Supplemental Figure 10. Novel *C. remanei* miRNAs.

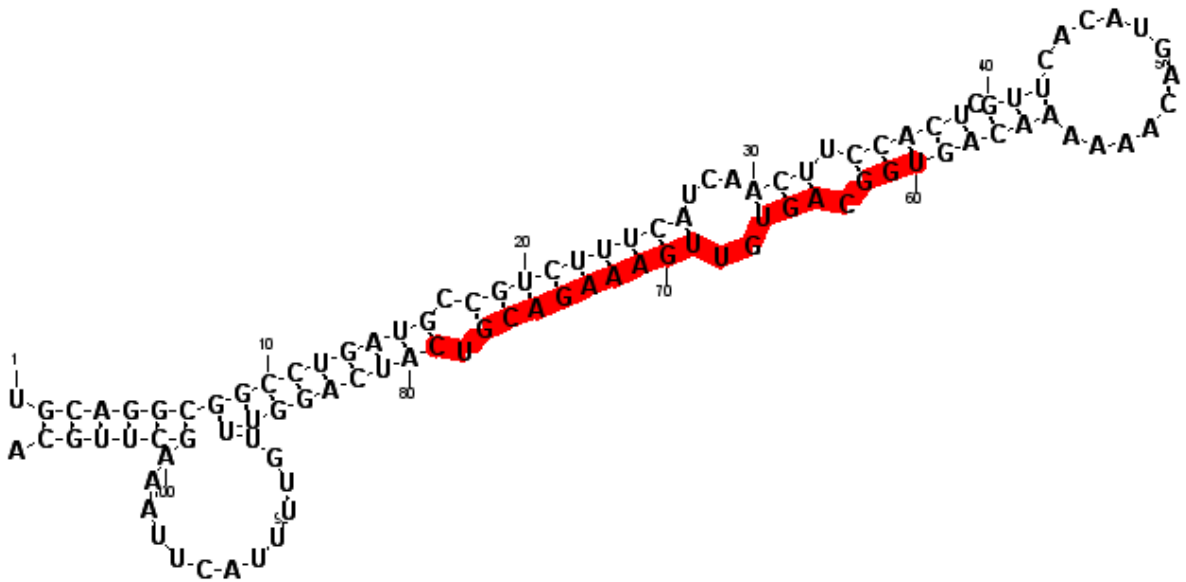
block990 [novel_cloningOK_randfoldOK]

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	0.45/0.50	19/22/0.88	0.0	0.0	6	0	1	0	28	5	3arm	1	nd	0.20	2	8	1	na	na

Families

Member of family miR-34 (seed GGCAGUG): cbr-mir-34, block990_novel



```
                                                                                                                reads   miRBase family seed
seed        ------------------------------------------------------------GGCAGUG----------------------------------------   8       miR-34
                                                                                                                len     cloning frequencies
                                                                                                                        EM464
            ------------------------------------------------------------TGGCAGTGTTGAAAGACGTC-----------------------------  20      6
            ------------------------------------------------------------TGGCAGTGTTGAAAGACGTCAT--------------------------  22      1
            ------------------------------------------------------------TGGCAGTGTTGAAAGACGT------------------------------  19      1
cremanei    tgcaggcggcctgatgccgtctttcatcaacttccactcgttcacatgacaaaaaacagTGGCAGTGTTGAAAGACGTCatcaggtttgttttacttaaagcttgca
            ****************************************************************************************************************
          ------------------------------------------------------------------------------------------------------------------ NM_060965
cremanei    .(((((((((((((((.(((((((((...(((.(((((.(((...........)))))))).)))..)))))))))).)))))))))).............)))))))).     0.540
                                                                                                                            -44.61
```

cremanei	chromosome:chrUn:63363025:63363131:-1	Opposite_strand|Intronic_coding|NM_060965|spr-5 ## {Repeats: no}

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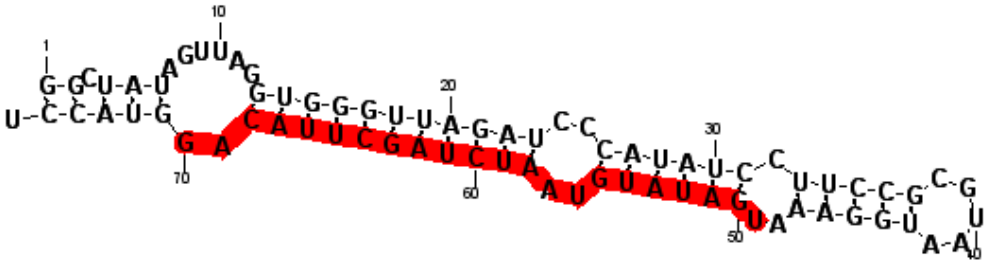
block1727 [novel_cloningHIGH_mirtron_randfoldOK]

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	0.002	no	no	0.26/0.32	19/22/0.89	0.0	0.0	25	0	1	0	6	6	3arm	1	0	0.18	2	37	1	na	na

