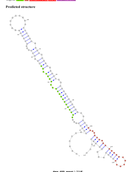
ID	Coordinates	Confidence	Class	Genomic Locus
dme_409	**chr3R:18559940-18560080 -**	**candidate-rescued**	**Canonical miRNA**	**CDS**

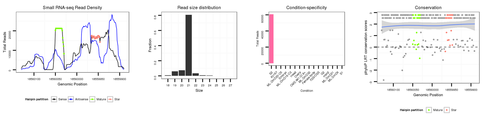
Click on GENE Genome Browser (Locus/GBrowse)

Legend: 5p 3p Terminal loop Mature Star

Predicted structure



dme_409_pred | 51nt



Show Alternate Folds

Flybase annotation

CR31541 | chr3:18559_409_dme(+)

5x Drosophila sources hsa2

Sense Strand Reads

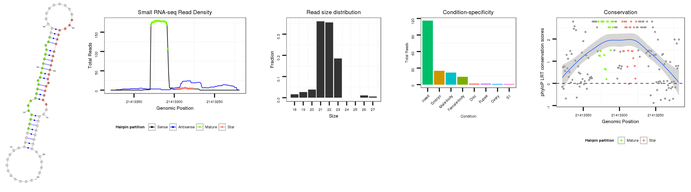
Hide Sp reads | Hide mid mismatch reads

| Sp | Coordinate | Strand | Length | Reads | Sense | 5p Offset | 5p Seq | 3p Offset | 3p Seq | Mid Mismatch | Mid Mismatch Count | Mid Mismatch Positions | 3p Trimmed | 5p Trimmed | Terminal Loop | Sense Start | Sense End | Sense Seq | Sense Qual | Sense Mapq | Sense Nh | Sense Nm | Sense Nmd | Sense Jc | Sense Jd | Sense Ih | Sense Ni | Sense Vp | Sense Vq | Sense Vc | Sense Xs | Sense Ts | Sense Rg | Sense Rx | Sense Cb | Sense Ub | Sense Cr | Sense Cy | Sense Ur | Sense Uy | Sense Hi | Sense Mc | Sense Md | Sense Nn | Sense Pa | Sense Pm | Sense Pn | Sense Pq | Sense Pr | Sense Ps | Sense Pt | Sense Qa | Sense Qb | Sense Qc | Sense Qd | Sense Qe | Sense Qf | Sense Qg | Sense Qh | Sense Qi | Sense Qj | Sense Qk | Sense Ql | Sense Qm | Sense Qn | Sense Qo | Sense Qp | Sense Qq | Sense Qr | Sense Qs | Sense Qt | Sense Qu | Sense Qv | Sense Qw | Sense Qx | Sense Qy | Sense Qz | Sense Ra | Sense Rb | Sense Rc | Sense Rd | Sense Re | Sense Rf | Sense Rh | Sense Ri | Sense Rj | Sense Rk | Sense Rl | Sense Rm | Sense Rn | Sense Ro | Sense Rp | Sense Rq | Sense Rr | Sense Rs | Sense Rt | Sense Ru | Sense Rv | Sense Rw | Sense Rx | Sense Ry | Sense Rz | Sense Sa | Sense Sb | Sense Sc | Sense Sd | Sense Se | Sense Sf | Sense Sg | Sense Sh | Sense Si | Sense Sj | Sense Sk | Sense Sl | Sense Sm | Sense Sn | Sense So | Sense Sp | Sense Sq | Sense Sr | Sense Ss | Sense St | Sense Su | Sense Sv | Sense Sw | Sense Sx | Sense Sy | Sense Sz | Sense Ta | Sense Tb | Sense Tc | Sense Td | Sense Te | Sense Tf | Sense Tg | Sense Th | Sense Ti | Sense Tj | Sense Tk | Sense Tl | Sense Tm | Sense Tn | Sense To | Sense Tp | Sense Tq | Sense Tr | Sense Ts | Sense Tt | Sense Tu | Sense Tv | Sense Tw | Sense Tx | Sense Ty | Sense Tz | Sense Ua | Sense Ub | Sense Uc | Sense Ud | Sense Ue | Sense Uf | Sense Ug | Sense Uh | Sense Ui | Sense Uj | Sense Uk | Sense Ul | Sense Um | Sense Un | Sense Uo | Sense Up | Sense Uq | Sense Ur | Sense Us | Sense Ut | Sense Uu | Sense Uv | Sense Uw | Sense Ux | Sense Uy | Sense Uz | Sense Va | Sense Vb | Sense Vc | Sense Vd | Sense Ve | Sense Vf | Sense Vg | Sense Vh | Sense Vi | Sense Vj | Sense Vk | Sense Vl | Sense Vm | Sense Vn | Sense Vo | Sense Vp | Sense Vq | Sense Vr | Sense Vs | Sense Vt | Sense Vu | Sense Vv | Sense Vw | Sense Vx | Sense Vy | Sense Vz | Sense Wa | Sense Wb | Sense Wc | Sense Wd | Sense We | Sense Wf | Sense Wg | Sense Wh | Sense Wi | Sense Wj | Sense Wk | Sense Wl | Sense Wm | Sense Wn | Sense Wo | Sense Wp | Sense Wq | Sense Wr | Sense Ws | Sense Wt | Sense Wu | Sense Wv | Sense Ww | Sense Wx | Sense Wy | Sense Wz | Sense Xa | Sense Xb | Sense Xc | Sense Xd | Sense Xe | Sense Xf | Sense Xg | Sense Xh | Sense Xi | Sense Xj | Sense Xk | Sense Xl | Sense Xm | Sense Xn | Sense Xo | Sense Xp | Sense Xq | Sense Xr | Sense Xs | Sense Xt | Sense Xu | Sense Xv | Sense Xw | Sense Xx | Sense Xy | Sense Xz | Sense Ya | Sense Yb | Sense Yc | Sense Yd | Sense Ye | Sense Yf | Sense Yg | Sense Yh | Sense Yi | Sense Yj | Sense Yk | Sense Yl | Sense Ym | Sense Yn | Sense Yo | Sense Yp | Sense Yq | Sense Yr | Sense Ys | Sense Yt | Sense Yu | Sense Yv | Sense Yw | Sense Yx | Sense Yy | Sense Yz | Sense Za | Sense Zb | Sense Zc | Sense Zd | Sense Ze | Sense Zf | Sense Zg | Sense Zh | Sense Zi | Sense Zj | Sense Zk | Sense Zl | Sense Zm | Sense Zn | Sense Zo | Sense Zp | Sense Zq | Sense Zr | Sense Zs | Sense Zt | Sense Zu | Sense Zv | Sense Zw | Sense Zx | Sense Zy | Sense Zz | Sense AA | Sense AB | Sense AC | Sense AD | Sense AE | Sense AF | Sense AG | Sense AH | Sense AI | Sense AJ | Sense AK | Sense AL | Sense AM | Sense AN | Sense AO | Sense AP | Sense AQ | Sense AR | Sense AS | Sense AT | Sense AU | Sense AV | Sense AW | Sense AX | Sense AY | Sense AZ | Sense Ba | Sense Bb | Sense Bc | Sense Bd | Sense Be | Sense Bf | Sense Bg | Sense Bh | Sense Bi | Sense Bj | Sense Bk | Sense Bl | Sense Bm | Sense Bn | Sense Bo | Sense Bp | Sense