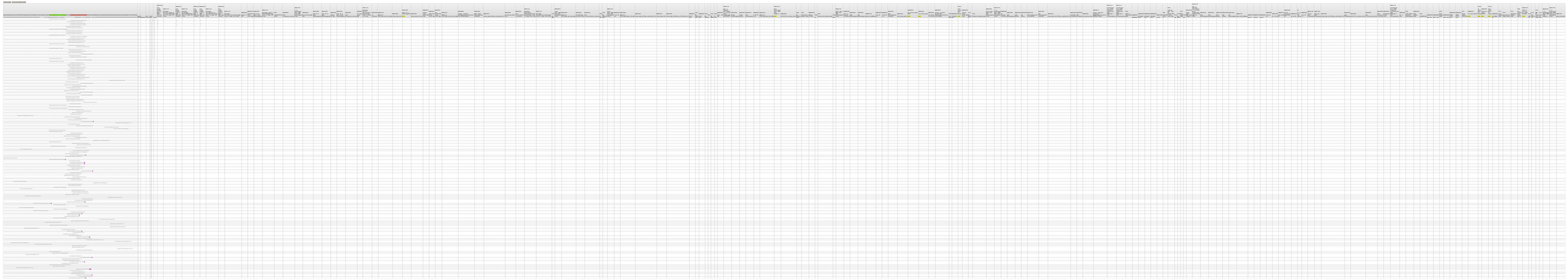
Other Annotations

Fly-Base Phenotype Class: LOF, PHENOTYPE

Fly-Base Gene Group: miRNA

Gene Ontology Group:

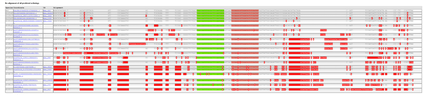
Show Alignment



Individual Small Reads

Multiple Alignment Overview

Alignment of 20 sequences

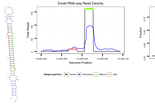


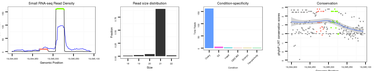
Generated on 2019-Apr-19

ID	Confidence	Strand	Genome Score
chbias211612 chr38:19094949-19095041 = **Known Ortholog**	**antisense_to_CHN antisense_to_CHN**	+	0.00 (vs GCDC Genome Bonus: 2.2 and Bias)

Length: **93 nt** (**0.0 % of the input sequence**)

Predicted structure:





Show Alignment Array

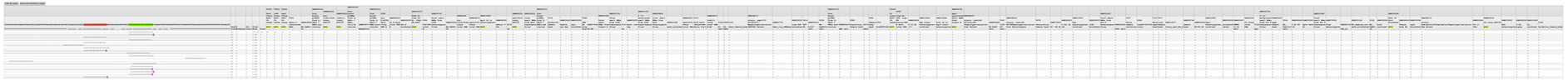
Pairwise ensemble

Helices in 5'-3'order with, helices in 3'-5'order and, helices in 5'-3'order only, helices in 3'-5', pairs, 3'-5'-pairs

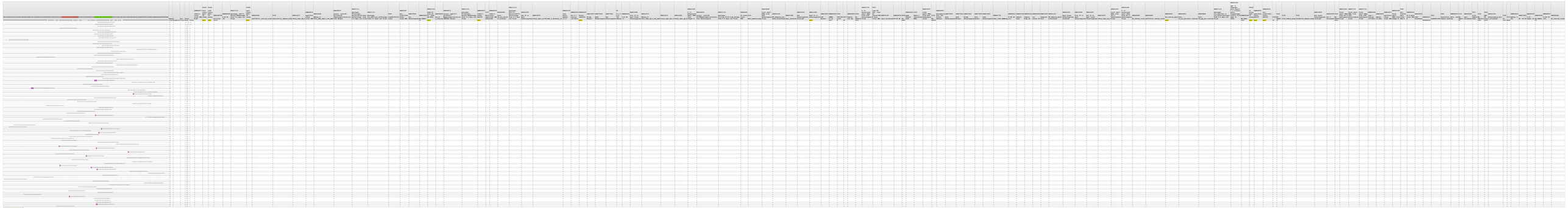
In Transcript Strand Coord

Main Strand Mode

Hide Ss-Sorted | Show SS-Sorted Coord | Hide

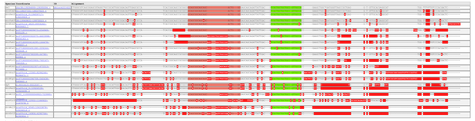


Full-seq-of-leaf mode



Show Alignment With Rnafoldz

Multiple Sequence Alignment

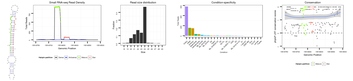


Alignment RMSD=0.0, 0.27 MB

Project	Project ID	Date	Sample Name(s)
[Illumina MiSeq] Lib_CDS_CFTR_EPCR_v_CFG_NGS_Exon Amplicon_Dna_group_2 CN_Set 1 R1			Lib_CDS_CFTR_EPCR_v_CFG_NGS_Exon Amplicon_Dna_group_2 CN_Set 1 R1

Run is **PASSED** **Complete**

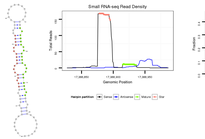
Analysis is **Complete**

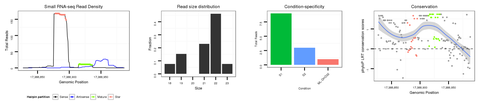

Lib_CDS_CFTR_EPCR_v_CFG_NGS_Exon Amplicon_Dna_group_2 CN_Set 1 R1

ID	Condition	Confidence	Class	Genomic Locus
dme_228	chrX:17388877-17388937 +	confident	Canonical miRNA	antisense_to_intron

Legend: Stem 5p Terminal loop Stem 3p

Predicted structure:





Show Alignment Fields

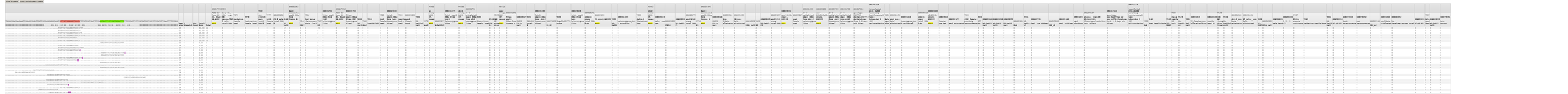
Filtered annotations

Indexes to data[2/5/8/9/14]: 0=dpm2 (Dp(3)CP(CP)CP(3)CP), Indexes to data[2/5/8/9/14]: 1=dpm2, Indexes to data[2/5/8/9/14]: 2=dpm2, Indexes to data[2/5/8/9/14]: 3=dpm2

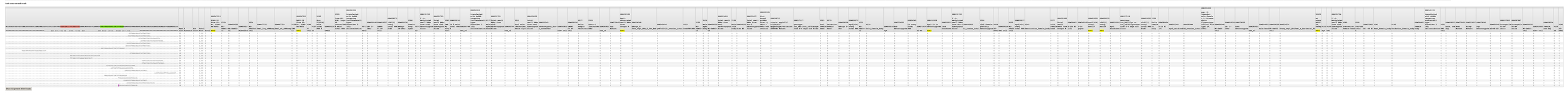
To Bigwig (Genome Coo

Sense Strand Reads

Hide No Indel | Hide read strand in reads

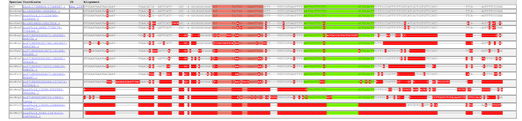


Anti-sense strand reads



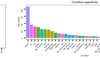
Show Alignment With Reads

Re-alignment of all predicted arrhitmiy:


Genome Coordinates
CO
Re-alignment
dmel_mel_Dp(3)CP(CP)CP(3)CP_dpm2

ID	Name	Description	Date	Covariance model
URS0A3JW2YC	rna:156 RNAcentral; RNA;mt;	Acanthocephala; Pan_pristis; 1 hit; 16 TR		Infernal v1.1rc4 (Nov-2013)

CC-BY-4.0 CC0 RNACENTRAL LICENCE



Show/hide instructions

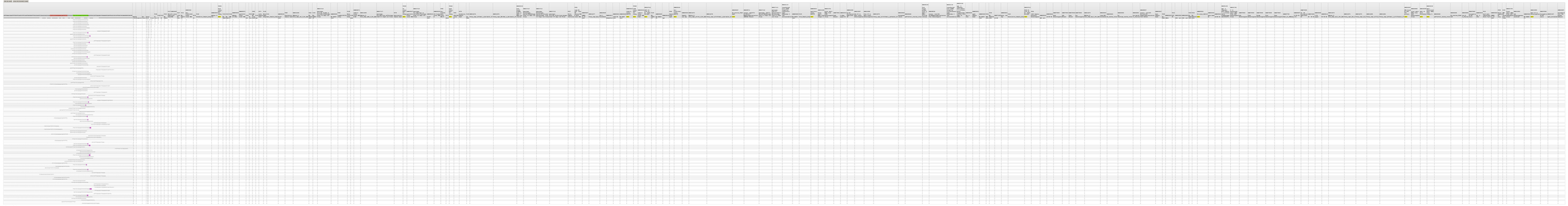
Filters (unavailable)

Hide: Hide all | Show all | Show or hide partially shown alignments and Rfam/Infernal SS/CM/CT cons

Hide/show Rfam/Infernal cons

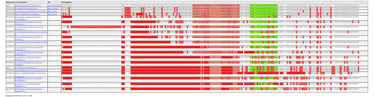
Hide/show Rfam SS

Show/hide all | Show/hide/reset sort order



Show/hide all | Show/hide/reset sort order

Show/hide all | Show/hide/reset sort order

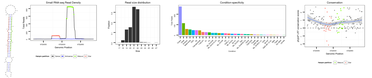


Support: RNAcentral Support, Help

Name	Description	Author	Date
Alex_CIT_chr15_ATCTGCT-ATCTGCT	Custom	Created with Sarek	2025-05-19 08:40:00 +0100

Type: germline Status: unknown

Analysis Groups:



Alignment Overview

Alignment Overview

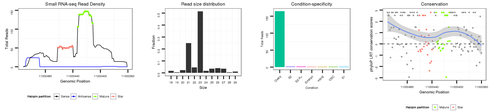
Alignment Overview for 1 sets, 2 Filtered ON, 0 sets, 2 Filtered OFF, Alignment Overview, Alignment Overview, Alignment Overview

ID	Coordinate	Confidence	Class	Genomic Locus
dme_199	chr2L:11000411-11000462	confident	Canonical miRNA	CDS

Flybase gene: FBgn0262739 Ago1-RB

Legend: Seed Mature 5' Mature 3' Loop Star

Predicted structure



Show Alternate Folds

Flybase annotation

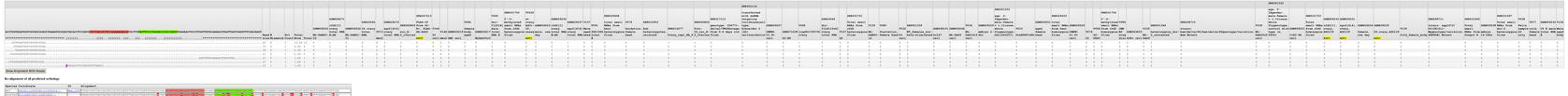
ncrna_fragment:pmiRNA:21-1194 [attr=id;] ncrna_fragment [Ref=X:+:0]

To Flybase Jbrowse Load

Some Overall Reads

Hide Sp reads | Show Mol Mismatch reads

Antisense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

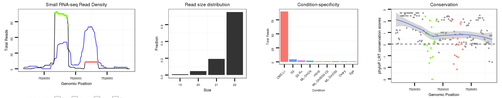
Generated 07/07/20 at 12:20 AM

ID	Condition	Confidence	Class	Genome Locus
dme_233	chrX:7528964-7529033 -	confident	Canonical miRNA	antisense_to_intron

Flybase:CG33C Genome Browser (GrameneMaize)

Length: **69** | Arm: **-** | Precursor: **chrX:7528964-7529033** | Annotation:

Predicted structure



Show Alignment Profile

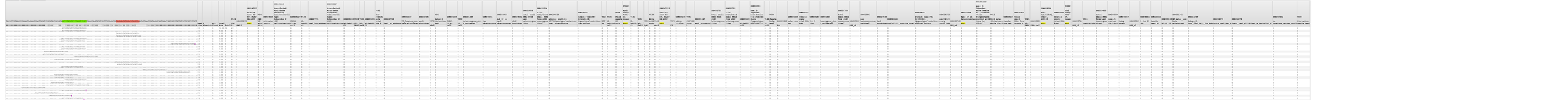
Flybase annotation

Hsalgene:Dbr:FLYB:FBGN0 TTAACC, Indicus:in sense(+sq):Hsalgene:Dbr:FLYB:FBGN TTAACC, Hsalgene:Dbr:FLYB:FBGN TTAACC, Indicus:in sense(+sq):Hsalgene:Dbr:FLYB:FBGN TTAACC

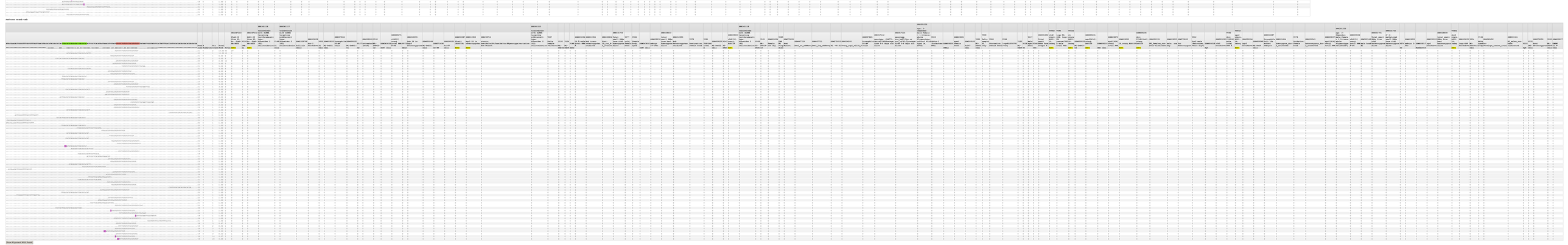
Sample Mature Read

Sample Hairpin Reads

Hide Sp reads | Hide Hit mismatch reads



Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

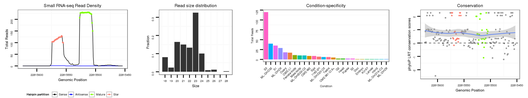
Generated 09/09/2025 at 15:26:16E

ID	Coordinates	Confidence	Class	Genetic Locus
dme_136	**chr3R:22815504-22815574 -**	**confident**	**Canonical miRNA**	**5pUTR**