Families

Member of family miR-50/62/90 (seed GAUAUGU): cbr-mir-90, cbr-mir-50, block1727_novel



```
                                                                                                                reads   miRBase family seed
seed        ------------------------------------------------------------------GAUAUGU----------------------------   37      miR-50/62/90
                                                                                                                len     cloning frequencies
                                                                                                                        EM464
            ------------------------------------------------------------------TGATATGTAA----TCTAGCT----TACAG------   22      25
            ------------------------------------------------------------------TGATATGTAA----TCTAGCT----TAC--------   20      7
            ------------------------------------------------------------------TGATATGTAA----TCTAGCT----TA---------   19      4
            ------------------------------------------------------------------TGATATGTAA----TCTAGCT----TACA-------   21      1
cremanei    GGCTATAGTTAGGTGGGTTAGATCCCATATCCTTC--------------CGCGTAATGGAAATGATATGTAA----TCTAGCT----TACAGGTACCT
ppacificus  --------------------GTTCCCGCACCCTTCTTTACATATCGTCTCGCTCGAGCGAGACGATATGTAAAGACCCTAGGGAAGATAAGGGAAC--
                                 * ****  * *****              ***   *  ** * *********     ****      **  ** **
            >>>>>>>>>>>>>>>>>>>>+++++++++++++++++++++          +++++++++++++++++++++++    +++++++    +++++>>>>>>>>>>>> NM_171786
            >>>>>>>>>>>>>>>>>>>>+++++++++++++++++++++          +++++++++++++++++++++++    +++++++    +++++>>>>>>>>>>>> NM_077717
cremanei    ((.(((.....(((((((((((..((((((.(((                ((.....)))))..)))))))..)    )))))))    )))..)))))).      0.890
                                                                                                                        -25.70
ppacificus                          ((((((...(((((((((((((((((((((....))))))))))))))))))))....))))).......))))))        0.955
                                                                                                                        -44.00
```

cremanei	chromosome:chrUn:111447780:111447855:-1	Same_strand|UTR_coding|NM_171786|ugt-50 ## {Repeats: no}
ppacificus	chromosome:chrUn:174340307:174340382:-1	intergenic

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block2421 [novel_cloningOK_randfoldOK]

Hairpin parameters

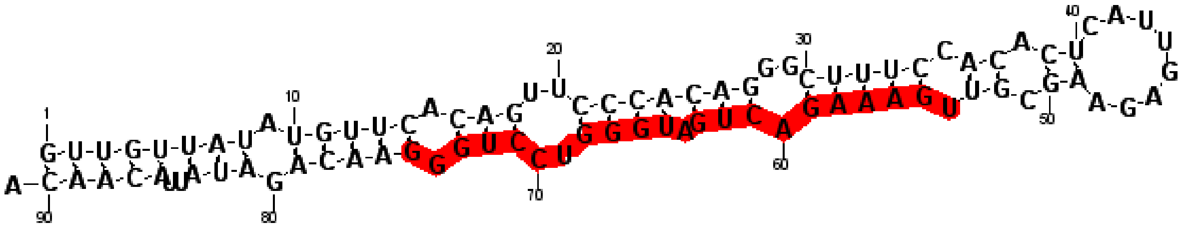
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.47/0.55	19/22/0.83	0.0	0.3	10	0	1	0	16	5	3arm	1	nd	0.23	2	12	1	na	na

Clusters

Located in cluster 5: block2421_novel, block2422_cand

Families

Member of family miR-71 (seed GAAAGAC): cbr-mir-71, block2421_novel



```
                                                                                                              reads   miRBase family seed
seed          ------------------------------------------------------GAAAGAC------------------------------   12     miR-71
                                                                                                              len     cloning frequencies
                                                                                                                            EM464
              -----------------------------------------------------TGAAAGACTGATGGGTCCTGGG----------------   22      7
              -----------------------------------------------------TGAAAGACTGATGGGTCCTGG-----------------   21      3
              -----------------------------------------------------TGAAAGACTGATGGGTCCT-------------------   19      2
cremanei      GTTGTTATATGTTCACAGTTCCCACAGGGCTTTCCACACTCATTGAGAAGCGTTGAAAGACTGATGGGTCCTGGGAACAGATATTACAACA
cbriggsae     ------AAAGGAT----------ACATTGCAATAAACATGAATTGAGGA-TGTAGAAAGAC-AATGTATACCTAG----------------
                    * * * *          ***  **  *  ***   ****** *  ** *******  ***  * *   *
          ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_057309
cremanei      (((((....(((((.(((..(((((((..(((((.((.((........)).)).))))).))).))))..))).)))))......))))).      1.000 -33.50
cbriggsae           ..(((((          ((((((......((((.........) ))).......) ))))))).)))..                     0.992 -11.02
```

cremanei	chromosome:chrUn:2910785:2910875:1	Same_strand|Intronic_coding|NM_057309|slou ## {Repeats: no}
cbriggsae	chromosome:chrX:15746922:15747052:-1	Same_strand|Intronic_coding|NM_001030307