Bq | Sense Br | Sense Bs | Sense Bt | Sense Bu | Sense Bv | Sense Bw | Sense Bx | Sense By | Sense Bz | Sense Ca | Sense Cb | Sense Cc | Sense Cd | Sense Ce | Sense Cf | Sense Cg | Sense Ch | Sense Ci | Sense Cj | Sense Ck | Sense Cl | Sense Cm | Sense Cn | Sense Co | Sense Cp | Sense Cq | Sense Cr | Sense Cs | Sense Ct | Sense Cu | Sense Cv | Sense Cw | Sense Cx | Sense Cy | Sense Cz | Sense Da | Sense Db | Sense Dc | Sense Dd | Sense De | Sense Df | Sense Dg | Sense Dh | Sense Di | Sense Dj | Sense Dk | Sense Dl | Sense Dm | Sense Dn | Sense Do | Sense Dp | Sense Dq | Sense Dr | Sense Ds | Sense Dt | Sense Du | Sense Dv | Sense Dw | Sense Dx | Sense Dy | Sense Dz | Sense Ea | Sense Eb | Sense Ec | Sense Ed | Sense Ee | Sense Ef | Sense Eg | Sense Eh | Sense Ei | Sense Ej | Sense Ek | Sense El | Sense Em | Sense En | Sense Eo | Sense Ep | Sense Eq | Sense Er | Sense Es | Sense Et | Sense Eu | Sense Ev | Sense Ew | Sense Ex | Sense Ey | Sense Ez | Sense Fa | Sense Fb | Sense Fc | Sense Fd | Sense Fe | Sense Ff | Sense Fg | Sense Fh | Sense Fi | Sense Fj | Sense Fk | Sense Fl | Sense Fm | Sense Fn | Sense Fo | Sense Fp | Sense Fq | Sense Fr | Sense Fs | Sense Ft | Sense Fu | Sense Fv | Sense Fw | Sense Fx | Sense Fy | Sense Fz | Sense Ga | Sense Gb | Sense Gc | Sense Gd | Sense Ge | Sense Gf | Sense Gg | Sense Gh | Sense Gi | Sense Gj | Sense Gk | Sense Gl | Sense Gm | Sense Gn | Sense Go | Sense Gp | Sense Gq | Sense Gr | Sense Gs | Sense Gt | Sense Gu | Sense Gv | Sense Gw | Sense Gx | Sense Gy | Sense Gz | Sense Ha | Sense Hb | Sense Hc | Sense Hd | Sense He | Sense Hf | Sense Hg | Sense Hh | Sense Hi | Sense Hj | Sense Hk | Sense Hl | Sense Hm | Sense Hn | Sense Ho | Sense Hp | Sense Hq | Sense Hr | Sense Hs | Sense Ht | Sense Hu | Sense Hv | Sense Hw | Sense Hx | Sense Hy | Sense Hz | Sense Ia | Sense Ib | Sense Ic | Sense Id | Sense Ie | Sense If | Sense Ig | Sense Ih | Sense Ii | Sense Ij | Sense Ik | Sense Il | Sense Im | Sense In | Sense Io | Sense Ip | Sense Iq | Sense Ir | Sense Is | Sense It | Sense Iu | Sense Iv | Sense Iw | Sense Ix | Sense Iy | Sense Iz | Sense Ja | Sense Jb | Sense Jc | Sense Jd | Sense Je | Sense Jf | Sense Jg | Sense Jh | Sense Ji | Sense Jj | Sense Jk | Sense Jl | Sense Jm | Sense Jn | Sense Jo | Sense Jp | Sense Jq | Sense Jr | Sense Js | Sense Jt | Sense Ju | Sense Jv | Sense Jw | Sense Jx | Sense Jy | Sense Jz | Sense Ka | Sense Kb | Sense Kc | Sense Kd | Sense Ke | Sense Kf | Sense Kg | Sense Kh | Sense Ki | Sense Kj | Sense Kk | Sense Kl | Sense Km | Sense Kn | Sense Ko | Sense Kp | Sense Kq | Sense Kr | Sense Ks | Sense Kt | Sense Ku | Sense Kv | Sense Kw | Sense Kx | Sense Ky | Sense Kz | Sense La | Sense Lb | Sense Lc | Sense Ld | Sense Le | Sense Lf | Sense Lg | Sense Lh | Sense Li | Sense Lj | Sense Lk | Sense Ll | Sense Lm | Sense Ln | Sense Lo | Sense Lp | Sense Lq | Sense Lr | Sense Ls | Sense Lt | Sense Lu | Sense Lv | Sense Lw | Sense Lx | Sense Ly | Sense Lz | Sense Ma | Sense Mb | Sense Mc | Sense Md | Sense Me | Sense Mf | Sense Mg | Sense Mh | Sense Mi | Sense Mj | Sense Mk | Sense Ml | Sense Mm | Sense Mn | Sense Mo | Sense Mp | Sense Mq | Sense Mr | Sense Ms | Sense Mt | Sense Mu | Sense Mv | Sense Mw | Sense Mx | Sense My | Sense Mz | Sense Na | Sense Nb | Sense Nc | Sense Nd | Sense Ne | Sense Nf | Sense Ng | Sense Nh | Sense Ni | Sense Nj | Sense Nk | Sense Nl | Sense Nm | Sense Nn | Sense No | Sense Np | Sense Nq | Sense Nr | Sense Ns | Sense Nt | Sense Nu | Sense Nv | Sense Nw | Sense Nx | Sense Ny | Sense Nz | Sense Oa | Sense Ob | Sense Oc | Sense Od | Sense Oe | Sense Of | Sense Og | Sense Oh | Sense Oi | Sense Oj | Sense Ok | Sense Ol | Sense Om | Sense On | Sense Oo | Sense Op | Sense Oq | Sense Or | Sense Os | Sense Ot | Sense Ou | Sense Ov | Sense Ow | Sense Ox | Sense Oy | Sense Oz | Sense Pa | Sense Pb | Sense Pc | Sense Pd | Sense Pe | Sense Pf | Sense Pg | Sense Ph | Sense Pi | Sense Pj | Sense Pk | Sense Pl | Sense Pm | Sense Pn | Sense Po | Sense Pp | Sense Pq | Sense Pr | Sense Ps | Sense Pt | Sense Pu | Sense Pv | Sense Pw | Sense Px | Sense Py | Sense Pz | Sense Qa | Sense Qb | Sense Qc | Sense Qd | Sense Qe | Sense Qf | Sense Qg | Sense Qh | Sense Qi | Sense Qj | Sense Qk | Sense Ql | Sense Qm | Sense Qn | Sense Qo | Sense Qp | Sense Qq | Sense Qr | Sense Qs | Sense Qt | Sense Qu | Sense Qv | Sense Qw | Sense Qx | Sense Qy | Sense Qz | Sense Ra | Sense Rb | Sense Rc | Sense Rd | Sense Re | Sense Rf | Sense Rg