Show miRDB Genome Browser (Loaded Mirror)

Legend: Seed Mature Loop Mature Seed

Predicted structure:



Show Alternative Folds

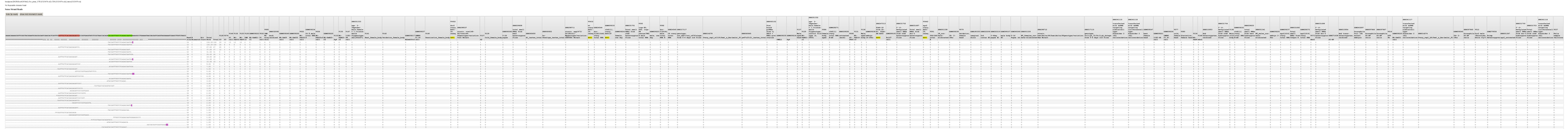
Flybase annotation

Hairpin:FBSN0041878 FlyBase:FlyBase_FTR:FCS0076 pfy:CR41533 FlyTF:fly_zinc2:CG7475 dsi:dsi2:CG7475 mj:

No Ensembl Genome Gene

Notes Virtual Reads

Hide Sp reads | Show Sp mismatch reads



Anti-sense strand reads

Show Sp reads match hairpin

Re-alignment of all predicted miRnAps

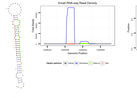
Generated: 2019-12-17 at 21:14 - CET

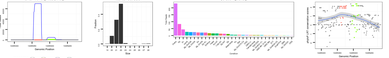
ID	Name	Updated	Rfam	Type
RF00177	**zfmr-sstr-97b-sc (rfc7b_1145572245-1145572345-1)**	Sunsea Ochoaing	Genus	sp7.9b

Family | Model | Seed | Structure | Maps | GC | Rscape | Cons | WUSS | CM | Info | Tree | HMM | Logo | Alignment | Text | History

Rfam-style SS-cons alignment

Predicted structure





Alignment

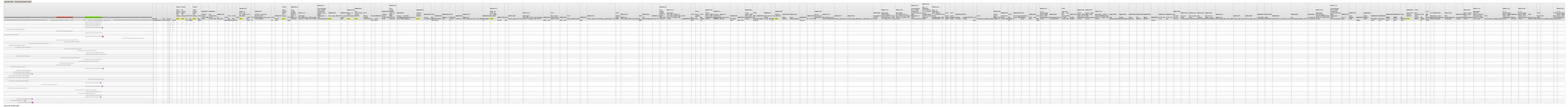
Alignment: 1145572245-1145572345-1 (Genus, sp7.9b)

MLI=0.000 TOI=0.000 (0.0% Genus, 0.0% sp7.9b), pairs=100, FOLD=0.0 pairs, CM=0.000 (0.0% Genus, 0.0% sp7.9b), Genus=0, sp7.9b=100, FP=0.0

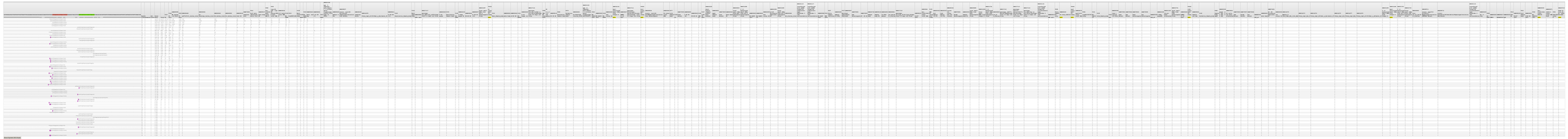
0 Top hits, Genus: 0, sp7.9b: 100

Sorted by: Genus, sp7.9b

Sorted by: Genus, sp7.9b



Sort over small (left)

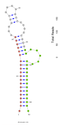


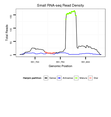
Alignment of all plants of Genus

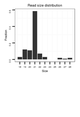
Sorted by: Genus, sp7.9b, score

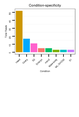
ID	CORRID	Coordinates	Strand	Genome Size
zfb2_tak_chr4:59172S-55178S	**Kawra-Orthdeg_intron_intron**	chr4:55178S-59172S	Minus	1,000,000

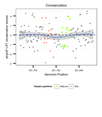
Predicted structure











Show Alignment Help

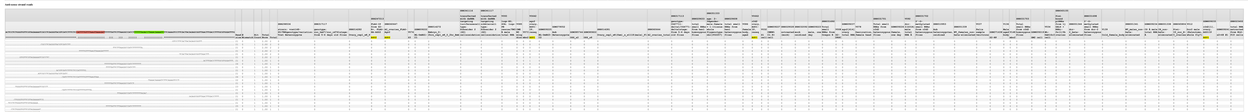
Parse annotation

MIRCHECK: Mem=8GB, Cpu=1, Time=1:00 | CPU=100.0% | RSS=1,376 | VSZ=2,852 | Exit=0 | Wall=0:00

Hide Target Rows

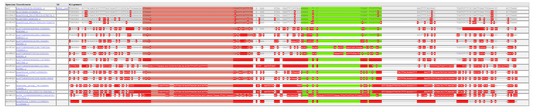
Hide Target | Show Target | Hide Query | Show Query | Reset Order

Call mirna: small node



Show Alignment MSA Panel

Re-alignment of all predicted orthologs



Hairpin: 0.000-0.000 (1.0*0.0*0)

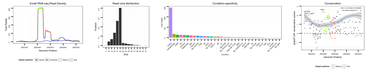
id	coordinate	condition	rna	score 0-100
dme_237	**chr2R:18987526-18987684 +**	**condition_1**	**C-seesaw-mdt9-1_unknown_rx_0.3%**	100.0

Sequence: CCCC

ID	Name	Description	Author	Date	Sample Count
1	**Rfam - RNA Jan 2020, 2170CG16, 2170CG16**		**Lindblad, P**	**Kaushik and Pro**	**2020-Feb-04, 10:00**

Type: **cis** Strand(s): **Both** Structure: **Structured**

2170CG16 (2170CG16)



Length: 100 nt (1 - 100)

Alignment

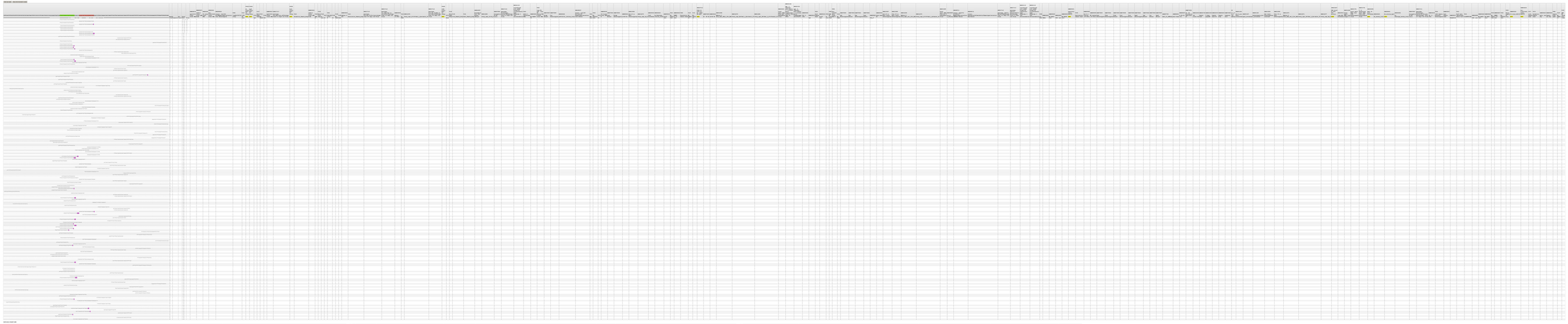
Alignment Statistics

Alignment of 2170CG16 (2170CG16) against Rfam 14.2 family RF00174 (cis): Alignment of 2170CG16 (2170CG16) against Rfam 14.2 family RF00174 (cis) Alignment: -mxnsf -mlocal --dna --rna --cmfile /tmp/cmsearch.cm.2170CG16.2170CG16.1579.cm --cmscore --nonbanded --noprofmx --noevhmmer --hmmfilter --hmmtblout /tmp/cmsearch.2170CG16.2170CG16.1579.tbl --hmmnoprofmx --hmmnonbanded --nohmmonly --noexpand --nosmall --cyksearchfb 100.0 --noscan --nofixed --rfam --cut ga --nohmmfb --hmmfb 0 --hmmwidthmax 4000 --hmmnegmin -0.1 --hmmseed 0 --hmmdna --hmmfast --hmmpvm --hmmcpu 1 --hmmscore sum --hmmfilter --hmmtblout /tmp/cmsearch.2170CG16.2170CG16.1579.tbl --hmmnoprofmx --hmmnonbanded --nohmmonly --noexpand --nosmall --cyksearchfb 100.0 --noscan --nofixed --rfam --cut ga --nohmmfb --hmmfb 0 --hmmwidthmax 4000 --hmmnegmin -0.1 --hmmseed 0 --hmmdna --hmmfast --hmmpvm --hmmcpu 1 --hmmscore sum --hmmfilter

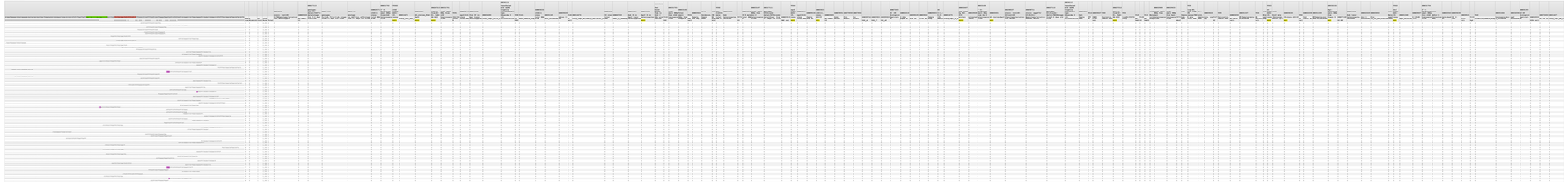
Total Hits: 10 Hits

Hits Overlapping Hits Non-Overlapping Hits

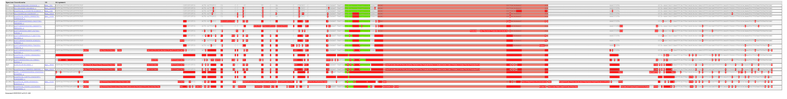
Hits Overlapping Hits



Hits Non-Overlapping Hits



Hits Alignment of Best Hits (Clustal)



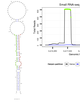
ID	Genome	Coordinates	Strand	Length
chloe_219	chr19: 6172473-6172527 +	**Candidate 2 canonical miRNA**	+	55

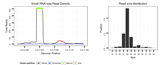
CCCC

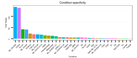
	Length	Distribution	Strand	Motif Score
dna__TTT_chr18:AC:AT:GC:AT:GC:TBPB	7	Conditional	3 canonical and 4 non-canonical	0.0

Consensus: **CCCCCCC** Reverse complement: **GGGGGGG**

Motif Logo





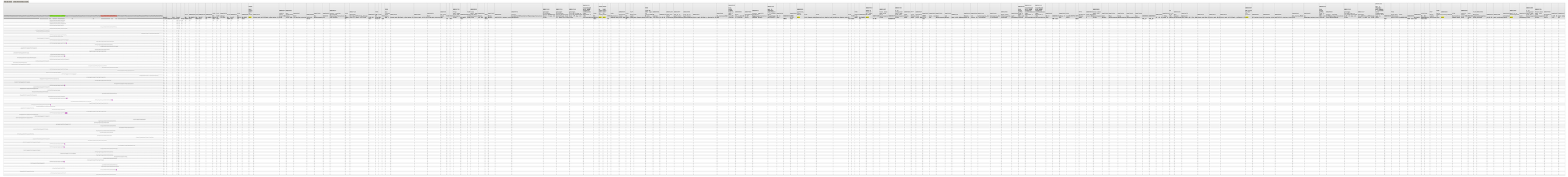


Show/hide Genome Browser

Other parameters:
--flank 0 --mm 0 --bowtie2 --bowtie2-N 0
--bowtie2-mp 1,0 --bowtie2-rdg 1,0,1,0
--bowtie2-rfg 1,0,1,0 --bowtie2-dpad 0

Initial Read Mapping:

Show/hide Initial Read Mapping Locations

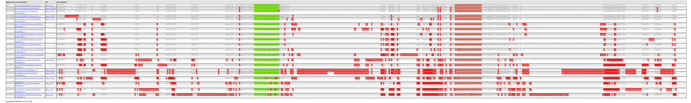


Left-over Small RNA

Show/hide Left-over Small RNA

De-depleted of all abundant RNAs:

Genome Coverage

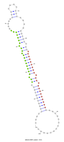


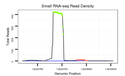
Generated 2020-05-21 21:21:08

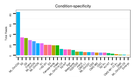
ID	Confidence	Flag	Sample Group
dbback124071 | chr38:142434645-142437331	Known Orthology	Serious	Serious

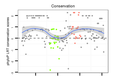
Legend: Exon Intron Intergenic

Predicted structure:









Show Alignment Chain

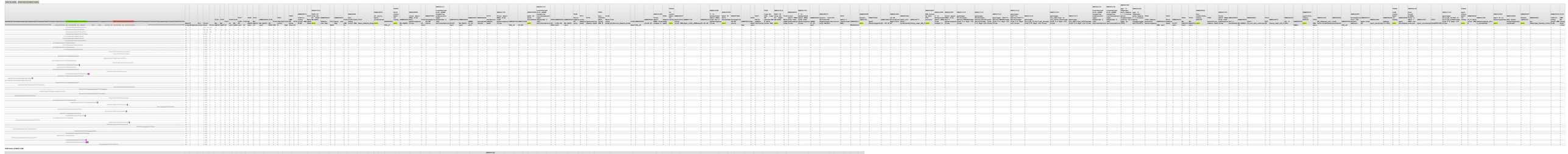
Fit Score: unavailable

Fold Energy: unavailable

No Reliable Hairpin Call

Intra-Strand Reads

Hide Reads Show Non-Hairpin Reads



Cell-cross strand reads

Show Hairpin With Reads

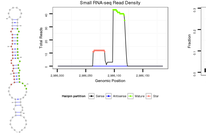
Re-alignment of all predicted orthologs

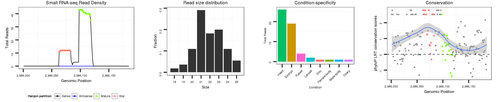
Species Sequence
Hairpin
Mature
Multiz Conservation
Consensus
Mature
Hairpin
Mature
Hairpin
Mature
Hairpin

