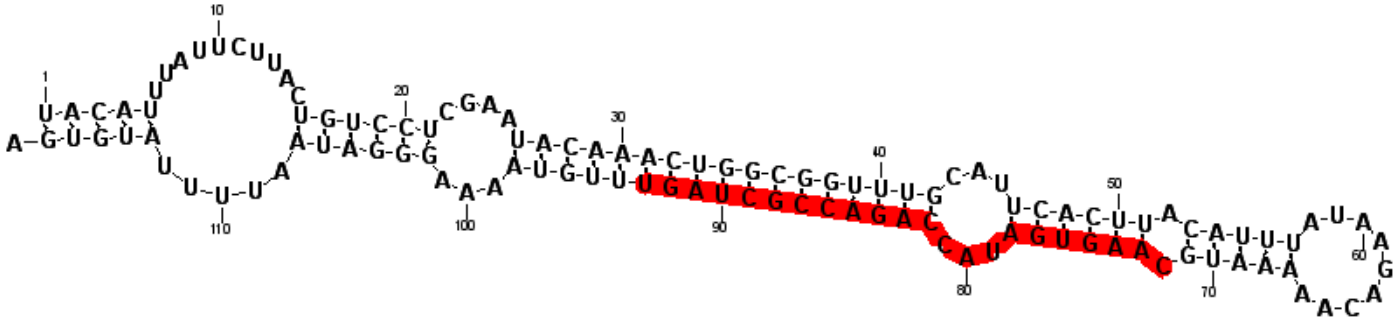
Supplemental Figure 8. Novel *C. elegans* miRNAs.

block8153 [novel_cloningOK_randfoldOK]

Hairpin parameters

miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.50/0.50	22/22/1.00	0.0	0.0	6	0	1	0	25	5	3arm	1	nd	0.14	3	6	1	na	na



```
                                                                                                                                                                  reads   miRBase family seed
seed            ------------------------------------------------------------------------------------AAGUGAU-------------------------------------------   6       novel
                                                                                                                                                                  len     cloning frequencies
                                                                                                                                                                          CE1
                ------------------------------------------------------------------------------------CAAGTGATACCAGACCGCTAGT-------------------------   22      6
celegans        TACATTTATTCTTACTGTCCTCGAATACAAACTGGCGGTTTGCAT--TCACTTACATTT-----ATAAGACAA-----AAATGCAAGTGATACCAGACCGCTAGTTTGTAAAAGGGATAATTTTATGTGA
cremanei        --------------GCATACATGAATTTCTTCCAGACATTTGTGC--TTTAGCAGATATAACCATTAATGCAG-----CAAAGAAAGTGATC----------------TGGTAGAGGAATGTA-------
cbriggsae       --------------GTGCGTAGAAAATTATGATAACATTTGGAATTATTGTTTAAAGTT-----TGGAAGAAGACACACAAAACAAGTGATC----------------CGGAAAATGTTATCG-------
cjaponica       -----------------------AATTTTTG---GCTATTAGCCG--TCGATT-----------TCAATGCAACTGCCAAATTCAAGTGATGGC--------------TAATAGCCAAAAATT-------
ppacificus      ----------------------------TGGCTGCTGTCAGCAT--TCCTTCTCTTGT-----TCGAGACAA-----AAAGTGAAGTGATC-------------------AACTGATCAGCTC------
                                                          *  *     *                 *   *       **   *******                     *
celegans        (((((.........((((((....(((((((((((((((...  ((((((.(((((     .........     )))))./////////...)))))))))))))))))...//////.....))))))).   0.930 -42.46
cremanei                   ...(((((...(((((.(((((((((.(((  (...((((.............)))))     ))....)))))./))                 )))./////////.)))))        0.999 -22.44
cbriggsae                  ................((((((((((((....((((((...(((     (......))))).....//////....))                 ))...)))))))))).        0.968 -17.10
cjaponica                           ((((((((   ((((((((((  ((.(((           (.(((((....))).../////////.))))))))))              ))))))))))))))        0.999 -32.00
ppacificus                                .(((((..((((((...  ((((((.((((..     .........     .))).)))).)))..                    ..)))))))))).        0.997 -16.80
```

celegans	chromosome:X:1390843:1390960:1	intergenic ## {SimpF: WRM0636bA02 1 fosmid,WRM0639aA01 1 fosmid,WRM064cE08 1 fosmid,WRM063cH01 1 fosmid,WRM0629aD05 1 fosmid,WRM0638dE02 1 fosmid,WRM0625bG09 1 fosmid}
cremanei	chromosome:chrUn:40953794:40953879:1	Opposite_strand|Exonic_coding|NM_062585 ## Same_strand|Intronic_coding|NM_062681
cbriggsae	chromosome:chrX:7915695:7915782:-1	Same_strand|Intronic_coding|NM_133381
cjaponica	chromosome:chrUn:70185177:70185246:1	intergenic ## {SimpF: trf,trf}
ppacificus	chromosome:chrUn:121899751:121899908:1	Same_strand|Intronic_coding|NM_001080348 ## Opposite_strand|Intronic_coding|NM_213308