ID	Coordinate	Confidence	Class	Genome Locale	
dme_166	**chr3R:21413269-21413329 -**	**candidate-rescued**	**Canonical miRNA**	**antisense_to_intron**	View on UCSC Genome Browser (GeneID/Mirez)

Legend: Sense Antisense Mature Star

Predicted structure



Show Alternate Folds

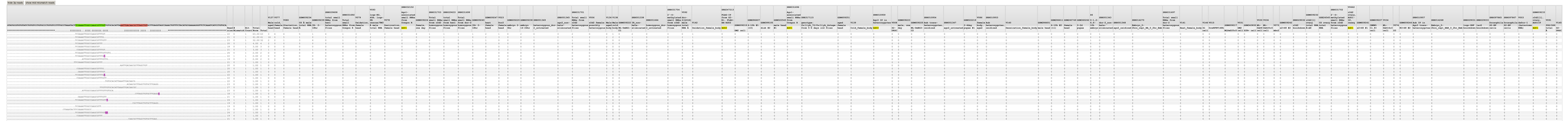
Flybase annotation

Inference is intron[no id], Inference is intron[no id], Inference is intron[no id]

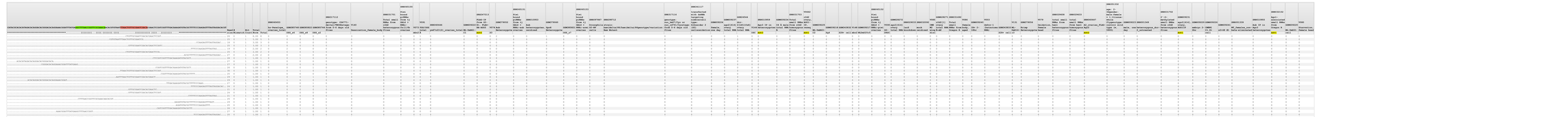
No Flypaddle cluster found

Sense Strand Reads

Sort by reads | show red mismatch reads



Anti-sense strand reads



Show Alignment With Reads

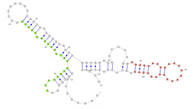
Re-alignment of all predicted orthologs

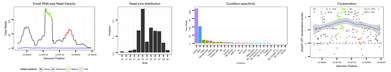
Generated 2019/05/24 at 03:01 AM

ID	Accession	Genome	Strand	Genome Coords
dme_398_chr3R:12164853-12164279	**;candidate-miscarf;Canonical miRNA;**	**hp1.V6**		chr3R:12164853-12164279 (Genome Browser, ExtraFetch)

Score: **0.000** **0.000** **0.000** **0.000** **0.000**

Predicted structure:





dme_398_annot [- 32.6]

Show/hide genome browser

Fetch sequences

dm6 (dme) 3'R:20-21 (+), (dme) 3'R:19-20 (+), (dme) 3'R:18-19 (+), (dme) 3'R:17-18 (+)

hp1.V6 (hp1.V6) Scaf1:1-1

Show/hide Scaffold

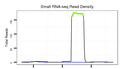
Hide Scaffold **Show 5'/3' Flanking Sequence**

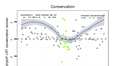
| | | |

ID	Coordinate	Confidence	Strand	Genome Length
dme_160 chr3R:24819412-24819471 -	**candidate-rescued**	**Metazoan**	**intron**	View on UCSC Genome Browser (GenomeMatch)

Legend: Stem Loop Terminal Loop Mismatch

Predicted structure





Show Structure Data

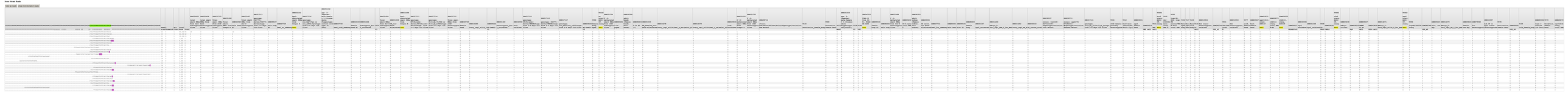
Flybase annotation

intersection (FB Genes and FB Exons)

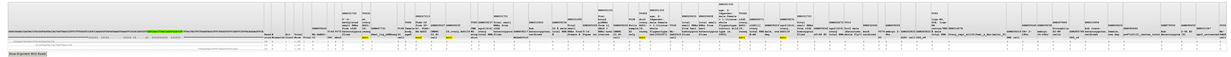
No Exon/Gene Linked Gene

Gene Sense Reads

Hide Sense | Show Sense Reads

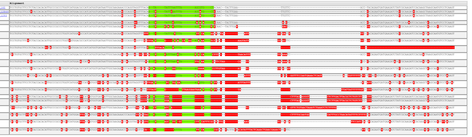


Anti-sense strand reads



Show Alignment Blocks Hexam

Bp alignment of all predicted orthologs

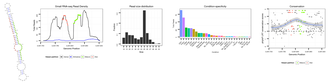


Date	Location	Weather	Operator
Wed, 17th Jan 01 - Sat, 17th Feb 01	Lambton County	Various (with ice)	Jim W.