ID	Coordinate	Confidence	Class	Genome Locus
dme_430_chr2R:2986051-2986135 +	**chr2R:2986051-2986135 +**	**confident**	**Canonical miRNA**	**intron**

Legend: 5p 3p 5p-iso 3p-iso loop-seq terminal-loop

Predicted structure





Show Alternate Folds

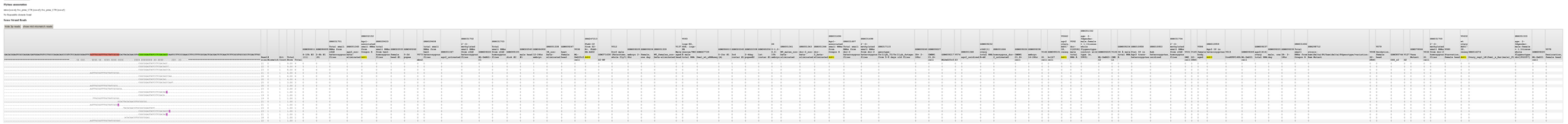
Flybase annotation

annotation:fly_pilot_178 (strand):fly_pilot_178 (overall)

No Expandable Genome found

Sense Strand Reads

Sort By reads Show Mid-Mismatch reads



Anti-sense strand reads

Show alignment With Reads

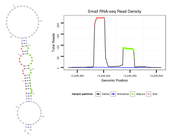
Re-alignment of all predicted orthologs

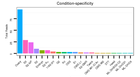
Generated 2025-07-21 17:17 -0400

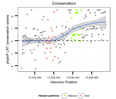
ID	Coordinate	Confidence	Class	Possible Scale
dme_159	**chr21:13245383-13245459 +**	**confident**	**Canonical snRNA**	**intergenic**

Legend: **Stem** **Loop** **Pri-miRNA Stem** **mature miRNA**

Predicted structure:







Show Alternative Folds

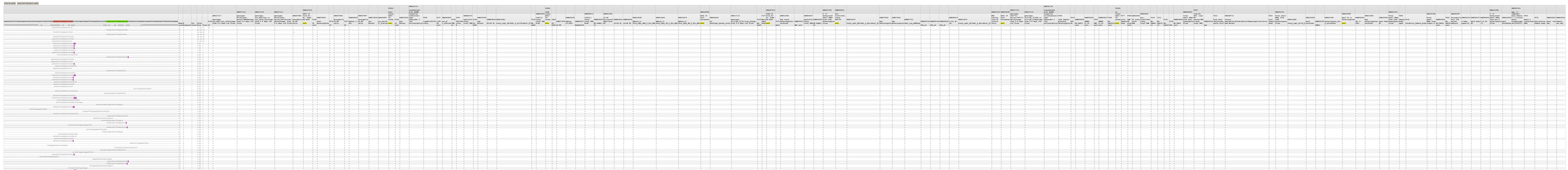
FASTA annotation

>dme_159

TA Expression (Genome Total)

Notes Small RNA

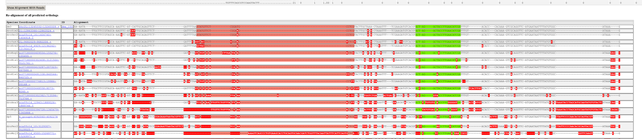
Hide Tip Notes Show Hint Information Hands



Sort score: Small RNA

Show Alignment With Genes

Re-alignment of all predicted siblings

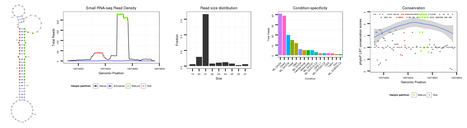

Species Scientific name
Alignment
Consensus
Hsapiens Homo sapiens
Ptroglodytes Pan troglodytes
Ggorilla Gorilla gorilla
Ppygmaeus Pongo pygmaeus
Nleucogenys Nomascus leucogenys
Rroxellana Rhinopithecus roxellana
Cjacchus Callithrix jacchus
Mmulatta Macaca mulatta
Mfascicularis Macaca fascicularis
Mnemestrina Macaca nemestrina
Mleucophaeus Macaca leucophaeus
Mfuscata Macaca fuscata
MmonkeyB Macaca mulatta monkeyB
MmonkeyK Macaca mulatta monkeyK
MmonkeyP Macaca mulatta monkeyP
MmonkeyR Macaca mulatta monkeyR
MmonkeyT Macaca mulatta monkeyT
Pkinji Pan troglodytes kinji
Pvereschagini Pongo pygmaeus verschagini
Pabelii Pongo abelii
Nnasalis Nasalis larvatus
Tgelada Theropithecus gelada
Csabaeus Chlorocebus sabaeus
Csyntheticus Chlorocebus sp. tantalus
Csaltuensis Chlorocebus aethiops
Csoonosus Chlorocebus pygerythrus
Csunicus Chlorocebus sp. pygerythrus
Csp Chlorocebus sp.
Csp2 Chlorocebus sp.
Csp3 Chlorocebus sp.
Csp4 Chlorocebus sp.
Csp5 Chlorocebus sp.
Csp6 Chlorocebus sp.
Csp7 Chlorocebus sp.
Csp8 Chlorocebus sp.
Csp9 Chlorocebus sp.
Csp10 Chlorocebus sp.
Csp11 Chlorocebus sp.
Csp12 Chlorocebus sp.
Csp13 Chlorocebus sp.
Csp14 Chlorocebus sp.

id	structure	conditions	time	version
dbm__432	**((((((((((.((((((.((((((.

ID	Locus/Alias	Condition	Class	Structure Source
dme_253_chr3:16574858-16574920	**chr3:16574858-16574920**	**condition 1**	**Canonical miRNA**	**CSS**

Flank: 20 bp 20 bp

Predicted structure



Show Enlarged Plots

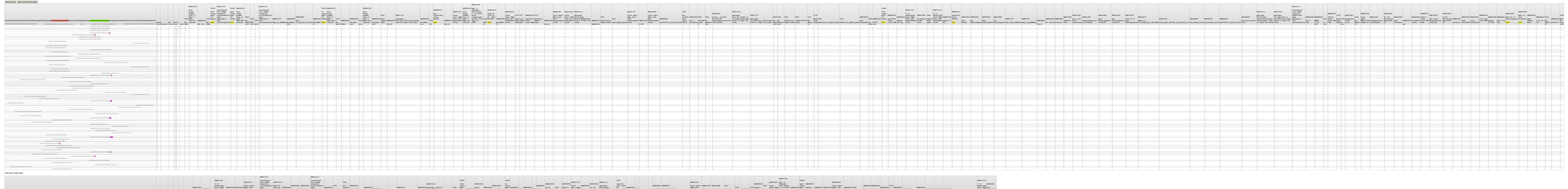
Plots

Total reads mapped: 1,000,000 (1000k) CPM (Mm: 0.00) (Mature: 0.00k), gmin: 2 FB (log 2)

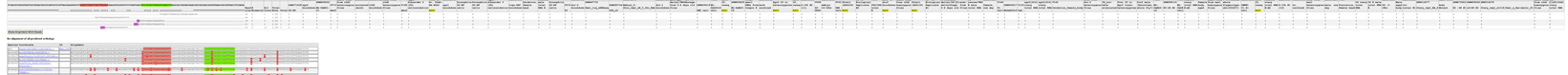
No Bootstrap Consult Tool

Some Overall Reads

Hide Tip Hands | show Non-Homologous Hairpin



Add some Overall Reads



Show Alignment With Hairpin

No alignment of all predicted miRNAs

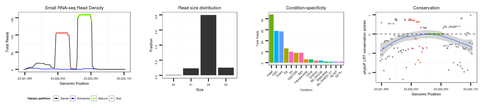
Species	Consensus	CS	Alignment
dme_253_chr3:16574858-16574920			
dme_253_chr3:16574858-16574920			
dme_253_chr3:16574858-16574920			

ID	Name	Condition	Size	Secondary structure
chloa_414_chr5.1.1593469-1593600	**c.[rnfbnm] ; [cmmcat]**	**rnfbnm ; [cmmcat]**	**[ ]**	((((((

ID	Coordinate	Confidence	Class	Genome Locus
dme_146	**chr3L:23221998-23222085 +**	**confident**	**Canonical miRNA**	**intron**

Legend: Stem 5p Terminal loop 3p Mature

Predicted structure:



Show Alignment Folds

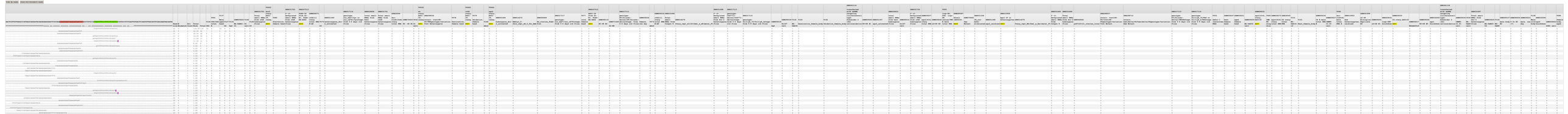
Fasta annotation

dme|147|Hairpin:-|dme|147|Mature:-|dme|147|Mature:-|

5p Expanded sheets fold

Sense Strand Reads

Hide 5p reads Show mid-stranded 5p reads



Anti-sense strand reads

Show Alignment With Reads

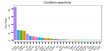
Re-alignment of all predicted orthologs

Created MEME5.5.4 [1] 2 MB

ID	dataset_ID	condition	Date	Genome name
dbss_296	dbss_0074774-0074827	condition	Canonical mRNA Spl-18	Drosophila melanogaster Release 6 plus ISO1 MT

Total: 54 **Canonical** **Alternative**

Feature structure:



Show/hide table

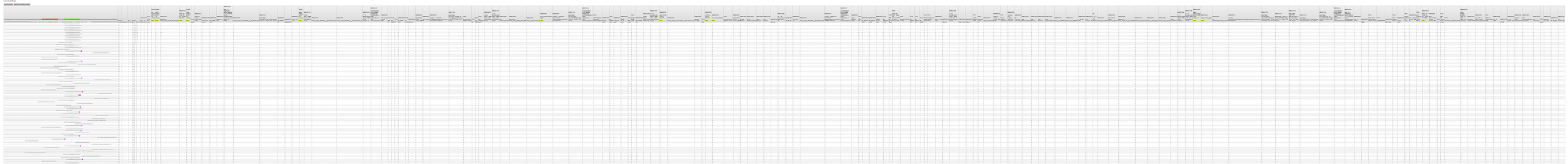
Filter selection

Fr: pass, CT:0.05,bg:0.01

Fr: pass, CT:0.05,bg:0.01

Total Small Reads

Hide full table Show/hide table



Add new small RNA

Show/hide alignments

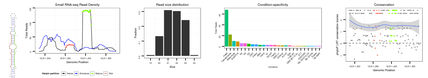
Alignment of all product isoforms

Created 2020/05/12 at 21:21:38

ID	Location	Condition	Size	Variable Sites
dmu_378_ctg/50:1401133:1401425 =	**condition**	**Canonical mRNA**	**uniform_ss_1 Bb**	chr1:1401170, chr1:1401174, chr1:1401178, chr1:1401182, chr1:1401186, chr1:1401190, chr1:1401194, chr1:1401198, chr1:1401202, chr1:1401206, chr1:1401210, chr1:1401214, chr1:1401218, chr1:1401222, chr1:1401226, chr1:1401230, chr1:1401234, chr1:1401238, chr1:1401242, chr1:1401246, chr1:1401250, chr1:1401254, chr1:1401258, chr1:1401262, chr1:1401266, chr1:1401270, chr1:1401274, chr1:1401278, chr1:1401282, chr1:1401286, chr1:1401290, chr1:1401294, chr1:1401298, chr1:1401302, chr1:1401306, chr1:1401310, chr1:1401314, chr1:1401318, chr1:1401322, chr1:1401326, chr1:1401330, chr1:1401334, chr1:1401338, chr1:1401342, chr1:1401346, chr1:1401350, chr1:1401354, chr1:1401358, chr1:1401362, chr1:1401366, chr1:1401370, chr1:1401374, chr1:1401378, chr1:1401382, chr1:1401386, chr1:1401390, chr1:1401394, chr1:1401398, chr1:1401402, chr1:1401406, chr1:1401410, chr1:1401414, chr1:1401418, chr1:1401422

Length **293** **CDS:1-293 (293)** **coding:293**

Predicted structure:



Show alignment frame

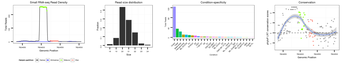
Hidden sequences:

HBAD:1:1:1:1:0:0:0

Name	Length	Strand	Type	Source	Score
Locus1:7160-7260 chr5:70_70140bp 70140bp	100	+	Repeats-Tandem	Tandem Repeats Finder	[score=0.0] [ACGCGCCCGCACGCACGCCCGCGCCCGCG]

Total **1** sequences, **100** bp, **100.00%** GC content

Sequence



Sequence Details

Primer associations

No primer data

Transposon Associations

No transposon data

Genomic Annotations

- Chr5:70000000-70140000 (+)
- Chr5:70000000-70140000 (+) Genes

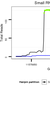
Gene Model Data

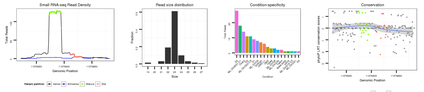
Gene ID	Name	Type	Strand	Chr	Start	End	Length	Exons	Introns	Coding Length	Coding Exons	Coding Introns	Coding %	Intergenic Upstream	Intergenic Downstream	Nearest Upstream Gene	Nearest Downstream Gene	Upstream Distance	Downstream Distance
Chr5:70000000-70140000	Chr5:70000000-70140000	Genes	+	Chr5	70000000	70140000	140000	1	0	0	0	0	0.00						

