Supplemental Figure 11. Novel *P. pacificus* miRNAs.

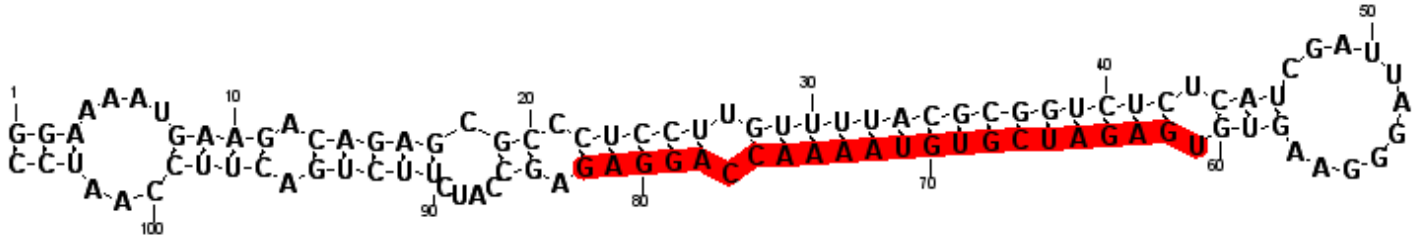
block15136 [novel_cloningOK_randfoldOK]

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	0.42/0.45	19/22/0.83	0.0	0.0	8	0	1	0	23	3	3arm	1	nd	0.09	1	12	1	na	na

Clusters

Located in cluster 28: block15133_cand, block15135_cand, block15136_novel



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seed            ------------------------------------------------------------------------------------------GAGAUCG-----------------------------------
                ------------------------------------------------------------------------------------------TGAGATCG---------------TGTAAAACCAG----GAG--
                ------------------------------------------------------------------------------------------TGAGATCG---------------TGTAAAACCAG----G----
                ------------------------------------------------------------------------------------------TGAGATCG---------------TGTAAAACCAG--------
ppacificus      GGAAAATGAAGACAGAGCGCCCTCCTTGTTTTACGCGGTCTCTCATCGA----------------------TTAGGGAAGTG---TGAGATCG---------------TGTAAAACCAG----GAGA
cremanei        ---------------TTTGAATTTCAAGGTT-----------------------------------------TCCAGAAAATG---AGAGATCGA--------------TATGAAATTTG----AA---
cbriggsae       ------GAAACGTGCTGTGATTTCATTGTGAGCTTCAGTACGATATCGA----------------------TTATGAACATCCATTGAGATCG---------------TGTAAAGCTGGCGAAGAGA
celegans        --------------------CTTCCAAATGCGACCAATCAGCGATTCACTCCGCCCACTTTTCAACCAATCAGAAGAAGTGGGCGGAGATCGAAGACGCTGATTGGTCGTGGATTTTG----GAGG
cbrenneri       ------------GGGCACTAGTTTCGTGTGTGTGTGTATGTATGTTCCTCTCTTTTGGT-----------CTTGTGAGATAATAATAGACTG---------------TGTAGAATCGA----GAGA
cjaponica       --------------------CCTCATCGTTTACACGCTTGTAAGTTCGCATA------------------TTGGCGATG-----TGAGATCG---------------TGTAAG---CG----AAGA
                                          *                                                     *         ***  *                 *            *
                ------------------------------------------------------                  -----------   --------                -----------    ----
                ------------------------------------------------------                  -----------   --------                -----------    ----
                ------------------------------------------------------                  -----------   --------                -----------    ----
ppacificus      (((....((((.(((((.((.(((((.(((((((((((((((.(((...                       ........)))   .)))))))                ))))))))..))    )))..
cremanei                     ((..(((((((.((((                                           ((((.....))   .)))))))..                ..))))))))..    ))
cbriggsae             .....((....(((((((.((((.(((((...((((((.((((                       (...........)))))).))))                )).....))))).))))
celegans                          ((((((((.((((((((((((((.((((.((((((((((((((.........)))))).))))))))))...))))..))))))))))))))....))))    ))))
cbrenneri                   ((((.......(((.(((.(((...((((.((((((((((((((((                (((.((((....(((.......))                ).....))).    ))))
cjaponica                         .(((.((((((((((((..((...((((...                          ...))))))     ..))..))                ))))))   ))    ).))
```

ppacificus	chromosome:chrUn:136661723:136661827:1	Opposite_strand|Intronic_non-coding|NM_001108718|Alkbh ## {Repeats: no}
cremanei	chromosome:chrUn:139358349:139358493:-1	intergenic

cbriggsae	chromosome:chrI:5315777:5315874:-1	Same_strand|Intronic_coding|NM_001011629 ## Opposite_strand|Intronic_coding|NM_033488 ## Opposite_strand|Boundary_coding|NM_001012940 ## Opposite_strand|Exonic_coding|NM_132275
celegans	chromosome:chrV:16959125:16959226:1	Opposite_strand|Intronic_coding|Y102A5C.18
cbrenneri	chromosome:chrUn:110630909:110631036:-1	intergenic
cjaponica	chromosome:chrUn:51398755:51398899:-1	intergenic

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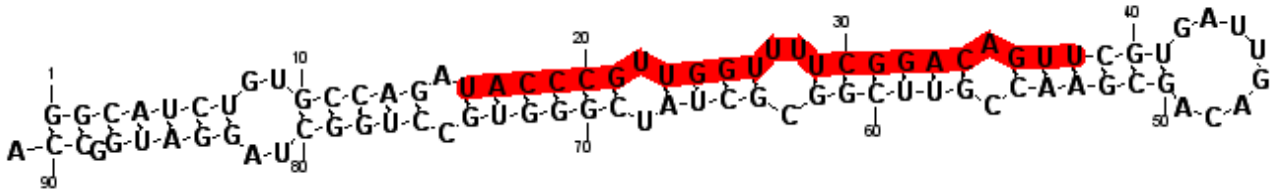
block9540 [novel_cloningHIGH_randfoldOK]

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	0.48/0.50	23/24/1.00	0.0	0.0	23	0	1	0	15	3	5arm	1	nd	0.17	2	30	1	na	na

Clusters

Located in cluster 17: block9537_cand, block9538_novel, block9539_novel, block9540_novel, sblock213_novel, block9543_cand, block9544_novel



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   seed      ---------------------------------------ACCCGUU-------------------------------------------------------------------------------------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                ---------------------------------------TACCCGTT------------------GGTTT--------------TCGGA--CAGTT------------------------------
                ---------------------------------------TACCCGTT------------------GGTTT--------------TCGGA--CAGTTC-----------------------------
ppacificus      GGCATCTGTGCCAGA------------------------TACCCGTT------------------GGTTT--------------TCGGA--CAGTTCGTG---------ATTGACAGCGAACCGTT
cbriggsae       -----CAAAACCAAAAACGATCCACTTTGAACCGAGTTATACCCGTTTGACATTGGTGGCCTAGAAATTTGAAATTCTAGGCCACCGGATACAAATCGCTGTAACTCTGCTTG-AAGTAGTCCA--
celegans        ---------------------------------------TACCCGTT------------------GTTT------------CATTTGAT-CAAATCACC---------CTTGTAAATAGTGCAAT
                                                        ********                   ***                 **  **  **             ***  *      *
                +++++++++++++++++++                     ********                 +++++              +++++  +++++++++         +++++++++++++++
                +++++++++++++++++++                     ********                 +++++              +++++  +++++++++         +++++++++++++++
                +++++++++++++++++++                     ********                 +++++              +++++  +++++++++         +++++++++++++++
                -------------------                     --------                 -----              -----  ---------         ---------------
                +++++++++++++++++++                     ********                 +++++              +++++  +++++++++         +++++++++++++++
                +++++++++++++++++++                     ********                 +++++              +++++  +++++++++         +++++++++++++++
ppacificus      (((((((..(((((.                         ((((((.(                 (((..              (((((  (.(((((((.         .......))))))..)))
cbriggsae           ((((((((((..((((..(((((((...((((((((...((((((...((((((((((((((.......)))))))))))))))...))))))...))))))))...))))  ))))..))))..
celegans                                                .((((((..                 ((.(             ((..(((( .....(((.         ..........))))....
```

ppacificus	chromosome:chrUn:49876653:49876743:1	Same_strand|Intronic_coding|NM_008140|Gnat1 ## Opposite_strand|Intronic_non-coding|NM_001086814|pl10 ##

		{Repeats: no}
cbriggsae	chromosome:chrV:2716798:2716927:1	Opposite_strand|Intronic_coding|NM_070879
celegans	chromosome:chrX:16845310:16845440:-1	Same_strand|Exonic_coding|T20F7.5

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block676 [novel_cloningOK_randfoldOK]

Hairpin parameters

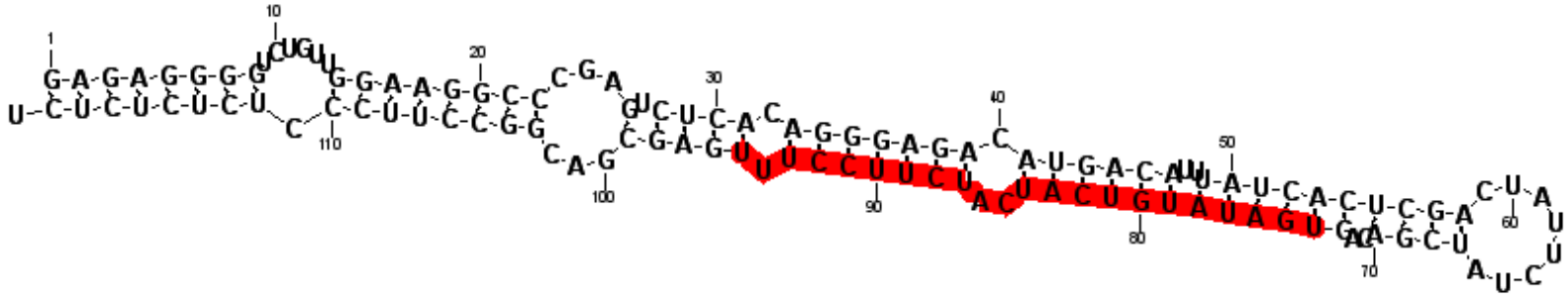
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.32/0.33	21/22/1.00	0.0	0.0	14	0	1	0	25	7	3arm	1	nd	0.14	2	15	1	na	na

Clusters

Located in cluster 5: block676_novel, block677_novel

Families

Member of family miR-50/62/90 (seed GAUAUGU): block676_novel, block677_novel



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seed        ----------------------------------------------------------------------------------------------------GAUAUGU----------------------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
            ----------------------------------------------------------------------------------------------------TGATATGTCATC--------------------ATCT
            ----------------------------------------------------------------------------------------------------TGATATGTCATC--------------------ATCT
ppacificus  -----------------GAGAGGGGTCTGTTGGAAGGCCCGAGTCTCACAGGGAGACATGACATTTATCACTCGACTATTCTATCGACAGTGATATGTCATC--------------------ATCT
cremanei    GAAGTTTCGTCACCAATTATAGGAAAATTTCCATAGCTTTATG---AAAAAAAACATATCACTAGTACGGGTTGATTATGCTAAATAAGTTGATATGTTTTTTTCCTATAAAGTTTCGCAAATTT
celegans    -------------------------------------------------------------ATATCACTTTTAGACATTCAATTTACCCATTAGATTGATATGTCAC--------------------------
cjaponica   -------------------CGAGGGGAACGT--------------------GGATCCATATCGTAT--------------------------CCGATATGTCTCC--------------------ATTC
                                                                  * **                                      *******
      +++++                 ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++                    ++++
      +++++                 ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++                    ++++
      +++++                 ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++                    ++++
ppacificus                  (((((((.....(((((((.....((((.(((((((.((((((..(((((((((.......))))..))))))))))).                    .)))
cremanei    ...(((((((((((((((((.((((((....(((((((((   (((((((((((((((((.((...((.......)))..)).)))).))))))))))))))..))))))))....))))))
celegans                                                                ...((((((((.((((((((((((.....)))))))).))))))..
cjaponica                    ..((((((..((                    (((..(((((((...                        .)))))))..)))                    ))))
```

ppacificus	chromosome:chrUn:24360839:24360958:-1	Same_strand|Intronic_coding|NM_126491|AT2G04620 ## Same_strand|Intronic_non-coding|NM_001033238|Cblb ## {Repeats: no}
cremanei	chromosome:chrUn:79418872:79419018:-1	Opposite_strand|Intronic_coding|NM_003428 ## {SimpF: trf}
celegans	chromosome:chrIII:4671854:4672013:-1	intergenic
cjaponica	chromosome:chrUn:75834811:75834970:1	Opposite_strand|Intronic_coding|NM_001027968

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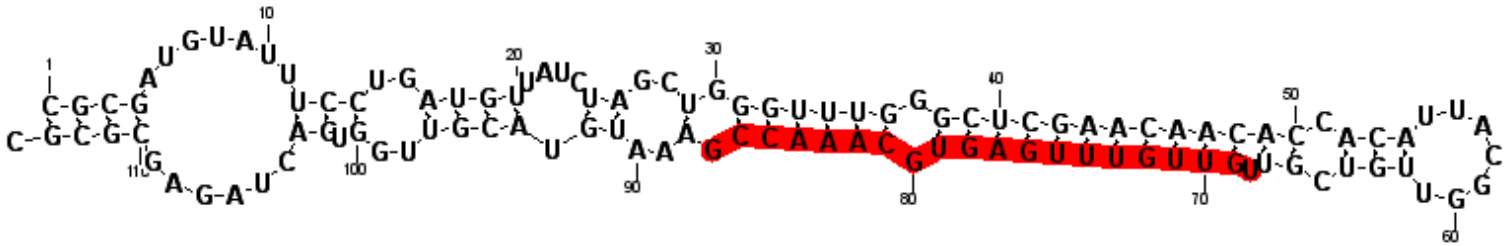
block3570 [novel_cloningOK_randfoldOK]

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	0.010	no	no	0.45/0.45	20/20/1.00	0.0	0.0	11	0	1	0	27	6	3arm	1	nd	0.15	2	11	1	na	na



```
seed          ------------------------------------------------------------------------------------GUUGUUU----------------------------
                                                                                                  TGTTGTTTGAGTGCAAACCG----------------
ppacificus    --------CGCGATGTATTTCCTGATGTTATCTAGCTGGGTTTGGGCTC---------GAACAACAC------CACATTACGGTTGTCGTTGTTGTTTGAGTGCAAACCGAAATGTACGTTGGTGA
cremanei      GAGCTTTCAGAAAAGTATAATCATGGCTAGGTTCCGGCGGCATTGGGTCCCGCCACGAAAACTACAGTAACCCAATGTTTGGTGTAC---TGTTGTTTTCGTGGTGAGACCCAATGTTGTCAGAAT
cbriggsae     -------------------------------------GCAAGTTAATTC----------AACAGTAA-----CCGAGCTAGGGAAGCCGTCGTTGTTTG------------AATTTACGTGGGG---
celegans      --------TGTTGTTTTTTTTTTTTTGAAAATTCCAAAAAAATCGGTTTTCT------AAACGACAC---TCCGATATTCCGCCGGCACGTGTTGTTTA---------GTAGAATGTCGTTTTTCG
cjaponica     -------------------------------------GGGCATGCGCTT---------AAATTAGAG------AAAATACGGTGTATTCTCGTTGTTTC--------------------------C
                                                    *    *           **    *               *         *******
              +++++        ++++++++++++++++++++++++++++++++++++         +++++++++      ++++++++++++++++++++++++++++++++++++++++++++++++++
              +++++        ++++++++++++++++++++++++++++++++++++         +++++++++      ++++++++++++++++++++++++++++++++++++++++++++++++++
              +++++        ++++++++++++++++++++++++++++++++++++         +++++++++      ++++++++++++++++++++++++++++++++++++++++++++++++++
              +++++        ++++++++++++++++++++++++++++++++++++         +++++++++      ++++++++++++++++++++++++++++++++++++++++++++++++++
ppacificus                 ((((.......(((((((((.........(((((.((((      (((((((((      .(((.......)))).)).)))))))))))).)))))).......)))))))).))
cremanei      ((((((((((((((((((((((((((((((.(((((((((((((.((((((((((((.((((((((((.((((..(((.....)))..)))   )))).))))))))))))).))))))))))))))).))))
cbriggsae                                          .((.((.(((((          (((((..(     (...(((.....))).)).)..)))))).)            )))).)).)).....
celegans                   (((((.(((((((...((..((((.((((.....(((((((      (((((((((   .(((.........)))...)))))))))))          ).))))).....))))).)
cjaponica                                          ...((((.((((          ((((..(((      ((.(((.....)).)))))...)))).                                .
```

ppacificus	chromosome:chrUn:90382507:90382620:-1	Same_strand|Intronic_coding|NM_067727|Y41D4A.5 ## {Repeats: no}
cremanei	chromosome:chrUn:54454799:54454951:-1	intergenic
cbriggsae	chromosome:chrV:5721884:5722037:-1	Opposite_strand|Intronic_coding|NM_068772 ## Same_strand|Intronic_coding|NM_112328
celegans	chromosome:chrII:12300866:12300991:-1	intergenic
cjaponica	chromosome:chrUn:82941792:82941945:-1	intergenic

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block7028 [novel_cloningHIGH_randfoldOK]

Hairpin parameters

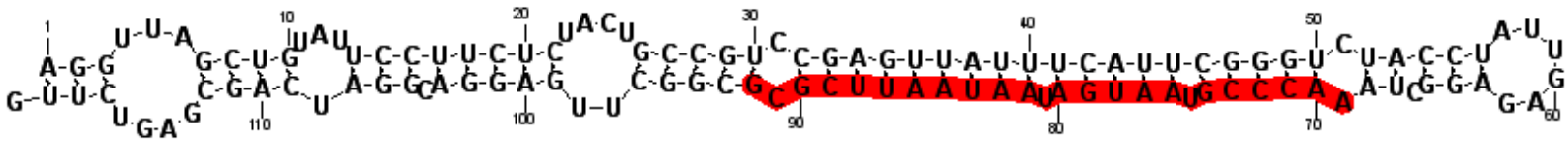
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.35/0.39	20/25/0.90	0.0	0.0	61	0	1	0	28	6	3arm	1	nd	0.12	1	71	1	na	na

Clusters

Located in cluster 14: block7028_novel, block7029_novel, sblock162_novel

Families

Member of family miR-51/52/55 (seed ACCCGUA): block7028_novel, block7029_novel, block9544_novel, block15318_novel, block15319_novel, sblock162_novel, sblock213_novel, sblock279_novel, sblock280_novel, block9543_cand



```
seed        ----------------------------------------------------------------------------------------ACCCGUA----------------------
seed        ---------------------------------------------------------------------------------------AACCCGU----------------------
seed        ------------------------------------------------------------------------------------------GUAAUG-----A-------------
seed        ----------------------------------------------------------------------------------------CCCGUAA----------------------

            ----------------------------------------------------------------------------------------AACCCGTAATG-----ATAATAATTCGCG-
            ---------------------------------------------------------------------------------------AAACCCGTAATG-----ATAATAATTCGCG-
            ----------------------------------------------------------------------------------------ACCCGTAATG-----ATAATAATTCGCG-
            ----------------------------------------------------------------------------------------AACCCGTAATG-----ATAATAATTCGC--
            ------------------------------------------------------------------------------------------CGTAATG-----ATAATAATTCGCG-
ppacificus  -----------------------AGGTTAGCTGTATTCCTTCTCTACTGCCG------TCCGAGTTATTTCATTCGGGTCTACCTATTGAGAGGCTAAACCCGTAATG-----ATAATAATTCGCG
celegans    GGAAGTTTGACAAATGGGACCCCGGGTGAGAAAAAAGAGGACACTGCGGCCGACACCTACCGGGATCCTCCGAGTATGTCTAGAACCCGTAAGGTGTCGGCCGCTATGTATGTATCGCAAATCCCA
cbrenneri   -------------------------------AAAAAAGTTGTCAACTACAAAAA-----------------------------------------------------TGATGTTCGTTTGATACGCCCAA
                                                *         *  *  *                                                      ***      *   *   *
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            -----                          ------------------------------      -----------------------------------------------------      --------------
ppacificus                                 (((...((((...(((((((((....((((      (.(((((((((((((((((((.(((((.....))).)).)))))).))))      ).))))))))).)
celegans        (((....(((((((((((.((...((.((.......((..(((..((((((((((((..((((.((.....(.....)).)).)))))..))))))))))))..)))).....)).....)))).
cbrenneri                                    ..((((((((...(((((((((                                                  (..((..(((.....)))..)).
```

ppacificus	chromosome:chrUn:2088313:2088432:1	Same_strand|Intronic_non-coding|NM_080105|cpo ## Same_strand|Intronic_coding|NM_169781|cpo ## Opposite_strand|Intronic_non-coding|NM_010570|Irs1 ## Opposite_strand|Intronic_coding|NM_184109|Rtl1 ## {Repeats: no}
celegans	chromosome:chrV:3733588:3733738:-1	Same_strand|Intronic_coding|Y39H10A.4
cbrenneri	chromosome:chrUn:168069557:168069716:-1	intergenic

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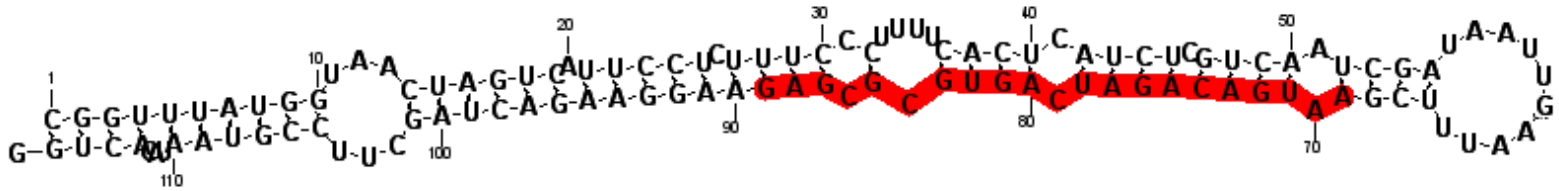
block6545 [novel_cloningOK_randfoldOK]

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	0.52/0.53	19/21/0.79	0.0	0.0	15	0	1	0	29	3	3arm	5	nd	0.24	3	19	1	na	na

Families

Member of family novel3 (seed AUGACAG): block6545_novel, block6555_novel, block6559_novel, block6568_novel, block16444_novel, block16447_novel, block16470_cand



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seed            ------------------------------------------------------------------------------------------AUGACAG-----------------------------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
ppacificus      ------CGGTTTATGGTAACTAGTCATTCCTCTTT----CCCTTTTCACTCA----TCTCGTCAATCGATA--ATTGAATTTCGAATGACAGA-----TCAGTGCGCGAGAAGG------AAGACTA
cjaponica       GCGTAGAGTTTTCTTGGAGTGTCGAATTTGTATTTATGGACCTATTCAAGCGAGTTTTTTGTCATTTTAAACCAATGAA-----AATGACAGAAAATTTCATTGAATAAATAGATACATCAAAACGA
```