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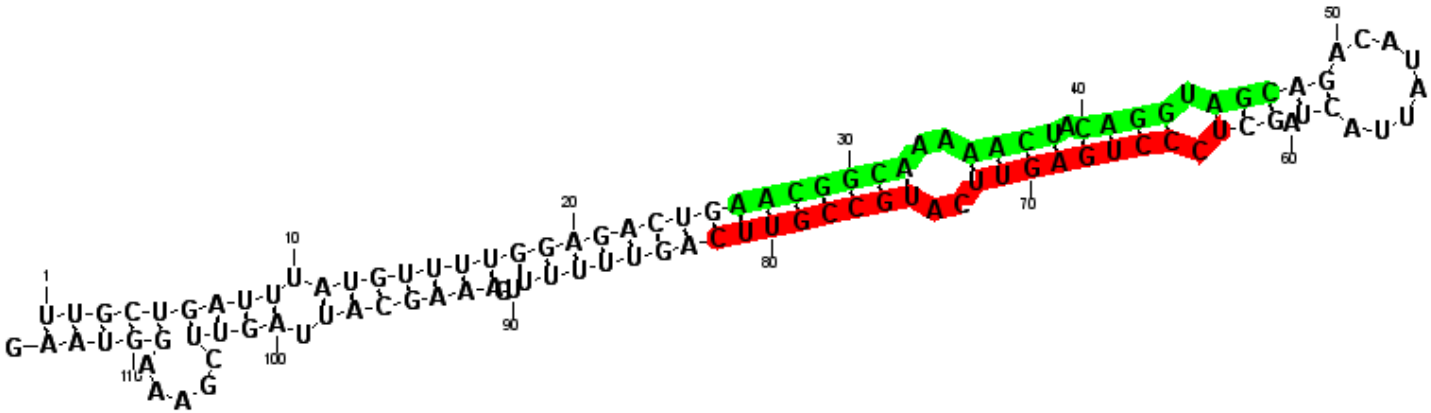
sblock45 [novel_cloningHIGH_multiarm_DicerOK_randfoldOK]

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	0.45/0.55	19/22/0.93	0.0 0.0	0.0 0.0	2 48	0 0	1 1	0 0	25 32	2 5	5arm 3arm	1 1	nd nd	0.18 0.15	2 2	54	1	2	1

Families

Member of family lin-4 (seed CCCUGAG): cel-mir-237, cbr-lin-4, sblock45_novel



```
seed      ------------------------------------------------------------------------------------------CCCUGAG-------------------------------------------
seed      -------------------------------------------ACGGCAA-------------------------------------------------------------------------------------------

          ------------------------------------------------------------------------------------------TCCCTGAGTTC-ATGCCGTTC-----------------------------
          ------------------------------------------------------------------------------------------TCCCTGAGTTC-ATGCCGTT------------------------------
          -------------------------------------------AACGGCAAAAACTAC-AGGTAGC-------------------------------------------------------------------------------
cremanei  ----------TTGCTGATTTATGTTTTG-------GAGACTGAACGGCAAAAACTAC-AGGTAGCAGACATA-TTACTAGC-------TCCCTGAGTTC-ATGCCGTTCAGTTTTTT------GAAAGCATTAGTTC
cbrenneri --------GCTTGCTTGAGAGAATCCAGGGGTACGGTCATAGTGCAACCAAA-------------------------------------TCCCTGAG-------------AATTTCTTATTTGCAAT-------CTTC
cjaponica --AGTAGAACCGCCTG----AAATTGAGCTGTACCGACACTTAACAGCCGGAACAACTCAACAACTTACTTATTTACTGGTTTGTGAGTCCCTGAGTTCTATTTCGTGCAGTGTTTTTCTCAATACAGCTCTATTTC
ppacificus AAACAAGAAGAGGCTGAGGAAAAATAAG--------------GACAATCGGAACCT--------------------------------TCCCTGAGTTT----------AGTCTCGTTT------------------
                      **            *               *      *                                 *******            * * *  *

cremanei            (((((((((.((((((((       (((((((((((((..((((.( (((.(((((..... ...)).))       ).)))))))). .)))))))))))))))).      .)))))))).)))).

cbrenneri         ..(((((.(((((((.(((((((((..(((.........)))..)                                  ))))))..)             ).))))))).....)))).       ....

cjaponica    (((((((((...(((    ((((.(((((((((..(.....((((((((((.((((((...((((((..(((....)))..))))))...))))))...))))))..))..))))....))..))))))))).))))))

ppacificus ((((.((((..(((((.(((.....(((              (..........)))                                ).))).)))))          ..))).))))
```

cremanei	chromosome:chrUn:103840413:103840526:-1	{Repeats: no}
cbrenneri	chromosome:chrUn:18512601:18512680:1	intergenic
cjaponica	chromosome:chrUn:130573784:130573927:1	intergenic
ppacificus	chromosome:chrUn:103937040:103937193:-1	Opposite_strand|Intronic_coding|NM_004535

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sblock79 [novel_cloningHIGH_multiarm_DicerOK_randfoldOK]

Hairpin parameters

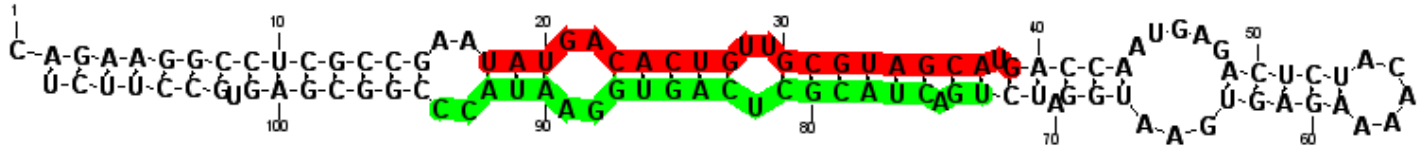
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.41/0.50	18/22/0.98	0.0 0.0	0.0 0.0	352 2	0 0	1 1	0 0	17 15	14 14	5arm 3arm	1 1	nd nd	0.23 0.27	2 2	384	1	2	2