Total Km	Total Hours	Average Speed
1,000.00 Km	1,000.00 Hours	1.00 Km/Hr

Legend: Excellent Good Average Poor Very Poor

Broken Connection



Show operator

Sat, 20th Jan 01 to Fri, 26th Jan 01 (7 days)

Total Distance: 1,000.00 Km

Total Duration: 1,000.00 Hours

Show Broken Connections

Show Operator Summary

Operator	Date	Start Time	Finish Time	Duration	Distance	Average Speed	Comments
Jim W.	Sat, 20th Jan 01	08:00	18:00	10.00	1,000.00	100.00	

Show Operator Summary

Operator	Total Hours	Total Km	Average Speed
Jim W.	10.00	1,000.00	100.00

Show Broken Connections

Broken Connection	Date	Start Time	Finish Time	Duration	Comments
Broken Connection	Sat, 20th Jan 01	08:00	18:00	10.00	

Show Broken Connection Summary

Broken Connection	Total Hours
Broken Connection	10.00

Show Operator Summary

Operator	Total Hours	Total Km	Average Speed
Jim W.	10.00	1,000.00	100.00

Show Broken Connection Summary

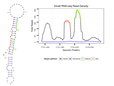
Broken Connection	Total Hours
Broken Connection	10

ID	Name	Description	Length	Type
1	hairpin		30	DNA

Hairp_ATT_dye-Dir-CTU-FHA-CTU-DCR | Length: 30 nt | Created: 2 months ago | Updated: 2 months ago | Access: Viewing | Modified: Editing | Access: Full Access

Total: 30 nt, 30 nucleotides, 0 pairs

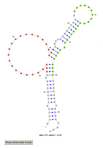
Predicted structure

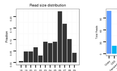


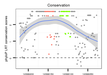
ID	Coordinate	Confidence	Class	Structural Motif
dme_417	chr31:12396075-12396172	candidate-conserved	Canonical miRNA	Apl TR

Strand: + Length: 98 Hairpin: 35 Stem: 21 Loop: 14 Mature: 21 Star: 21

Predicted structure







Hairpin positions: Stem Arm Loop Mature Star

Show Advanced Fields

Fitness annotation

Mut_count: 0 Pos:[0,0,0,0,0,0,0,0]

Fit: 0 p-value: 0 Sig: 0 Conf: 0.000

Tissue Overall Reads

Total: 0 Samples: 0

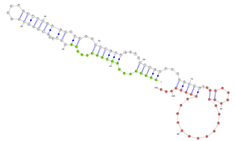
Show Tissue Details Show Hairpin Details

| | | |

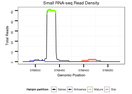
ID	Coordinate	Coordinate +	Size	Genome Locus	
dme_407	**chr2R:5788375-5788476**	**candidate**	**101**	**NDRX4**	**intron**

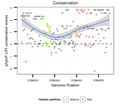
Genome: **dm6** on **Drosophila melanogaster**

Predicted structure:



dme_407_annot [-33.9]





Show Minimum Folds

FASTaim annotation

hairpin:chr2R:5788375-5788476:dme-mir-CR12344+dme-mir-CR12344+dme-mir-CR12344+

ID	Location	Confidence	Class	Strand	Score
dme_382	**chr38:9137261-9137361**	**candidate-reversal**	**Canonical miRNA**	**antisense_to_ENS**	Filter score 0.99, Genome Balance, Exclude Repeats

Sequence ACCCC

ID	Location	Candidates	Strand	Number Length
dme_38k_ufa38k.1:40291615-40292138	...	candidates removed	Canonical and GT/AG	524

Length: 524 GTAGCTCTCT

ID	Name	Cluster	Type	Genome size
dme_408_annot	**Dme_408_Chr3R:17467414..17467621 +	candidate consensus	Unassigned and 0%	1 Genome**	Drosophila melanogaster (taxid:7227)

Length: 208 (208 bp)

Total Copy number: 1 (1 copies)

dme_408_annot [- 66.2]

Alias consensus

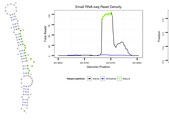
Alias annotation

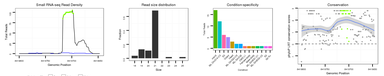
chr3:17467414-17467621:TTATGCTGCGCCGTTCGCGGCCGTCGCGGCGCGC

id	comment	confidence	flag	review level
dme_234 chr3R:8419697-8419750	**, candidate-removed_C-neutral mRNA v. intron**			Filter out CR, Create Review (Local Blast)

Score **-10.00** (**-10.00 / 0.00**) **[-10.00,-10.00]**

Predicted structure:





Show/hide alignment

Pfam domains

dmel2R:dmel2R:dm:gene:FBGN0261274:rna_gene:LTR:dm:Gmr:R1:

TE:Rootless:Jockey:Tc1

Gene Ontology

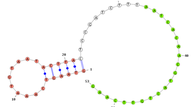
Hide GO terms Show term-enrichment matrix

| id | score | strand | ss | ss_ref | ss_ref_ref | ss_ref_ref_ref | ss_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref | ss_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref_ref

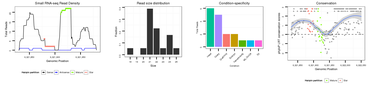
ID	Location	Strand	Length	Type
dme_399	chr2R:6321187-6321931	+	745	Intron

Length mod 3 = 2 (Intron length = 745 bases)

Predicted structure:



dme_399_amino (-2.8)



Hide Alignment Details

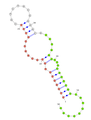
PRIMARY ALIGNMENTS

>chr2R:6321187-6321931 (+) [0:0,0,0,

ID	Locus	Candidates	Strand	Genome Length
dme_379	chr28:4220035-4220092	2 candidates covered	NEG's	Intron

Rfam: RF00379 - Intron group IIB

Predicted structure



MFE: 27.20 kcal/mol

Show structure help

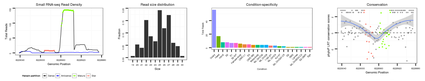
Primer assessment

Mean Tm 64.8°C (sd: 0.0°C) GC% 40.0 (sd: 0.0) MFE -4.0

Tm Score(0): 100.0 (sd: 0.0)

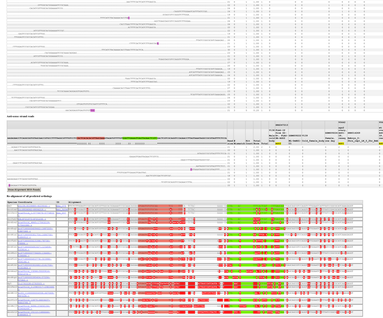
Gene Ontology

Hide GO terms Show GO terms and IDs



Sorted genome BAM Browser

Multiple alignment of all pre-miRNA in a Rfam family

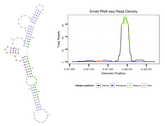


Consensus sequence

ID	Condition	Confidence	Class	Genome Locus
dme_406	chr X:8491906-8492812 >	condition-record	Canonical miRNA	intron

UCSC Genome Browser: chrX:8491906-8492812

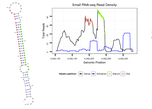
Predicted structure

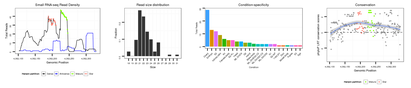


ID	Name	Kingdom	Size	Random Seed
dme_405_rfa/26:40621/52:40622380	**candidate-rescued_Canonical miRNA_CDS**	Eukaryota	1,759	1543141236, Sunday, November, 11,2018 9:00:36