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                 * *** * * *       ***  * ***     *** ****  *     * * **** *  * *  * ****     *********     *** **    *  **       ** ** 
+++++      ++++++++++++++++++++++++++++++    +++++++++++++    +++++++++++++++  +++++++++++++++++++++  +++++++++++++++++      ++++++
```

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                  *                    * *  *  *    ******   * *        **   *        *      **  **    *        *       *     *****
          +++++   ++++++               +++++++++++++++++++   +++++++++++++++++++++++++++++++++++++++++++++++++++++++++++   +++++++
ppacificus        ((((((               .....((((.((.((((((   .((.((((((((((((..((((.((....)))))).............)))))))))))).   )))))).
cbriggsae         .((...(((((.  ....(((.(((....(((((((((((.((.((((((((((.(((((....((((.....))))).  .......))))))))))))..))))..)).)))))).))))))
celegans       (((...(((((.((((..(((((((((.....((((..((((((.   ...((((..((((((..((((((((.((      ....)).)))))..)))...))))))).)))   )))))))))))))))
```

ppacificus	chromosome:chrUn:37971356:37971462:-1	Same_strand|Intronic_non-coding|NM_031349|Agtrl1 ## {Repeats: no}
cbriggsae	chromosome:chrX:11068434:11068573:-1	Same_strand|Intronic_coding|NM_014930 ## Opposite_strand|Intronic_coding|NM_011438 ## Opposite_strand|Exonic_coding|NM_076586
celegans	chromosome:chrV:18176877:18177014:-1	Same_strand|Boundary_coding|C31G12.4

---

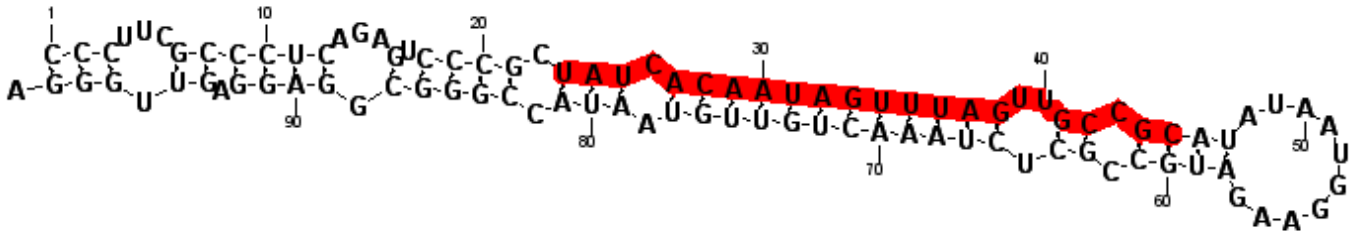
block12316 [novel_cloningOK_randfoldOK]

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	0.002	no	no	0.39/0.39	23/23/1.00	0.0	0.0	7	0	1	0	22	2	5arm	1	nd	0.17	2	7	1	na	na

Clusters

Located in cluster 25: block12316_novel, cel-mir-65, block12318_cand



```
                                                
```

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

ppacificus	chromosome:chrUn:95556118:95556217:1	Same_strand|Intronic_non-coding|NM_175692|A930034L06Rik ## {Repeats: no}
cremanei	chromosome:chrUn:144588271:144588410:-1	Opposite_strand|Boundary_coding|NM_005135 ## Opposite_strand|Intronic_coding|NM_009194 ## Opposite_strand|Exonic_coding|NM_068509
cbriggsae	chromosome:chrX:11616482:11616621:1	Same_strand|Intronic_coding|NM_010459 ## Opposite_strand|Intronic_coding|NM_001122952 ## Opposite_strand|Exonic_coding|NM_076657
celegans	chromosome:chrX:14712663:14712802:1	Same_strand|Boundary_coding|F33C8.1b
cbrenneri	chromosome:chrUn:138462303:138462442:1	intergenic
cjaponica	chromosome:chrUn:99604108:99604241:-1	Same_strand|Intronic_coding|NM_001114122

---

sblock123 [novel_cloningHIGH_multiarm_DicerOK_randfoldOK]

Hairpin parameters

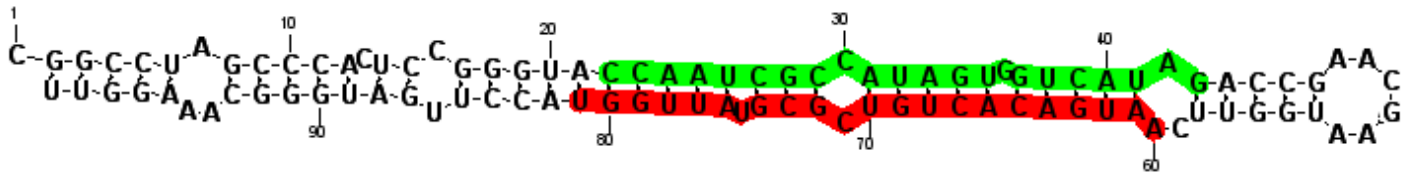
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.42/0.50	18/23/0.99	0.0 0.0	0.0 0.0	2 321	0 0	1 1	0 0	21 19	4 6	5arm 3arm	1 1	nd nd	0.14 0.09	1 1	335	1	1	1

Clusters

Located in cluster 10: sblock123_novel, cel-mir-63

Families

Member of family miR-64 (seed AUGACAC): cel-mir-63, cel-mir-63, cel-mir-63, cel-mir-63, cel-mir-63, cel-mir-63, cel-mir-63, cel-mir-63, cel-mir-63, cel-mir-63, cel-mir-65, block387_novel, sblock123_novel, block385_cand, sblock77_cand



```
seed    ------------------------------------------------------------------------------AUGACAC--------------------------------
seed    ----------------------CAA-------------------UCGC-------------------------------------------------------------------
seed    ------------------------------------------------------------------------------UGACAC---------------U----------------
```

```
   seed        ----------------------------------------------------------------------------------------CAC---------------UGUC--------------
               ------------------------------------------------------------------------------------AATGACAC---------------TGTCGCGTATTGGT----
               ------------------------------------------------------------------------------------AATGACAC---------------TGTCGCGTATTGG-----
               ----------------------------------------------------------------------------------ATGACAC---------------TGTCGCGTATTGGT----
               ---------------------CCAA-------------------TCGCCATAGTGGTCATAG-------------------------------------------------------------
               ------------------------------------------------------------------------------------AATGACAC---------------TGTCGCGTATT-------
               ------------------------------------------------------------------------------------AATGACAC---------------TGTCGCGTATTGGTA---
               ------------------------------------------------------------------------------------AATGACAC---------------TGTCGCGTAT--------
               ----------------------------------------------------------------------------------ACAC---------------TGTCGCGTATTGGTA---
ppacificus     CGGCCTAGCCCACTCCGGGTACCAA------------------TCGCCATAGTGGTCATAGACCG-AACGA-------ATGGTTCAATGACAC---------------TGTCGCGTATTGGTACC
cremanei       ------------------GTGCAAC----------------ACCCGAATGTATCTATTTGAACGCAAGACGG---------TTATAAATGACAC-----------------------ACGGGTGTA
cbriggsae      TTGGTTCGATTCCTTCTGGTCTAGCA----TACGGTATTTGAATTTAATATCATTTTGTAGGACTG-GACGAAATCTACA-----AAATGACACTAAATTCAAATACCGTATACCAAACCAGATCC
celegans       ----------TTCTTTAAAAACAAAAATCCAAAAAAATTCTATCGTGGTATTTCTGTCATGGACTGTGGCAGTAGCTGAAGTCTTGAATGACAC---------------AGTCGCCAGAAAGA---
cbrenneri      ----------------------------------------TATTTTGGGATAGATATGTCAAGTTTCAACGATA-----AAATTCAAATGACAC---------------TGTCCCAAATTAGA----
                                                            *     *           *               *******                         *
          ------------------------------                  ----------------------- -----       ---------------                 ------------------
          ------------------------------                  ----------------------- -----       ---------------                 ------------------
          ------------------------------                  ----------------------- -----       ---------------                 ------------------
          ------------------------------                  ----------------------- -----       ---------------                 ------------------
          ------------------------------                  ----------------------- -----       ---------------                 ------------------
          ------------------------------                  ----------------------- -----       ---------------                 ------------------
          ------------------------------                  ----------------------- -----       ---------------                 ------------------
ppacificus     .(((((.(((((.((.(((((((((                  ((((.(((((.(((((.((((( .....       .)))))..)))))))                ))).))).)))))))))
cremanei                        .((((((                 ((((((..((((.((.((((((((........)         )).))))))).))                        ))))))))..
cbriggsae      .(((((((..((((((((((.....(    ((((((((((((((((((...((((((((((((.... .......))))))     )))))))...)))))))))))))))))).....))))))...
celegans                  ...........((...((((.......(((.((.((((..((.((((((((((.((((....)))))).)))))...)))))))).                )))..))))))).)))
cbrenneri                                            ((.((((((((((...((((((((((........     )))))).....))))))                )))))))))).))..
```

ppacificus	chromosome:chrUn:122024147:122024246:-1	Opposite_strand|Intronic_coding|NM_001080348|POU3F2 ## Opposite_strand|Intronic_non-coding|NM_001014991|Dscam ## {Repeats: no}
cremanei	chromosome:chrUn:51101436:51101575:1	intergenic
cbriggsae	chromosome:chrUn:6618676:6618810:-1	Same_strand|Intronic_coding|NM_202770 ## Opposite_strand|Intronic_coding|NM_065688
celegans	chromosome:chrIV:9221933:9222038:-1	intergenic
cbrenneri	chromosome:chrUn:23481745:23481884:1	Opposite_strand|Intronic_coding|NM_058831 ## Same_strand|Intronic_coding|NM_059307

---

block16493 [novel_cloningHIGH_randfoldOK]

Hairpin parameters

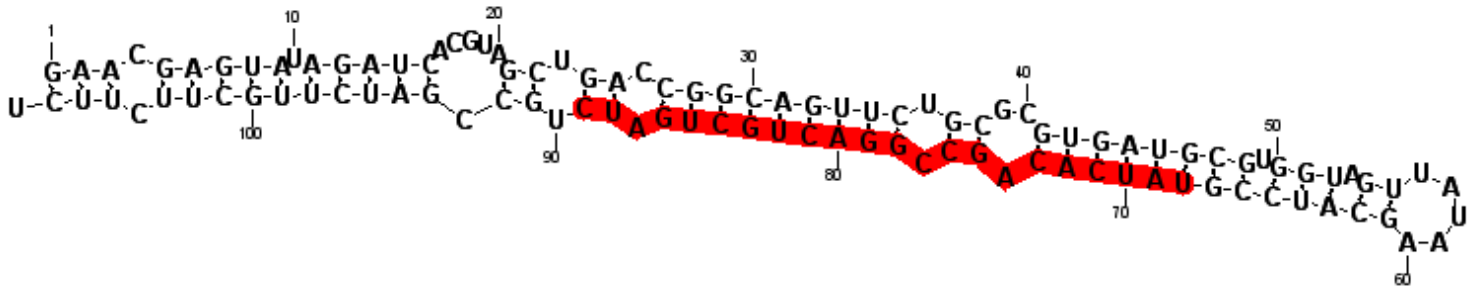
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.002	no	no	0.52/0.61	18/22/0.97	0.0	0.0	378	0	1	0	19	7	3arm	1	nd	0.18	1	418	1	na	na

Clusters

Located in cluster 30: sblock390_novel, block16493_novel

Families

Member of family miR-43 (seed AUCACAG): block8236_novel, block16493_novel, block8237_cand



```
seed        ------------------------------------------------------------------------------AUCACAG-------------------------------------
seed        -----------------------------------------------------------------------------UCACAGC-------------------------------------
seed        ----------------------------------------------------------------------------CAGCCGG-------------------------------------

            ------------------------------------------------------------------------------TATCACAGCCGGACTGCTGATC-----------------------
            -----------------------------------------------------------------------------TATCACAGCCGGACTGCTGAT------------------------
            ------------------------------------------------------------------------------TATCACAGCCGGACTGCTG--------------------------
            -----------------------------------------------------------------------------TATCACAGCCGGACTGCT---------------------------
            ------------------------------------------------------------------------------ATCACAGCCGGACTGCTGATC-----------------------
            ----------------------------------------------------------------------------ACAGCCGGACTGCTGATC-------------------------
ppacificus  -----------GAACGAGTATAGATCACGTAGCTGACCGGCAGTTCTGCGCGTGATGCGTGG---TAGTTATAAGCATCCGTATCACAGCCGGACTGCTGATCTGCCGATCTT--GCTTCTTCT---
cremanei    TGCTGTTATTCGAAGGTCTTCGGACCGC-------CCCTTCAGTT-GACTCGTGATCCGCCGACTTTGATATATGGA--CGAATCACAGTCA----CCTGATGGTACGGTCTTTGAATTCCTATAT
                        *** *  *   ** * *        **  *****   * ****** **  *   * * **** * *  ** ******* *      *****    ** ****    *** * *
      +++++             ++++++++++++++++++++++++++++++++++++++++++++++   ++++++++++++++++++++++++++++++++++++++++++++++  +++++++++
      +++++             ++++++++++++++++++++++++++++++++++++++++++++++   ++++++++++++++++++++++++++++++++++++++++++++++  +++++++++
ppacificus              (((.(((((.(((((.....((.((.(((((((((.((..((((((((.((   (.((.....)))))))))))))).)).)))))))))).)).)).))))))  )))).)))).
cremanei    ((((((.......(((..(((((((((.        .((.(((((.( ((((.(((((.(((((...........))))).  )).))))))))))    .)))).)).)..))))))..))))..))).....
```

ppacificus	chromosome:chrUn:160261330:160261437:1	Same_strand|Intronic_coding|NM_001109726|zgc:171740 ## {Repeats: no}
cremanei	chromosome:chrUn:126692870:126692991:-1	Opposite_strand|Intronic_coding|NM_073652 ## Same_strand|Intronic_coding|NM_067460

---

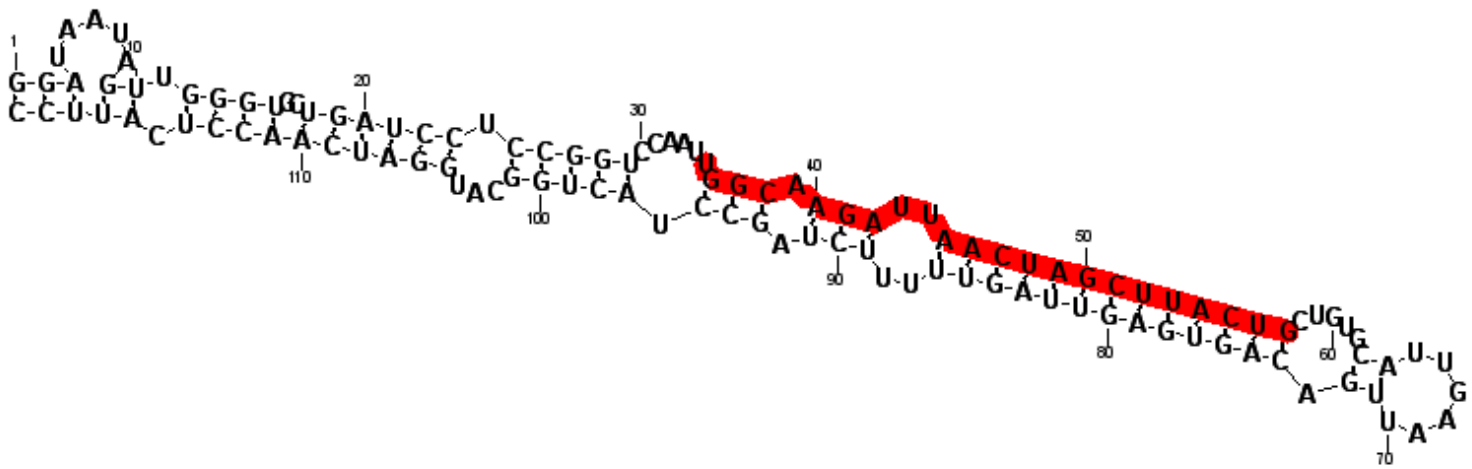
block5428 [novel_cloningHIGH_randfoldOK]

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	0.36/0.39	22/23/1.00	0.0	0.4	47	0	1	0	34	7	5arm	1	nd	0.14	2	47	1	na	na

Families

Member of family miR-73/74 (seed GGCAAGA): cel-mir-72, block5428_novel, block398_cand



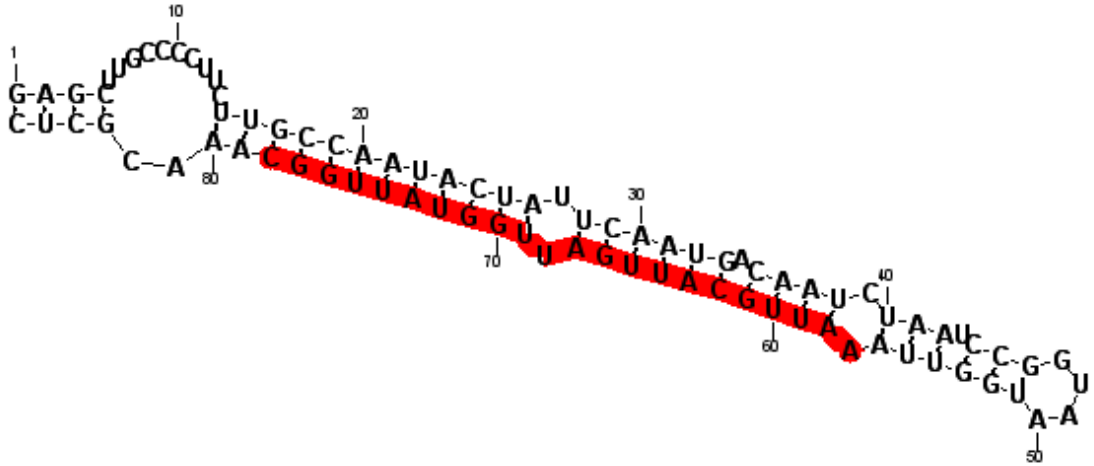
```
seed          ----------------------------------GGCAAGA-------------------------------------------------------------------------------
                                                                                                                                        
                                                                                                                                        
                                                                                                                                        
              ----------------------------------TGGCAAGATTAACTAGCTTACTG-------------------------------------------------------------
              ----------------------------------TGGCAAGATTAACTAGCTTACT--------------------------------------------------------------
ppacificus    GGATAATAGTTGGGTGCTGATCCTCCGGTCCAATTGGCAAGATTAACTAGCTTACTGCTGTGCATTGAATTGACAGTGAGTTAGTTTTTCTAGCCTACTGGCATGGATCAACCTCATTCC------
cremanei      ----------------------------------GGGCAAGAGTTATCAGCCT---------------------------GGCAGTTGCACGAGCCTCCTGGTGTTGGTTCTCCTCCT---------
celegans      ----------------------------------TGGCAAGATG-------------------------------TGTATTTGTGCAGCTCTCTTTCCATGTGTTCTTTAACTGCCAAAAAT(
cbrenneri     ----------------------------------TGGCAAGAACAATCGAAATGAC-----------------------ATCGTCAATACGAGCAT-------TTGATTCTCTCGTTT---------
                                                 *******                                                *     *       *   *        *
          ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
          ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
          ------------------------------------------------------------------------------------------------------------------------------
          ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++
ppacificus    (((.....((.(((((..((((((.(((((.....(((.((((..(((((((((((((.....((......)).))))))))))))..))))).))))).(((((...)))))))))))).(((((
cremanei                                       (((...((((..((((((((                          ((.((..((....)))).)))).)).)))))).))).))).
celegans                                       .((((..((.(                                   (((.((((.((((.......................)))))))).))
cbrenneri                                      .(((.((((..((((.(((((..                       .((((....)))))..)))       )))))).))).))).
```

ppacificus	chromosome:chrUn:128942353:128942472:-1	Same_strand|Intronic_non-coding|NM_022416|Stk32b ## Opposite_strand|Intronic_non-coding|NM_024598|C16orf57 ## {Repeats: no}
cremanei	chromosome:chrUn:41425731:41425890:-1	Opposite_strand|Exonic_coding|NM_062758 ## Same_strand|Intronic_coding|NM_062757
celegans	chromosome:chrX:13263671:13263830:-1	Opposite_strand|Boundary_coding|K09A11.1
cbrenneri	chromosome:chrUn:94869277:94869436:-1	Opposite_strand|Intronic_coding|NM_003428 ## Opposite_strand|Boundary_coding|NM_059343

block3569 [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	0.36/0.36	22/22/1.00	0.0	0.0	10	0	1	0	8	6	3arm	1	nd	0.05	1	10	1	na	na



```
                                                
```

ppacificus	chromosome:chrUn:90337401:90337486:-1	Opposite_strand|Intronic_coding|NM_001127378|RAP1A ## Same_strand|Intronic_coding|NM_001014722|peb ##

		Opposite_strand|Intronic_non-coding|NM_213405|zgc:56630 ## {Repeats: no}
cremanei	chromosome:chrUn:91386178:91386290:1	Opposite_strand|Intronic_coding|NM_202978
cbriggsae	chromosome:chrIII:1065049:1065174:-1	Same_strand|Intronic_coding|NM_061083 ## Opposite_strand|Intronic_coding|NM_001010845 ## {SimpF: trf}
celegans	chromosome:chrIV:12941316:12941441:1	Opposite_strand|Boundary_non-coding|C32H11.12
cbrenneri	chromosome:chrUn:74524331:74524456:1	intergenic
cjaponica	chromosome:chrUn:48172873:48172998:1	Opposite_strand|Intronic_coding|NM_021343

---

sblock390 [novel_cloningHIGH_multiarm_DicerOK_randfoldOK]

Hairpin parameters

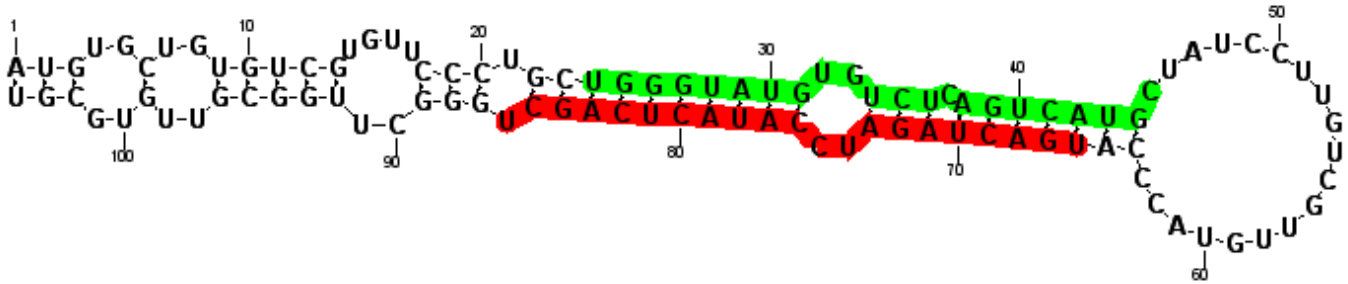
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.41/0.50	21/22/1.00	0.0 0.0	0.0 0.0	1 214	0 0	1 1	0 0	23 18	-1 2	5arm_loop 3arm	1 1	nd nd	0.23 0.14	2 2	226	1	3	3