Clusters

Located in cluster 7: sblock79_novel, sblock80_novel, sblock81_novel, cel-mir-65, cbr-mir-64, block2522_novel

Families

Member of family miR-64 (seed AUGACAC): cel-mir-65, cbr-mir-64, cel-mir-63, block2522_novel, sblock79_novel, sblock80_novel, sblock81_novel



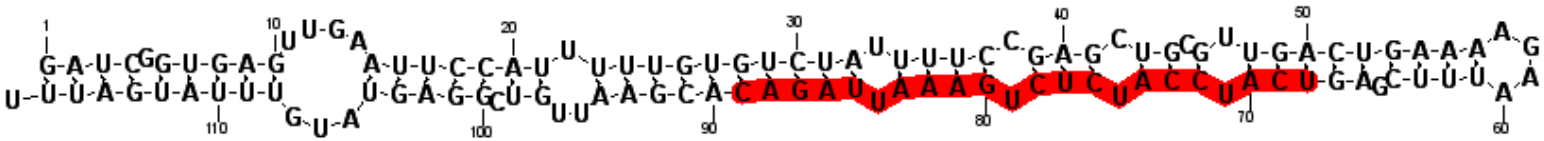
```
         ------------------------------AUGACAC-------------------------------------------------------------------------------------
seed     ------------------------------UGACACU------------------------------------------------------------------------------------
seed     ------------------------------------------------------------------------------------------GACUACG-------------------------
seed     ------------------------------UAUGACA------------------------------------------------------------------------------------

         ------------------------------TATGACACTGTTGCGTAGCATG----------------------------------------------------------------------
         ------------------------------TATGACACTGTTGCGTAGCAT-----------------------------------------------------------------------
         ------------------------------TATGACACTGTTGCGTAG--------------------------------------------------------------------------
         ------------------------------TATGACACTGTTGCGTAGC-------------------------------------------------------------------------
         ------------------------------ATGACACTGTTGCGTAGCATGA----------------------------------------------------------------------
         ------------------------------TATGACACTGTTGCGTAGCA-------------------------------------------------------------------------
         ------------------------------------------------------------------------------------------TGACTACGCTCAGTGGA-----ATACC-------
         ------------------------------ATGACACTGTTGCGTAGCAT-----------------------------------------------------------------------
         ------------------------------ATGACACTGTTGCGTAGCATG----------------------------------------------------------------------
         ---------------------A--------TATGACACTGTTGCGTAGCAT-----------------------------------------------------------------------
cremanei -----CAGAAGGCCTCGCCGAA-------TATGACACTGTTGCGTAGCATGA---CCAATGAGACTCTACAAAAGAGTGAATG------GATCTGACTACGCTCAGTGGA-----ATACCCGGCG--AGTGCCTTCT--
cbriggsae ------------------------------TATGACACTGTTT----AAATGA-----------------------------------AACAGGACTTTCTCTAAC--------ACACCGGGTTCCTGCTCATTTCA(
cjaponica TTTTCCACGAAATTTCTTGAAGCGCATTTTATGACACAGTTG----AAATGAGTGCGACCGTAACCCTATTAAAAAATGGATGGGATACGGTAGCACTCCTTTCAACTGTGTCATAAAATGTGCTTCGATGCATTTC-(
                                        ******** ***       ****                                                ***      *          * *    *        * **

cremanei       .(((((((((((((..       (((..(((((..(((((((((.((   (((.....(((((.....)))))...))       ).)))).)))))).)))))..     )))..)))))  )).)))))))

cbriggsae                              .(((((((((...    ((((((                                     ..(((((....(((....        .....))).)))))).))))))))

cjaponica .(((((((((((...(((((((((((((((((((((((((    (((.((((((.((((((.(((.(((........)))))).)))))).)))))).))))))))))))))))))))))))...))))) )
```

cremanei	chromosome:chrUn:10328652:10328760:1	{Repeats: no}
cbriggsae	chromosome:chrIII:218627:218775:-1	Same_strand|Intronic_coding|NM_001102902 ## Opposite_strand|Intronic_coding|NM_001077612
cjaponica	chromosome:chrUn:31496648:31496788:-1	Same_strand|Intronic_coding|NM_064705

block1645 [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	0.003	no	no	0.36/0.36	22/22/1.00	0.0	0.0	5	0	1	0	28	7	3arm	1	nd	0.23	2	5	1	na	na



```
seed      ----------------------------------------------------------------------------------------CAUCCAU----------------------------------------
          ----------------------------------------------------------------------------------------TCATCCATCTCTGAAATTAGAC-------------------------
cremanei  --------------GATCGGTGAGTTGAA---TTCCATTTTTGTGTCTATTTTCCGAGCTGCGTTGACTGAAAAGAATTTCGAG-----TCATCCATCTCTGAAATTAGAC-ACGAATTGTCGGAGTATGTTTATGA
cbriggsae GGTTCCGGCTTGGATGCCGGCGAGTTGGAAAACCGGAAGACGGCGC-----------------------CGAAGAGATTCGAGC-----TCATCCATTTTTCAACACTGCTGACACAGCGACGGGTCGAGAACC---
celegans  ----------------------------AAAAACTGAAA-----------------------AAAATTGGATGAAATTTGAGAAATTTTCATCCATTTTTTTCAGTTTTT-------------------------
cbrenneri -----TGGTTTTTTTGTCTGCAA----AATAATTGGAATTATGTGT---------------GGTAGATCCGAAGGGCATCTAGG-----TCATCCAT-GATCCAATTATTTGATAACAGGACAAA------------
ppacificus -----------------GGATGATTTTAAAGATGGCACTTGTG-------------------------CAGGAACATTACAAA-----CCATCCAT---TAAAAATATTC-------------------------
                                  *       *                                        *           *******   *

cremanei                 ((((.(((((....(   ((((((.(((((((((.((((.(((.((...(((((((((....)))).))     )))..)).))).))))).))))) )))))..)).))))).....))))))))
cbriggsae  ((((((((((..((((((((.(((((((((..(((.((..((..                        ((((....)))).))     )).))).))))))))..)))))).....))).))))))).))))))
celegans                              ((((((((((                        ((((.(((((((((.((....)).))))))))))))))))))))))
cbrenneri       .......(((((((...(    (((((((((.((((((..(                ((((((((....)).)))))..     )))..))))  )))))))))))))).......)))))))
ppacificus                  (((((.((((((.((((((...(((((                        .........)))))).     ))))))..)   )))))).))))))
```