Length **1759 NUCLEOTIDES - CONTINUE**

Predicted structure





Show INTERACTIVE

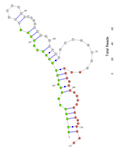
Hairpin sequence

CTGCGAT>ath_hairpin-405_dmel_bantam_dp:25:16:25:0:0:0

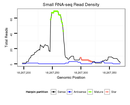
ID	Coordinates	Coordinates	Class	Genome Locus
dme_425	**chr/X:18267247-18267319 +**	**candidate-cocoat**	**MIRNA**	**novel**

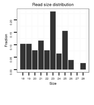
Legend: DICER HAIRPIN SEED MISMATCH

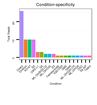
Predicted structure

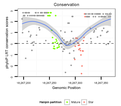


dme-X1-dme1-1R1









Show Minimum Folds

FlyBase annotation

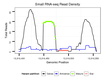
Hairpin:FlyBase:FBMI:FBM0017963, Hairpin:FlyBase:FBMI:FBM0017963, Hairpin:FlyBase:FBMI:FBM0017963, mature:FlyBase:FBMI:FBM0017964, mature:FlyBase:FBMI:FBM0017964, mature:FlyBase:FBMI:FBM0017964

id	condition	subfamily	Rfam	Sample Size
dme_42x_chr28:13516449-13516567 +	candidate-crossed	**NMWA-Intron**		2024-10-29, Double Bonus (CAMERMan)

Length: **119 nt** (**CAMERMan suggested**)

Predicted structure:

MFE: -50.10 kcal / mol



Show full-screen view

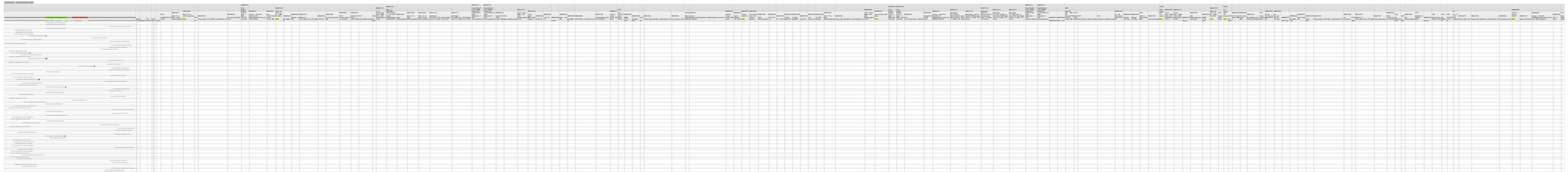
Flankers assembled:

5p flanker: chr28:13516394-13516422 (+) 5'hp: chr28:13516422-13516449 (+) loop: chr28:13516449-13516463 (+) 3'hp: chr28:13516463-13516490 (+) 3p flanker: chr28:13516490-13516518 (+)

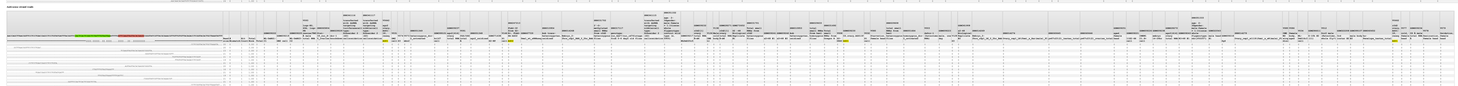
5p flanking sequence: ccccc 3p flanking sequence: ccccc

Hairpin Small RNA-seq

Show Small RNA-seq hairpin in Trackviewer



Alignment Small RNA-seq



Show alignment in IGV Browser

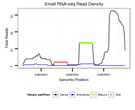
Per alignment of all gp-dme-x-chr28bp:

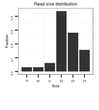
Generated MAMMOTH on 2024-10-29

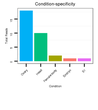
ID	Candidate	Coordinates	Size	Genome Locus
dme_431	**chr3R:24863516-24863579**	**-conditions-rescued**	**NORNA**	**mrom**

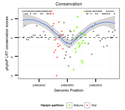
Legend: **Stem** **Loop** **5' Flank** **3' Flank** **mature/star**

Predicted structure:









Show Alignment Plots

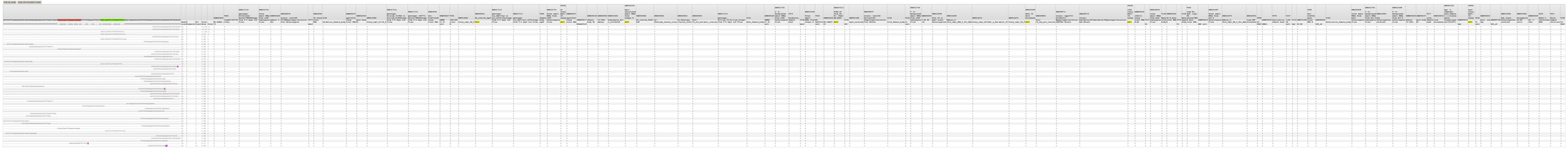
Filter accession

dme:DM1 dsi:CK00JM1 sdz:CK00JM1 vdr:CK00JM1

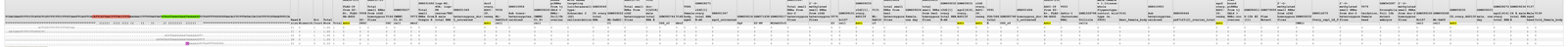
To Bundle-Unsure Food

Sense Strand Reads

Hide Sp Header | Show Hide Alternatch Header



Anti-sense strand reads



Show All Aligned With Reads

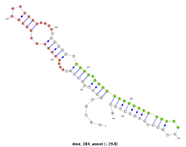
Multiple alignment of all predicted orthologs

Species	Coordinates	ID	Alignment
dme	chr3R:24863516-24863579	dme_431	ACTGTTCGAGGACGTCTGCGAGCGCGC

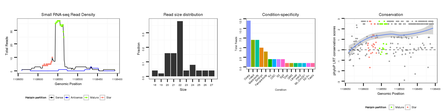
ID	Coordinate	Confidence	Class	Genome Locus
dme_384 chr3R:11108456-11108591 -	**candidate-rescued**	**Canonical miRNA**	**intron**	chr3R:11108456-11108591 (-) (Genome Browser) (Ensembl Browser)

Length: 136 bp | Strand: - | Arm: 3p | Loop: 4 nt

Predicted structure:



dme_384_amot (-29.8)