Clusters

Located in cluster 30: sblock390_novel, block16493_novel

Families

Member of family miR-44/45/61 (seed GACUAGA): cbr-mir-45, sblock390_novel



```
seed        ------------------------------------------------------------------------GACUAGA-------------------------------------
seed        ------------------------------------------------------------------------UGACUAG-------------------------------------
seed        -----------------------------------GGGUAUG-------------------------------------------------------------------------------

            ------------------------------------------------------------------------TGACTAGATCCATACTCAGCT-------------------------
            -----------------------------------------------------------------------ATGACTAGATCCATACTCAGCT-------------------------
            -----------------------------------------------------------------------ATGACTAGATCCATACTCAGC--------------------------
            -----------------------------------TGGGTATG-TGTCTCAGTCATGC-----------------------------------------------------------
ppacificus  ATGTGCTGTGTCGTGTTC-------C--CTGC--TGGGTATG-TGTCTCAGTCATGCTATCC---TTGTCGTTGTACCCATGACTAGATCCATACTCAGCTGGGCTT-----------GGCGTTGTC
cremanei    ----TCTTTGGGGATTCCATGAATTC--GTGA--TAATTAT------TCAATCACC--------------------CACACGACTAGAC-----------------------------AATTCTCAA
cbriggsae   GTGCTCTTTGGAGGCGTCAGAGCACCTACCGA--CAAATATGTCTTATCAGTTTTCTTGGAT---CAGAGAT--------TGACTAGATTTGTTTTTGGTGAGGTCGCTTTTTTTGGAGGTTCTCTC
cbrenneri   ---GGCCAAGGAGACGAAGAGAGAATGGCCGATCTGGATGTG-CTCGTTAGTCATAGACGATACACAGAGAACGGTCATATGACTAGAGACACATTCAGCTTGGCCT-----------GGATCTC--
```

```
                 *   *  *                 *       * *      * * *                              *******                                  *
            +++++++++++++++++++++++       +  ++++  ++++++++ +++++++++++++++++++   +++++++++++++++++++++++++++++++++++++++++++           ++++++++
            +++++++++++++++++++++++       +  ++++  ++++++++ +++++++++++++++++++   +++++++++++++++++++++++++++++++++++++++++++           ++++++++
ppacificus      ((((((..((((((....(       (  (.((  (((((((( ..(((.(((((((......   .............))))))))))..))))))))))).)))..)           ))))..))
cremanei           ..(((((((((.........((  (((.  .......       .........                    ..))))).......                           ))))))))
cbriggsae       ((((...(((((((((.(((((((((((((((  .(((((.((((..((((.(((((.....   .)))))))        )))..)))).))))))))))).)))).)))))....)).)).))))
cbrenneri          ...............((((....((((((.(((((((((( (((..(((((((((((.................))).))))))))))).))))))))).)))))))).           ...))))
```

ppacificus	chromosome:chrUn:160261176:160261279:1	Same_strand|Intronic_coding|NM_001109726|zgc:171740 ## {Repeats: no}
cremanei	chromosome:chrUn:21269534:21269677:-1	Same_strand|Intronic_coding|NM_180914 ## Opposite_strand|Intronic_coding|NM_001031159
cbriggsae	chromosome:chrV_random:1139821:1139942:1	Opposite_strand|Intronic_coding|NM_070863 ## Same_strand|Intronic_coding|NM_062358
cbrenneri	chromosome:chrUn:172696445:172696554:1	intergenic

---

sblock219 [novel_cloningOK_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	0.56/0.58	18/24/0.89	0.0 0.0	0.3 0.0	7 1	0 0	1 1	0 0	19 18	7 7	5arm 3arm	1 1	nd nd	0.26 0.19	3 2	9	1	3	1

Clusters

Located in cluster 18: sblock218_novel, block9864_cand, sblock219_novel, block9867_cand, block9868_novel

```
                                                
```

```
                +++++     ++++++     +++++++++++++++++++++++++++++++++++++++++++++++++++++  +++++++++++++                    ++++++++++++++++++++++++
                -----     ------     -----------------------------------------------------  -------------                    ------------------------
                +++++     ++++++     +++++++++++++++++++++++++++++++++++++++++++++++++++++  +++++++++++++                    ++++++++++++++++++++++++
ppacificus                .((((..     ((((.....((((((((((...((.((((((.((((...(((((...))))))))  )).)))))).))..                    )))))))))))).....))))..)
cremanei            ......(((((((...(   ((((((((.((....(                    (((.......))))))    .)))))))...))))..                    )))))))
cbriggsae                  ((((((((((((((((((((((((....                                  ))))))))))))))))..)))          )))))))
celegans               ((( ((((.....((((.((((.((((((.((((.              .((((((....((...(((..(((((....)))))).))))...))))))))))))))))).))))..))))...
cbrenneri                  (((((((.                    ..((                (((((.((((..((.....)))))))))))).                    )))))))
cjaponica                  (((((.(((((.(((((.(((((..((.....))..))).....)))   .))))))..))))))..))))).............                    ....
```

ppacificus	chromosome:chrUn:57291904:57292002:1	Same_strand|Intronic_non-coding|NM_053103|Entpd7 ## Opposite_strand|Intronic_coding|NM_001081764|COL2A1 ## Same_strand|Intronic_coding|NM_000421|KRT10 ## {Repeats: no}
cremanei	chromosome:chrUn:146216710:146216779:-1	Same_strand|Boundary_coding|NM_060035
cbriggsae	chromosome:chrI:2105032:2105170:-1	Same_strand|Intronic_coding|NM_174569 ## Opposite_strand|Intronic_coding|NM_001107428
celegans	chromosome:chrV:17325808:17325924:1	intergenic
cbrenneri	chromosome:chrUn:20877422:20877560:-1	Opposite_strand|Intronic_coding|NM_004834
cjaponica	chromosome:chrUn:140207356:140207438:-1	Same_strand|Intronic_coding|NM_066364 ## Opposite_strand|Intronic_coding|NR_003947

---

block7029 [novel_cloningOK_randfoldOK]

Hairpin parameters

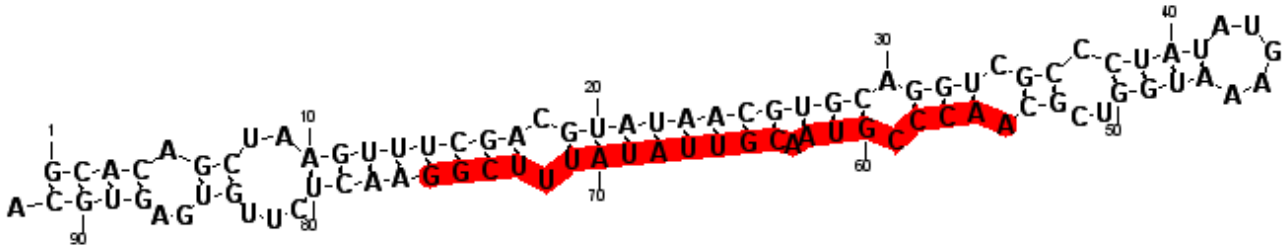
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.38/0.41	21/22/1.00	0.0	0.0	16	0	1	0	16	8	3arm	1	nd	0.14	1	21	1	na	na

Clusters

Located in cluster 14: block7028_novel, block7029_novel, sblock162_novel

Families

Member of family miR-51/52/55 (seed ACCCGUA): block7028_novel, block7029_novel, block9544_novel, block15318_novel, block15319_novel, sblock162_novel, sblock213_novel, sblock279_novel, sblock280_novel, block9543_cand



```
seed      ----------------------------------------------------------------------ACCCGUA-----------------------------------------
```

```
                 ----------------------------------------------------------------------AACCCGTA------------------ACGTTATATTTCGG------------
                 ----------------------------------------------------------------------AACCCGTA------------------ACGTTATATTTCG-------------
ppacificus       -----------------GCACAGCTAAGT---TTCGACGTATAACGTGCAGGTCGCCCTATATGAAATGGTCGCAACCCGTA------------------ACGTTATATTTCGGAACTCTTGTGAG
celegans         ATTCTAGTTTATTACAGGTTCTGTTACGCATGTTCCACATATGGCGTGGTACTCGGTC-ATAAGATTTATTGCAAACCCGTATGTAGGAAATGTGGTGACAAATTAGGTTGGAGATGTGTTGGGAT
                                 *  * * ** *    *** ** ***  ****    ***  * *** **  *  *   ********                  *  ***  **   **  * *** **
            +++++                ++++++++++++   ++++++++++++++++++++++++++++++++++++++++++                  ++++++++++++++++++++++++++
            +++++                ++++++++++++   ++++++++++++++++++++++++++++++++++++++++++                  ++++++++++++++++++++++++++
            +++++                ++++++++++++   ++++++++++++++++++++++++++++++++++++++++++                  ++++++++++++++++++++++++++
            +++++                ++++++++++++   ++++++++++++++++++++++++++++++++++++++++++                  ++++++++++++++++++++++++++
            +++++                ++++++++++++   ++++++++++++++++++++++++++++++++++++++++++                  ++++++++++++++++++++++++++
            +++++                ++++++++++++   ++++++++++++++++++++++++++++++++++++++++++                  ++++++++++++++++++++++++++
            +++++                ++++++++++++   ++++++++++++++++++++++++++++++++++++++++++                  ++++++++++++++++++++++++++
            +++++                ++++++++++++   ++++++++++++++++++++++++++++++++++++++++++                  ++++++++++++++++++++++++++
            +++++                ++++++++++++   ++++++++++++++++++++++++++++++++++++++++++                  ++++++++++++++++++++++++++
            -----                ------------   --------------------------------------------------                  --------------------------
            +++++                ++++++++++++   ++++++++++++++++++++++++++++++++++++++++++                  ++++++++++++++++++++++++++
            -----                ------------   --------------------------------------------------                  --------------------------
ppacificus                       ((((.((..(((   (((((.(((((((((((.(((.((.((((.....))))..)).)))).)))                  .)))))))).))))))))...))..)
celegans         (((((((..(((((.(((.((.(((((((((.((((((((((((.((.(((...(((( ....)))))...)))..))))))))))).))))))))).))))....)).))))..)))))..)))))))
```

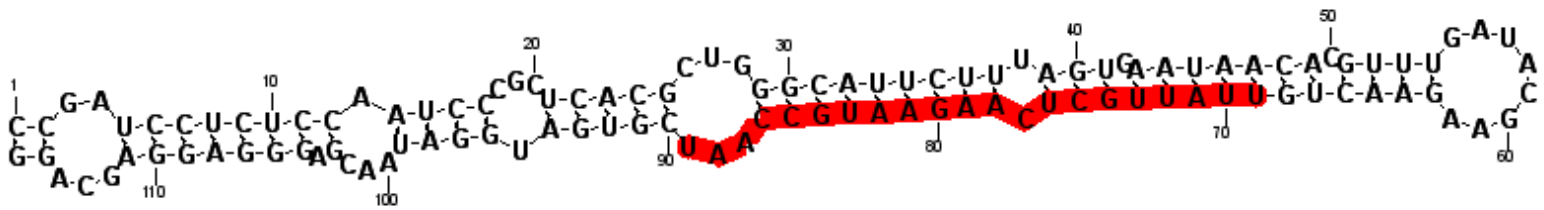
ppacificus	chromosome:chrUn:2088476:2088567:1	Same_strand|Intronic_non-coding|NM_080105|cpo ## Same_strand|Intronic_coding|NM_169781|cpo ## Opposite_strand|Intronic_non-coding|NM_010570|Irs1 ## Opposite_strand|Intronic_coding|NM_184109|Rtl1 ## {Repeats: no}
celegans	chromosome:chrV:19429504:19429628:-1	Same_strand|Boundary_coding|C25F9.1

---

block6855 [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	0.33/0.39	18/21/0.71	0.0	1.0	12	0	1	0	27	6	3arm	1	nd	0.11	1	14	1	na	na



```
seed             ----------------------------------------------------------------------UAUUGCU-----------------------------------------
```

```
                 ------------------------------------------------------------------------------TTATTGCTCAA-GAATGCCAAT--------------------------
                 ------------------------------------------------------------------------------TTATTGCTCAA-GAATGCC-----------------------------
                 ------------------------------------------------------------------------------TTATTGCTCAA-GAATGCCAA---------------------------
ppacificus       CCGATCCTCTCCAATCCCGCTCACGCTGGGCATTCTTT----AGTGAATAACACGTTTGATACGAAGAAC-----TGTTATTGCTCAA-GAATGCCAATCGTGATGGATAACGAGGGAGGAGCAGG
cremanei         ---------------------------ATGAGCCTATTCACAAGGTTGCCAAAAAAAAC-AAAAGGCGAT--------TTATTGCTAAT-AGTAGCTAGT---------------------------
cbriggsae        ---------------------------TGATTCTGATTCAGAAGCCGTATCGAGAATTTTGTTC------------TGGTATTGCTAGA-AAGAAAAA-----------------------------
cbrenneri        ------------------------AAACGGTATTCTTT----GGTTAATAATAAGGATGGCATCACGACTCATTATATTATTGCTCAA-GAATACCCTTT--------------------------
cjaponica        -----------------------GCTAAGAGCCATCTTC----GGCGGGTAATAGCCAT-ATACGACGGC------TAATATTGCTTAATGGCTAACAGC---------------------------
                                                   **                                                 *******
                 ---------------------------------------------    ----------------------------     -------------- ---------------------------------------
                 +++++++++++++++++++++++++++++++++++++++++++++    ++++++++++++++++++++++++++++     ++++++++++++++ +++++++++++++++++++++++++++++++++++
                 ---------------------------------------------    ----------------------------     -------------- ---------------------------------------
                 +++++++++++++++++++++++++++++++++++++++++++++    ++++++++++++++++++++++++++++     ++++++++++++++ +++++++++++++++++++++++++++++++++++
                 ---------------------------------------------    ----------------------------     -------------- ---------------------------------------
                 +++++++++++++++++++++++++++++++++++++++++++++    ++++++++++++++++++++++++++++     ++++++++++++++ +++++++++++++++++++++++++++++++++++
                 ---------------------------------------------    ----------------------------     -------------- ---------------------------------------
ppacificus       ((..(((((((..((((...((((((...(((((((((.    (((.(((((((.((((........))))     )))))))))).)) )))))))...)))))).))))).....)))))))...))
cremanei                                   ...(((((((((..((((.((((((.......... ....))))))))        ...))))..))))  ))..))))...
cbriggsae                                  ...((((..((((...((((.((((((.((((((...))))))             ))))))).))).)) )))))...
cbrenneri                                ....(((((((((.    (((.(((((((((..(((((.........))))).))))))))))).)) )))))))....
cjaponica                             (((...(((((((....    (((.((((.((((((.. .......)))      )).))))))))..))))))...)))
```

ppacificus	chromosome:chrUn:170378240:170378355:-1	Opposite_strand|Intronic_non-coding|NM_000209|PDX1 ## Same_strand|Intronic_non-coding|NM_016248|AKAP11 ## {Repeats: no}
cremanei	chromosome:chrUn:70810702:70810857:-1	intergenic
cbriggsae	chromosome:chrV:13083902:13084057:1	Same_strand|Intronic_coding|NM_063725 ## Opposite_strand|Intronic_coding|NM_074696 ## Same_strand|Boundary_non-coding|NM_074680
cbrenneri	chromosome:chrUn:164687999:164688154:-1	intergenic
cjaponica	chromosome:chrUn:88304351:88304506:-1	intergenic

---

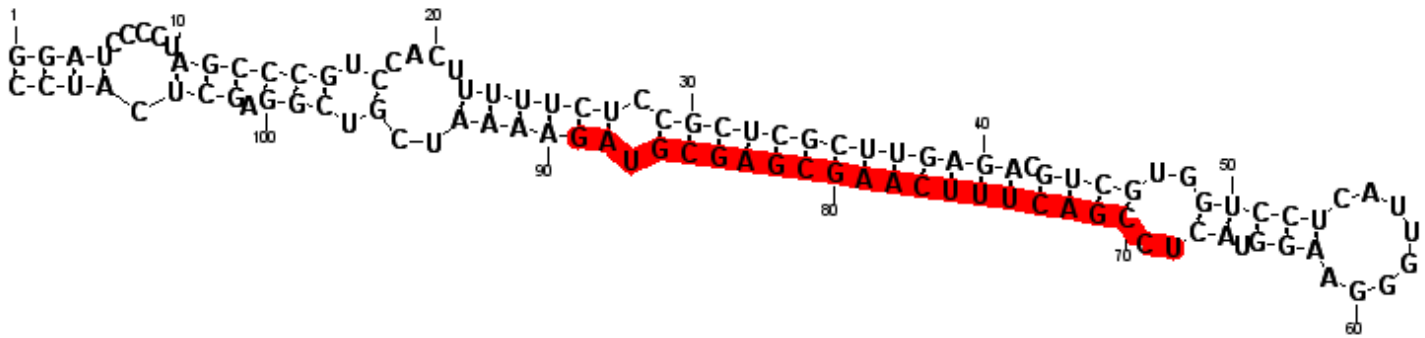
block3107 [novel_cloningHIGH_randfoldOK]

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	0.52/0.55	20/22/1.00	0.0	0.0	117	0	1	0	20	6	3arm	1	nd	0.09	1	140	1	na	na

Clusters

Located in cluster 6: block3104_novel, block3105_cand, cel-mir-63, block3107_novel, sblock77_cand, cel-mir-63



```
seed          ------------------------------------------------------------------------------CCGACUU----------------------------------
              ------------------------------------------------------------------------------TCCGACTTTCAAGCGAGCGTAG--------------------
              ------------------------------------------------------------------------------TCCGACTTTCAAGCGAGCGT----------------------
              ------------------------------------------------------------------------------TCCGACTTTCAAGCGAGCGTA---------------------
ppacificus    GGATCCCCTAGCCCGTCCACTTTTTCTCCGCTCGCTTGAGACGTCGTGGTC---CTCATTGGGAAG-----------GTACTCCGACTTTCAAGCGAGCGTAGAAAATCGTCGGAGCTCATCC
cremanei      ----------------------------------------CCGGCTTCGACAGAAAGATTGCGAAGCAGAACGATCTGTGCACCGACTTTCAAGCGA-----------AGACGG---------
celegans      ------------------------------GCGCGGTCGGGTCGTGGCCGTC-GGCGCCCTGGGTAG-----------G--CGCCGACTTGCACCCG------------CGGCGA---------
cjaponica     ------------------------------GGCGTTGTTGCCGTAGTCGAT-GTCACAATTTGATG-----------GATTTCCGACTTACGA----------------CTTCAG-----CTCA
                                                                  **     *          *  *  *           *    ******* *                      *
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++   +++++++++++           +++++++++++++++++++++++++++++++++++++++++++++++
            ------------------------------------------------------------   ------------           ------------------------------------------------
            ------------------------------------------------------------   ------------           ------------------------------------------------
            ------------------------------------------------------------   ------------           ------------------------------------------------
ppacificus    ((((.....((((((.....((((((.(((((((((((((.(((((..(((   ((........))           ).))..))))))))))))))))).)))))).....))).))).))))
cremanei                                                  (((.((((((...(((((.(((....((((((....))))))....)))))))))...)))           )).)))
celegans                                        .(((.((.(((((.(((((..((( (((((((.......)           )  )))))))))))))))           ).)))).
cjaponica                                        ...((((....(((((((((.. (((.(((.......))           )))...))))))).))))).                ...)))     ).....
```

ppacificus	chromosome:chrUn:81422821:81422929:-1	Same_strand|Intronic_coding|NM_209655|AGOS_ADR206W ## Opposite_strand|Intronic_non-coding|NM_001108251|Ubqln2 ## Opposite_strand|Intronic_coding|NM_001064407|Os06g0561200 ## {Repeats: no}
cremanei	chromosome:chrUn:12039729:12039877:-1	Same_strand|Intronic_coding|NM_069070
celegans	chromosome:chrIII:10634025:10634173:1	intergenic
cjaponica	chromosome:chrUn:78866317:78866465:1	Same_strand|Intronic_coding|NM_000092

---

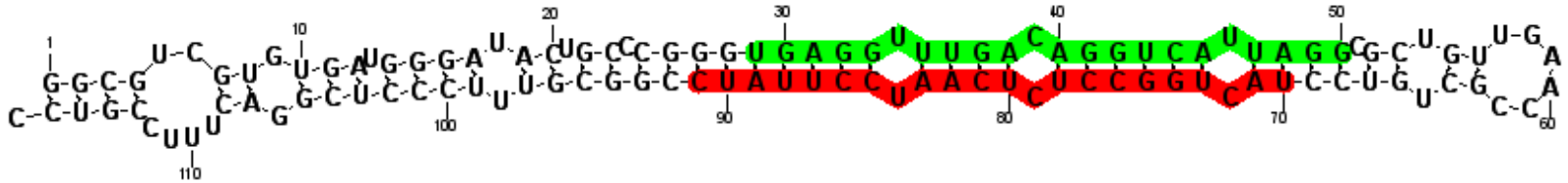
sblock125 [novel_cloningHIGH_multiarm_DicerOK_randfoldOK]

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	0.45/0.45	22/22/1.00	0.0 0.0	0.0 0.0	11 18	0 0	1 1	0 0	28 26	6 7	5arm 3arm	1 1	nd nd	0.18 0.14	1 1	29	1	2	2

Clusters

Located in cluster 12: block5311_cand, sblock125_novel



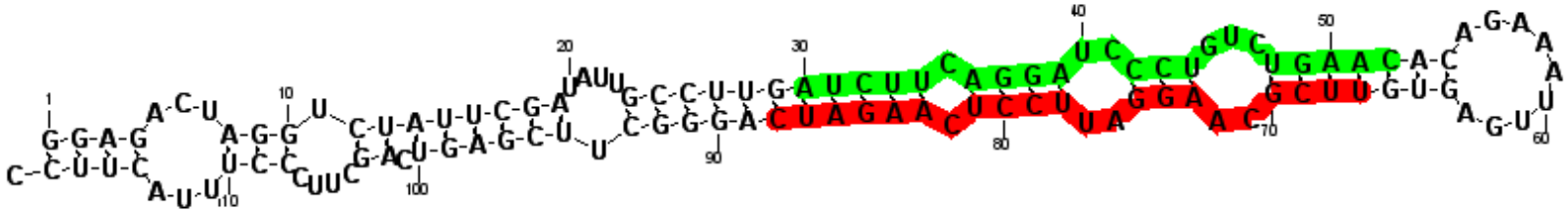
```
                                                
```

Clusters

Located in cluster 21: sblock239_novel, sblock240_novel, sblock241_novel, sblock242_novel, sblock243_novel