ID	Coordinate	Confidence	Class	Genome Locus
dme_239 (chr28:11579868-11579928 -)	**coordinate**	**Canonical miRNA**	**antisense_to_CDS**	UCSC hg19 UCSC Genome Browser (Lowell Mitnick)

Legend: **miRNA** **Canonical miRNA** **antisense_to_CDS**

Predicted structure





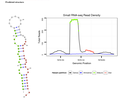
Show Minimum Image

Pri-hairpin sequence

AATCCCTCCCTCCATCCATCCTTTTTTTCTTTTTTT

Sample	Sample type	Genome	Size	Coverage	Sequencing platform
Chlamydomonas reinhardtii CC-1690 21 gr mt+	Lab strain	Chlamydomonas reinhardtii v5.5 (JGI Phytozome)	15.8 Mb	1000x	Illumina, Nanopore, Sanger

Comment: Chlamydomonas reinhardtii CC-1690 21 gr mt+ Lab strain Illumina, Nanopore, Sanger 1000x Chlamydomonas reinhardtii v5.5 (JGI Phytozome) 15.8 Mb

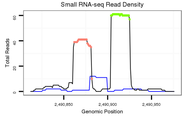


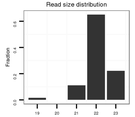
ID:	Coordinate:	Confidence:	Class:	Genome Locale:
dme_239	**chr3L:2490862-2490926 +**	**confident**	**Canonical miRNA**	**intron**

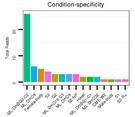
[View on UCSC Genome Browser (Cons8:Mmu)]

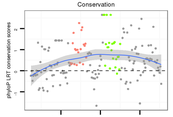
Legend: Loop 5p 3p Mismatch to 3p/loop Mismatch to 5p

Predicted structure









Show Alternate Folds

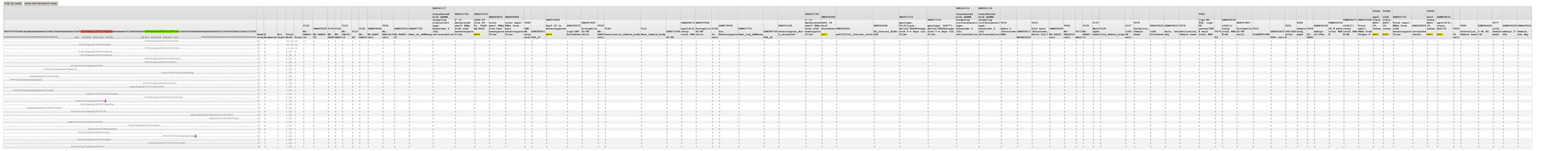
Flybase annotation

intron [CG31686-RA] intron [CG31686-RB] intron [CG31686-RC] intron [CG31686-RD] five_prime_UTR [CG31686-rf]

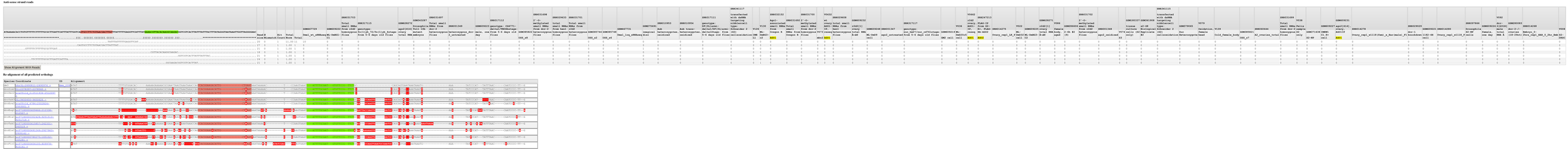
No Repeatable elements found

Sense Strand Reads

Hide 3p reads Show mid-mismatch reads



Anti-sense strand reads



Show Alignment With Reads

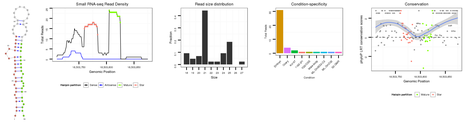
Re-alignment of all predicted orthologs

Generated 09/09/2019 at 12:55 AM

ID	Accession	Prediction	Flank	Strand	Score
dme_415 / chr3R:18503750-18503825 +	**candidate**	**NORNA**	**intron**		

Legend: Stem Loop Terminal loop Bulge/Internal loop

Predicted structure



Show Alignment Tracks

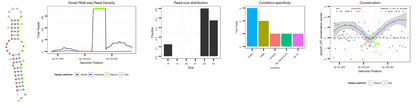
Fit Rna annotation

Fit Rna Annotation: chr3R:18503750-18503825:+,chr2L:17001319-17001391:+,chr2L:17001319-17001391:+,chr2L:17001319-17001391

ID | Candidates | Class | Genome Size
dme_163 | chr16:12741988-12742837 = candidate | Microsat | larvae | 1 | 1 | Drosophila melanogaster (GenBank/Refseq)

Locus **dme_163 chr16:12741988-12742837** (+) **CAGCAGCAGCAGCAGCAG**

Predicted structures



Show/Hide Sequences

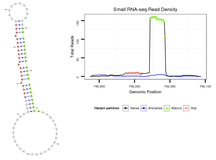
Primer parameters

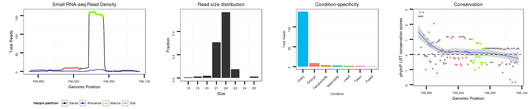
Mature:GTCTTCACGACGACG

ID	Coordinate	Confidence	Class	Genome Locus
dme_173	chr4:745987-746044 +	confident	Canonical miRNA	intron

Legend: 5'arm 3'arm 5'Flank 3'Flank miRNA Seed

Predicted structure





Show Alternate Folds

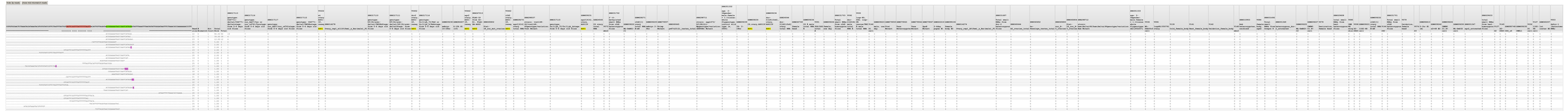
Flybase annotation

dme:FlyLeafDescR:fly_gtex_173 [ln:4]

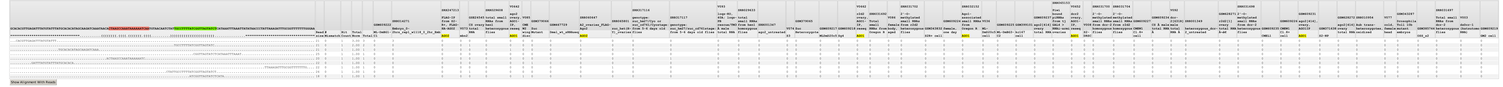
No Expression Attribute found

Some Viewed Reads

Sort By reads show mid mismatch reads

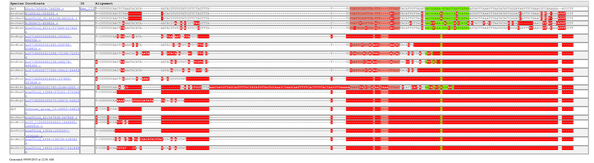


Antisense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

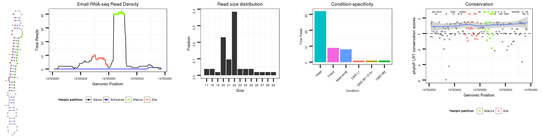


Created 09FEB2017 at 12:56 GMT

ID	Coordinate	Confidence	Class	Genome Groups
sblock87333	**chr31:16726056-16726097 -**	**Known Orthologs**	**CDS**	**CDS**

Legend: **Intron** **Exon** **Intergenic** **Intergenic Extension**

Predicted structure



Show Alignment Panel

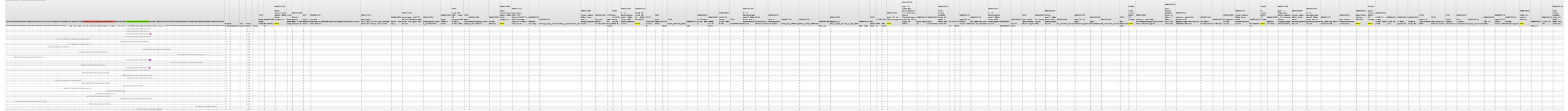
Flybase annotation

CDS:FBrB0 (dm.ala)

No flybase stands-trial

Sense Small Reads

Show Tip Reads Show Not mismatch reads



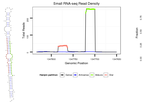
Anti-sense strand reads

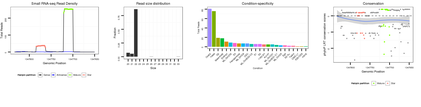
Show Alignment With Reads

Bar alignment of all pre-sheet orthologs

ID	Condition	Cluster	Genome Length
dme_149 chr3L:16:+:1347786-1347786 ; .;intron ;Canonical mRNA; intron			
Score **100.00** Strand **+** Structure		Click on GENE Genome Browser (UseGtfile)	

Predicted structure





Show Annotation Table

Flybase annotation

dme:FBGN0087044

5L:Scaffold:Genome Total

Gene Ontology Terms

Show Gene Ontology Terms

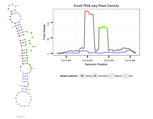
Gene Ontology Terms

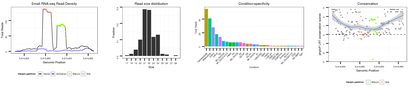
Term	Ontology	Evidence	Qualifier	Source
GO:0005634 nucleus	CC	IDA		FlyBase
GO:0006397 mRNA processing	BP	IMP

ID	Name	Evalue	Size	Blocks length
dme_T74_chr3R:19196228-19199913 +	condition_Control mRNA vs. Intergenic	7.6e-1	3	1

Motif 1 was **not** found in the primary sequences

Predicted structure:





Show/hide motif logo

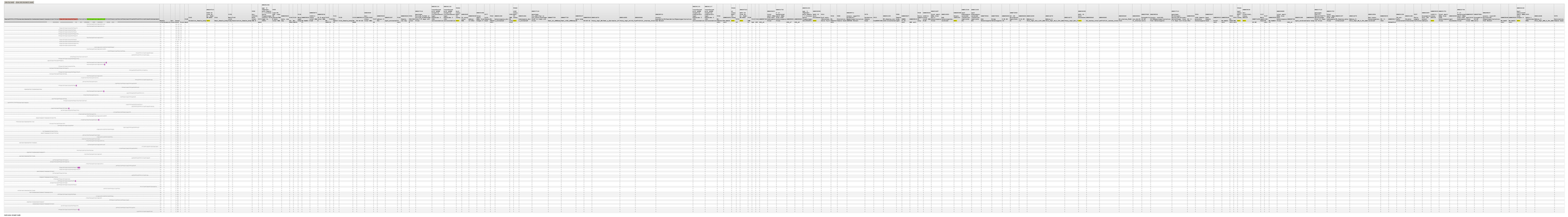
Flyber annotation

No flyber annotation found for this motif.

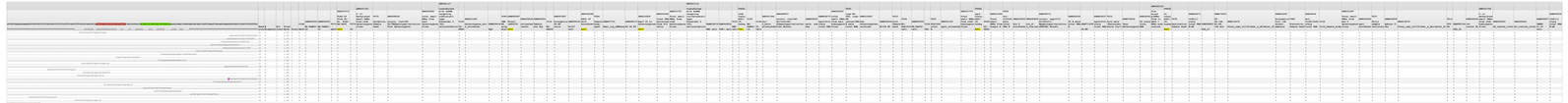
No flyber annotation found.

Gene Ontology Search

Filter by GO term: enter GO term and click Update



Sort by score, strand, length



Show/hide gene data through

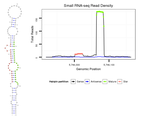
Gene Ontology Search

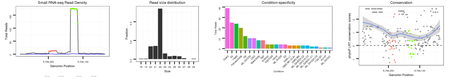
Generated 2019-03-11 21:01 +00

ID	Confidence	Strand	Strand Code	
sbbm21649_chr21:5745968-5746114 =	**Score Ortholog**	**Same**	**Same**	Show in UCSC Genome Browser (Linked Mirror)

Length: 147 bp

Predicted structure





Show Alternative Hits

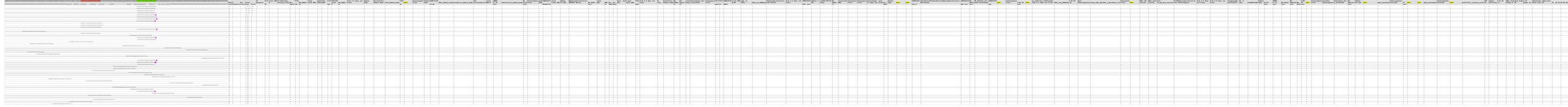
FitGoro annotation

sbbm21649_chr21:5745968-5746114 (1:5745968-5746114)

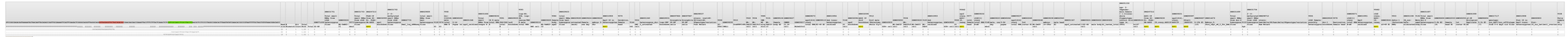
Score: 0.000 Strand: Same

Score Vienna Rnark

Code: No Valid Alternative Hits



Hairpin arms strand Cuts



Show Expressed MiRS Hairpin

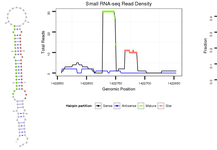
Alignment of all predicted miRNAs

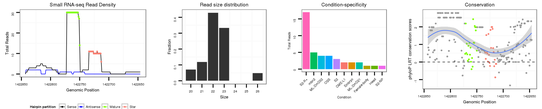
Species Consensus	ID	Alignment
hsa-mir-1-1 hsa-mir-133a-1 hsa-mir-206 hsa-mir-133b	MIR1-1	ccugcuacuuuacauacacuuccuuacauuccccagcgcgcg

ID	Coordinates	Coordinates+	Class	Genome Locale	
xblock1407	**chr21:.1422696-1422793 -**	**Known Ortholog**	**intergenic**	**intergenic**	View on UCSC Genome Browser (Local Mirror)