Show Structure Tools

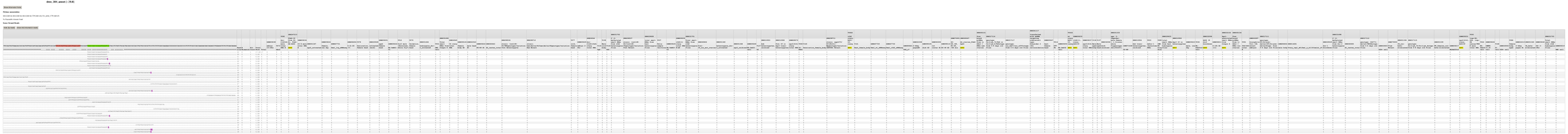
Fictious annotation

Annotation accession: dme-mir-384-3-1-TR-1340-1441-1-1-1, gene_1-TR-1340-1441

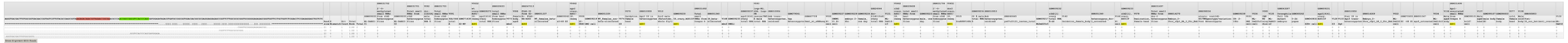
No Bulgeminer character found

Some Overall Blocks

Hide Tip Labels Show Child Alignment Details



Self-score overall vsulb



Show Alignment Block Details

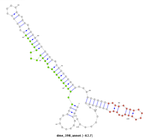
Re-alignment of all predicted orthologs

Generated 2026-05-01 at 21:05:-08

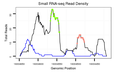
ID	Coordinates	Confidence	Type	Genomic Locus
dme_398	chr3L:16004487-16004598 (-)	candidate-rescued	Canonical miRNA	CDS

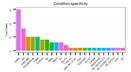
Flank: 60nt up 60nt down

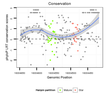
Predicted structure



dme_398_mature (-) 42,37







Show Advanced Scroll

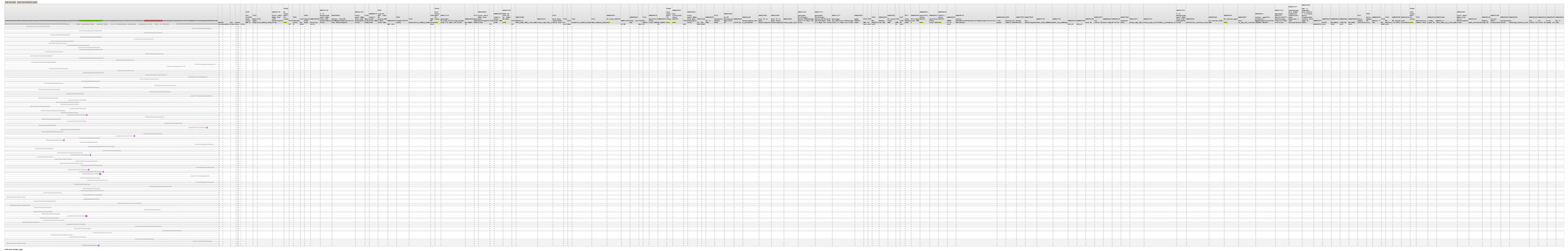
Flybase annotations

1 Exon(s)

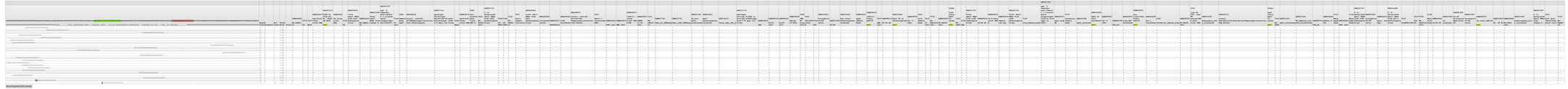
No Available Jackrab Scaff

Name Sorted Reads

Hide Sp Hairpin | Show Not Aligned Hairpin

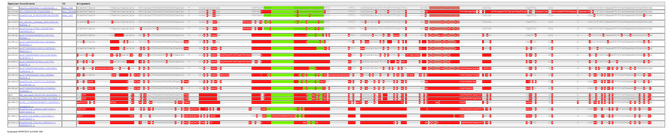


Sub-score dot-dot-rank



Show Alignment Sort Rules

Alignment of all pri-miRNA sRNAs

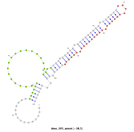


Generated 2019-09-23 at 04:46, JBB

ID	Confidence	Strand	Genome Location
dme_399	**candidate-rescued**	**Canonical miRNA**	**chr3R:9921075-9921205**

Score: **100.00** [0 | 0 | 100] **100.00%**

Predicted structure



dme_399, score: 100.00

Show Structure Image

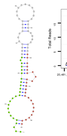
Pri-miRNA sequence

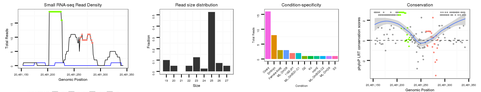
dme_399:2:79:20:-:gi|10|+|dme_gene:2:79:20:-:gi|10|dme_gene:2:79:20:-:gi|10|dme_gene:2:79:20:-:gi|10

ID	Coordinate	Confidence	Class	Genome Locus
dme_423	**chr3R:20481203-20481293 +**	**candidate**	**MIRNA**	**intron**

Legend: Exon Intron Mature Star Hairpin

Predicted structure:





Show Alignments Table

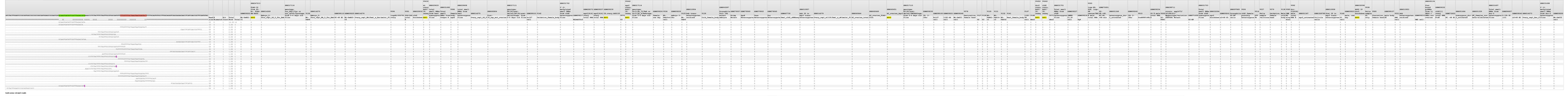
Fixture annotation

MIR12:FBMI:dme_CR12:FBMI:FlyBase_CR12:FBMI:FlyBase_

Target Gene Ontology

Hairpin Reads

Hide 10 reads | Show AND MISMATCH reads



Add-none strand reads

Show Alignment With Reads

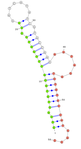
Re-alignment of all predicted orthologs

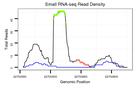
Generated 2019-06-21 at 17:41 PM

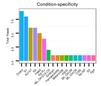
ID	Candidate	Candidate	Size	Genome Locus
dme_416	**chr38:22700824-22700895**	**candidate-rescued**	**MIRNA**	**intron**

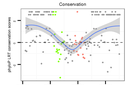
Strand: + - Predicted by ALL tools Predicted by two tools

Predicted structure:









Show Alternate Folds

Flybase annotation

dme-MIR-iab-4 (FB:MIR:FBrf0114842) (FB:SNR:FBrf0114842) (FB:SNR:FBrf0114842) (FB:SNR:FBrf0114842) (FB:SNR:FBrf0114842)

No Repeatmasker Overlap Found

Same Strand Reads

Hide Tic reads Show 500 Mismatch reads

Anti-sense strand reads

Show Alignment With Reads

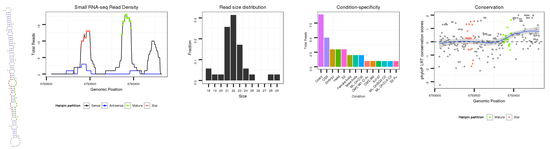
Re-alignment of all predicted orthologs

Species	Coordinates	ID	Alignment
dmel	chr38:22700824-22700895(+)	FBrf0114842	
dsim	chr38:22700824-22700895(+)		
dsec	chr38:22700824-22700895(+)		
dyak	chr38:22700824-22700895(+)		
dere	chr38:22700824-22700895(+)		
dvir	chr38:22700824-22700895(+)		
dpse	chr38:22700824-22700895(+)		
dpse	chr38:22700824-22700895(+)		
dpse

Dr	Coordinate	Coordinate	Class	Female Locus
dme_435	**chr21:6793585-6793539 -**	**candidate-rescued**	**Canonical miRNA**	**intron**

Legend: [illegible] **Dme_435_3p** [illegible]

Predicted structure



Show Alternate Folds

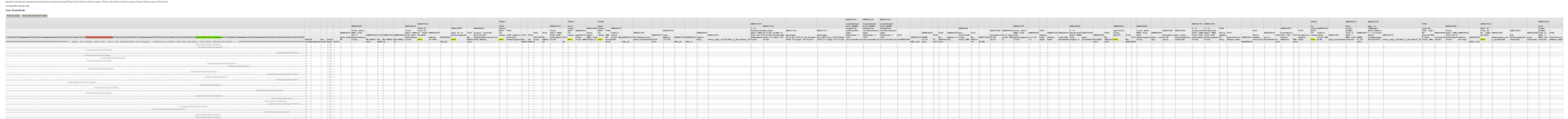
Flybase annotation

mmu-let-7a1 mmu-let-7a2 mmu-let-7a3 mmu-let-7b1 mmu-let-7b2 CR9 [mt:1:cds] CR9 [mt:1:exon] fru_pma_1TR [mt:1:cds] fru_pma_1TR [mt:1:exon]

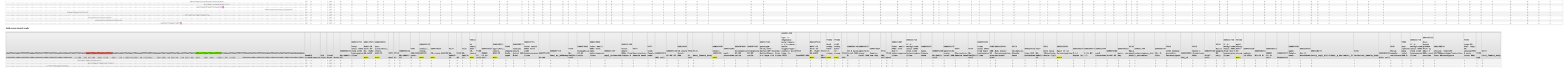
No Repeatmasker elements found

Name Variant Reads

Note 3p reads show mid-mismatch reads



Anti-sense strand reads



Show alignment MSA Reads

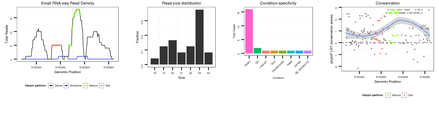
Re-alignment of all predicted orthologs

Generated 2020-09-24 at 02:36 -0400

ID	Coordinate	Confidence	Class	Strand/Length
dme_303	**chr28:+:15620295-15565311**	**candidate/rescued**	**Canonical miRNA**	**intron**

Legend: **Mature** **Loop** **Hairpin extension** **Flank**

Predicted structure



Show Alternative Folds

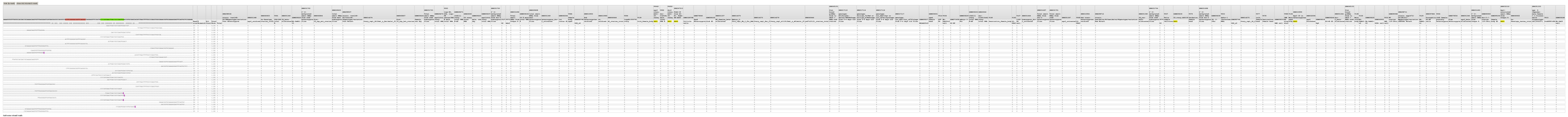
FUSion annotation

miRNA:Dmg:CTR3:FUSION:+:chr2:15620295-chr2:15620295-chr2:15620295-chr2:15620295-chr2:fus_gene_CTR:FUSION:+chr2:fus_gene_CTR:FUSION:+chr2:fus_gene_CTR:FUSION:+chr2:fus_gene_CTR:FUSION:+chr2:

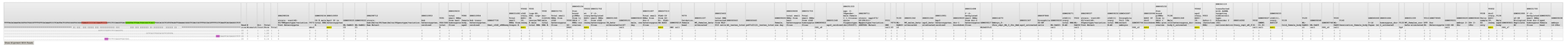
Vs. Expectable Junction Total:

Vector Overall Reads

Hide Vp reads | Show NM MISMATCH reads

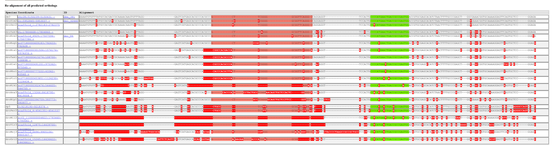


Sort vector strand reads



Show Ungrouped SEQ Reads

Re-alignment of all predicted reliables



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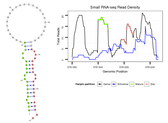
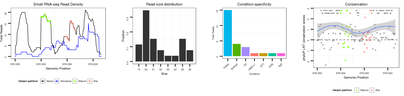
ID	Coordinate	Condition	Size	Genome Length
dme_433	**chr3L:5761234-5761300**	**combine-crossed**	**50bNA**	**intron**

Flags: **MERGED** **FORWARD** **REVERSE** **HAS_INTRON**

Predicted structure





Show Structure Code

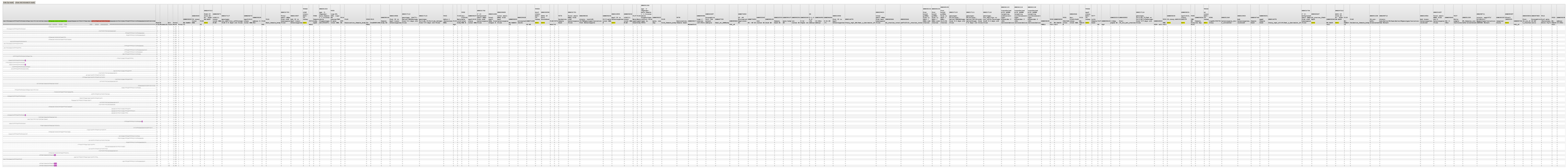
Fold Stats - annotation

structure=hairpin;mfe=-27.00;pfunc=1.00;ref=-27.00;alt=NA;delta=0;length=66;_stack_lectures_ids_0%3Ac_0%3Ab_0%3Ad_0%3Ae=NA%3BNA