Families

Member of family novel2 (seed UCGCAAG): sblock239_novel, sblock240_novel, sblock241_novel, sblock242_novel, sblock243_novel, sblock5_novel, sblock6_novel, sblock9_novel, sblock7_cand



```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
seed      ------------------------------------------------------------------UCGCAAG-----------------------------------------------
seed      ------------------------------------------------------------------CGCAAGG-----------------------------------------------
seed      -------------------------------UCUUCAG-------------------------------------------------------------------------------

          ------------------------------------------------------------------TTCGCAAGGA----TTCCTCAAGATC-----------------------------
          ------------------------------------------------------------------TCGCAAGGA----TTCCTCAAGATC-----------------------------
          ------------------------------------------------------------------TTCGCAAGGA----TTCCTCAAGAT------------------------------
          ------------------------------ATCTTCAGGATCCCTGTCTGAAC-----------------------------------------------------------------
ppacificus -GGAGACTAGGTCTATTCGATATTGCCTTGATCTTCAGGATCCCTGTCTGAACACAGAAATTGAGTGTTCGCAAGGA----TTCCTCAAGATCAGGGCTTCGAGTCAGCTTCCCTTTACTTCC
cremanei  TGGAAGAT-----------------------------GGACTCCTGAAGGAACACTGAAAATTGTGGATCGCAAGAAGCACATCTTCAA-----------------------------
cjaponica -GGCCTATCGCGCAACCTATTATAGGCCTATCGCGCAAAA--CCTGTGGGATC-------------GGTCGCAAGGA----AGCGTCAT-----------------------------TGCC
           **    *                                 *  ****   ** *             * ******* *      * ***
          ----- ------------------------------------------------------------------------------    ---------------------------------------------
ppacificus  ((((...(((.(((((((((....(((((((((.((((..(((...(((((((.........)))))))..))).    .)))).))))))))))).)))))).))....)))...)))).
cremanei  ..((((((                                (..((.((...((..(((........)))..))...)).))..))))))).
cjaponica   (((..((.((((..(((.....((((.(((.((((...  ..)))).))).             ))))...))).    .)))).))                                .)))
```

ppacificus	chromosome:chrUn:70644944:70645061:1	Opposite_strand|Intronic_coding|NM_077023|sulp-3 ## {SimpF: trf}
cremanei	chromosome:chrUn:17135136:17135293:1	Same_strand|Exonic_coding|NM_001011069 ## Same_strand|Boundary_coding|NM_001004599 ## Same_strand|Boundary_non-coding|NM_001050414
cjaponica	chromosome:chrUn:9659728:9659885:1	intergenic

---

block15318 [novel_cloningHIGH_randfoldOK]

Hairpin parameters

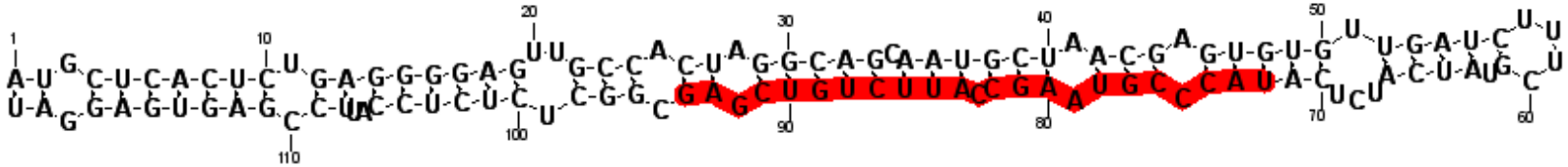
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.47/0.55	18/23/0.99	0.0	0.0	1042	0	1	0	26	9	3arm	1	nd	0.22	1	1137	1	na	na

Clusters

Located in cluster 29: block15318_novel, block15319_novel

Families

Member of family miR-51/52/55 (seed ACCCGUA): block7028_novel, block7029_novel, block9544_novel, block15318_novel, block15319_novel, sblock162_novel, sblock213_novel, sblock279_novel, sblock280_novel, block9543_cand



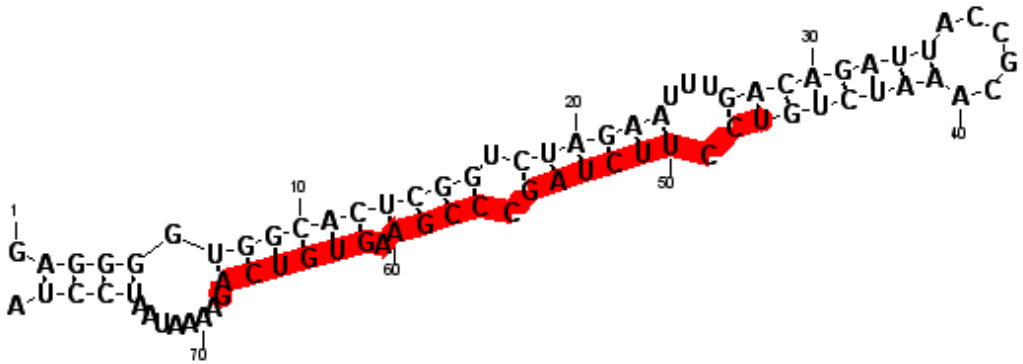
```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
seed        ------------------------------------------------------------------------ACCCGUA----------------------------------------
seed        ------------------------------------------------------------------------------GUAAGCC-----------------------------------
seed        ------------------------------------------------------------------------CCCGUAA----------------------------------------
seed        ------------------------------------------------------------------------UACCCGU----------------------------------------

            ------------------------------------------------------------------------TACCCGTAAGCCATTCTGTCGAG-------------------------- 2
            ------------------------------------------------------------------------TACCCGTAAGCCATTCTGTCG----------------------------- 2
            ------------------------------------------------------------------------TACCCGTAAGCCATTCTGTC------------------------------ 2
            ------------------------------------------------------------------------TACCCGTAAGCCATTCTGT------------------------------- 1
            ------------------------------------------------------------------------------CGTAAGCCATTCTGTCGAG-------------------------- 1
            ------------------------------------------------------------------------TACCCGTAAGCCATTCTG-------------------------------- 1
            ------------------------------------------------------------------------ATACCCGTAAGCCATTCTGTCG----------------------------- 2
            ------------------------------------------------------------------------TACCCGTAAGCCATTCTGTCGA---------------------------- 2
            ------------------------------------------------------------------------ACCCGTAAGCCATTCTGTCGAG---------------------------- 2
ppacificus  atgctcactctgaggggagttgccactaggcagcaatgctaacgagtgtgttgatctttcgtatcatctcaTACCCGTAAGCCATTCTGTCGAGcggctctctccattccgagtgaggat
            ***********************************************************************************************************************
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ N
            ---------------------------------------------------------------------------------------------------------------------------- N
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ N
            ---------------------------------------------------------------------------------------------------------------------------- N
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ N
ppacificus  ((.(((((((.((((((((..(((.((.(((((.((((((.(((.(((((.((((.......)))).....))))).))).))).))))))))..))).))))).))))))..)).))))))).))  1
```

ppacificus	chromosome:chrUn:139887484:139887603:1	Same_strand|Intronic_coding|NM_023879|Rpgrip1 ## Opposite_strand|Intronic_non-coding|NM_100443|5PTASE13/AT5PTASE13 ## Same_strand|Intronic_non-coding|NM_019711|Rbms2 ## {Repeats: no}

block268 [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	0.55/0.55	22/22/1.00	0.0	0.0	19	0	1	0	12	6	3arm	1	nd	0.23	2	19	1	na	na



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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
seed        ------------------------------------------------------------------------CCUUCUA----------------------------------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
            ------------------------------------------------------------------------TCCTTCTAGCC-----------CGAAGTGTCAG----------------
ppacificus  -----------GAGGGGTGGCACTCGGTCTAG-----AATTTGACAGATTACCG---CAAATC--------TGTCCTTCTAGCC-----------CGAAGTGTCAGAAAATAATCCTA----
cremanei    --------------------TTCTAGATTTGAGAGGAGAACTTAAAAACTT------AAAACATCATGTATTTTCCTTCTAGCC-----------TCAATTCTGAA----------------
cbriggsae   -----------AGGGAGAAGTATTAGACTTTAGGATTAATCTTACGTACCCGA----AAAACA--------AGACCTTCTAACG-----------TCATCTGCCCA----------------
cbrenneri   AGTTTGAAAAAAAAAAAAAGTTTTTTGAGCTCGCGCTTCTCCTAAAGGGTGTTTGTTTTAAAAA--------CATCCTTCTAGTGGTGCTGGGTTTTCAGATATCTTTCACTCATTTTGGATT
                                      * *   *           * *              ***             *******                *  *
        -----           ---------------------     -----------------   ------        -------------           ------------------------    -----
ppacificus              .(((((.(((((((((((.((((     ((...(((((((((....   ..))))        ))))).)))))))..)           )))).))))))........)))).
cremanei                         ...((((.(((((...((((...((((.((..      ..........)).)))...))))...)           ))))).))))..
cbriggsae               .(((...((.....(((.((((((....((((..........    .....)        )))..)))))))..)           ))..)).))).
cbrenneri   (((((..(((.....((((...(((((((((((((((....((((((((((((.......)))        )))))))..))).))))).))))..))))))...))))).....)))..))))
```

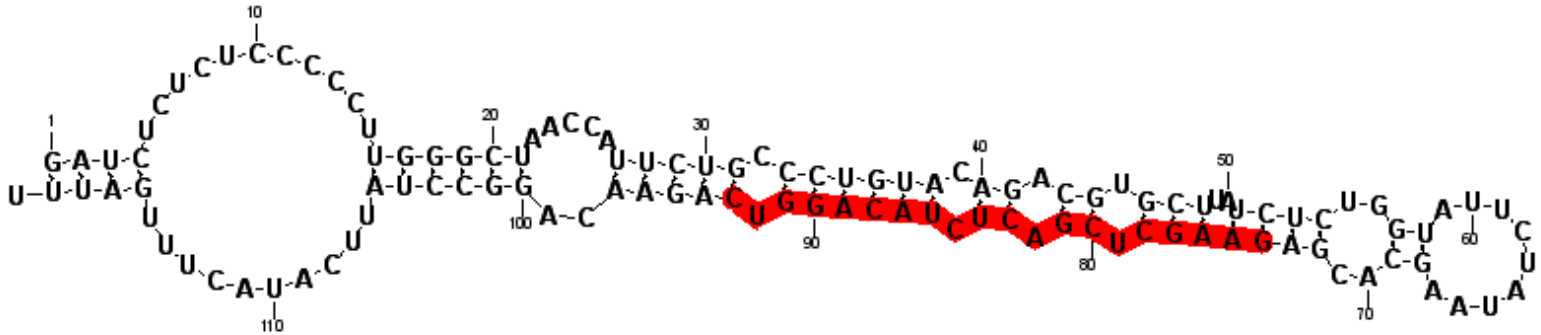
ppacificus	chromosome:chrUn:11709201:11709280:-1	Opposite_strand|Intronic_non-coding|NM_172085|Pou3f2 ## {Repeats: no}
cremanei	chromosome:chrUn:53741562:53741681:1	Same_strand|Intronic_coding|NM_067125
cbriggsae	chromosome:chrV:565452:565571:-1	Opposite_strand|Intronic_coding|NM_071035 ## Same_strand|Intronic_coding|NM_001847
cbrenneri	chromosome:chrUn:188247856:188247969:-1	intergenic

---

block15468 [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	0.006	no	no	0.53/0.55	19/20/0.81	0.0	0.0	26	0	1	0	27	6	3arm	1	nd	0.20	1	32	1	na	na



```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
seed                 ------------------------------------------------------------------------AAGCUCG--------------------------------------
                     ------------------------------------------------------------------------GAAGCTCGACTCTACAGGTC----------------------------  2
                     ------------------------------------------------------------------------GAAGCTCGACTCTACAGGT-----------------------------  1
ppacificus           gatctctctccccttgggctaaccattctgccctgtacagacgtgcttatctctggtattctataagcacgaGAAGCTCGACTCTACAGGTCagaacaggcctattcatactttgattt
                     ***********************************************************************************************************************
                     ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ N
                     ------------------------------------------------------------------------------------------------------------------------ N
                     ------------------------------------------------------------------------------------------------------------------------ N
                     ------------------------------------------------------------------------------------------------------------------------ N
                     ------------------------------------------------------------------------------------------------------------------------ N
                     ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ N
                     ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ N
                     ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ N
                     ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ N
                     ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ N
                     ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ N
                     ------------------------------------------------------------------------------------------------------------------------ N
                     ------------------------------------------------------------------------------------------------------------------------ N
ppacificus           ((((...........((((((.....(((((.(((((((.((.((.(((..((((..((.........))..))))))).)).)).)))))).)))))..)))))).........)))).      0
```

ppacificus	chromosome:chrUn:143574306:143574425:1	Same_strand|Intronic_coding|NM_067172|php-3 ## Opposite_strand|Intronic_coding|NM_007674|Cdx4 ## Opposite_strand|Intronic_non-coding|NM_010461|Hoxb8 ## {Repeats: no}

---

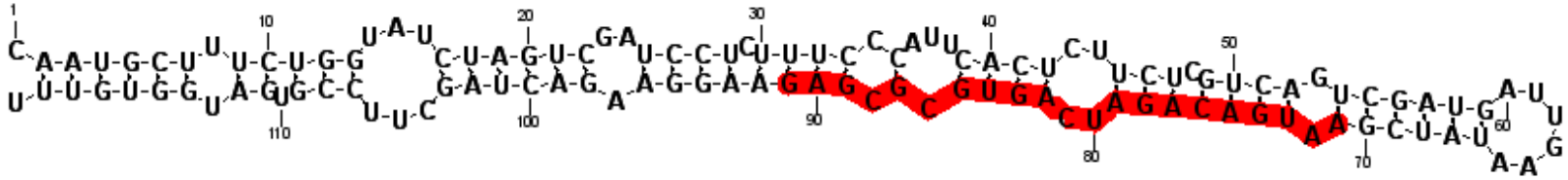
block16447 [novel_cloningOK_randfoldOK]

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	0.52/0.53	19/21/0.79	0.0	0.0	15	0	1	0	29	5	3arm	5	nd	0.29	3	19	1	na	na

Families

Member of family novel3 (seed AUGACAG): block6545_novel, block6555_novel, block6559_novel, block6568_novel, block16444_novel, block16447_novel, block16470_cand



```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
seed        ------------------------------------------------------------------------AUGACAG-----------------------------------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
            ------------------------------------------------------------------------AATGACAGATCAGTGCGCGAG------------------------------ 2
            ------------------------------------------------------------------------AATGACAGATCAGTGCGCG------------------------------- 1
ppacificus  caatgctttctggtatctagtcgatcctctttcccattcactcttctcgtcagtcgatgattgaatatcgAATGACAGATCAGTGCGCGAGaaggaagactagcttccgtgatggtgttt
            ****************************************************************************************************************************
            ---------------------------------------------------------------------------------------------------------------------------- N
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ N
ppacificus  .(((((((.(((((...(((((((..((((.((((.....((((..(((.((((.((((((.....)))))))).)))))))..))))...)))))))))).))))))...))))..)).))))))).  1
```

ppacificus	chromosome:chrUn:158438638:158438757:1	Opposite_strand|Intronic_non-coding|NM_001106424|RGD1562890 ## Same_strand|Intronic_non-coding|NM_005654|NR2F1 ## {Repeats: no}

---

sblock146 [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	0.33/0.57	20/23/1.00	0.0 0.0	0.0 0.0	49 1	0 0	1 1	0 0	24 19	3 5	5arm 3arm	1 1	nd nd	0.09 0.09	1 1	52	1	2	2

```
seed        -------------------------AUGGUAA-------------------------------------------------------------------------------
seed        ------------------------------------------------------------------------------CGCUCAA-----------------------------------

            ------------------------AATGGTAAGAGA------------TTGAAGTGACT-------------------------------------------------------------23
            ------------------------AATGGTAAGAGA------------TTGAAGTG----------------------------------------------------------------20
            ------------------------AATGGTAAGAGA------------TTGAAGTGA---------------------------------------------------------------21
            ------------------------------------------------------------------------------CCGCTCAATCTCCTTGCCATAGC-------------------23
ppacificus  CGCAGATTTCTGAGTGAGTCCGGTAATGGTAAGAGA------------TTGAAGTGACTGTTGCACATTGAAGGCAGCCGCTCAATCTCCTTGCCATAGCCGGCAACTCAGAAAGACGA
cremanei    -------------------------AATGGTAAGAGAGGCTGA-TGACAATCGTCTAACAAAGACG-ATTGAGCGCACGTAGCCTTTGACTGTGCCGTA---------------------
cbriggsae   -GGACGCCCTCCATCAGAAAGTGCAATGGTAAGAGT-TCTGA-TGTGGTCAGCCACAACACGGTACGCCATATCAACTCCGTCCTTATCTTCGTCTCCAATGTGTCC------------
celegans    -----------------------GAAATGGTAAGAGA-------GGTCGTTATTGTGACTAGGACACACTAGGCGACTCCACTTATTCATCATTCAATAACCCACT--------------
cjaponica   -------------------------AATGGTAATCGATCGTGAGTATCTTCTGCTCGAAGAGGATA--------GAACACAGTCTATGACCACG---------------------------
                                      ********  *                     *                               *
            ++++++++++++++++++++++++++++++++++++++++++++            ++++++++++++++++++++++++++++++++++++++
```

Hairpin parameters

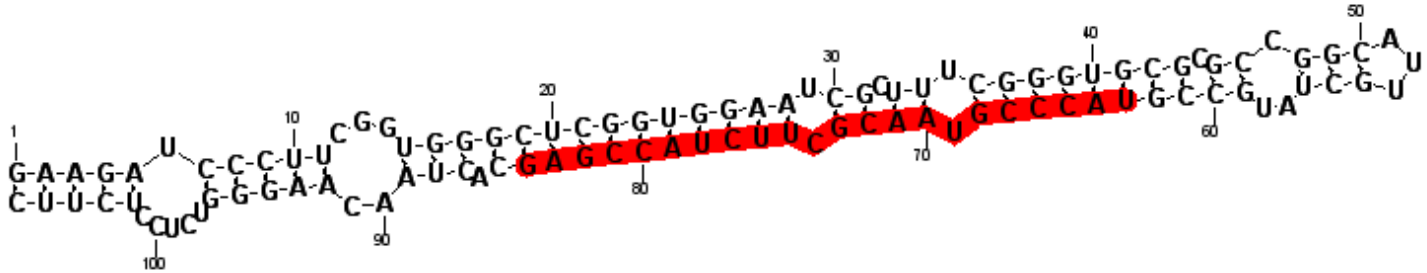
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.55/0.55	20/22/1.00	0.0	0.0	28	0	1	0	22	9	3arm	1	nd	0.09	1	32	1	na	na

Clusters

Located in cluster 29: block15318_novel, block15319_novel

Families

Member of family miR-51/52/55 (seed ACCCGUA): block7028_novel, block7029_novel, block9544_novel, block15318_novel, block15319_novel, sblock162_novel, sblock213_novel, sblock279_novel, sblock280_novel, block9543_cand



```
                                                                                                                                                                  n
seed        ------------------------------------------------------------------ACCCGUA-----------------------------------------------
                                                                                                                                                                  
                                                                                                                                                                  
                                                                                                                                                                  
            ------------------------------------------------------------------TACCCGTA-ACGCTTCTACCGAG-----------------------------  22
            ------------------------------------------------------------------TACCCGTA-ACGCTTCTACCG------------------------------  20
ppacificus  GAAGATCCCTTCGGTGGGCTCGGTGGAATCGCTTTCGGGTGCGCGCCGGCA--TTGC-TAT-GCCGTACCCGTA-ACGCTTCTACCGAGCACTAACAAGGGTCTCCTCTTC-------
celegans    ----------CTCGTAAAAGCAACTGGAACTC-TTAGTGTTTCATTCGAAATGTTTCGAAT-GCCACACCCGTACACATTT-GAATGAG-----------------------------
cjaponica   TAGGG-----TCAGGGGACTCGGCTGAAGC---TTATCGTGTTTATCTGCA--TTTTGTATAGATATACCCGTATAAGTTTCCGCTGAGC--------------CCCCTTTGACTCTA
                          *      *    * * *   **   **      *   *  **    ** *    ******* *   **     ***
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++  ++++ +++ ++++++++++++ +++++++++++++++++++++++++++++++++++       +++++ NM_
            ------------------------------------------------------  ---- --- ------------ -----------------------------------       ----- NM_
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++  ++++ +++ ++++++++++++ +++++++++++++++++++++++++++++++++++       +++++ NM_
            ------------------------------------------------------  ---- --- ------------ -----------------------------------       ----- NM_
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++  ++++ +++ ++++++++++++ +++++++++++++++++++++++++++++++++++       +++++ NM_
ppacificus  (((((.((((((...(((((((((((((.((.((.(((((((((.((.((((.  ..)) ).. )))))))))).) )))).))))))))))).))))..)))))....)))))             1.0
                                                                                                                                              -51
celegans                ((((((.....(((.((...... ...((((..(((((((((....))))))) )..))))).......)).)) ).))))                                  0.7
                                                                                                                                              -15
cjaponica   (((((     (((((((.((((((.(((((   ((((((.((.(((((((.  ....))..))))).))).)).))))))))).))))))).              ))))))..))))))      1.0
                                                                                                                                              -45
```

ppacificus	chromosome:chrUn:139887636:139887741:1	Same_strand|Intronic_coding|NM_023879|Rpgrip1 ## Opposite_strand|Intronic_non-coding|NM_100443|5PTASE13/AT5PTASE13 ## Same_strand|Intronic_non-coding|NM_019711|Rbms2 ## {Repeats: no}
celegans	chromosome:chrIV:9107636:9107781:-1	intergenic
cjaponica	chromosome:chrUn:66592796:66592889:-1	Same_strand|Intronic_coding|NM_001027065

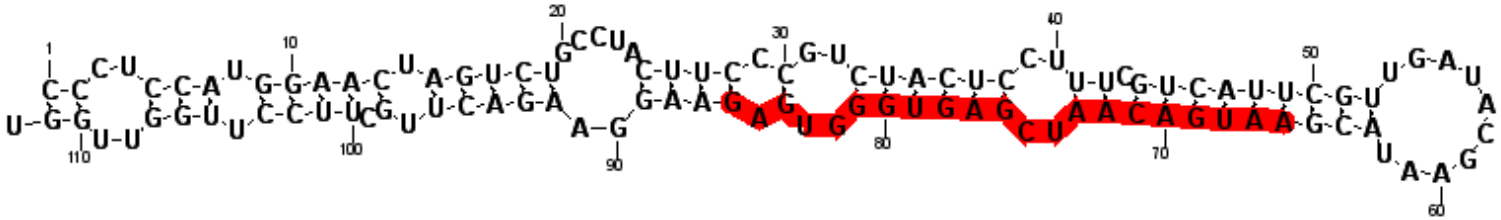
block4989 [novel_cloningOK_randfoldOK]

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	0.48/0.50	20/21/1.00	0.0	0.0	11	0	1	0	26	3	3arm	2	nd	0.14	2	12	1	na	na

Families

Member of family novel5 (seed AUGACAA): block4989_novel, block11618_novel, block13895_novel



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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
seed        ------------------------------------------------------------------------AUGACAA----------------------------------------
seed        ------------------------------------------------------------------------UGACAAU---------------------------------------

            ------------------------------------------------------------------------A--ATGACAATC-GAGTGGGTGAG--------------------------  21
            ------------------------------------------------------------------------ATGACAATC-GAGTGGGTGAG--------------------------  20
ppacificus  CCCTCCATGGAACTAGTCTGCCTACTTCCCGTCTACTCCTTTCGTCATTCGTTGATAC---GAATACGA--ATGACAATC-GAGTGGGTGAGAAGGAAGACTTGCTTCCTTGGTTGGT
cbriggsae   --------------------------------GATCGTCGTCTTCTTTGTC--TGAAAC----AAAACATTCATGACAATT-GGATTGATATG-------------------------T
celegans    --------------------------------CCTCCTCACTTCCTCTATTGTTGCTACCGTAAACACGGTCATGACAACTAGAGTGGGGATG--------------------------
                                                 *  **   *  *   *   **  **    ** **    *******   *  * *    *
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++   ++++++++  +++++++++ ++++++++++++++++++++++++++++++++++++++ NM_
            ------------------------------------------------------------------   --------  --------- ------------------------------------------ NM_
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++   ++++++++  +++++++++ ++++++++++++++++++++++++++++++++++++++ NM_
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++   ++++++++  +++++++++ ++++++++++++++++++++++++++++++++++++++ NM_
            ------------------------------------------------------------------   --------  --------- ------------------------------------------ NM_
ppacificus  ((..((((.((((..(((((.....((((.(((((((((..((.(((((((((.....   ....))))  )))))))).. )))))))))..))))..))))))...))))..))).      1.0
cbriggsae                                   ....(((((((...(((((  ((((..     .....))))).))))))..  ))))..))))...                    .      1.0
celegans                                    ..((((((((....((((((((((..((((((....))))))..))))))).))))))))))..                            1.0
```

ppacificus	chromosome:chrUn:118520890:118521001:-1	Same_strand|Intronic_coding|NM_102771|ARF6 ## Opposite_strand|Intronic_non-coding|NM_214682|pscd1 ## {Repeats: no}
cbriggsae	chromosome:chrIV:14996368:14996519:1	Same_strand|Intronic_coding|NM_080629 ## Opposite_strand|Intronic_coding|NM_067727
celegans	chromosome:chrII:6170007:6170158:1	intergenic

sblock218 [novel_cloningHIGH_multiarm_DicerOK_randfoldOK]