Legend: **Seed** **Stem** **Terminal Loop** **Bulge/Loop**

Predicted structure





Show Alternate Forms

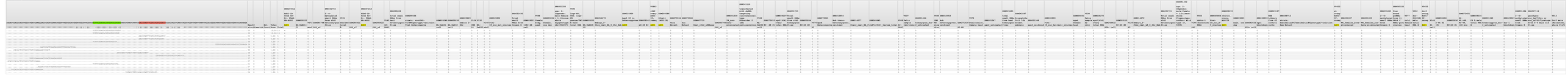
Flybase annotation

intergenic

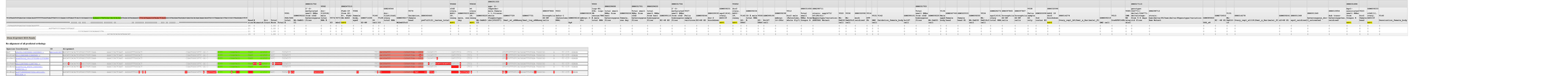
No Repeatmasker elements found

Sense Strand Reads

Hide Bp reads | show mid mismatch reads



Anti-sense strand reads



Show Argument With Reads

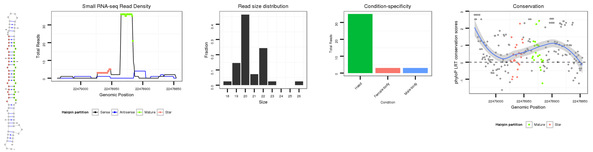
Re-alignment of all predicted orthologs

Species Coordinate
ID
Alignment
Consensus GUGCACC-g-CCA-AG
mmulatta
mfascicularis
mnemestrina
cnehalis
pnemeistrina
tbrachyura
macaque
pcynomolgus
pnemestrina
pleonina
pfascicularis
pfuscata
pnemeistrina
pnemestrina
pnemestrina
pnemest

ID	Coordinates	Confidence	Class	Genome Loci
sblock91942	**chr31:22478896-22478988 -**	Known Ortholog	Interprande	Interprande

Score: 0.000 Ex: 0 Cons: 0.000 Cons: -0.000

Predicted structure



Show Alternate Folds

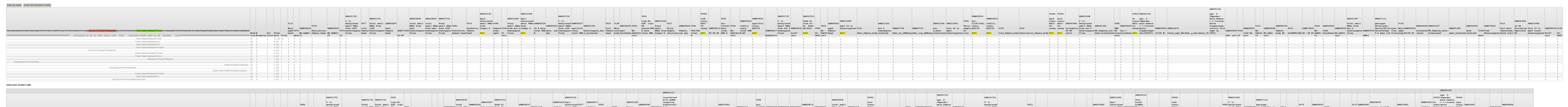
Flybase annotation

interprna

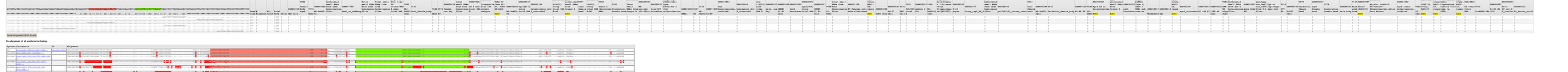
No Repeatmk elements found

Some Strand Reads

Hide Sp reads Show this mismatch reads



Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

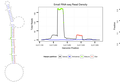
Generated 2019-12-11 at 12:26 AM

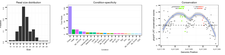
Name	Length	Strand	Genome	Date	Nucleotide content
Alex_Vel_Ala-tRNA-AGY-TYA-4-27TYA-5	73	Cytosol	Cytosol (Cytosol and mt)	Sunday, 2 Nov 2025	29% A 23% C 23% G 25% T

Alex_Vel_Ala-tRNA-AGY-TYA-4-27TYA-5 | Cytosol | Cytosol (Cytosol and mt) | Sunday, 2 Nov 2025 | 29% A 23% C 23% G 25% T

Score: 0.0 bits (0) | Expect: 1.0 | Method: Compositional matrix adjust. | Identities: 73/73(100%) | Strand: Plus/Minus

Product: tRNA-Ala (AGC)





Secondary structure

Primary sequence:

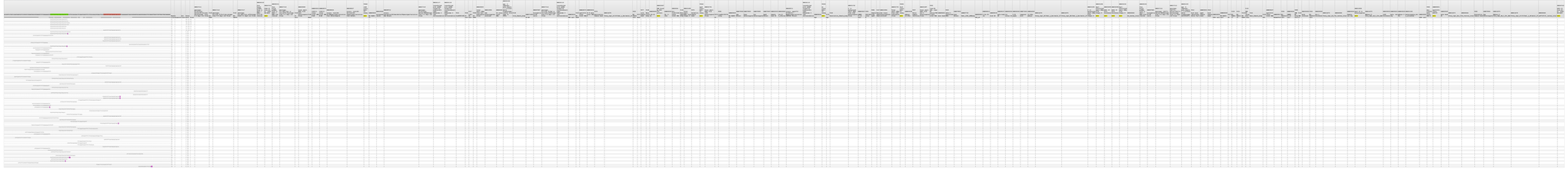
AGCGGGGGUGUCUCUAGCUCAGCGGUAGAGCGCGCGCUCAGACGCGAGGGUCGCGGGUUCGAUUCCCGCCCCCGCUCCA

Secondary structure:

((((((((((,,,,,,,,,,)))))))))),((((((((,,,,,,,,)))))))),((((((((,,,,,,,,))))))))

Alignment

Show alignment

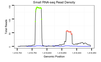


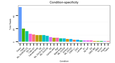
Show alignment: Show sequence logo

Sequence logo

ID	Alias	Confidence	Size	Genome Coords
chbank9157 / chr19_:14138752-14138871 +	Reverse Orthologs	Strong	Intron	chr19:14138752-14138871 (Human Mar.2009 (GRCh37/hg19))

Predicted structure:





Show/hide help

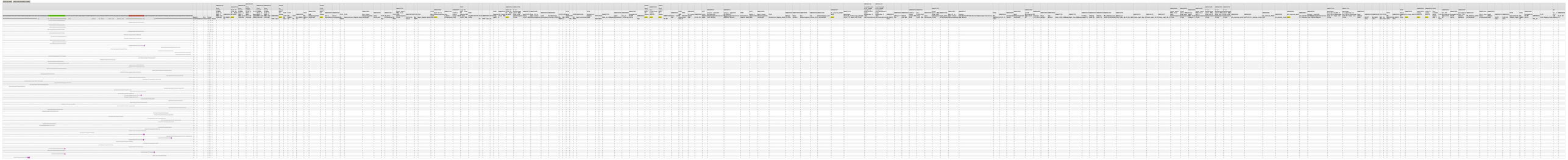
Filters assessed

Min 10 RPM in 1 sample (10:20:0 as 1x, yes, 1:0:0:0:0:0:0:0 as 1:0:0:0:0:0:0:0, not)

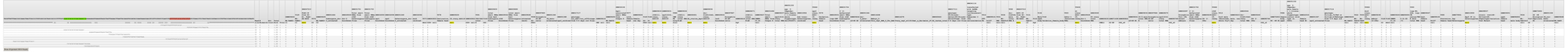
Min 1 RPM in 1 sample (1:0:0:0:0:0:0:0 as 1:0:0:0:0:0:0:0, not)

Sets through filters

Show/hide details Show/hide/reset/save/load

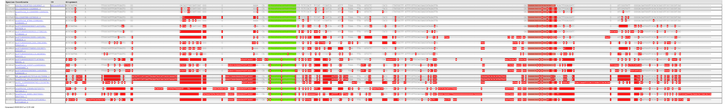


Left-over small reads



Show/hide alignment

Multiple alignment (Muscle)

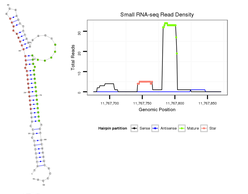


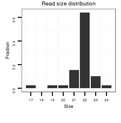
Powered by MUSCLE v3.8.31 (edit)

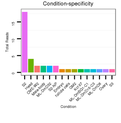
ID	Coordinate	Confidence	Class	Genome Locus
sblock204826	**chrX:11767725-11767821 +**	**Known Ortholog**	**intron**	**intron**	[View on UCSC Genome Browser (GenomeMirror)](#)

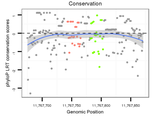
Legend: Donor Acceptor Canonical Non-canonical

Predicted structure









Show Alternate Folds

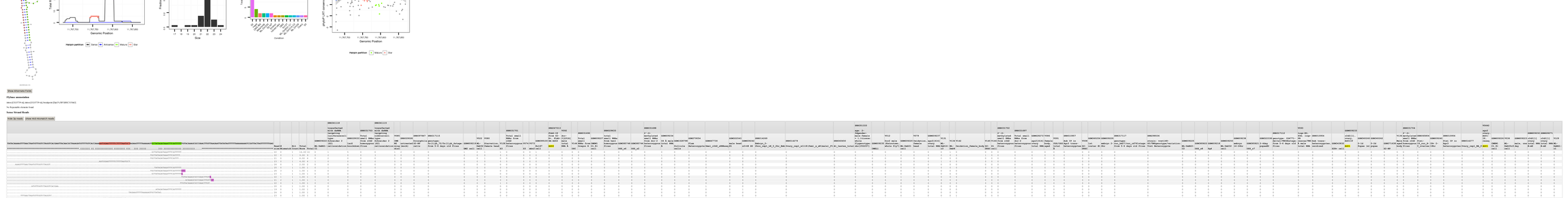
Flybase annotation

intron [CG37739-xg], intron [CG37739-xg], broad-spec [Dip7%3BY3BIC7370%2]

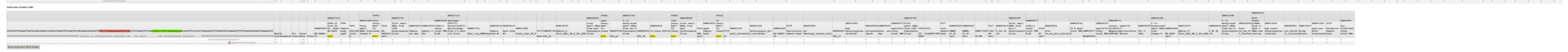
No Repeatmasker elements found

Sense Strand Reads

Hide 3p reads | show read mismatch reads



Antisense strand reads



Show Alignment With Reads

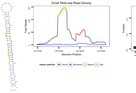
Re-alignment of all predicted orthologs

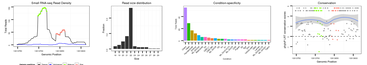
Generated 2026-05-27 00:00:00 UTC

ID	Name	Location	Strand	Length
dme_7.49	**chr31:1,783,626-1,783,7762**	**condition 2 normal mRNA 1.526**	+	150

Score: **0.9**

Predicted structure:





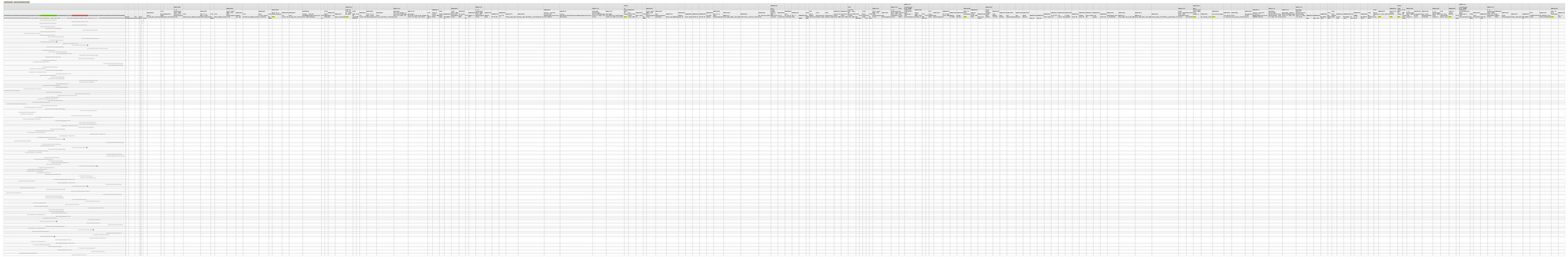
Show/hide this tab

Probe sequences

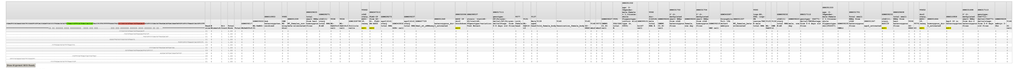
CTCGAAGC GAUCTGCAUCAC

Probe Target Site

Hide Target Site Show/hide target sites



Hide Gene Structure Show/hide gene structure



Show/hide this tab

Multiple Alignment of Predicted Orthologs

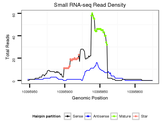
Hide Multiple Alignment

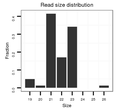
Hide/show MAF(PHAST) or .ps .pdf

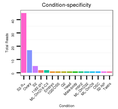
ID	Coordinate	Confidence	Class	Genomic Locale	
sblock1#1949	**chrX:10395825-10395903 -**	**Known Orthologs**	**intron**	**intron**	[View on UCSC Genome Browser (Grmh38/Mmu1)](#)

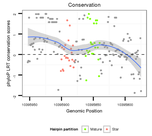
Legend: **Mature** **Star** **Conserved** **Alternative**

Predicted structures









Show Alternate Folds

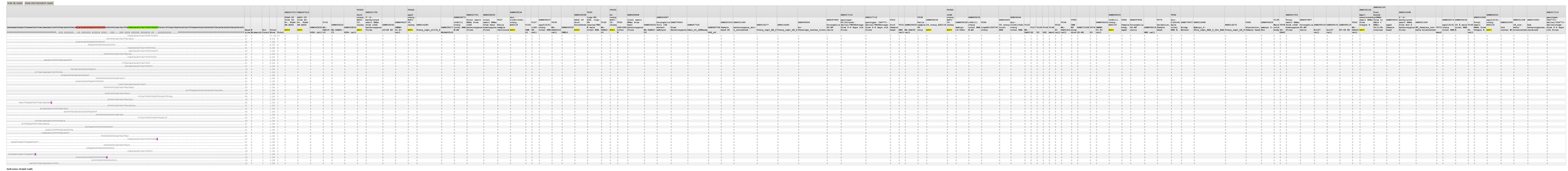
Flybase annotation

Intergenic [Dbz/5:/97:IR9/6:V36/7] Intergenic [Dbz/5:/97:IR9/6:X36/7] Intergenic [Dbz/5:/97:IR9/7:2136/7] mirn [cpn-mi]