cremanei	chromosome:chrUn:105689030:105689146:-1	{Repeats: no}
cbriggsae	chromosome:chrX:3584522:3584627:1	Opposite_strand|Intronic_coding|NM_001027419 ## Same_strand|Intronic_coding|NM_181874 ## Same_strand|Exonic_coding|NM_077275
celegans	chromosome:chrIII:11153220:11153376:1	Same_strand|Intronic_coding|Y47D3A.29
cbrenneri	chromosome:chrUn:102193689:102193783:1	intergenic
ppacificus	chromosome:chrUn:156932186:156932342:1	intergenic

sblock80 [novel_cloningHIGH_multiarm_DicerOK_randfoldOK]

Hairpin parameters

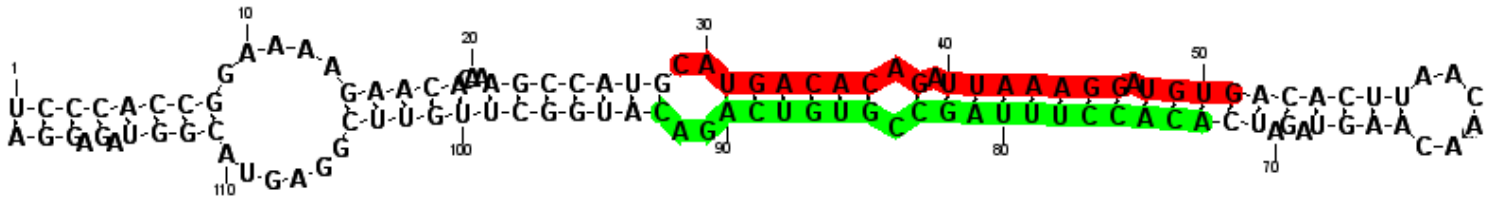
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.33/0.53	18/23/0.93	0.0 0.0	0.0 0.7	602 9	0 0	1 1	0 0	28 27	6 9	5arm 3arm	1 1	nd nd	0.22 0.19	3 2	707	1	1	1

Clusters

Located in cluster 7: sblock79_novel, sblock80_novel, sblock81_novel, cel-mir-65, cbr-mir-64, block2522_novel

Families

Member of family miR-64 (seed AUGACAC): cel-mir-65, cbr-mir-64, cel-mir-63, block2522_novel, sblock79_novel, sblock80_novel, sblock81_novel



```
                                                                                                                                reads   miRBase family seed
seed   ----------------------------AUGACAC-------------------------------------------------------------------------------------686     miR-64
seed   ------------------------------------------------------------------------------CACCUUU-------------------------------------9       novel
seed   --------------------------------CACAGAU-------------------------------------------------------------------------------------9       novel
seed   -------------------------------GACACAG-------------------------------------------------------------------------------------2       novel
seed   -------------------------------UGACACA-------------------------------------------------------------------------------------1       novel
                                                                                                                                len     cloning frequencies
                                                                                                                                        EM464
       ----------------------------CATGACACAGATTAAAGGATGTG-------------------------------------------------------------------------23      602
       ----------------------------CATGACACAGATTAAAGG-----------------------------------------------------------------------------18      42
       ----------------------------CATGACACAGATTAAAGGATGT-------------------------------------------------------------------------22      35
       ---------------------------------ACACAGATTAAAGGATGTGA-------------------------------------------------------------------------20      9
       ------------------------------------------------------------------------A-CACCTTTAGCCGTGTCAGAC-------------------------21      6
       ----------------------------CATGACACAGATTAAAGGA---------------------------------------------------------------------------19      5
       ------------------------------------------------------------------------A-CACCTTTAGCCGTGTCAG----------------------------19      3
       ----------------------------ATGACACAGATTAAAGGATGTGA-----------------------------------------------------------------------23      1
       ----------------------------CATGACACAGATTAAAGGATG-------------------------------------------------------------------------21      1
       ------------------------------TGACACAGATTAAAGGAT---------------------------------------------------------------------------18      1
       ----------------------------CATGACACAGATTAAAGGAT-------------------------------------------------------------------------20      1
       ------------------------------TGACACAGATTAAAGGATGTG-----------------------------------------------------------------------21      1
cremanei  TCCCACCGGAAAAGAACACAAAGCCATGCATGACACAGATTAAAGGATGTGACACTTAACAACAAGTAGATCA-CACCTTTAGCCGTGTCAGACATGGCTTGTTCGGAGTACGGTAGAGGA
cbriggsae ----------------------------CATGACACTGATGTTTAAACACTGC---CCATGGGAAAACACTCA-TGCAGATAAACGGGTCAAA---------------------------
celegans  ----------------------------CATGACACGGGGAAAAGTAAGCCGTTCT------GAAAACCAGCG-AGGTTTCGAATGTTTAACAAGTGACATA-------------------
cbrenneri ----------------------------CATGACACCG--TCGGAAAGGCGATCGTTCACTCTACAGTAGGCG-ATTCTCTCGATGTGCTTCAAG---------------------------
cjaponica ----------------------------CATGACACATGTCTAGA----------TCGTAATGAAAGCATCACAGCCTGCGCAGACACTTACGGTGGAGTGTTG----------------
                                      *******                                   *
cremanei  (((.((((.....((((((...(((((((..((((((...(((((((.(((((.((((.....))))...))) )))))))))..))))))..))))))))))))).....))))...))) 1.000 -46.00
cbriggsae                             ..((((.....((((((....((((   ..(((((.....)))) )))))..)))))).)))))..                          0.654 -14.30
celegans                              .(((.(((.........((((.(((((.      ((.((((.... .))))))))))))))....))).))).                  0.933 -11.42
cbrenneri                             ..((((((.((  (((...(((.((((((..((((....)))).)))  )))).))))))))))..))))..                    0.999 -16.60
cjaponica                             ...((((((...(((..(           ((((((((...(((.........)))).....)).)))))))))))))).           0.661 -12.30
```