Hairpin parameters

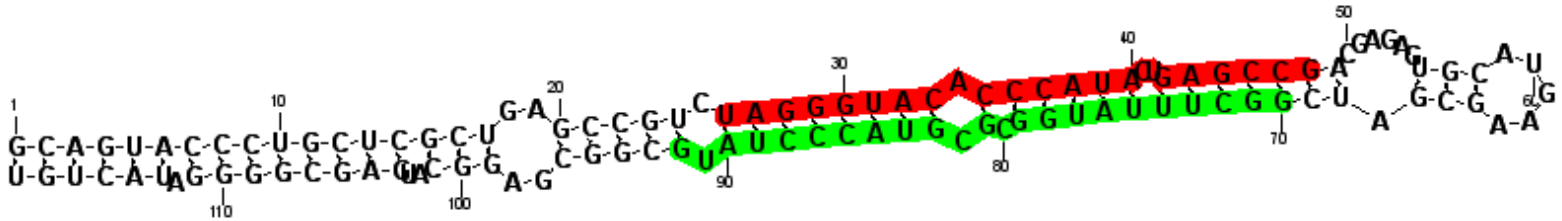
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.57/0.57	23/23/1.00	0.0 0.0	0.0 0.0	84 1	0 0	1 1	0 0	25 26	10 6	5arm 3arm	1 1	nd nd	0.17 0.17	2 3	85	1	1	2

Clusters

Located in cluster 18: sblock218_novel, block9864_cand, sblock219_novel, block9867_cand, block9868_novel

Families

Member of family novel10 (seed AGGGUAC): block9868_novel, sblock218_novel



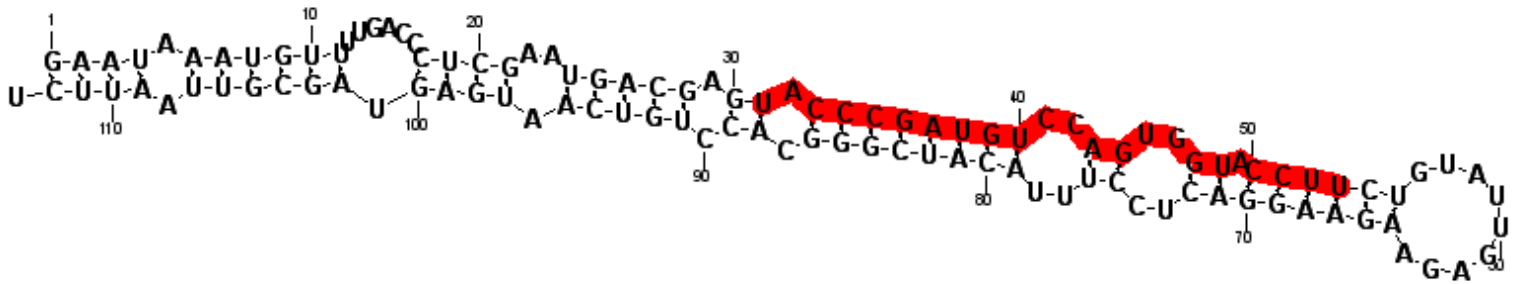
```
                                                
```

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	0.52/0.54	23/24/1.00	0.0	0.0	15	0	1	0	30	2	5arm	1	nd	0.26	2	16	1	na	na

Families

Member of family novel4 (seed ACCCGAU): block6478_novel, block9539_novel, block9537_cand, sblock169_cand



```
                                                                                                                                                  
seed                 ------------------------------ACCCGAU-------------------------------------------------------------------------------
                                                                                                                                                  
                                                                                                                                                  
                                                                                                                                                  
                     ------------------------------TACCCGATGTCCAGTGGTACCTT-------------------------------------------------------------------  23
                     ------------------------------TACCCGATGTCCAGTGGTACCTTC------------------------------------------------------------------  24
ppacificus           GAATAAATGTTTTGACCCTCGAATGACGAGTACCCGATGTCCAGTGGTACCTTCTGTATT----GAGAAGAAGGACTCCTTTACATCGGGCACCTGTCAATGAGTAGCGTTAATTCT
cbrenneri            ------------------------------ACCCGATGT------GTCGTCTCCGTATTGAACGGATAGATGACCTCATTCAC----------------GGAG-------------
cjaponica            ------------------------------TACCCGAT---------TCATCTGAAAATT----GGGTATTTGATCAGTTTTTC---------GTGTATACGGGTA-----------
                                                     *******         *    *    ***    *   *   *  *   **  *                  * *
                     ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++    ++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_1
                     ------------------------------------------------------------    ------------------------------------------------------------ NM_0
                     ------------------------------------------------------------    ------------------------------------------------------------ NM_0
                     ------------------------------------------------------------    ------------------------------------------------------------ NM_0
                     ------------------------------------------------------------    ------------------------------------------------------------ NM_0
                     ------------------------------------------------------------    ------------------------------------------------------------ NM_0
                     ------------------------------------------------------------    ------------------------------------------------------------ NM_0
                     ------------------------------------------------------------    ------------------------------------------------------------ NM_1
ppacificus           ((((.(((((((.....((((..(((((.((.(((((((((..((..((.(((((((.....    ....)))))))).)).)).))))))))..)).)))))).)))).)))))))..))))).      0.94
cbrenneri                                                 ..(((((((.       ((((((((((.....)))))..)))))))..)))...)                 )).. 
cjaponica                                                (((((((          .((((..(((((((    ((........)))))))))).         )))..)).)))))))      0.99
```

ppacificus	chromosome:chrUn:153749595:153749707:-1	Same_strand|Intronic_coding|NM_133373|PLCD3 ## Opposite_strand|Intronic_coding|NM_013355|PKN3 ## {Repeats: no}
cbrenneri	chromosome:chrUn:33825956:33826108:-1	Opposite_strand|Boundary_coding|NM_064504
cjaponica	chromosome:chrUn:147296861:147297013:1	Opposite_strand|Boundary_non-coding|NM_058635

block677 [novel_cloningHIGH_randfoldOK]

Hairpin parameters

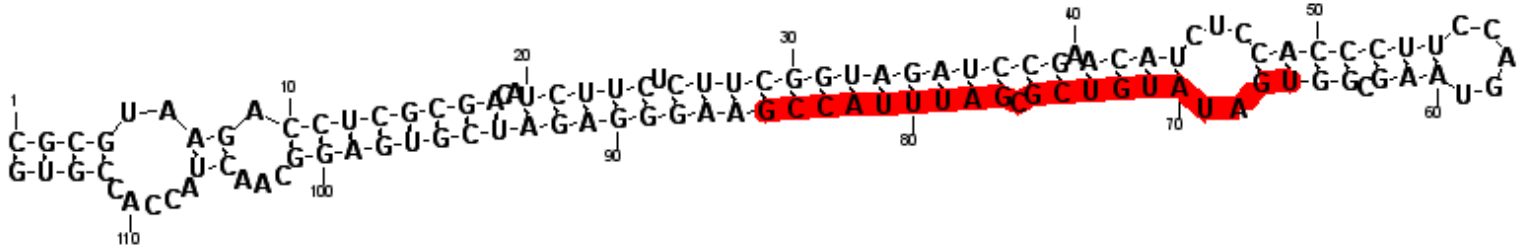
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.45/0.45	20/20/1.00	0.0	0.0	34	0	1	0	30	6	3arm	1	nd	0.15	2	34	1	na	na

Clusters

Located in cluster 5: block676_novel, block677_novel

Families

Member of family miR-50/62/90 (seed GAUAUGU): block676_novel, block677_novel



```
                                                                                                                                                  
seed                ------------------------------------------------------------------GAUAUGU-----------------------------------------
                                                                                                                                                  
                                                                                                                                                  
                                                                                                                                                  
                    ------------------------------------------------------------------TGATATGTCGCGATTTACCG-------------------------------  20
ppacificus          --CGCGTAAGACCTCGCGACATCTTCTCTTCGGTAGATCCGAACATCTCCACCCTTCCAGTAAGCGGTGATATGTCGCGATTTACCGAAGGGAGATCGTGAGGCAACTACCACCGTG
cremanei            GAAGTGTGGATTATCAGAAAATT---------GCA--------------------TGCGATCAGCTTCGATATGTCTTGAT-----GAAGCCGAAACTTCAATTGAATCGA------
cbriggsae           -------------CTACAGTACTCTTTCTACAGTA--------------------TCCAGTTA---CTGATATGTAAAAGT-----GCAGGTAG-----------------------
cbrenneri           --CTCTTTATTCATGACAGAATCCATGGCCGGGTG------------------------GCTCTCGTTGATATGTTTTGA------AAAAAGAG-----------------------
                                  *           *                                  *******             *
                +++++  ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_1
                +++++  ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_0
                +++++  ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_0
ppacificus          ((((..((.((((((((..(((((.(((((((((((((.((((...(((((((.....)))).)))))..)))))).))))))))))))))))))))...)).....))))      0.98
cremanei          (((((.(((.(((((((.....          (((                    (((((.....)))).)))))).))))))     )).)))).))))).........           0.98
cbriggsae                     ((((.(((((.((..(((((((                    ......))   )))).))...)).)))     )).))))                           0.99
cbrenneri           ((((((.((((.((((..((((.(((((((....)                    )).....)))).)))).)))).)))      ).)))))))                          0.99
```

ppacificus	chromosome:chrUn:24360964:24361078:-1	Same_strand|Intronic_coding|NM_126491|AT2G04620 ## Same_strand|Intronic_non-coding|NM_001033238|Cblb ## {Repeats: no}
cremanei	chromosome:chrUn:148217589:148217665:-1	intergenic
cbriggsae	chromosome:chrX:17328103:17328257:-1	Opposite_strand|Intronic_coding|NM_001011629 ## Same_strand|Intronic_coding|NM_001003133
cbrenneri	chromosome:chrUn:117489689:117489750:-1	intergenic

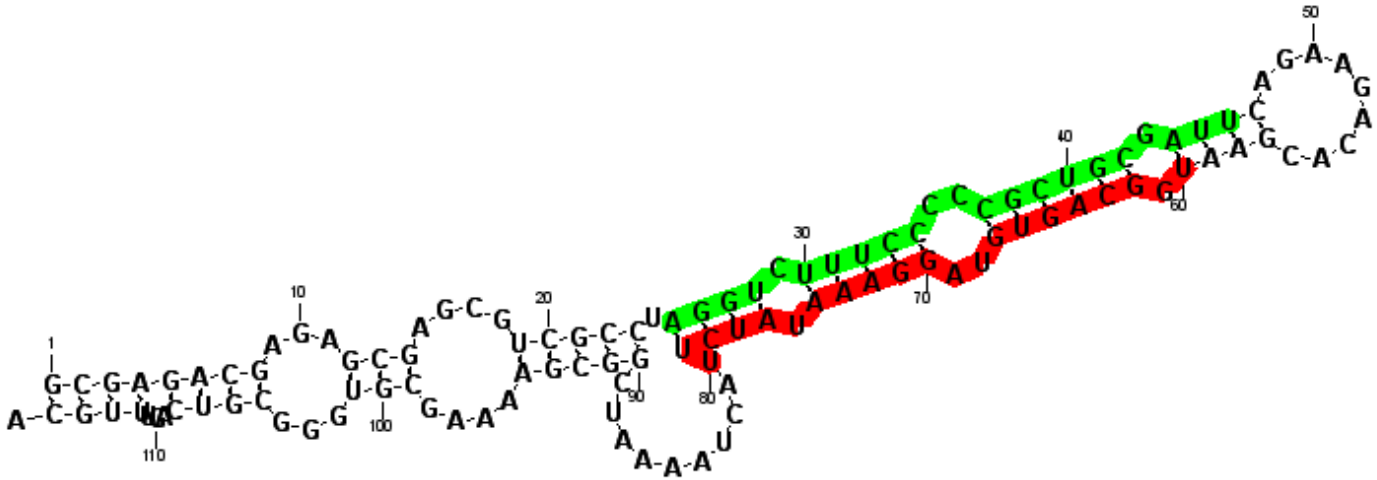
sblock21 [novel_cloningHIGH_multiarm_DicerOK_randfoldOK]

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	0.009	no	no	0.36/0.59	18/24/0.98	0.0 0.0	0.0 0.0	1 51	0 0	1 1	0 0	24 36	1 3	5arm 3arm	2 2	nd nd	0.18 0.29	2 2	60	1	2	1

Families

Member of family novel7 (seed GGUCUUU): sblock21_novel, sblock395_novel



```
                                                
```

```
            ++++++
```

		coding|NM_001048860|Os01g0201700 ## {Repeats: no}
cbrenneri	chromosome:chrUn:82165233:82165300:-1	Opposite_strand|Exonic_coding|NM_068919 ## Same_strand|Intronic_coding|NM_001083844

---

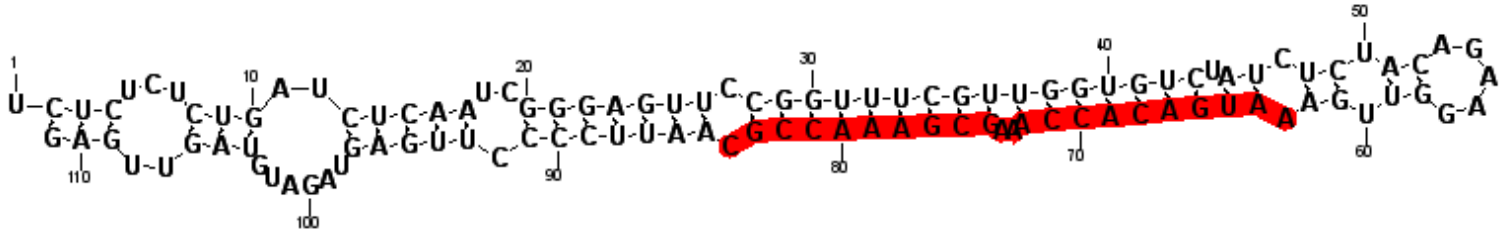
block387 [novel_cloningHIGH_randfoldOK]

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	0.39/0.52	18/25/0.97	0.0	0.0	691	0	1	0	27	5	3arm	1	nd	0.14	2	761	1	na	na

Families

Member of family miR-64 (seed AUGACAC): cel-mir-63, cel-mir-63, cel-mir-63, cel-mir-63, cel-mir-63, cel-mir-63, cel-mir-63, cel-mir-63, cel-mir-63, cel-mir-63, cel-mir-65, block387_novel, sblock123_novel, block385_cand, sblock77_cand



```
                                                                                                                                                                  rea
seed        ------------------------------------------------------------------AUGACAC----------------------------------------------------------------  74
seed        -----------------------------------------------------------------AAUGACA-----------------------------------------------------------------   6
seed        ---------------------------------------------------------------------CACCAAA-------------------------------------------------------------   5
seed        ------------------------------------------------------------------UGACACC----------------------------------------------------------------   2
                                                                                                                                                                  le

            ------------------------------------------------------------------AATGACACCAAAGCGAAACCGC---------------------------------------------  22
            ------------------------------------------------------------------AATGACACCAAAGCGAAACCGCAAT-------------------------------------------  25
            ------------------------------------------------------------------AATGACACCAAAGCGAAACCGCAA--------------------------------------------  24
            ------------------------------------------------------------------AATGACACCAAAGCGAAACCG-----------------------------------------------  21
            ---------------------------------------------------------------------ACACCAAAGCGAAACCGCAA--------------------------------------------  20
            ------------------------------------------------------------------AAATGACACCAAAGCGAAACCG----------------------------------------------  22
            ------------------------------------------------------------------AATGACACCAAAGCGAAA---------------------------------------------------  18
            ------------------------------------------------------------------AAATGACACCAAAGCGAAACCGC----------------------------------------------  23
            ------------------------------------------------------------------ATGACACCAAAGCGAAACCGC-----------------------------------------------  21
            ------------------------------------------------------------------AAATGACACCAAAGCGAAACCGCAA---------------------------------------------  25
ppacificus  ---TCTCTCTCTGATCTCAATCGGGAGTTCCGGTTTCGTTGGTGTCTATCTCTACAGAAGGTTGAAATGACACCAAAGCGAAACCGCAATTCCCCTTGAGTAGATGTAGTTGAG
cremanei    ---------CCTCACTTC---CTCTATTGTTGCTACCGT-----------------AAACATGGTCATGACACCAAGAG----------------TGAAGAGG-----------
cbriggsae   --------------ACACCA--CGGGCGGTCAGTTTTCTT-----------------AAAAGGCAAAATGACACAAAAAC----------------TTTGGTGC-----------
celegans    GGGTATATTTGAAATGTC-----GGAATGTCGATTCAGCAG---------------TAAATTTGATATGACACTCTGAC------------TTTTTTAAATGT-----------
                        *   *             * *                        **       *******                    *
            +++++   ++++++
```

```
           +++++   ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_1346
           -----   ---------------------------------------------------------------------------------------------------------------------------------- NM_0287
           +++++   ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_0288
           -----   ---------------------------------------------------------------------------------------------------------------------------------- NM_2045
           -----   ---------------------------------------------------------------------------------------------------------------------------------- NM_1983
           -----   ---------------------------------------------------------------------------------------------------------------------------------- NM_0018
           +++++   ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_0318
           +++++   ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_0113
           -----   ---------------------------------------------------------------------------------------------------------------------------------- NM_0010
           -----   ---------------------------------------------------------------------------------------------------------------------------------- NM_0297
           +++++   ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_1114
           -----   ---------------------------------------------------------------------------------------------------------------------------------- NM_0097
           +++++   ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_0002
           +++++   ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_0721
ppacificus         .(((...(((..((((((..(((((((.(((((((((((((((.((.((.((.....)).)).)))))))))..)))))))))).)))))))).)))))).....)))..)))      1.000 -
cremanei                 ((((..(((   ((((..((((((..(((((                 ....)))))..)))))...))))                 .)))))))                 0.983 -
cbriggsae                    .(((((  .((...((((.(((.((.                 ....)).))).))))........)                 ).)))))).                0.999 -
celegans        ....((((((((((.(((     (((.((((((..((((...               .....))))..)))))).))))))             ..)))))))))                1.000 -
```

ppacificus	chromosome:chrUn:16229155:16229265:-1	Same_strand|Intronic_non-coding|NM_198493|ANKRD45 ## Opposite_strand|Intronic_coding|NM_026191|Dhx40 ## Opposite_strand|Intronic_non-coding|NM_028737|4931406B18Rik ## Same_strand|Intronic_coding|NM_134696|CG2839 ## {Repeats: no}
cremanei	chromosome:chrUn:132991715:132991865:-1	intergenic
cbriggsae	chromosome:chrV:12630934:12631084:1	Same_strand|Intronic_coding|NM_001021523
celegans	chromosome:chrX:8114476:8114546:1	Same_strand|Exonic_coding|K07E3.1

---

block373 [novel_cloningOK_randfoldOK]

Hairpin parameters

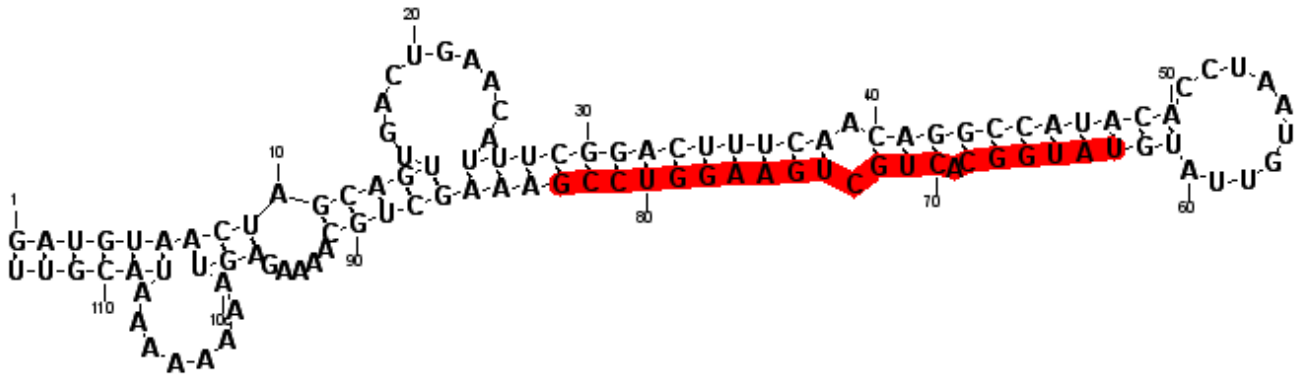
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.57/0.58	19/21/0.96	0.0	0.0	23	0	1	0	30	2	3arm	2	nd	0.10	1	24	1	na	na