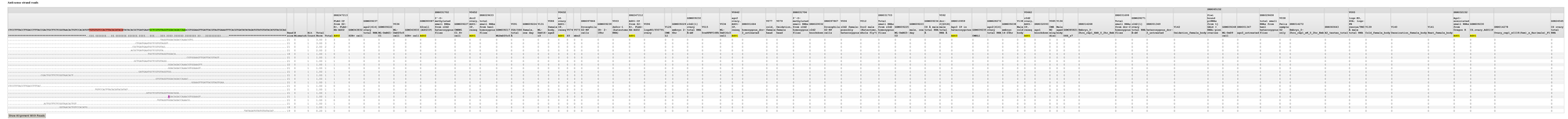
To flyapollo chrome load

Sense Strand Reads

Hide Sp reads | Show mismatch reads

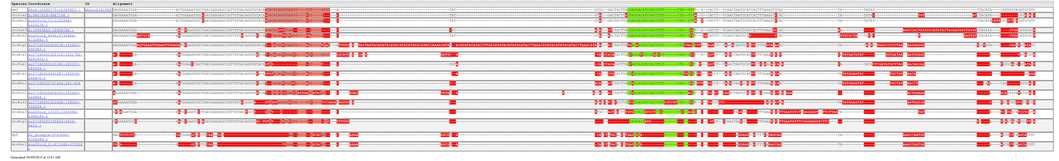


Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

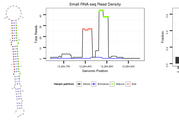


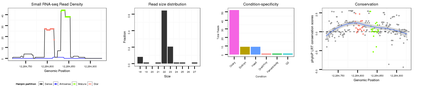
Generated PRSW [2.0 at 12:41 AM]

ID	Confidence	Class	Strand	Genome Coords
dbtech26554 / chr21:12284769-12284877 =	**Known Orthology**	intron	intron	Show in UCSC Genome Browser (Linked Mouse)

Type: **intron** **CONSERVATION** **ORTHOLOGY**

Predicted structure





Show Alignments Hide

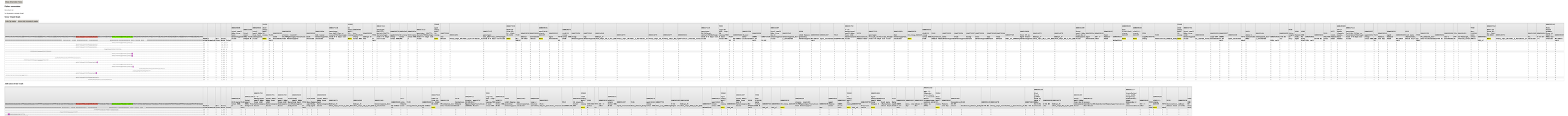
Fetch sequences

hg19:chr21:12284769-12284877

No Repeatmasker masking found

Select Strand Reads

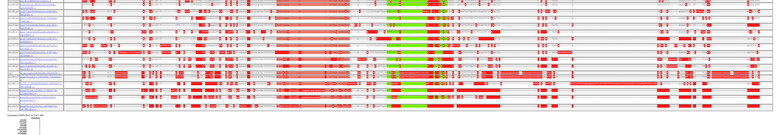
Hide All Reads Show Fetch Mismatch Reads



Add more strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs



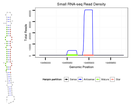
Updated 2/20/2020 at 12:01 AM

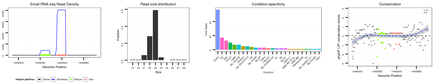
ID	Condition	Cell/Strain	Date	Sample Amount
dmo-mir-979-ps	chrX:19455870-19455964	Kasco Ortiboug	dmo_prime_5 TR	1pl TR

Filter on GTF: Genes Retrieve Gene (Ctrl+Shift+Enter)

Genes: dmo-mir-979-ps

Predicted structure





Show Alignment Help

FASTA sequences

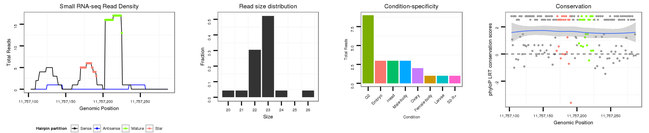
>1 Genome: chrX:19455870-19455964 (+) dmo-mir-979-ps dmo-chrX:19455870-19455964 (+) dmo-mir-979-ps, pdf=0.1,bw=TF,ldist=0,rdist=0,lbp=0,rbp=0,ldir=TF,rdir=TF,lfold=0,rfold=0,lfold=0,rfold=0,lfold=0,rfold=0

ID:	Coordinate:	Confidence:	Class:	Genome Locale:
sblock147283	**chr3R:11757153-11757237 +**	**Known Ortholog**	**CDS**	**CDS**

View on UCSC Genome Browser (Local/Mirror)

Legend: Sense Antisense Mature Star

Predicted structure



Show Alternate Folds

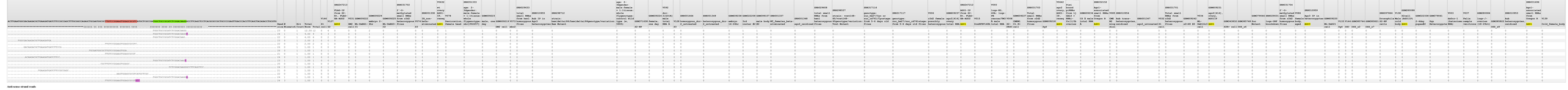
Flybase annotation

CDS:CG4223-mRa

No Exposible chrom found

Sense Strand Reads

Hide 3p reads Show mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

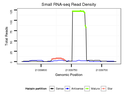
Re-alignment of all predicted orthologs

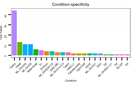
Species Coordinate	ID	Alignment
Ref	Ref_chr3R:11757153-11757237_+	ACCTTGAAGTGGCGACGAAGCGCTTCAAGATGACTTTTCCGCCAACTTTTGCCGCCAACTTTTGCCGCCAACTTCAATTGCCGCCAACTTCAATTGCCGCCAACTTCAAT

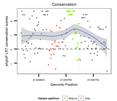
ID	Coordinate	Confidence	Class	Secondary Locus(s)
dme_312	**chr3L:21339724-21339782 (-)**	confident	**Canonical miRNA**	**embrace_in_intron**

Legend: 5p 3p Terminal loop Other

Predicted structure:







Show 20 hairpin fields

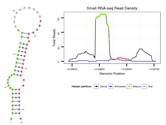
Fields: mouseover, click to pin

hairpin_id dme312-DS1 | ds_idx=1 | ref_id=1 | ref_strand=- | ds_ID=ds:1 | PRI=MI0013707 | hairpin=ath_chr4:8_chr4:8_+_1_1_0_0_0

ID	Confidence	Strand	Genome Size
dme_397_chr3L:14128796-14128857	**confident**	**MIRNA**	**intron**

Genome Browser: Flybase

Predicted structure

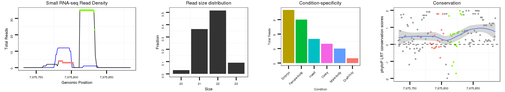


ID	Coordinate	Confidence	Class	Genome Locus
dme_194	**chrX:7975782-7975834 +**	**confident**	**Canonical miRNA**	**Intergenic**

View on UCSC Genome Browser (GenomeMirror)

Strand: **Arm** **Loop** **Stem 5p** **Stem 3p** **mature miRNA**

Predicted structure



Show Genomic Data

Flybase annotation

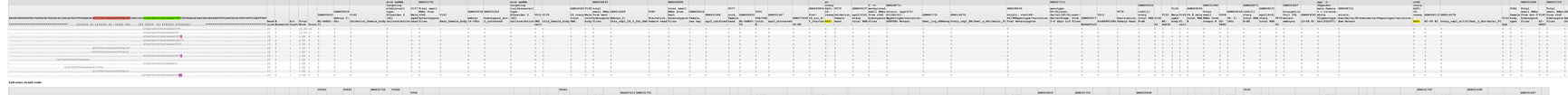
Sequence:ZinFLY8:5892:5914(+)

No Ensembl/Gencode Gene

Sense Strand Reads

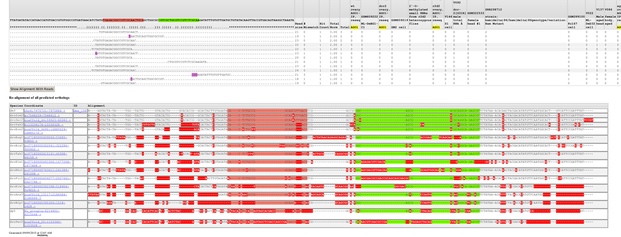
Hide Sp reads Show Hid mismatch reads

Antisense strand reads



Show Alignment With Reads

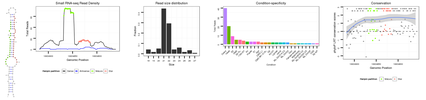
Re-alignment of all predicted miRNAs


Species Coordinate
Sp
Alignment
Consensus
dme_194 chrX:7975782-7975834 +
Drosophila melanogaster
Drosophila simulans
Drosophila sechellia
Drosophila yakuba
Drosophila erecta
Drosophila ananassae
Drosophila pseudoobscura
Drosophila persimilis
Drosophila willistoni
Drosophila mojavensis
Drosophila virilis
Drosophila grimshawi
Drosophila rhopaloa
Drosophila ehrenoberi
Drosophila kikkawai
Drosophila biarmipes
Drosophila bipectinata
Drosophila eugracilis
Drosophila ficusphila
Drosophila takahashi
Drosophila rhizodoxa
Drosophila prolongata
Drosophila santomea
Drosophila yamatoana
Drosophila lutescens
Drosophila tsacasi
Drosophila camerounensis
Drosophila sechellia mauritiana
Drosophila simulans sim
Drosophila simulans mau
Drosophila simulans syn
Drosophila melanogaster ref
Drosophila melanogaster iso-1
Drosophila melanogaster iso-2
Drosophila melanogaster iso-3
Drosophila melanogaster iso-4
Drosophila melanogaster iso-5
Drosophila melanogaster iso-6
Drosophila melanogaster iso-7
Drosophila melanogaster iso-8
Drosophila melanogaster iso-9
Drosophila melanogaster iso-10
Drosophila melanogaster iso-11
Drosophila melanogaster iso-12
Drosophila melanogaster iso-13
Drosophila melanogaster

ID	Name	Description	Date	Drawing Scale
dme_352	**ubr56_1160d011-1160d020**	**combine 2 control mRNA 1.5hr**		1:10,000,000

Length: **1160** nucleotides

Predicted structure



Show Predicted Structure

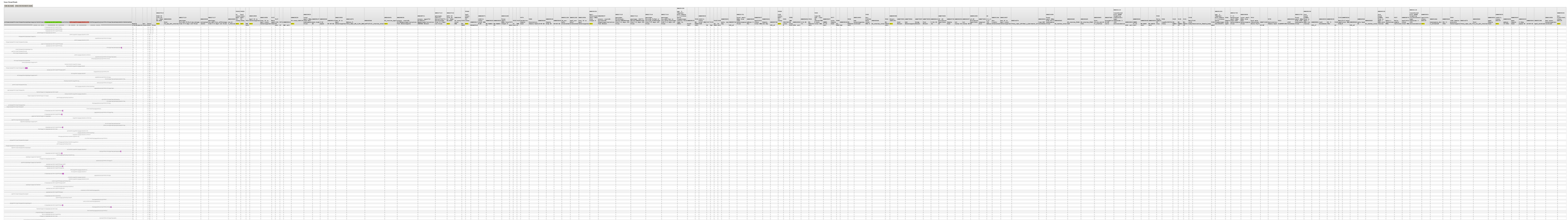
Primer annotation

Primer: Dsp1(1-20)-R1-T7-R2-Dsp1(1-20)

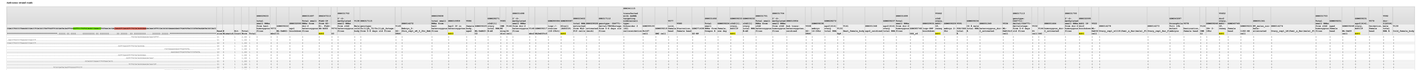
Primer: Dsp1(1-20)-R1-T7-R2-Dsp1(1-20)

Trace Visual Audit

Hide Tag Legend Show Hide Hairpin Legend

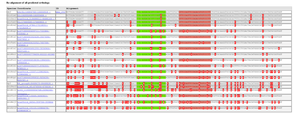


Audit notes: **no audit made**



Show Alignment Hide Alignment

No alignment of aligned sRNA(s)

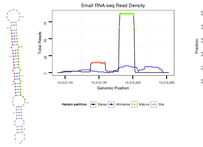


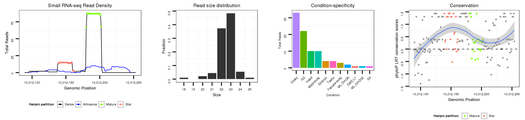
Alignment length: 1160

ID	Coordinate	Strand	Confidence	Class	Genome Locus
dme_179	chrX:10012139-10012203	+	confident	Canonical miRNA	antisense_to_intron

Legend: DICER HAIRPIN PRECURSOR

Predicted structure





Show Alternate Folds

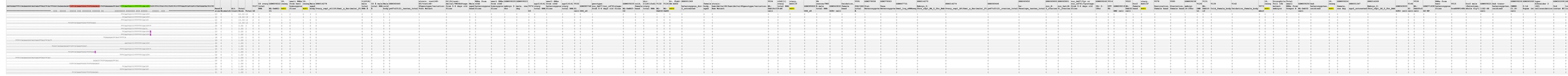
Flybrex annotation

Antisense to uhm(CR34999.4d), Antisense to uhf(NM_078999.4/EL), intron [Dm(+) ch], intron [Dm(+) ch], Intergenic [Dm(+)X:8F:8C:7F8C]