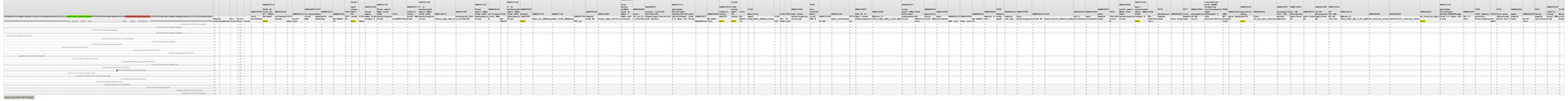
To Scientific Genome Code

Trans Strand Reads

Hide Sp Reads | Show Not Homologs Reads

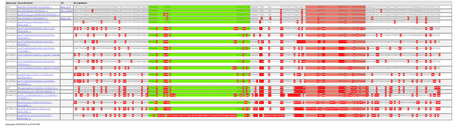


Anti-sense strand reads



Show Expanded MSA Reads

Sp alignment of all predicted orthologs

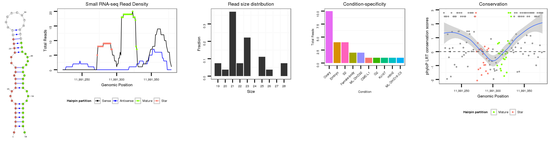


Generated 2026-06-23 at 07:58:56

ID	Condition	Condition-1	Chr	Genome Loc
dme_429 | chr2L:11991272-11991329 +	**candidate-rescued**	**MIRNA**	**intron**	Flybase|UCSC Genome Browser|GenomeBrowse

Legend: DICER 5' DICER 3' MIRNA PRIMARY

Predicted structure



Show Alternate Folds

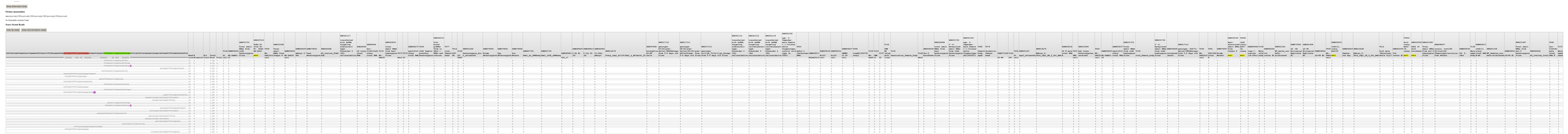
Fisher assessMiRna

intron (sum adj.CDR (sum)|adj.CDR (sum)|adj.CDR (sum)|adj.CDR (sum)|adj.

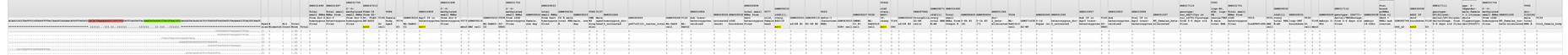
No Repeats-check-free!

Sense Strand Reads

Hide 3p reads | Show mid mismatch reads



Anti-sense strand reads



Show Alignment With Reads

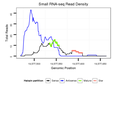
Re-alignment of all predicted orthologs

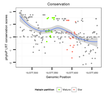
ID	Coordinate	Strand	Source Type
dme_414_chr3:19577319-19577614	**chr3:19577319-19577614**	**+**	**candidate-rescued_5-neutral-mRNA**

Genome	Source Version
dmelanogaster_r6_Apr_FB	Other ucsc2fb Genome Browser (Local Mirror)

Flank: **GGCGCG** **CCGCGC** **GGGCGCGCGC**

Predicted structure





Show Alignment(0/48)

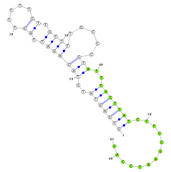
Fichas anonimas

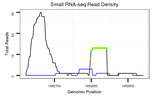
Analysis Date:2025-08-13 08:11:00PM, Valorous no seqpacutoffs, chrom_sections, (as of May 1 2014) (1:1:0:0:1:0:1:0:1), Sacagna dp:Flat:1:0:0:0:0:1:0:0:0:1:0:1:0:1

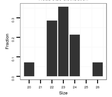
ID	Coordinate	Confidence	Class	Genome Locus
dme_387	chr3L:16652629-16652689 +	candidate-rescued	MIRNA	intron

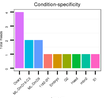
Score: 0.000 (0.000 to 0.000) Mature arm: 5p

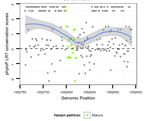
Predicted structure











dme_387_mature | 5:4

Show Alternate Fields

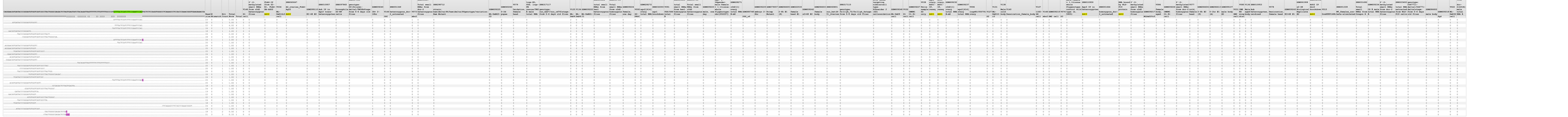
Flybase annotation

intron(FCR7wg:CR0:2:7967-cds):CR:2:5767-cds

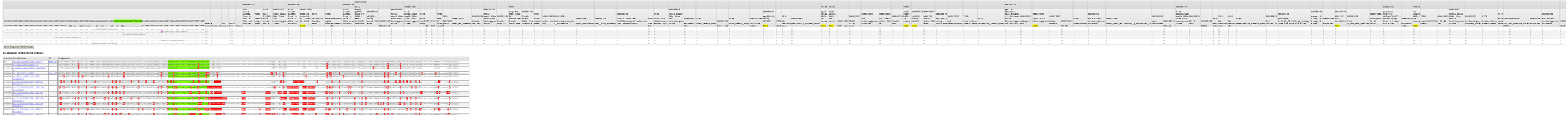
No Repeatds clusters found

Some Strand Reads

Sort by reads | show red mismatch reads



Anti-sense strand reads



Show Alignment With Reads

Re-alignment of all predicted orthologs

Generated: 09/08/2021 at 07:09 PM