Clusters

Located in cluster 3: block373_novel, block374_cand

Families

Member of family miR-228 (seed AUGGCAC): block373_novel, block2819_novel, block10249_novel, block374_cand, block8794_cand, block10251_cand



```
                                                                                                                                                                  reac
seed        ------------------------------------------------------------------AUGGCAC-------------------------------------------------                      23
seed        ------------------------------------------------------------------UGGCACU-------------------------------------------------                       1
                                                                                                                                                                  le
                                                                                                                                                                  
            ------------------------------------------------------------------TATGGCACTGCTGA-AGGTCCG------------------------------                      21
            ------------------------------------------------------------------ATGGCACTGCTGA-AGGTCC-------------------------------                      19
ppacificus  GATGTAACTAGCAGTTGACTGAACATTTCGGACTTTCAACAGGCCATACACCTAATGTTATGTATGGCACTGCTGA-AGGTCCGAAAGCTGCAAAAGAGTAAAAAAAATACGTT
cremanei    ---------------------GAAATATGATATTGTAGTCCAATT--------------AGGTATGGCACTGCGGTCCAGTTTC------------------------------
celegans    --------------------CGGTATATCTACTTTGTTGCATTTC---------AATTGAAGTATGGCACT------TAGTATCACCG---------------------------
cbrenneri   ---------------------CAAGTGTTAGAGCCACGTCAGC----------------ATCGATGGCACTGCTGAACCATTTG------------------------------
cjaponica   ---------------------CGAATTCGAGACGTGCGCCAAAT---------------ACATATGGCACACGTGT-CGATTCG------------------------------
                                      *              *                   *   *******          *
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_0010
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_0104
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_0659
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_0010
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_0010
ppacificus  (((((((((.(((((.........((((((((((((.((((((((((.........)))))))).))).))) )))))))))))))).....))).........))))))      0.590 -
cremanei                            (((((.((..(((((((((((...              .....))).)))))))).))))))                                1.000 -
celegans                           (((((((.(((...(((((..(((((         ....)))))..)))))..      )))))).))))                        1.000 -
cbrenneri                           ((((((((((.(((((.....                ..)).))))....)))))..))))))                              0.998 -
cjaponica                           (((((.(((((.(((((.(((((...               .....)))).)))))).) )))))))                              1.000 -
```

ppacificus	chromosome:chrUn:15255644:15255756:-1	Same_strand|Intronic_non-coding|NM_001055022|Os02g0813800 ## Same_strand|Intronic_coding|NM_010455|Hoxa7 ## {Repeats: no}
cremanei	chromosome:chrUn:99940193:99940345:1	intergenic
celegans	chromosome:chrII:12411870:12412022:-1	Same_strand|Boundary_coding|Y57A10C.1
cbrenneri	chromosome:chrUn:25945890:25946042:-1	Opposite_strand|Boundary_coding|NM_001030406 ## Opposite_strand|Intronic_coding|NM_001052424
cjaponica	chromosome:chrUn:148863762:148863914:1	intergenic

block9868 [novel_cloningOK_randfoldOK]

Hairpin parameters

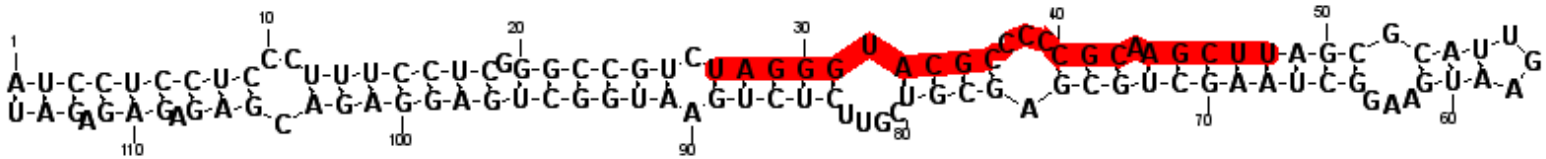
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.003	no	no	0.62/0.64	22/24/1.00	0.0	0.0	9	0	1	0	26	7	5arm	1	nd	0.23	3	10	1	na	na

Clusters

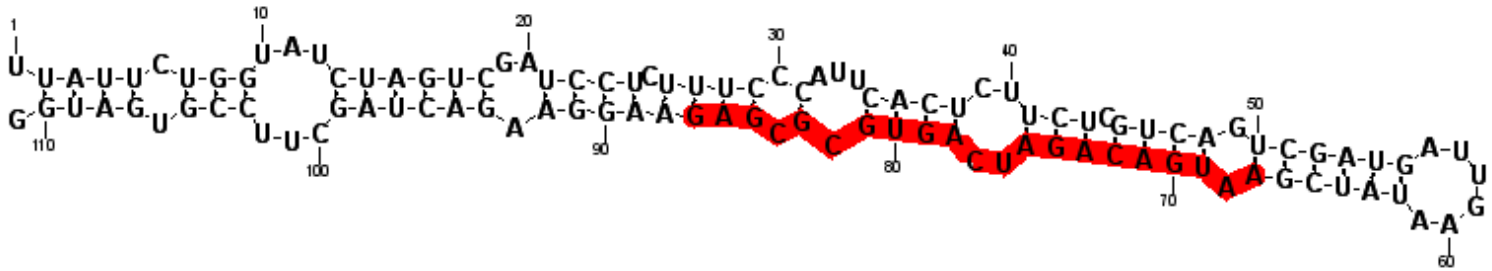
Located in cluster 18: sblock218_novel, block9864_cand, sblock219_novel, block9867_cand, block9868_novel

Families

Member of family novel10 (seed AGGGUAC): block9868_novel, sblock218_novel



```
                                                                                                                                                                  rea
seed          ---------------------------AGGGUAC-------------------------------------------------------------------------------------------------------      1
                                                                                                                                                                  1
                                                                                                                                                                  1
                                                                                                                                                                  1
              --------------------------TAGGGTACGCCCCCGCAAGCTT-------------------------------------------------------------------------------------------      22
              --------------------------TAGGGTACGCCCCCGCAAGCTTAG------------------------------------------------------------------------------------------      24
ppacificus    atcctcctccctttcctcgggccgtcTAGGGTACGCCCCCGCAAGCTTagcgcattgaatgaaggctaagctgcgagcgtcgttctctgaatggctgaggagacgagagagagat
              ***************************************************************************************************************************************
              ++++++
```



```
                                                                                                                                                                reads
seed        ------------------------------------------------------------------AUGACAG------------------------------------                                  19
                                                                                                                                                                len

            ------------------------------------------------------------------AATGACAGATCAGTGCGCGAG-----------------------                                   21
            ------------------------------------------------------------------AATGACAGATCAGTGCGCG--------------------------                                   19
ppacificus  ttattctggtatctagtcgatcctctttcccattcactcttctcgtcagtcgatgattgaatatcgAATGACAGATCAGTGCGCGAGaaggaagactagcttccgtgatgg
            ***************************************************************************************************************
          ------------------------------------------------------------------------------------------------------------------------------------------------------ NM_005654
                                                                                                                                                                1.000
ppacificus  .((((.(((...((((((..((((.((((.....((((..(((.((((.((((((.....)))))).)))))))..)))))...)))))))).))))))...))).)))))..                                -36.00
```

ppacificus	chromosome:chrUn:158621413:158621523:-1	Opposite_strand|Intronic_non-coding|NM_005654|NR2F1 ## {Repeats: no}	

---

sblock162 [novel_cloningHIGH_multiarm_DicerOK_randfoldOK]

Hairpin parameters

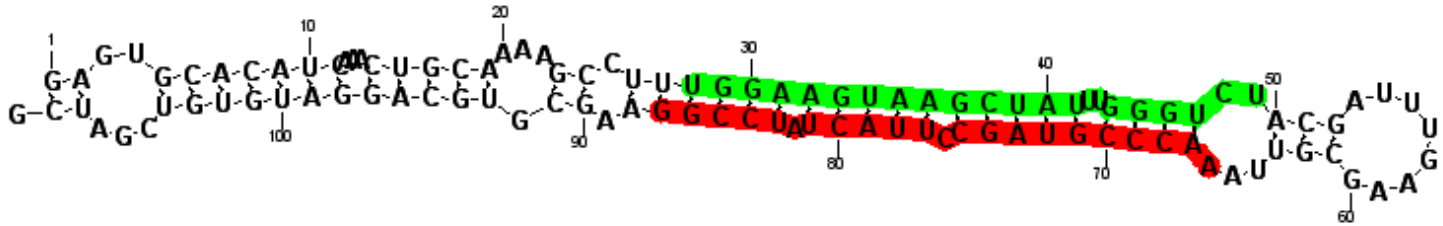
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.41/0.57	18/25/0.92	0.0 0.0	0.0 0.0	2 114	0 0	1 1	0 0	27 23	3 5	5arm 3arm	1 1	nd nd	0.18 0.09	2 1	131	1	1	1

Clusters

Located in cluster 14: block7028_novel, block7029_novel, sblock162_novel

Families

Member of family miR-51/52/55 (seed ACCCGUA): block7028_novel, block7029_novel, block9544_novel, block15318_novel, block15319_novel, sblock162_novel, sblock213_novel, sblock279_novel, sblock280_novel, block9543_cand



```
                                                                                                                                                                reads
seed        ------------------------------------------------------------------ACCCGUA-------------------------------------      118
seed        ------------------------------------------------------------------AACCCGU------------------------------------      10
seed        ----------------------------GGAAGUA-------------------------------------------------------------------------------      2
seed        ------------------------------------------------------------------CCCGUAG------------------------------------      1
                                                                                                                                                                len

            ------------------------------------------------------------------AACCCGTAGCCTTACTATCCGG-----------------------      22
            -----------------------------------------------------------------AAACCCGTAGCCTTACTA---------------------------      18
            -----------------------------------------------------------------AAACCCGTAGCCTTACTATCCGG-----------------------      23
            ------------------------------------------------------------------AACCCGTAGCCTTACTATCCGGAAG--------------------      25
            ---------------------------TGGAAGTAAGCTATTTGGGTCT-------------------------------------------------------------      22
            ------------------------------------------------------------------AACCCGTAGCCTTACTATCCG-----------------------      21
            ------------------------------------------------------------------AACCCGTAGCCTTACTAT---------------------------      18
            ------------------------------------------------------------------ACCCGTAGCCTTACTATCCGG-----------------------      21
            -----------------------------------------------------------------AAACCCGTAGCCTTACTAT---------------------------      19
ppacificus  GAGTGCACATCAAACTGCAAAAGCCTTTGGAAGTAAGCTATTTGGGTCTACGATTTGAAGCGTTAAACCCGTAGCCTTACTATCCGGAAGCGTGCAGGATGTGTCGATCG
cbrenneri   GAGT----------TTGTAGAGGC--------------------------------AATGCGTTCATTTTGTAGTTTTTGTACCC--------GTAGCCTCTACGAATTC
            ****           ** * * **                                 * ***** *    ****  **  ** **         * **  * *    **
            ++++++
```

sblock8 [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	0.41/0.48	19/23/0.95	0.0 0.0	0.0 0.0	1 34	0 0	1 1	0 0	21 17	2 3	5arm 3arm	10 10	nd nd	0.26 0.23	3 2	41	1	1	1

Clusters

Located in cluster 2: sblock5_novel, sblock6_novel, sblock7_cand, sblock8_novel, sblock9_novel

Families

Member of family novel1 (seed UCUUCAG): sblock239_novel, sblock240_novel, sblock241_novel, sblock242_novel, sblock243_novel, sblock5_novel, sblock6_novel, sblock8_novel, sblock9_novel, sblock7_cand

```
                                                                                                                                                                  reads
seed        ------------------------------------------------------------------UCACAAG-------------------------------------------  35
seed        ------------------------------------------------------------------CACAAG-----G---------------------------------------  4
seed        -------------------------UCUUCAG-------------------------------------------------------------------------------------  1
seed        ------------------------------------------------------------------AAG-----GU---UU-----------------------------------  1
                                                                                                                                  len
            ------------------------------------------------------------------TTCACAAG-----GT---TTCCTCAAGATC-----------------  22
            ------------------------------------------------------------------TCACAAG-----GT---TTCCTCAAGATC-----------------  21
            ------------------------------------------------------------------TTCACAAG-----GT---TTCCTCAAG--------------------  19
            -------------------------ATCTTCAGGATCCCTGTCTGAAC-------------------------------------------------------------  23
            ------------------------------------------------------------------CAAG-----GT---TTCCTCAAGATCA----------------  19
ppacificus  ---GCTCTATTCGATACGCCTCTGATCTTCAGGATCCCTGTCTGAACACAGAAATTG---AGTGTTCACAAG-----GT---TTCCTCAAGATCAGGGCTTCGAGTCAGCT
cremanei    ---ATTGCA---------------------AGTATGCTGAAATGAGAAAAACGAATTTGCAATTTTCACAAG-----GCATATTCTGCAAA--------------------
cbriggsae   ----TTGTA-----------------------ATCCAGGTCTAAATGAAATAAATG---GGATTTCACAAG-----G----TTCTTGATTGCTT----------------
cjaponica   AAAACTGTGTC----------------------ACGCCTGTTTTGTAGGAAACATTT---ATATTTCACAAGTAGACACCAGTTTT-------------------------
                 *                          *  *     *      *   * *        *******          **
            -----   ---------------------------------------------------   ------------     --   ------------------------------------ NM_141281
            -----   ---------------------------------------------------   ------------     --   ------------------------------------ NM_077023
ppacificus     (((..(((((...(((.((((((((.((((..(((...(((((((.......   .)))))))..))     ).   .)))).))))))))))).)))))).))).      1.000
                                                                                                                                  -44.90
cremanei       .(((((                    (((((((....((((((.............))))))...)     )))))))..)))))..                          1.000
                                                                                                                                  -15.94
cbriggsae       ..(((                       (((.((..((...((((((.....   ..)))))))...)     )    ..)).)))))).                      1.000
                                                                                                                                  -11.40
cjaponica   (((((((((((                     ((...((...((((((.....)))   )))...))...)).)))))).))))))                               0.753
                                                                                                                                  -12.40
```

ppacificus	chromosome:chrUn:8759695:8759791:-1	Opposite_strand|Intronic_coding|NM_141281|PEK ## {SimpF: trf}
cremanei	chromosome:chrUn:15150917:15151053:1	intergenic
cbriggsae	chromosome:chrUn:2861058:2861194:1	intergenic
cjaponica	chromosome:chrUn:71113291:71113427:1	Opposite_strand|Intronic_coding|NM_067309 ## Same_strand|Intronic_coding|NM_210683

---

block10920 [novel_cloningOK_randfoldOK]

Hairpin parameters

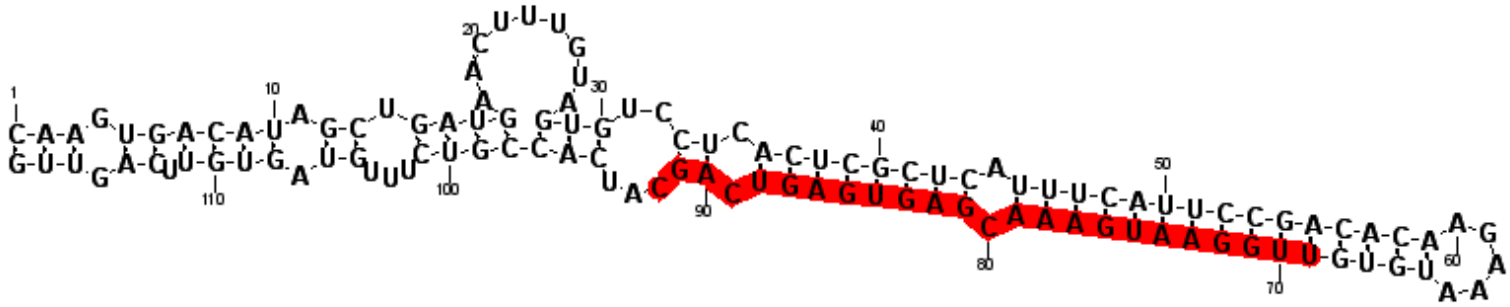
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.43/0.48	20/24/1.00	0.6	0.8	10	0	1	0	26	4	3arm	2	nd	0.10	1	12	1	na	na

Clusters

Located in cluster 23: block10919_novel, block10920_novel, block10921_cand

Families

Member of family novel12 (seed UGGAAUG): block10919_novel, block10920_novel



```
          ------------------------------------------------------------------------------------------UGGAAUG-----------------------------------
seed      ------------------------------------------------------------------------------------------GGAAUGA-----------------------------------

          ------------------------------------------------------------------------------------------TGGAATGAAACGA-------------GTGAGTCAGC------
          ------------------------------------------------------------------------------------------T--TGGAATGAAACGA-------------GTGAGTC---------
          ------------------------------------------------------------------------------------------T--TGGAATGAAACGA-------------GTGAGTCAG-------
          ------------------------------------------------------------------------------------------T--TGGAATGAAACGA-------------GTGAGTCAGC------
          ------------------------------------------------------------------------------------------TGGAATGAAACGA-------------GTGAGTCAG-------
          ------------------------------------------------------------------------------------------TGGAATGAAACGA-------------GTGAGTC---------
ppacificus --------------CAAGTGACATAGCT-----GATGAACTTTGTAGTGTCCTCACTCGCTCATTTCATTCCGACACAAGAAATGTGT--TGGAATGAAACGA-------------GTGAGTCAGCATCACC
cremanei  GTAAATGTCACTTCGAATCGGTCCAGTTCCATTGATTCGTTCAATGATTGCAT--CAGATCCAGAATATTCCAAAACAGTGTCT------TGGAATGCAATTT---------GTTGTCGAGCCAAAGAGACT
cbriggsae ----------------------TCT---------GA-----TTCGACAGCAATC--CTTGGTCATAACATC-----------ACTT-----TGGAATGCAA--------------------------------
celegans  ------------CTCAAAAGATCG---------AAC----TTCATAACGAGAC--TTTG---AAAAAATGC--------AATTTT-----TGGAATG-------------------TCTCGTTATGAAATTC
```

```
cbrenneri  -------------------ATTCC---------GACATTTTTCGGAATGAAAT--TCCGACCGGAATATTCCGAGCAAAAAATTT-----TGGAATGAAATTCCGACCGGAATATTCCGAGCGAAAAATTT
cjaponica  ---------------ACGCTATGC---------GATTTTCTTTTTCTCAAAAA--TTATTTCATTTCACGTT-------GAATTTGCACGTGGAATGAAATAA-------------TTTGGTGACCAAAAT
                                             *     *                          *               *      *******
ppacificus               (((.(((((((.((.     ((((.........(((..((.(((((((((.((((((((((((((.....))))))  )))))))))).))              )))))).))...)))
cremanei   (((((((((.(((((((((.((..((.(((((((((..((((..(((((((((((  ....((((..(((((.......)))))..      )))))))))))).          )))).))))..))).....
cbriggsae                        (((         ..     ((((((.((((.((  (..(((.........            )))).     .))).))))..
celegans               (((((((..(((         ((.    ((((((((((((  (((.   (((((....        ..))))     ).))).)                   )))))))))))).))
cbrenneri                     (((((         ((.((((((((....(((((  ((((..(((((((((((((((.........))     ))))))...)))))))..)))))))).)))....))))))))).)
cjaponica                 (((((((.(         ((((((((((..(((.(((  (((((((((((((((.(       (......))))))))))))))))))              )))..)))..))))).
```

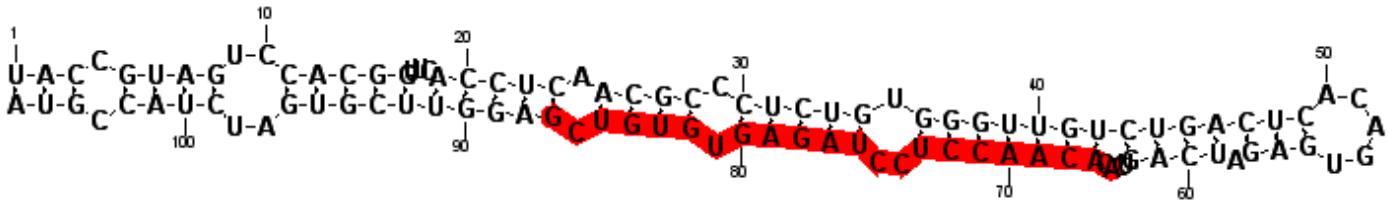
ppacificus	chromosome:chrUn:75760447:75760564:1	{Repeats: no}
cremanei	chromosome:chrUn:146831717:146831866:1	Opposite_strand|Boundary_non-coding|NM_175314 ## Opposite_strand|Exonic_coding|NM_069391 ## Opposite_strand|Intronic_coding|NM_001127433 ## Same_strand|Intronic_coding|NM_032085 ## Opposite_strand|Boundary_coding|NM_001106810
cbriggsae	chromosome:chrV:9407784:9407941:-1	Same_strand|Exonic_coding|NM_001029031 ## Same_strand|Intronic_coding|NM_001011629 ## Opposite_strand|Intronic_coding|NM_005334
celegans	chromosome:chrIII:4997561:4997647:-1	Same_strand|Intronic_coding|C27F2.8
cbrenneri	chromosome:chrUn:156053843:156053958:-1	intergenic ## {SimpF: trf}
cjaponica	chromosome:chrUn:71593210:71593310:-1	Opposite_strand|Intronic_coding|NM_136816

---

block13893 [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	0.002	no	no	0.50/0.55	20/23/1.00	0.0	0.0	8	0	1	0	19	10	3arm	1	nd	0.22	2	10	1	na	na



```
                                                                                                                                                                reads   mi
                                                                                                                                                                        fa
seed    ------------------------------------------------------------------CACAACC-----------------------------------   8     mi
seed    ------------------------------------------------------------------ACAACCU-----------------------------------   1     no
seed    ---------------------------------------------------------------------ACCUCCU-------------------------------   1     no
                                                                                                                        len   cl
                                                                                                                              fr
```

```
                 ------------------------------------------------------------------ACACAACCTCCTAGAGTGTGTCG-------------------   23   8
                 ------------------------------------------------------------------CACAACCTCCTAGAGTGTGTCG-------------------   22   1
                 -----------------------------------------------------------------AACCTCCTAGAGTGTGTCGA------------------   20   1
ppacificus       TACCGTAGTCCACGGTTCACCTCAACGCCCTCTGTGGGTTGTCTGACTCACAGTGA---GATCAGTCACACAACCTCCTAGAGTGTGTCGAGGTTCGTGATCTACCGTA
cremanei         ----------------TCTTTTTTTCTCCTTCTGTTG----------TCACCGTCACTTAATTGATAACACAACCTCCGAGGATAAAAAAAGA----------------
                                 **   *   * ** ***** *          **** ** *    **   * *********** **  *      **
                 ------------------------------------------------------------   ------------------------------------------------------- NM_080760
                 ------------------------------------------------------------   ------------------------------------------------------- NM_007475
                 ------------------------------------------------------------   ------------------------------------------------------- NM_004392
                 ------------------------------------------------------------   ------------------------------------------------------- NM_080759
                 ------------------------------------------------------------   ------------------------------------------------------- NM_135607
                 ------------------------------------------------------------   ------------------------------------------------------- NM_012634
ppacificus       (((.(((((..(((((...(((((.((((.(((((.(((((((((((((((.....))   ).))))....)))))))..)))))).))))).))))))))))..)))).)))      1.000
                                                                                                                                        -44.80
cremanei                         (((((((((.(((((..((((          (....((((.....))))...)))))....)))))).)))))))))                      1.000
                                                                                                                                        -17.10
```