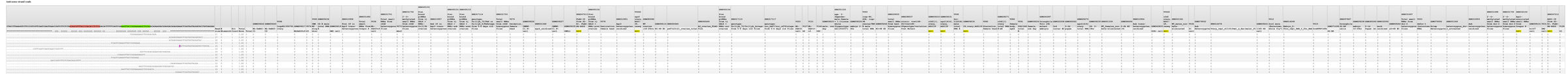
No Repeatmk elements found

Sense Strand Reads

Scale By reads | Show mid-mismatch reads

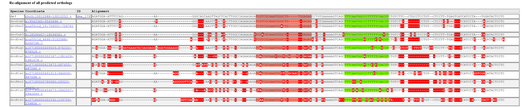


Antisense strand reads



Show Alignment With Reads

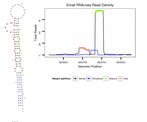
Re-alignment of all predicted etrnbigs

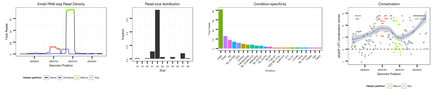


ID	CLASSIFIER	Confidence	Flag	Genome Locus
dme_376	**chr3L:28056673-28057788**	**conflicted**	**Canonical mRNA**	**intron**

Genome: **dmel** Assembly: **dmel_r6.22_FB2018_03**

Predicted structure





Show/Hide Hairpin Plot

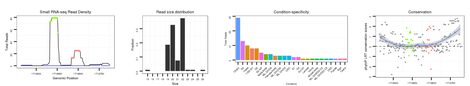
Fold-Back Alignment

GGCCTCGTTGCAGCCGTGTGTCTCGCTGCGTTCGTTTCGCTGCGCCGTTGTTTCGCTGCGCCGTTGTTTCGCTGCGCCGTT

ID	Coordinates	Conditions	Class	Structure Length
dme_418 (chr3L:17199774-17199886 -)	**conditions=['control' 'oxidative' 'starvation']**	**mRNA**	**intron**	113

Legend: **Stem** **Loop** **Bulge** **Internal** **Multi**

Predicted structure



Show Alignments Details

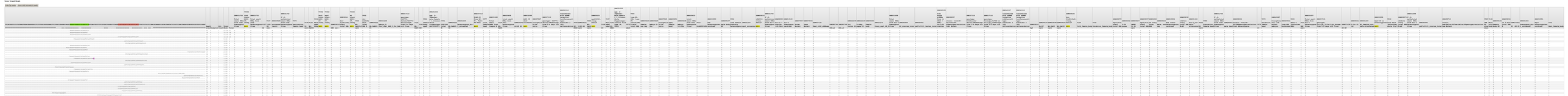
Picture annotation

mfe=[for vl: dme=[for vl: dme=[for vl: dme=[for vl: 2.700 (dan=-inf,) 2.700 (dan=-inf,) 2.700 (dan=-inf,) 2.700 (dan=-inf,) 2.700 (dan=-inf,) 2.700 (dan=-inf,)

No Secondary structure found

Static Variant Results

Show Variant Results **Show Alignment Details**



Anti-sense strand traffic

Show Alignment With Reads

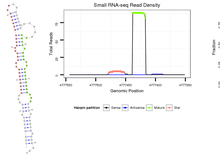
Sw alignment of all protein coding

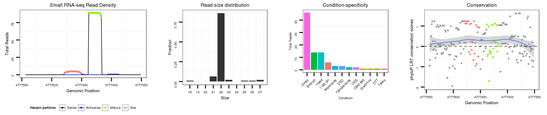
Generated 2019-09-23 21:22:31 -0400

ID	Coordinate	Confidence	Class	Genome Locale
block2035391	**chr3R:4777401-4777494 -**	**Known Orthologs**	**ncRNA**	**hsTR**

Legend: Seed Mature Loop Mismatch Bulge

Predicted structure





Show Alternate Folds

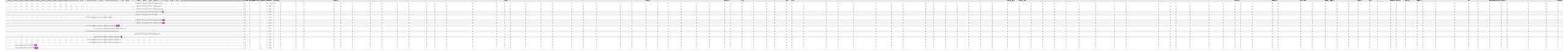
Flybase annotation

dme_pre_CTR [CG7884-cd]

5x Expanded, Genome Coord

Some Strand Reads

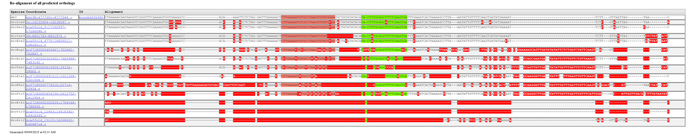
Hide Sp reads | Show mid-mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs



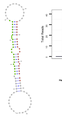
Created: 2025/05/22 at 11:11 AM

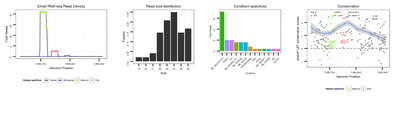
id	coordinate	strand	length	sequence	source locus
dme_249	**chr2L:7850678-7850863**	+	**condition**	**Canonical mRNA**	intronic_to_intron

Chr2L:14,131K: Kinase Mutant, Cultured Mid-L3

Length: 186 bp | **Strand: +** | **Canonical mRNA**

Predicted structure





Show Minimal Folding

Fasta sequence

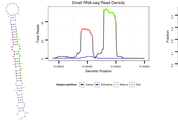
>dme_249 | 186 bp | 50.0% GC | 0.0% AT | 0.0% N

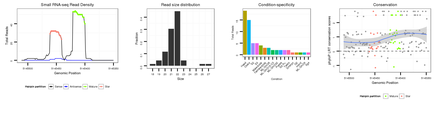
TCTGCGCCCCCGCCCCCGCCCC

ID	Location	Confidence	Class	Genome Locus
dme_259	**chr2R:14450001-14450013**	**confident**	**Canonical miRNA**	**intron**

Flank: **GGG** **GCTCCCCCCCCCCCC** **AGGGGGCCG**

Predicted structure:





Show Alignment Profile

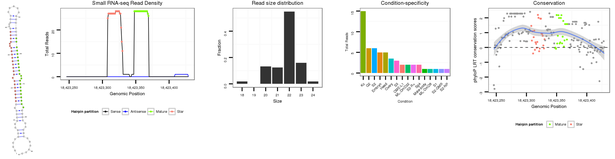
Flybase annotation

intron(Fbtr:dme-miR-iMe-iMe-iMe

ID	Coordinate	Confidence	Class	Genome Locale
sblock152513	**chr3R:18423296-18423379 +**	**Known Ortholog**	**intron**	**intron**

Score: **65.0** Bit **Known Ortholog** **intron/intron**

Predicted structure



Show Alternate Folds

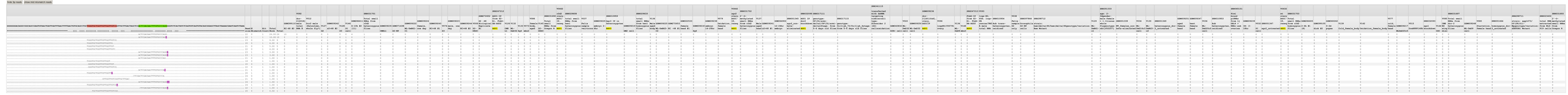
Flybase annotation

intron [Chr:4]

No Repeatile elements found

Some Strand Reads

Hide 3p reads | Show mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

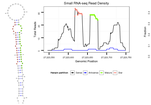
Re-alignment of all predicted orthologs

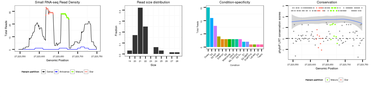
Conserved PRMT5R in 12dd-3rd

ID	Coordinate	Confidence	Strand	Cluster Score
chRnaA:1160001 - chr 10:27121596-27223699	**+**	**Known Orthology**	**+ 3.94**	**1.384**

Genome: **mm10 (GRCm38.p6 - GENCODE vM25)**

Predicted structure:





Show information tracks

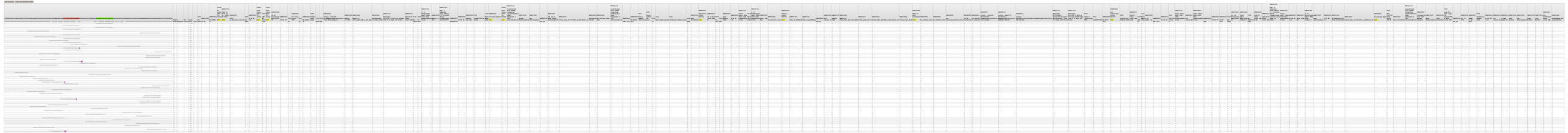
Filters: **unmodified**

Sort: **Alignment score**

To Expandto Genome view

Note: Small Reads

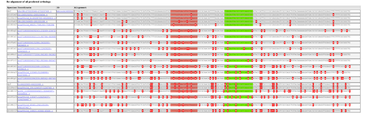
Hide Small Reads Show Non-Aligned Reads



Add Large Small Reads

Show Aligned Sets Only

Multiple Sequence Alignment



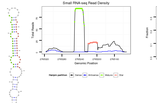
Generated MAFFM v1.1.847

ID	Locus	Cluster	Status	Strand
ebfsa4.2216 / chr21:27565182-27565267	chr21:27565182-27565267	Known-Strikeing	Intron	Intron

Genome Browser Links: Show on UCSC Genome Browser | E-mail Report

Locus: **chr21:27565182-27565267**

Predicted structure



ID	Coordinate	Confidence	Class	Consensus Locus
sblock96218	**chr3L:26331100-26331185 +**	**Known Ortholog**	**Intron**	**Intron**

Predicted structure

Show Alignment Paths

Flybase annotation

sacu(DP1:ch_sac;DP1:ch_sac;DSPR:ch_sac;dsim2:CAU01:ch_sac;dsim;DSPR:ch_sac;dsim;DSPR:ch_sac)

No flybase stories found

Some Strand Reads

Hide Tip reads | Hide mid mismatch reads

Antisense strand reads

Show Alignment With Reads

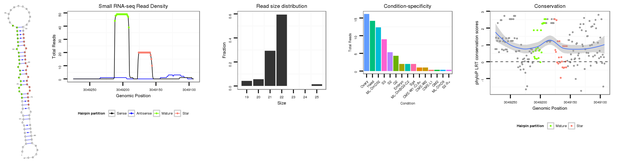
Re-alignment of all predicted orthologs

Generated 2020-08-21 at 12:01 AM

ID	Coordinate	Coordinate	Chr	Genome Locale	
sblock223863	**chrX:3049143-3049225 -**	**Known Ortholog**	**antisense_to_intron**	**antisense_to_intron**	Show on UCSC Genome Browser (Loaded Mmu)

Insert size: **min** 36 **median** 36 **max** 36 **MMR** 100.00%

Predicted structure



Show alternate Forms

FASTmm annotation

Antisense to intron_fragment [SQ:4Cx07N]; Intralignment [Dp:PLNT:IR:IR:NO]; Antisense to intron [N:4x]

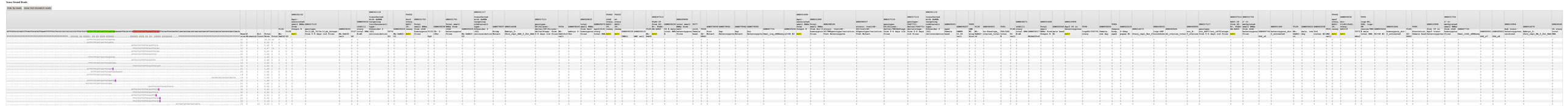
No Repeatmk element found

genome view

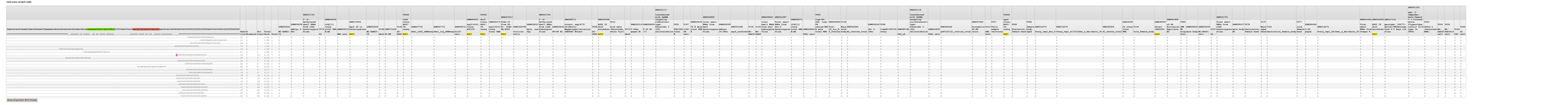
1. chr9:43563745-43563771
2. chr9:43563800-43563826
3. chr9:43563862-43563888; 3MM:N; 3MM:N;

Sense Strand Reads

Hide 36 reads | show mul mismatch reads



Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

Generated: 09/09/2025 at 02:28 AM

Mouse
Rat
Chinese hamster
Human
Pig
Cattle
Sheep
Dog
Cat
Horse
Chimpanzee
Gorilla
Orangutan
Gibbon
Rhesus macaque
Crab-eating macaque
Green monkey
Marmoset
Tarsier
Mouse lemur
Bushbaby
Tree shrew
Squirrel
Kangaroo rat
Guinea pig
Chinese hamster
Hamster
Naked mole-rat
Damaraland mole-rat
Cape golden mole
Tenrec
Cape elephant shrew
Rock hyrax (Bosch)
Rock hyrax (Ili)
Wild boar
Dolphin
Alpaca
Bactrian camel
Dromedary
Greater horseshoe bat
Pale spear-nosed bat
Big brown bat
Microbat
Hedgehog
Shrew
Cabbit
Ferret
Panda
Dog
Cat
Sea otter
Walrus
Weasel
Black flying fox
Red flying fox
Flying lemur
Alpine ibex
Sheep
Wild yak
Cattle
Nilgiri tahr
Nyala
Blackbuck
Pronghorn
Camel
Alpaca
Guanaco
Wheelers oarfish
Tasselled wobbegong
Whale shark
Bamboo shark
Small-spotted catshark
Spotted gar
Bichir
Bowfin
Human
Chimpanzee
Gorilla
Sumatran orangutan
Human
Chimpanzee
Gorilla
Sumatran orangutan
Human
Chimpanzee
Gorilla
Sumatran orangutan

ID	Coordinate	Confidence	Class	Genome Locus
CG1136_Ja2	**chr31:4057416-4057474 +**	**Known Ortholog**	**mitron**	**intron**

View on UCSC Genome Browser (GenbrMitron)

Score: 0.00 Strand: + Genome Length: 59 Mature Length: 59

Predicted structure

Show Antisense Folds

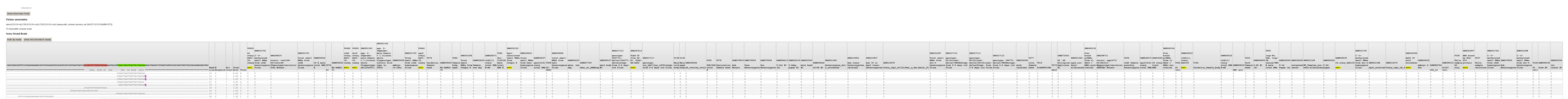
Fiches annotation

mirna:[CCCC-6], CDS:[CCCC0+-cds], CDS:[CCCC0+-cds], transposable_element_insertion_site:[MGETCCCCCHQMMCDST]