cremanei	chromosome:chrUn:10328768:10328887:1	{Repeats: no}
cbriggsae	chromosome:chrX:7081897:7082056:1	Opposite_strand|Intronic_coding|NM_153821 ## Same_strand|Intronic_coding|NM_001087279
celegans	chromosome:chrX:9065601:9065760:-1	Opposite_strand|Boundary_coding|F47E1.4
cbrenneri	chromosome:chrUn:18699017:18699176:1	intergenic
cjaponica	chromosome:chrUn:51553290:51553449:1	Opposite_strand|Intronic_coding|NM_015753 ## Same_strand|Intronic_coding|NM_001021294

sblock81 [novel_cloningHIGH_multiarm_DicerOK_randfoldOK]

Hairpin parameters

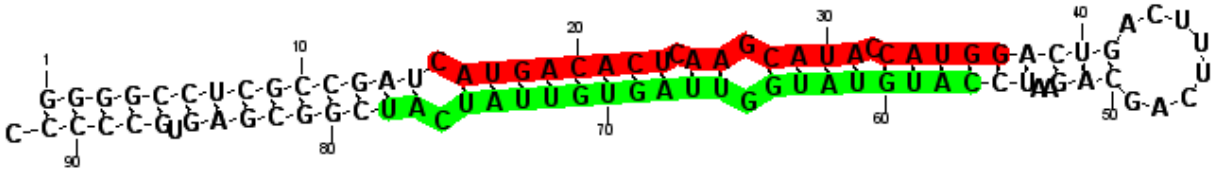
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.32/0.48	19/23/0.99	0.0 0.0	0.0 1.0	548 3	0 0	1 1	0 0	14 14	4 7	5arm 3arm	1 1	nd nd	0.13 0.09	1 1	579	1	1	2

Clusters

Located in cluster 7: sblock79_novel, sblock80_novel, sblock81_novel, cel-mir-65, cbr-mir-64, block2522_novel

Families

Member of family miR-64 (seed AUGACAC): cel-mir-65, cbr-mir-64, cel-mir-63, block2522_novel, sblock79_novel, sblock80_novel, sblock81_novel



```
                                                                                                                                  reads   miRBase family seed
seed    --------------------------AUGACAC-------------------------------------------------------------------------------------   566     miR-64
seed    ------------------------------CACUCAA-----------------------------------------------------------------------------------     6     novel
seed    ------------------------------------------------------------------------AUGUAUG-------------------------------------------     3     novel
seed    --------------------------UGACACU-------------------------------------------------------------------------------------     3     novel
seed    ------------------------------ACACUCA-----------------------------------------------------------------------------------     1     novel
                                                                                                                                  len   cloning frequencies
                                                                                                                                        EM464
        -------------------------CATGACACTCAAGCATACCATGG-------------------------------------------------------------------------  23    548
        -------------------------CATGACACTCAAGCATACCATG--------------------------------------------------------------------------  22    9
        ----------------------------ACACTCAAGCATACCATGGA-----------------------------------------------------------------------  20    6
        -------------------------CATGACACTCAAGCATACC----------------------------------------------------------------------------  19    4
        -------------------------CATGACACTCAAGCATACCAT--------------------------------------------------------------------------  21    3
        ------------------------------------------------------------------------CATGTATGGTTAGTGTTATCAT---------------------------  22    2
        --------------------------ATGACACTCAAGCATACCATG---------------------------------------------------------------------------  21    2
        -------------------------CATGACACTCAAGCATACCA---------------------------------------------------------------------------  20    2
        ----------------------------GACACTCAAGCATACCATGGA-----------------------------------------------------------------------  21    1
        --------------------------ATGACACTCAAGCATACCATGGA-------------------------------------------------------------------------  23    1
        ------------------------------------------------------------------------CATGTATGGTTAGTGTTAT-------------------------------  19    1
cremanei  -----------GGGGCCTCGCCGATCATGACACTCAAGCATACCATGGAC---TGACTTTCAGCAGAATCCATGTATGGTTAGTGTTATCATCGGCGAGTGCCCCC--------------
celegans  ---------------ATCCAGATATAATGACAC-------------GAAT------CGTTCAATTGGGTC----TCTGATAAAAGCAA--AACGAACGGTATCCGTGTCATTG-------
cbrenneri TCGCTGTTTCTCCGGCCTTGCCGATTATGACACTTAAGCATA-GGTGGACCATCGAAGATCA-TAGGCTCCAGCTATGATAAGTGGAATAGTCGGCGAGAGCCTGGAGCATTCCATTCGA
                                ** ******             * *          ***   *  **    * ** * *  *  *    **    *   *

cremanei            ((((((((((((((.((((((((.((.((((.(((((((   ((........)))..))))))))))).))))))))))).))))))))).))))).                1.000
                                                                                                                                      -53.30
celegans                .........(((((((((             (.((      (((((..(((.(((    ...)))).....)))  ...)))))))...))))))))))         0.994
                                                                                                                                      -18.10
cbrenneri .........(((((((((((((((((((..((((((..(((( (.((((((........... ..)).)))).)))))).))))))..))))))))))))).))).))))............ 0.986
                                                                                                                                      -52.72
```