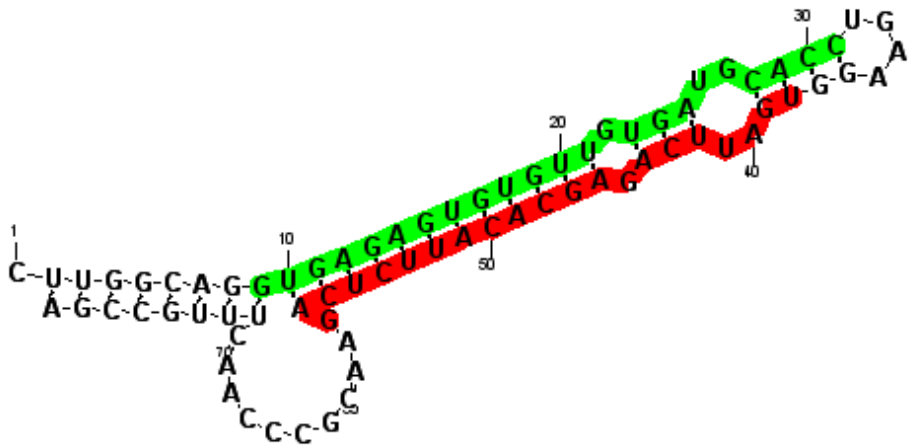
ppacificus	chromosome:chrUn:118105751:118105856:1	Opposite_strand|Intronic_coding|NM_080760|DACH1 ## Opposite_strand|Intronic_non-coding|NM_012634|Prps2 ## {Repeats: no}
cremanei	chromosome:chrUn:127475724:127475790:-1	Same_strand|Intronic_coding|NM_005692

---

sblock143 [novel_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	0.43/0.52	21/23/1.00	0.0 0.0	0.0 0.0	1 3	0 0	1 1	0 0	8 18	0 2	5arm 3arm	1 1	nd nd	0.17 0.24	2 2	4	1	2	0



```
                                                                                                                                reads   mi
                                                                                                                                        fa
   seed     ------------------------------------------------------------GAUUCAG-----------------------------------------      3      no
   seed     ------------------------------UGAGAGU-------------------------------------------------------------------------      1      no
                                                                                                                                len    cl
                                                                                                                                       fr

            ------------------------------------------------------------TGATTCAGAGCACATTCTCAG----------------------------     21      3
            ---------------------------GTGAGAGTGTGTTGTGATGCACC-------------------------------------------------------------     23      1
ppacificus  --------------------CTTGGCAGGTGAGAGTGTGTTGTGATGCACCTGAA---GGTGATTCAGAGCACATTCTCAGAACGCCCAACTTTGCCGA----------
cremanei    ------------------------------GAGAACGTGCTGGAGAGTAC--GAC---AATGATTCAGCCAG------------------TGTTGTTCAG---------
cbriggsae   --------------------------ATGTACAGATGTTCCCAGATTTCAGAAAA---GCTGATTCAGAGCA------------------TTTTCACCAT---------
celegans    ---------------------------GGAAAGAGTTGGCACAGATATTG--------AGAGATTCAGGCAA------------------ATTCTTTTA----------
cbrenneri   GGAACTATTATTACCTGAATTGTTGTGAGTGCCAGTTGATTTGATAACTTCAGAT---GGAGATTCAGAAGGGCTACTCTCTACAGATTGAGATGACGAAGCTGGTTCT
cjaponica   --------------------------GGGTTTGTTCTTTTTTGGTATTGCCTGAAACTGGCGATTCAGAAAAT------------------TTTTGACTA----------
                                                                 *******                                  *
            -----                    -----------------------------------   ----------------------------------------          ----- NM_023879
            +++++                    +++++++++++++++++++++++++++++++++++   ++++++++++++++++++++++++++++++++++++++++          +++++ NM_100443
            -----                    -----------------------------------   ----------------------------------------          ----- NM_019711
            +++++                    +++++++++++++++++++++++++++++++++++   ++++++++++++++++++++++++++++++++++++++++          +++++ NM_031473
            -----                    -----------------------------------   ----------------------------------------          ----- NM_184109
            -----                    -----------------------------------   ----------------------------------------          ----- NM_198493
ppacificus                           .(((((((((((((((((((.(((..((((....   ))))..))))..))))))))))))..........))))))))               1.000
                                                                                                                                -33.80
cremanei                                      ..(((((..(((((.((((.(  (..   ..)))))))..))))                  )...)))))..           0.880
                                                                                                                                -10.90
cbriggsae                                 ..((..(((((((...((..((((....   .))))..))..)))))                  )))..))...           1.000
                                                                                                                                -10.10
celegans                                   .(((((((((.((...((.(((.        ...))))))..))..)                  ))))))))..           1.000
                                                                                                                                -11.80
cbrenneri   (((((((((.(((.((.((((((...(((((((.....((((...((((....   ))))..))))))..))))..))))...))))..))..))..))))..))...))))))))  0.968
                                                                                                                                -24.40
cjaponica                                 .((((.....((((((((.((((((.......))))))))))))))).                  ....)))))..           0.999
                                                                                                                                -15.30
```

ppacificus	chromosome:chrUn:139827647:139827722:-1	Opposite_strand|Intronic_coding|NM_023879|Rpgrip1 ## Same_strand|Intronic_non-coding|NM_100443|5PTASE13/AT5PTASE13 ## Opposite_strand|Intronic_non-coding|NM_019711|Rbms2 ## {Repeats: no}
cremanei	chromosome:chrUn:102008305:102008420:-1	Same_strand|Intronic_coding|NM_202815 ## Same_strand|Exonic_coding|NM_179210 ## Same_strand|Boundary_coding|NM_006364 ## Same_strand|Boundary_non-coding|NM_123733
cbriggsae	chromosome:chrUn:1372202:1372317:-1	intergenic
celegans	chromosome:chrIII:8288498:8288613:-1	Opposite_strand|Intronic_coding|F10E9.6c
cbrenneri	chromosome:chrUn:154999200:154999305:-1	intergenic
cjaponica	chromosome:chrUn:142317091:142317206:-1	Same_strand|Intronic_coding|NM_065010

---

sblock213 [novel_cloningOK_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

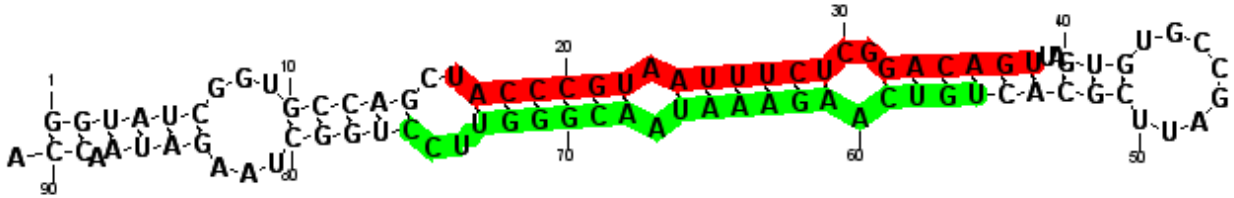
no	0.001	no	no	0.43/0.45	21/23/1.00	0.0 0.0	0.0 0.0	10 1	0 0	1 1	0 0	15 15	5 5	5arm 3arm	1 1	nd nd	0.18 0.19	2 2	13	1	2	2

Clusters

Located in cluster 17: block9537_cand, block9538_novel, block9539_novel, block9540_novel, sblock213_novel, block9543_cand, block9544_novel

Families

Member of family miR-51/52/55 (seed ACCCGUA): block7028_novel, block7029_novel, block9544_novel, block15318_novel, block15319_novel, sblock162_novel, sblock213_novel, sblock279_novel, sblock280_novel, block9543_cand



```
                                                                                                                reads
seed        ----------------ACCCGUA-------------------------------------------------------------------------------------------  12
seed        ------------------------------------------------------------------------------------GUCAAGA----------------------------  1
                                                                                                                 len

            ---------------TACCCGTAATTTC------TCGGACAGT-------------------------------------------------------------------------  22
            ---------------TACCCGTAATTTC------TCGGACAGTT------------------------------------------------------------------------  23
            ------------------------------------------------------------------------------TGTCAAGAAATAACGGGTTCC---------------  21
ppacificus  GGTATCGGTGCCAGCTACCCGTAATTTC------TCGGACAGTTAGTGT-----------GCCGATTCGCACTGTCAAGAAATAACGGGTTCCTGGCTAAGATAACCA
cbrenneri   ---------------TACCCGTAATTTCCAGAG-TAGTGGTGTTTGCGT--------------ACTTTACCCTATTATTCA-CGACGGGAA-----------------
cjaponica   -------------CGCAACCCGTAATTTCGAAAATTCGCGGTGTCAATATCGACATGAGTGGCGAAATGACGCGGTTTCGAAGCGTCGGGGAGC---------------
                          ************      * *    **     *                 *  * *  *     *    ****
            ++++++++++++++++++++++++++++++      ***************           ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_008140
            ++++++++++++++++++++++++++++++      ***************           ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_001108780
            ++++++++++++++++++++++++++++++      ***************           ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_204691
            ---------------------------------   ---------------           -------------------------------------------------------- NM_001086814
            ++++++++++++++++++++++++++++++      ***************           ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_144499
            ++++++++++++++++++++++++++++++      ***************           ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_000172
ppacificus  ((((((...((((((..((((((.(((((      (..(((((((..(((.           .......)))))))))).)))))).)))))).)))))...)))))).)).      1.000 -42.10
cbrenneri                     ..(((((.........(( (((.((((.......              ....))))))))))..... ..))))))..                      1.000 -15.49
cjaponica                  .((..((((...(((((((.....((.(((((((...(((.((....)).)))..)))))))).))))))))...))))..))                    0.865 -27.90
```

ppacificus	chromosome:chrUn:49876775:49876865:1	Same_strand|Intronic_coding|NM_008140|Gnat1 ## Opposite_strand|Intronic_non-coding|NM_001086814|pl10 ## {Repeats: no}
cbrenneri	chromosome:chrUn:115947694:115947824:1	intergenic
cjaponica	chromosome:chrUn:57108744:57108824:-1	Same_strand|Intronic_coding|NM_058707

---

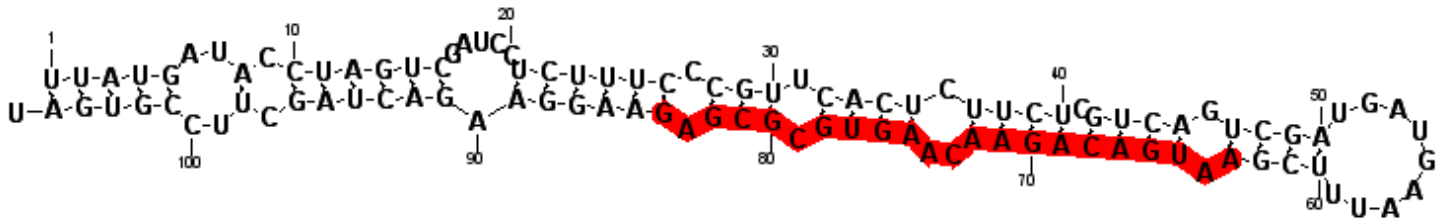
block6568 [novel_cloningOK_randfoldOK]

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	0.004	no	no	0.50/0.52	20/22/1.00	0.0	0.0	12	0	1	0	22	3	3arm	1	nd	0.23	2	14	1	na	na

Families

Member of family novel3 (seed AUGACAG): block6545_novel, block6555_novel, block6559_novel, block6568_novel, block16444_novel, block16447_novel, block16470_cand



```
                                                
```

Hairpin parameters

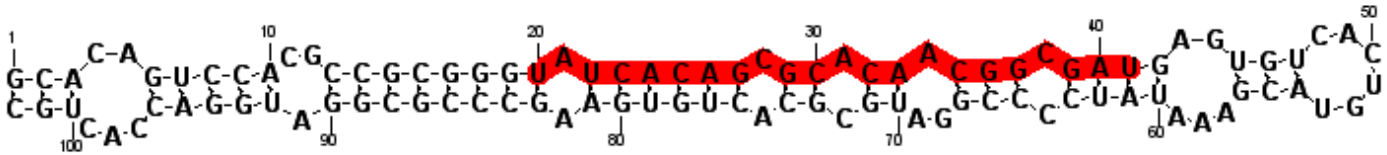
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.55/0.61	18/22/0.98	0.0	0.0	49	0	1	0	19	6	5arm	1	nd	0.23	1	54	1	na	na

Clusters

Located in cluster 16: block8236_novel, block8237_cand

Families

Member of family miR-43 (seed AUCACAG): block8236_novel, block16493_novel, block8237_cand



```
                                                                                                                    reads   mi
                                                                                                                            fa
seed        --------------------AUCACAG-------------------------------------------------------------------------   53      mi
seed        -------------------------CAGCGCA-------------------------------------------------------------------------   1       no
                                                                                                                    len     cl
                                                                                                                            fr

            -------------------TATCACAGCGCACAACGGCGAT-------------------------------------------------------------------   22      49
            -------------------TATCACAGCGCACAACGGCG----------------------------------------------------------------------   20      4
            -----------------------ACAGCGCACAACGGCGAT-------------------------------------------------------------------   18      1
ppacificus  GCACAGTCCACGCCGCGGGTATCACAGCGCACAACGGCGATGAGTGTCACTGTACGAAATATCCCCGGAT----GCGCACTGTGAAGCCCGCGGATGGACCACTGC
cremanei    -------------------TATCACAGGAAAACACTGA---AAATGAAAATGTTCGTAGAATTTCAGACA--------ACTGTGTATG------------------
cbriggsae   -------------------TATCACAGGAACTGATTTGGTTGAGTGGCAAC-TTCGTGTCGCTCAAGGAGAGAAGCTTCCTTTGAA--------------------
                                ********      *        * **  *   * **          *            ** ** *
            ------------------------------------------------------------------    ------------------------------------ NM_126491
            ------------------------------------------------------------------    ------------------------------------ NM_001086210
ppacificus  (((..((((((..(((((((.((((((.((.((.(((.((((..(((.....)))...)))))..))))..)    ).)).)))))).))))))))).))))))...))))   0.970 -49.70
cremanei                            ...(((((.......((((   (((((((....)))))....)))))))...        .)))))....                   0.998 -10.80
cbriggsae                           ..(((.(((((((..((((..(((((((((.. ....)))))))))))..)))).)).)))))).))).                   1.000 -25.00
```

ppacificus	chromosome:chrUn:24343647:24343748:1	Opposite_strand|Intronic_coding|NM_126491|AT2G04620 ## Opposite_strand|Intronic_non-coding|NM_001086210|Imf2 ## {Repeats: no}
cremanei	chromosome:chrUn:17348232:17348373:-1	Same_strand|Intronic_coding|NM_131292 ## Opposite_strand|Intronic_coding|NM_059223 ## Opposite_strand|Boundary_non-coding|NM_059242
cbriggsae	chromosome:chrIV:7989286:7989427:-1	Same_strand|Intronic_coding|NM_007735 ## Opposite_strand|Intronic_coding|NM_210229 ## Same_strand|Exonic_coding|NM_020166 ## Same_strand|Boundary_non-coding|NM_209500

---

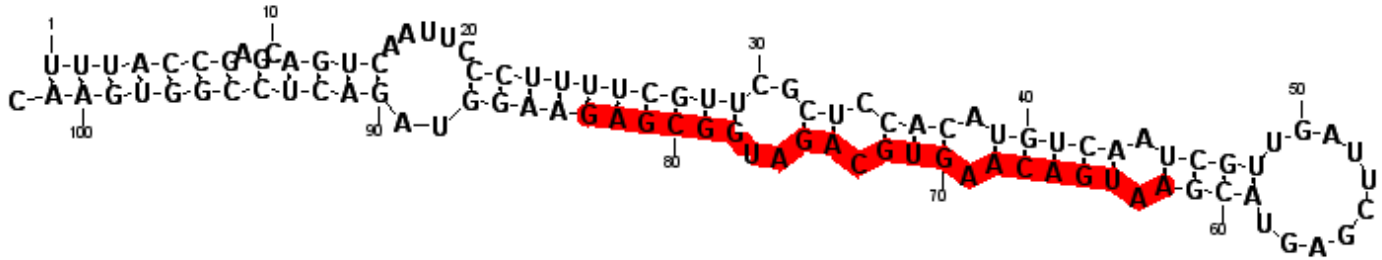
block11618 [novel_cloningOK_randfoldOK]

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	0.002	no	no	0.50/0.50	20/22/1.00	0.0	0.7	9	0	1	0	19	3	3arm	1	nd	0.23	2	10	1	na	na

Families

Member of family novel5 (seed AUGACAA): block4989_novel, block11618_novel, block13895_novel



```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
```

		reads	miRBase family
seed	----------AUGACAA----------	9	novel
seed	----------CAAGUGC----------	1	novel
		len	clonin freque
			PS3
	----------AATGACAAGTGCAGATGGCG----------	20	6
	----------AATGACAAGTGCAGATGGCGAG----------	22	3
	----------ACAAGTGCAGATGGCGAGAA----------	20	1

```
ppacificus      TTTACCGAGCAGTCAATTCCCTTTTCGTTCGCTCCACATGTCAATCGTTGATTCGAGTACGAATGACAAGTGCAGATGGCGAGAAGGTAGACTCCGGTGAAC
cremanei        --------ACAGTTCAT-----------------------TCGGTCATTGTATTGAG--------------ACAGATGACAAGAAAATTGA----AGTGA--
                         ****  **                       **  ** ***  * ***               ****** * ****  * **     ****
                ------------------------------------------------------------------------------------------------------ NM_001016583
ppacificus      (((((((...((((.....((((((((..((.((((.(((((.((((.........)))).)))))..))).))..))))))))))..)))).))))))).      1.000 -37.90
cremanei                .((.(((((                       ((.(((((((((.....              ))))).))))..)))...)))    ).)).        1.000 -11.30
```

ppacificus	chromosome:chrUn:85605707:85605808:1	Opposite_strand|Intronic_coding|NM_001016583|nkx6-1 ## {Repeats: no}
cremanei	chromosome:chrUn:120511191:120511332:-1	intergenic

---

sblock240 [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	0.42/0.48	19/23/0.99	0.0 0.0	0.0 0.0	1 117	0 0	1 1	0 0	21 17	2 3	5arm 3arm	10 10	nd nd	0.26 0.23	3 2	138	1	1	1

Clusters

Located in cluster 21: sblock239_novel, sblock240_novel, sblock241_novel, sblock242_novel, sblock243_novel

Families

Member of family novel2 (seed UCGCAAG): sblock239_novel, sblock240_novel, sblock241_novel, sblock242_novel, sblock243_novel, sblock5_novel, sblock6_novel, sblock9_novel, sblock7_cand

```
                                                                                                                reads   miRBase family seed
seed      ------------------------------------------------------------UCGCAAG--------------------------------   120     novel
seed      -------------------------------------------------------------CGCAAGG-------------------------------    16     novel
seed      ----------------------------------------------------------------AAGGU-UU---------------------------     1     novel
seed      -----------------------UCUUCAG-------------------------------------------------------------------     1     novel
                                                                                                                len     cloning frequencies
                                                                                                                          PS312
          ------------------------------------------------------------TTCGCAAGGT-TTCCTCAAGATC-----------------   22      117
          ------------------------------------------------------------TCGCAAGGT-TTCCTCAAGATC------------------   21      16
          ------------------------------------------------------------TTCGCAAGGT-TTCCTCAAGAT------------------   21      2
          ------------------------------------------------------------TTCGCAAGGT-TTCCTCAAGA-------------------   20      1
          ----------------------ATCTTCAGGATCCCTGTCTGAAC-------------------------------------------------------   23      1
          ------------------------------------------------------------------CAAGGT-TTCCTCAAGATCA----------------   19      1
ppacificus GCTCTATTCGATACGCCTCTGATCTTCAGGATCCCTGTCTGAACACAGAAATTG--AGTGTTCGCAAGGT-TTCCTCAAGATCAGGGCTTCGAGTCAGCT
cremanei  --------------------TCATTTGTGGGGTTACTTT---------GGAAATGATACCTTTCGCAAGTTGCTCTTGAATGA------------------
cbrenneri ----------------------ATGGGCGAAGAAGCCGAC--------GACGCTGGTGGCGTTCGCAAGGAGTTCTTCCTGAT------------------
                                 **           *            *    **      ********    ** *
          ---------------------------------------------------------  -------------- ---------------------------------- NM_077023
ppacificus (((..(((((((...(((.(((((((.((((..(((...(((((((........  .)))))))..))). .)))).))))))))))).)))))).))).      1.000
                                                                                                                          -44.20
cremanei                          (((((((.(((((.(((((          ((((........)))))).)))).))))))))))))                     1.000
                                                                                                                          -12.90
cbrenneri                           ((.((.(((((((.((..(        (((((.....)))).)).)...)).)..)))))))).))                   0.969
                                                                                                                          -17.00
```

ppacificus	chromosome:chrUn:70645090:70645186:1	Opposite_strand|Intronic_coding|NM_077023|sulp-3 ## {SimpF: trf}
cremanei	chromosome:chrUn:142319296:142319432:1	intergenic
cbrenneri	chromosome:chrUn:107495296:107495432:-1	Same_strand|Boundary_non-coding|NM_001076894 ## Same_strand|Boundary_coding|NM_058433

---

sblock242 [novel_cloningHIGH_multiarm_DicerOK_randfoldOK]

Hairpin parameters

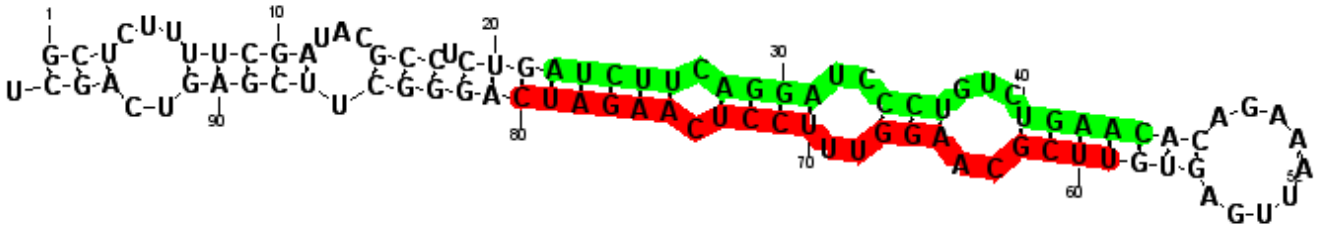
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.42/0.48	19/23/0.99	0.0 0.0	0.0 0.0	1 117	0 0	1 1	0 0	21 17	2 3	5arm 3arm	10 10	nd nd	0.26 0.23	3 2	138	1	1	1