No Rnaseqdb clusters found

Sense Strand Reads

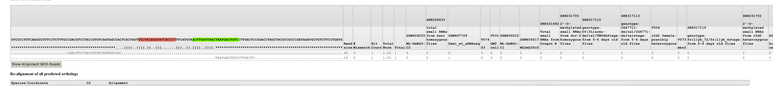
Sort: by reads Show mid mismatch reads



Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthologs



Generated 2016-06-23 at 5:41 PM

ID	Coordinate	Confidence	Class	Genome Graph
dme_256	**chr2R:19758846-19758904**	**confident**	**Canonical miRNA**	**intron**

Legend: **Mature** **Loop** **Star** **Miscleavage**

Predicted structure

Show Alternate Folds

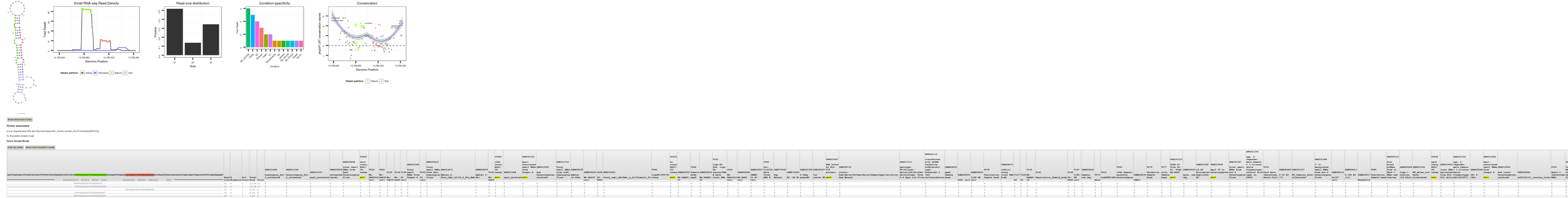
Flybase annotation

ovca: Ovgene[Ovc02]:Intro[Ovc02] transcribe_chrom_vector_vin [P-Gen9]:Ov[PA2701]

No Reputable cDNA 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

Species	Coordinate	ID	Alignment
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.1	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.2	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.3	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.4	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.5	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.6	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.7	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.8	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.9	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.10	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.11	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.12	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.13	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.14	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.15	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.16	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.17	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.18	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.19	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.20	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.21	--
Ovc	chr2:1.....-1.....(+)	ovgene0001.hom.mafft.22	--

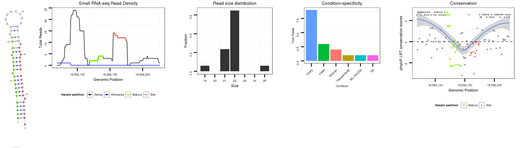
Generated MAFFT v7.475 (#1) (of 22)

```
ovgene0001.hom.mafft.1
ovgene0001.hom.mafft.2
ovgene0001.hom.mafft.3
ovgene0001.hom.mafft.4
ovgene0001.hom.mafft.5
ovgene0001.hom.mafft.6
ovgene0001.hom.mafft.7
ovgene0001.hom.mafft.8
ovgene0001.hom.mafft.9
ovgene0001.hom.mafft.10
ovgene0001.hom.mafft.11
ovgene0001.hom.mafft.12
ovgene0001.hom.mafft.13
ovgene0001.hom.mafft.14
ovgene0001.hom.mafft.15
ovgene0001.hom.mafft.16
ovgene0001.hom.mafft.17
ovgene0001.hom.mafft.18
ovgene0001.hom.mafft.19
ovgene0001.hom.mafft.20
ovgene0001.hom.mafft.21
ovgene0001.hom.mafft.22
```

ID	Coordinate	Strand	Class	Genome Locus
CG15160_in3	chr2L:18592119-18592176 +	+	Known Ortholog	mitrus / Intron

Legend: Exon Intron 5' UTR 3' UTR Annotation

Predicted structure



Show Alternate Folds

Fisher association

mirna:CG15160 seq:CTRLCG15160-seq:CTRLCG15160-seq

No Reproducible Arrows Found

Sense Strand Reads

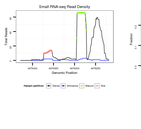
Hide Sp reads | Show read mismatch reads

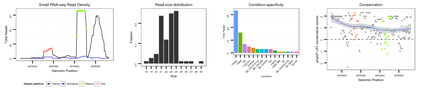
| | | |

ID	Confidence	Confidence	Class	Genomic Locus
chbtch177188 : chrX:49762618-49763379 : -	Known Orthologs	Intron	Intron	Other and UCSC Genome Browser (Local Mirror)

Legend: **Intron** **Exon** **Known Orthologs** **Known Orthologs**

Predicted structure





Show Minimum Inputs

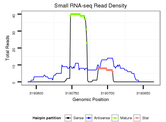
Picture annotation

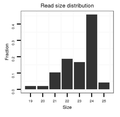
H:AQ:eyJ3b2JiIjp7IlRlbXAiOjIsIm9waWNpdHkiOjAuMjUsIlRlbXAiOjIsIiAgIiAgIiAg

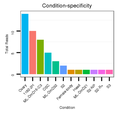
ID	Coordinate	Confidence	Class	Genome Locale
sblock1755500	**chrX:31906685-31907627 +**	**Known Orthologs**	**antisense_to_intron**	**antisense_to_intron**

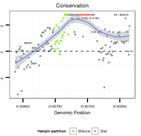
Legend: Mature Hairpin Flanking Sequence Structure

Predicted structure









Show Alternate Folds

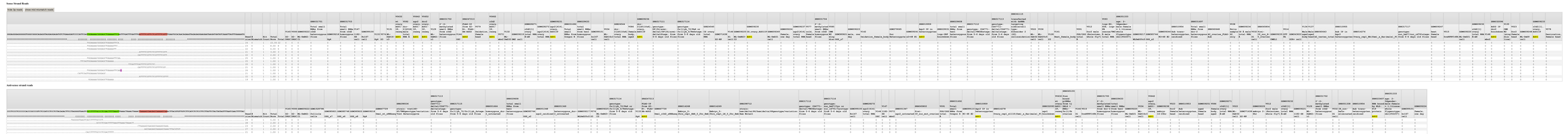
Flybase annotation

bocaljcan:[flyTS:FBTR0130563] Anticoding to intron:[dm-ad], Anticoding to intron:[dm-ad], Anticoding to intron:[dm-ad], Anticoding to intron:[dm-ad], Anticoding to intron:[dm-ad], Anticoding to intron:[dm-ad], Anticoding to intron:[dm-ad], Anticoding to intron:[dm-ad]

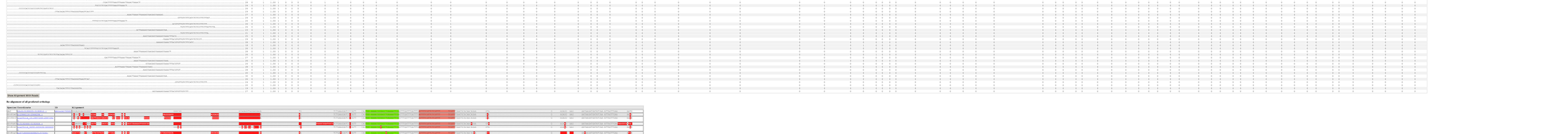
No Repeatmiler element found

Some Strand Reads

Sort By reads show mid mismatch reads

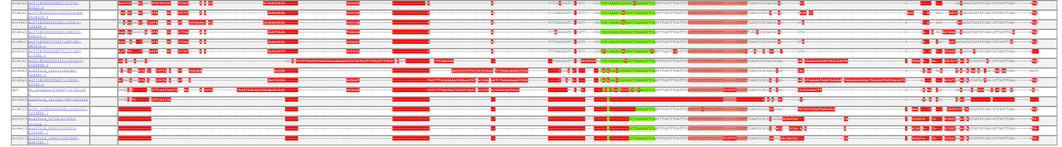


Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs



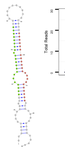
Generated 2019-09-24 at 12:56 AM

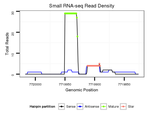
ID	Candidate	Class	Genome Count
vblock41610|chr28:7719876-7719967 -	**Known Ortholog**	**intron**	**intron**

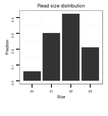
[View on UCSC Genome Browser (Local Mirror)]

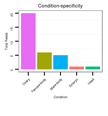
Length: **92** | **GC: 0.5435** | **Score: 0.7**

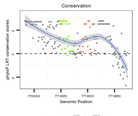
Predicted structure











Show Alternate Folds

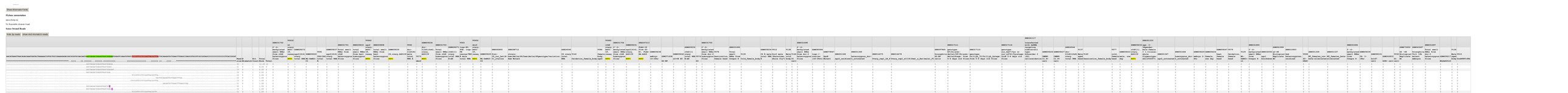
Flybase annotation

intra (3e-ln)

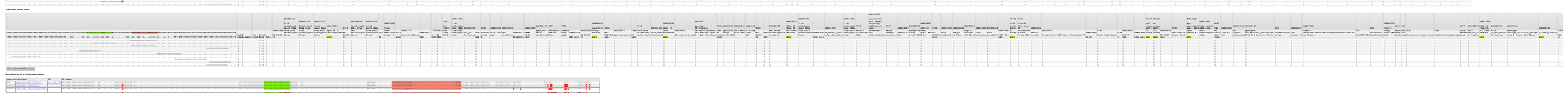
No flyanatomic clusters found

Sense Strand Reads

Hide 26 reads | Show mid mismatch reads

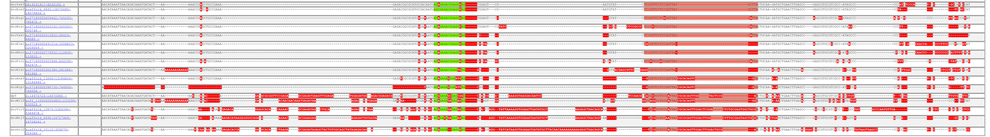


Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs



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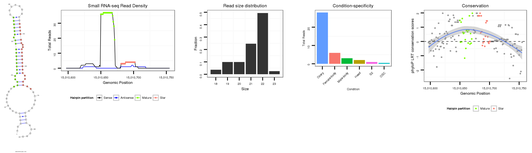
ID	Coordinate	Confidence	Class	Genome Locus
sblock2397585	**chrX:15010647-15010705 +**	**Known Orthology**	**intergenic**	**intergenic**	Chen and Chi, Genome Biology (2148)(2021)

Legend: Exon Intron Upstream Downstream

Predicted structure



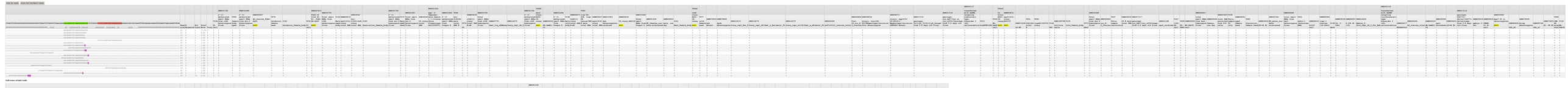
Show Alternative Folds

Flybase annotation

Drosophila melanogaster
Version(s)/Date(s)r6.54 Jul 2022

Some Overall Reads

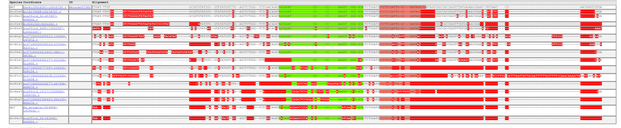
Sort By Reads | Hide Hit Mismatch reads



Self-cross overall reads

Show Alignment With Reads

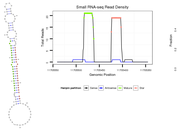
Re-alignment of all predicted orthologs

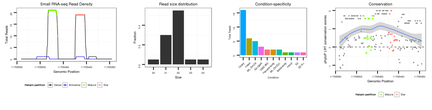


ID	Confidence	Confidence	Class	Genomic Locus
chlack45286_chr28:11705395-11705491 - Known OrthoDB	**interspecies**	**intronic_to_intron**		chr28:11705395-11705491

Length: 96 | 5' Flank: 20 | Core: 56 | 3' Flank: 20

Predicted structure:





Show Alignment Table

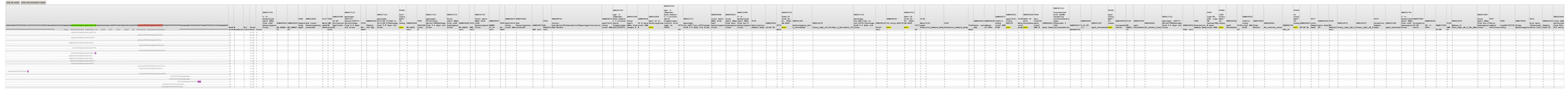
Fit Sites annotation

Fit Sites annotation

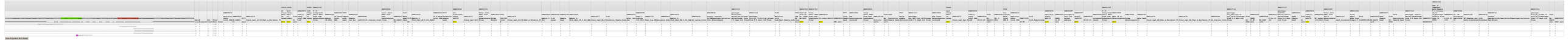
No Sites with a score > 0.0

Intra Strand Reads

Hide Sequence Show Full Alignment Hide Reads



Anti-sense strand reads



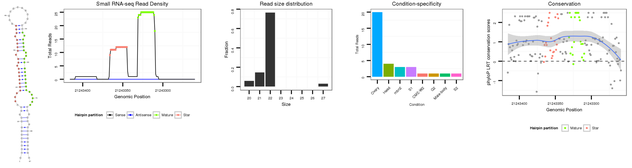
Show Alignment With Reads

Re-alignment of all predicted orthologs

ID	Coordinate	Confidence	Class	Genome Locale	
dme_196	**chr3R:21243310-21243366** +	**confident**	**Canonical miRNA**	**intron**	(View on UCSC Genome Browser (Local Mirror))

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

Predicted structure



Show Alternate Folds

Flybase annotation

mirna:Dme-mir-iab

No flyanatomy element found

Sense Strand Reads

Hide Sp-miRNA | Show 400 mismatch reads

Anti-sense strand reads

Show Alignment With Reads

Re-alignment of all predicted orthology

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