cremanei	chromosome:chrUn:10328912:10329003:1	{Repeats: no}
celegans	chromosome:chrV:7533985:7534057:-1	Opposite_strand|Exonic_coding|C54F6.3
cbrenneri	chromosome:chrUn:123880705:123880822:1	intergenic ## {SimpF: trf,trf}

---

block2522 [novel_cloningHIGH_randfoldOK]

Hairpin parameters

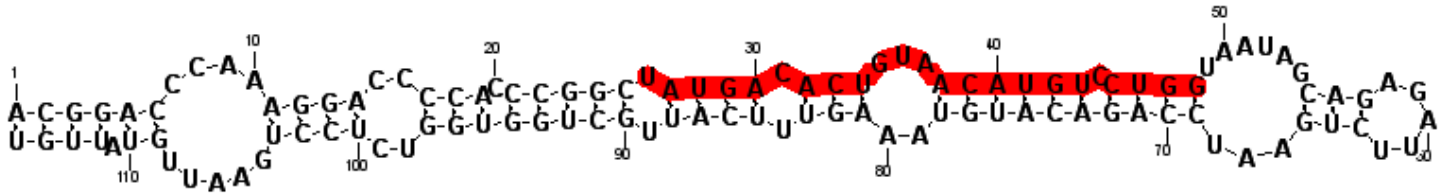
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.33/0.47	18/24/0.99	0.0	0.0	529	0	1	0	25	9	5arm	1	nd	0.26	3	568	1	na	na

Clusters

Located in cluster 7: sblock79_novel, sblock80_novel, sblock81_novel, cel-mir-65, cbr-mir-64, block2522_novel

Families

Member of family miR-64 (seed AUGACAC): cel-mir-65, cbr-mir-64, cel-mir-63, block2522_novel, sblock79_novel, sblock80_novel, sblock81_novel



```
                                                                                                                reads   miRBase family seed
seed      -------------------------AUGACAC-------------------------------------------------------------------------------------------  564     miR-64
seed      ------------------------------CACUGUA-------------------------------------------------------------------------------------------  4       novel
                                                                                                                len     cloning frequencies
                                                                                                                        EM464
          -------------------------TATGACACTGTAACATGTCCTGG-------------------------------------------------------------------------------  23      529
          -------------------------TATGACACTGTAACATGTCCTGGT------------------------------------------------------------------------------  24      24
          -------------------------TATGACACTGTAACATGTCCTG--------------------------------------------------------------------------------  22      5
          -------------------------TATGACACTGTAACATGTCCT---------------------------------------------------------------------------------  21      5
          ------------------------------ACACTGTAACATGTCCTGG-----------------------------------------------------------------------------  19      4
          -------------------------TATGACACTGTAACATGT------------------------------------------------------------------------------------  18      1
cremanei  ACGGACCCAAAGGACCCCACCCGGCTATGACACTGTAACATGTCCTGGTAATAGCAGAGATTCTGAATCC---AGACATGTAAAGTTTCATTGCTGGTGGTCTCCTGAATTGTATTGT
cbriggsae ------------------------TATGACACT--TGTACTTCCATGTGTGAGGAGACAAATGTACTCACTAGGGCAGGTAAG---TCATT--------------------------
ppacificus ------------------------ATGACACTGACATACTGC---------GGTTACTTGACGAATCCCTTGGAATGATAGCG--TCATT--------------------------
                                   *******     *   *         *   *       * **     *     **     *****
cremanei  ((((((....((((..((((.(((((.((((.((((...((((((.((((.....(((.....)))...))   ))))))))..))))..))))..))))))))..))))).....)).))))  1.000
                                                                                                                                        -40.90
cbriggsae                         .((((((...  ..(((((((....((((((...((....)).)))))...)).)))))..)   )))))..                            0.994
                                                                                                                                        -17.20
ppacificus                         (((((.(((.(((.((((.         ((..............)).)))).)))).)))).)   )))))..                            0.876
                                                                                                                                        -10.04
```

cremanei	chromosome:chrUn:10329302:10329416:1	{Repeats: no}

cbriggsae	chromosome:chrV:11490457:11490611:-1	Opposite_strand|Intronic_coding|NM_001011629 ## Same_strand|Intronic_coding|NM_007492 ## Same_strand|Boundary_coding|NM_001028559
ppacificus	chromosome:chrUn:20322976:20323130:-1	intergenic

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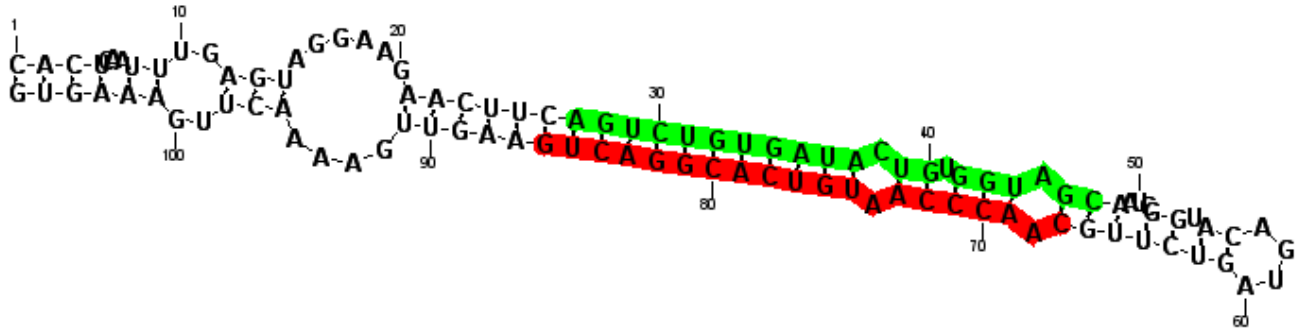
sblock123 [novel_cloningHIGH_multiarm_DicerOK_randfoldOK]

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	0.45/0.57	18/22/0.98	0.0 0.0	0.0 0.0	6 599	0 0	1 1	0 0	26 20	9 6	5arm 3arm	1 1	nd nd	0.14 0.10	1 1	624	1	1	1



```
                                                                                                                reads   miRBase family seed
seed   ------------------------------------------------------------------AACCCAA--------------------------------   611     novel
seed   --------------------------GUCUGUG-------------------------------------------------------------------------   7       novel
seed   -------------------------------------------------------------------ACCCAAU--------------------------------   3       novel
seed   ------------------------------------------------------------------CAACCCA--------------------------------   3       novel
                                                                                                                len     cloning frequencies
                                                                                                                        EM464
       -------------------------------------------------------------------CAACCCAATGTCACGGACTG--------------------   20      599
       -------------------------------------------------------------------CAACCCAATGTCACGGACT---------------------   19      9
       --------------------------AGTCTGTGATACTGTGGTAGC-------------------------------------------------------------   21      6
       -------------------------------------------------------------------AACCCAATGTCACGGACT---------------------   18      2
       -------------------------------------------------------------------CAACCCAATGTCACGGACTGAA-------------------   22      2
       ------------------------------------------------------------------GCAACCCAATGTCACGGACTG--------------------   21      1
       -------------------------------------------------------------------AACCCAATGTCACGGACTGA--------------------   20      1
       -------------------------------------------------------------------CAACCCAATGTCACGGACTGA--------------------   21      1
       ------------------------------------------------------------------GCAACCCAATGTCACGGA-----------------------   18      1
       --------------------------AGTCTGTGATACTGTGGTAG-------------------------------------------------------------   20      1
       ------------------------------------------------------------------GCAACCCAATGTCACGGACT----------------------   20      1
cremanei  CACTCAATTTGAGTAGGAAGAACTTCAGTCTGTGATACTGTGGTAGCAATCGGTACAGTAGTCTTGCAACCCAATGTCACGGACTGAAGTTGAAAACTTGAAAGTG
cbriggsae ---------------TCAGCCACTTCGGTTGTGGTTATACAAACAGAAGTTGAT-----------ATAACCCAA--TCACGAA---------AATGGCTGA-----
cjaponica CCCAAAATTTCAG--ACAAAAATATCGATTTTTAAAAAATTTTCAGAAA-AAATTCAATATTTTTAAAACCCAATATTTTTGTCTG------AACTGTTGGG----
                         *   *  **  *       *       ** *     *             *******  *               **    **
cremanei  ((((...((..(((.....(((((((((((((((((.((.(((.(((...((.((....)))))))).)))))).))))))))))))))....)))..)))))))   0.860
                                                                                                                        -39.70
```

```
cbriggsae                 (((((((.(((((((.(((((((..(((....)))..)            )))))))))  )..))))          ..))))))))      1.000
cjaponica (((((...(((((  ((((((((((....(((((((((.......(((. ...)))....)))))))))....))))))))))))))      ))...))))))     -25.00
                                                                                                                        0.986
                                                                                                                       -25.70
```

cremanei	chromosome:chrUn:105689755:105689860:1	{Repeats: no}
cbriggsae	chromosome:chrX:10977030:10977093:1	Opposite_strand|Intronic_coding|NM_027552 ## Same_strand|Intronic_coding|NM_011438
cjaponica	chromosome:chrUn:92512297:92512389:1	Same_strand|Intronic_coding|NM_001025854