Clusters

Located in cluster 21: sblock239_novel, sblock240_novel, sblock241_novel, sblock242_novel, sblock243_novel

Families

Member of family novel2 (seed UCGCAAG): sblock239_novel, sblock240_novel, sblock241_novel, sblock242_novel, sblock243_novel, sblock5_novel, sblock6_novel, sblock9_novel, sblock7_cand



```
                                                                                                                reads   miRBase family seed
seed        ------------------------------------------------------------UCGCAAG--------------------------------   120     novel
seed        -------------------------------------------------------------CGCAAGG--------------------------------    16     novel
seed        ------------------------------------------------------------------AAGGU-UU---------------------------     1     novel
seed        -----------------------UCUUCAG-------------------------------------------------------------------------     1     novel
                                                                                                                len     cloning frequencies
                                                                                                                        PS312
            ------------------------------------------------------------TTCGCAAGGT-TTCCTCAAGATC-----------------   22     117
            -------------------------------------------------------------TCGCAAGGT-TTCCTCAAGATC-----------------   21     16
            ------------------------------------------------------------TTCGCAAGGT-TTCCTCAAGAT------------------   21     2
            ------------------------------------------------------------TTCGCAAGGT-TTCCTCAAGA-------------------   20     1
            ---------------------ATCTTCAGGATCCCTGTCTGAAC-------------------------------------------------------   23     1
            -------------------------------------------------------------------CAAGGT-TTCCTCAAGATCA----------------   19     1
ppacificus  GCTCTTTTCGATACGCCTCTGATCTTCAGGATCCCTGTCTGAACACAGAAATTGA--GTGTTCGCAAGGT-TTCCTCAAGATCAGGGCTTCGAGTCAGCT
cremanei    --------------------TCATTTGTGGGGTTACTTT---------GGAAATGATACCTTTCGCAAGTTGCTCTTGAATGA------------------
cbrenneri   ---------------------ATGGGCGAAGAAGCCGAC--------GACGCTGGTGGCGTTCGCAAGGAGTTCTTCCTGAT------------------
                                  **           *            *    **       ********    ** *
            ---------------------------------------------------------  ------------- ---------------------------------- NM_077023
ppacificus  (((...((((((...(((.(((((((.((((..(((...(((((((.........  )))))))..))))). .)))).))))))))))).))))))..)))).     1.000
                                                                                                                        -43.50
cremanei                          (((((((.(((((.(((((         ((((.......)))))).)))).)))))))))))                        1.000
                                                                                                                        -12.90
cbrenneri                           ((.((.(((((((.((..(         (((((.....)))))).))...)))..)))))))).))                  0.969
                                                                                                                        -17.00
```

ppacificus	chromosome:chrUn:70645366:70645462:1	Opposite_strand|Intronic_coding|NM_077023|sulp-3 ## {SimpF: trf}
cremanei	chromosome:chrUn:142319296:142319432:1	intergenic
cbrenneri	chromosome:chrUn:107495296:107495432:-1	Same_strand|Boundary_non-coding|NM_001076894 ## Same_strand|Boundary_coding|NM_058433

sblock9 [novel_cloningHIGH_multiarm_DicerOK_randfoldOK]

Hairpin parameters

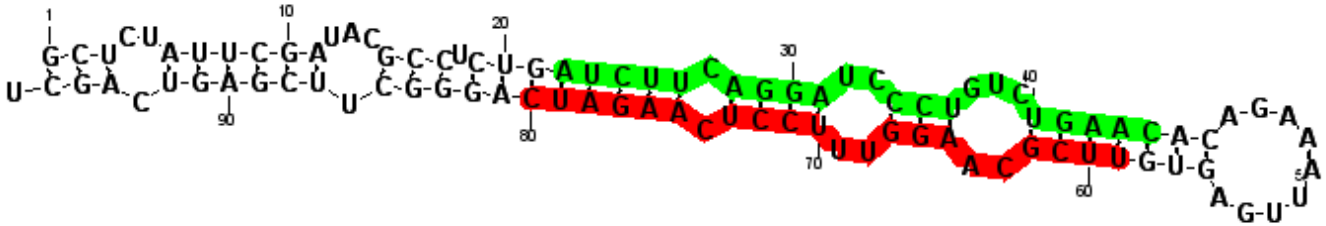
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.42/0.48	19/23/0.99	0.0 0.0	0.0 0.0	1 117	0 0	1 1	0 0	21 17	2 3	5arm 3arm	10 10	nd nd	0.26 0.23	3 2	138	1	1	1

Clusters

Located in cluster 2: sblock5_novel, sblock6_novel, sblock7_cand, sblock8_novel, sblock9_novel

Families

Member of family novel2 (seed UCGCAAG): sblock239_novel, sblock240_novel, sblock241_novel, sblock242_novel, sblock243_novel, sblock5_novel, sblock6_novel, sblock9_novel, sblock7_cand



```
                                                                                                                reads   miRBase family seed
seed      ------------------------------------------------------------UCGCAAG--------------------------------   120     novel
seed      ------------------------------------------------------------CGCAAGG-------------------------------   16      novel
seed      ------------------------------------------------------------AAGGU-UU-----------------------------   1       novel
seed      ----------------------UCUUCAG-------------------------------------------------------------------   1       novel
                                                                                                                len     cloning frequencies
                                                                                                                        PS312
          ------------------------------------------------------------TTCGCAAGGT-TTCCTCAAGATC-----------------   22      117
          ------------------------------------------------------------TCGCAAGGT-TTCCTCAAGATC-----------------   21      16
          ------------------------------------------------------------TTCGCAAGGT-TTCCTCAAGAT------------------   21      2
          ------------------------------------------------------------TTCGCAAGGT-TTCCTCAAGA-------------------   20      1
          ---------------------ATCTTCAGGATCCCTGTCTGAAC-------------------------------------------------------   23      1
          ------------------------------------------------------------CAAGGT-TTCCTCAAGATCA----------------   19      1
ppacificus GCTCTATTCGATACGCCTCTGATCTTCAGGATCCCTGTCTGAACACAGAAATTG--AGTGTTCGCAAGGT-TTCCTCAAGATCAGGGCTTCGAGTCAGCT
cremanei  --------------------TCATTTGTGGGGTTACTTT---------GGAAATGATACCTTTCGCAAGTTGCTCTTGAATGA------------------
cbrenneri ---------------------ATGGGCGAAGAAGCCGAC--------GACGCTGGTGGCGTTCGCAAGGAGTTCTTCCTGAT------------------
                                **          *            *    **      *******    ** *
          ---------------------------------------------------------  -------------- ---------------------------------- NM_141281
          ---------------------------------------------------------  -------------- ---------------------------------- NM_077023
ppacificus (((..(((((((...(((.(((((((.((((..(((...(((((((........  .)))))))..))))). .))))).))))))))))).)))))).))))).    1.000
                                                                                                                        -44.20
cremanei                          (((((((.(((((.(((((         ((((.......)))))).)))).)))))))))))                        1.000
                                                                                                                        -12.90
```

```
cbrenneri                    ((.((.(((((((.((..(        (((((.....)))).))...))..)))))))).))        0.969
                                                                                                    -17.00
```

ppacificus	chromosome:chrUn:8759833:8759929:-1	Opposite_strand|Intronic_coding|NM_141281|PEK ## {SimpF: trf}
cremanei	chromosome:chrUn:142319296:142319432:1	intergenic
cbrenneri	chromosome:chrUn:107495296:107495432:-1	Same_strand|Boundary_non-coding|NM_001076894 ## Same_strand|Boundary_coding|NM_058433

---

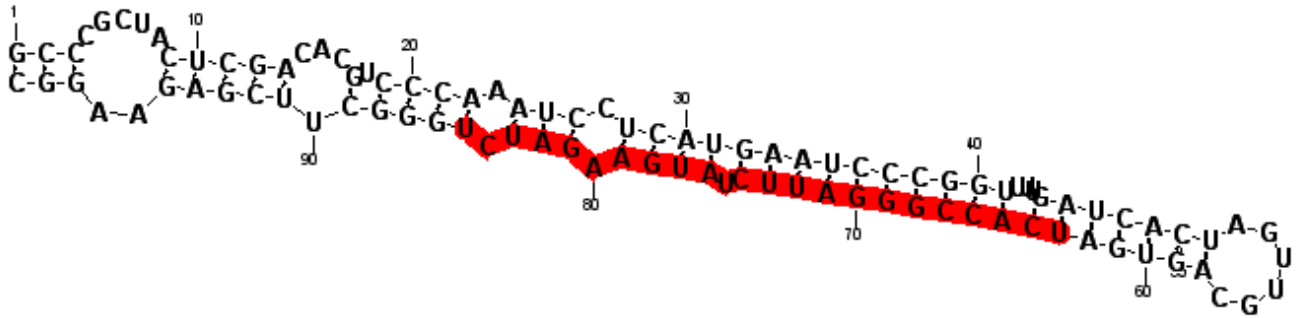
block16473 [novel_cloningOK_randfoldOK]

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	0.43/0.43	23/23/1.00	0.0	0.0	22	0	1	0	15	5	3arm	1	nd	0.13	1	22	1	na	na

Families

Member of family miR-35/36/38/39/40/41 (seed CACCGGG): cbr-mir-39, block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel, block6540_novel, block6541_novel, block13918_novel, block16473_novel, block19_cand



```
                                                                                                   reads   miRBase family seed
seed          ------------------------------------------------------------CACCGGG-----------------------------   22      miR-35/36/38/39/40/41
                                                                                                   len     cloning frequencies
                                                                                                           PS312
              ------------------------------------------------------------TCACCGGGATTCTATGAAGATCT---------------   23      22
ppacificus    GCCCGCTACTCGACACGTCCCAAATCCTCATGAATCCCGGTTTTGATCACTAGTTGCAGTGATCACCGGGATTCTATGAAGATCTGGGCTTCGAGAAGGC
cbriggsae     --------------------CTACAGACTCATAACTCGGTGTTTTCAAT----GTTGACTTGGTCACCGGGA--------------AGACGTCAAGAG---
cjaponica     GCGCACTT-----------GCATAGCAGCTCGCTGCGGGCCGCCGATC----ATATGAGCGGCCACCGGGGGTTTGTGA-------------AAGTGTGC
                                  * *    *      *         *       *      *  *******                        **
              ++++++
```

```
ppacificus     (((.....((((.....((((.(((.(((((((((((((((...((((((.....)))))))))))))))))).))))).))).))))..))))))..)))      1.000
                                                                                                                          -46.00
cbriggsae                          .....((((....(((((((...((((.     .....)))).)))))))).                .)).)))).....      0.999
                                                                                                                          -14.70
cjaponica      ((((((((            .((((..(((((.(((..(((((((...     ...)).)))))).))))))))))))).             ))))))))      0.998
                                                                                                                          -35.60
```

ppacificus	chromosome:chrUn:159226760:159226859:1	Same_strand|Intronic_non-coding|NM_011049|Pctk1 ## Opposite_strand|Intronic_non-coding|NM_078871|RpS26 ## {Repeats: no}
cbriggsae	chromosome:chrIII_random:574024:574163:-1	Opposite_strand|Intronic_coding|NM_001034977
cjaponica	chromosome:chrUn:116556444:116556515:1	Opposite_strand|Intronic_coding|NM_001027564

---

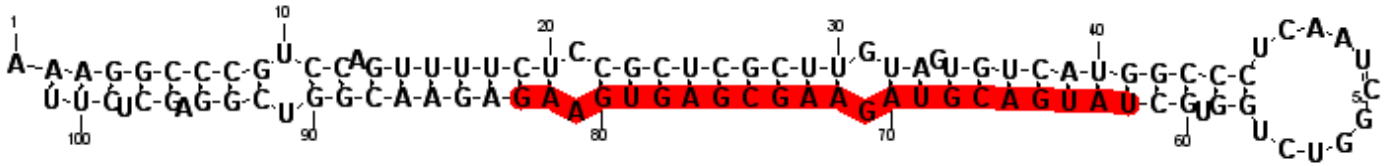
block3104 [novel_cloningOK_randfoldOK]

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	0.45/0.45	22/22/1.00	0.0	0.0	5	0	1	0	18	5	3arm	1	nd	0.09	1	5	1	na	na

Clusters

Located in cluster 6: block3104_novel, block3105_cand, cel-mir-63, block3107_novel, sblock77_cand, cel-mir-63



```
                                                                                                                  reads     miRBase
                                                                                                                            family
seed           ------------------------------------------------------------AUGACGU--------------------------------   5         novel
                                                                                                                  len       cloning
                                                                                                                            frequen
                                                                                                                                PS31
               ------------------------------------------------------------TATGACGTAGAAGCGAGTGAAG------------------  22        5
ppacificus     aaaggcccgtccagttttctccgctcgcttgtagtgtcatggccctcaatcggtctggtgcTATGACGTAGAAGCGAGTGAAGagaacggtcggagctctt
               ***********************************************************************************************************
               ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_209655
               ------------------------------------------------------------------------------------------------------- NM_001108251
               ------------------------------------------------------------------------------------------------------- NM_001064407
               ------------------------------------------------------------------------------------------------------- NM_001027696
ppacificus     .(((((((((.((.(((((((.(((((((((.((.((((((((((.....)).))))))))))).))))))))).))))))))).))))))).))).))).))      1.000 -52.30
```

ppacificus	chromosome:chrUn:81421754:81421854:-1	Same_strand|Intronic_coding|NM_209655|AGOS_ADR206W ## Opposite_strand|Intronic_non-coding|NM_001108251|Ubqln2 ## Opposite_strand|Intronic_coding|NM_001064407|Os06g0561200 ## {Repeats: no}

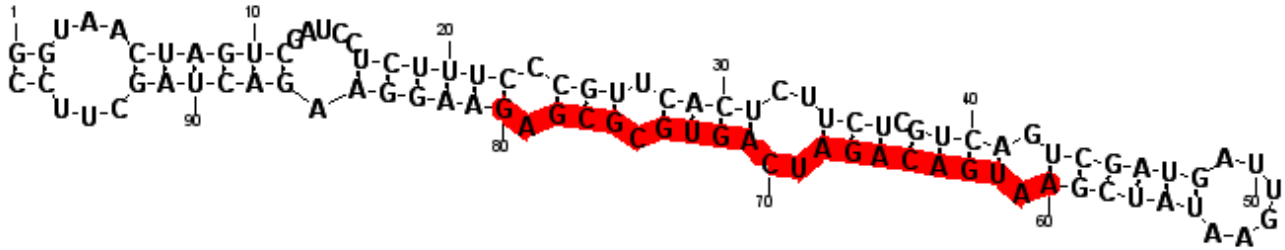
block6559 [novel_cloningOK_randfoldOK]

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	0.002	no	no	0.52/0.53	19/21/0.79	0.0	0.0	15	0	1	0	17	5	3arm	5	nd	0.24	2	19	1	na	na

Families

Member of family novel3 (seed AUGACAG): block6545_novel, block6555_novel, block6559_novel, block6568_novel, block16444_novel, block16447_novel, block16470_cand



```
                                                                                                                                                                                reads   miRBase family s
seed        ------------------------------------------------------------AUGACAG------------------------------                                                                19      novel
                                                                                                                                                                                len     cloning frequenc
                                                                                                                                                                                        PS312
            ------------------------------------------------------------AATGACAGAT-CAGTGCGCGAG-----------------                                                                21      15
            ------------------------------------------------------------AATGACAGAT-CAGTGCGCG-------------------                                                                19      4
ppacificus  GGTAACTAGTCGATCCTCTTTCCCG--TTCACTCTTCTCGTCAGTCGATGATTGAATATCGAATGACAGAT-CAGTGCGCGAGAAGGAAGACTAGCTTCC
cbriggsae   CTCAATCACTTACTCTTTTATACCCGCTGAAATATGCCCGTT------------------CAATGACAGATCCAGTGATTGCG-----------------
celegans    --GACGTAGCTACTGTGCTGTCAAGGCTTCAAGTTTTGAA--------------------AAATGACAGAA-CAGTGCTCGAG-----------------
cjaponica   CCGGTGTAGTGGTTCGTCAAACCAAATTGAAGACACCAAGT----------------------ATGACAGAT-CATCACAAGCGA----------------
                  *     *             *  *                                 *******  **      * *
            ------------------------------  ------------------------------------------- ---------------------------------- NM_001034853
            ++++++++++++++++++++++++++++++  +++++++++++++++++++++++++++++++++++++++++++ +++++++++++++++++++++++++++++++++ NM_028162
            ------------------------------  ------------------------------------------- ---------------------------------- NM_001104024
            ------------------------------  ------------------------------------------- ---------------------------------- NM_001104025
            ------------------------------  ------------------------------------------- ---------------------------------- NM_168038
            ------------------------------  ------------------------------------------- ---------------------------------- NM_204702
            ++++++++++++++++++++++++++++++  +++++++++++++++++++++++++++++++++++++++++++ +++++++++++++++++++++++++++++++++ NM_079714
            ++++++++++++++++++++++++++++++  +++++++++++++++++++++++++++++++++++++++++++ +++++++++++++++++++++++++++++++++ NM_169968
ppacificus  ((...((((((.....((((((.((  (.(((((..((((.(((((.((((((.....)))))).))))))). .)))).))).)))))).))))))...))      1.000 -36.60
cbriggsae   ..(((((((((...((((.((((((..((........)))..)).                  ..)))).))))...)))))))))..                      0.970 -12.30
celegans      ..((.((((.((((((.((((((....(((.....))))                     ...))))))).) )))))))))..                      0.998 -20.80
cjaponica   .((.((((.((((((..(((((.((....(((.......)))))                     .)))))..)) )))).))))..)).                     0.966 -13.30
```

ppacificus	chromosome:chrUn:158918302:158918398:-1	Opposite_strand|Intronic_coding|NM_001034853|RPGR ## Same_strand|Intronic_coding|NM_028162|Tbc1d5 ## {Repeats: no}
cbriggsae	chromosome:chrI_random:1634686:1634822:1	Same_strand|Intronic_coding|NM_070996 ## Opposite_strand|Intronic_coding|NM_111044 ## Opposite_strand|Boundary_coding|NM_053011
celegans	chromosome:chrII:11697032:11697168:1	Same_strand|Exonic_coding|C47D12.8
cjaponica	chromosome:chrUn:61820214:61820350:-1	intergenic

---

block9539 [novel_cloningHIGH_randfoldOK]

Hairpin parameters

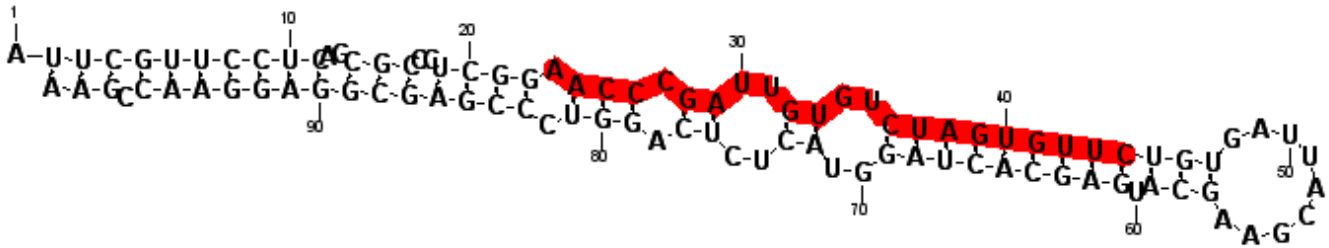
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.43/0.48	18/23/0.99	0.0	0.0	74	0	1	0	22	3	5arm	1	nd	0.23	2	99	1	na	na

Clusters

Located in cluster 17: block9537_cand, block9538_novel, block9539_novel, block9540_novel, sblock213_novel, block9543_cand, block9544_novel

Families

Member of family novel4 (seed ACCCGAU): block6478_novel, block9539_novel, block9537_cand, sblock169_cand



```
                                                
```

```
                 ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_000172
ppacificus       .(((((((((..(((..((((.(((.((..((..(((((((((((((.........))).)))))))))..))..)).)))).)))))))))
```

block13918 [novel_cloningOK_randfoldOK]

Hairpin parameters

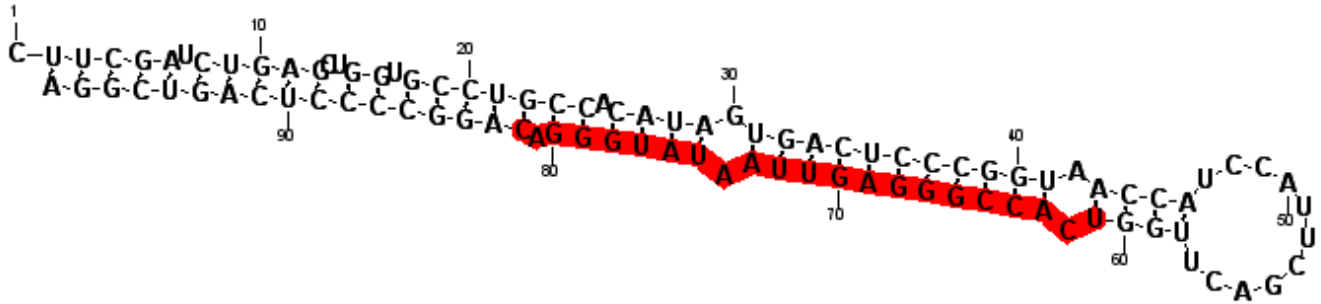
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.47/0.50	19/22/0.83	0.0	0.0	5	0	1	0	16	3	3arm	1	nd	0.14	1	6	1	na	na

Clusters

Located in cluster 27: block13916_cand, block13918_novel, cbr-mir-42, block13920_cand

Families

Member of family miR-35/36/38/39/40/41 (seed CACCGGG): cbr-mir-39, block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel, block6540_novel, block6541_novel, block13918_novel, block16473_novel, block19_cand



```
                                                                                                                reads   miRBase family seed
seed        ------------------------------------------------------------CACCGGG------------------------------   5       miR-35/36/38/39/40/41
seed        ---------------------------------------------------------------------GGGAGUU--------------------------   1       novel
                                                                                                                len     cloning frequencies
                                                                                                                        PS312
            ---------------------------------------------------------------TCACCGGGAGTTAATATGGGAC----------------   22      5
            ---------------------------------------------------------------------CGGGAGTTAATATGGGACA---------------   19      1
ppacificus  CTTCGATCTGAGCTGGTGCCTGCCACATAGTGACTCCCGGTAACCATCCATTCGACT-TGGTCACCGGGAGTTAATATGGGACAGGCCCCTCAGTCGGA
cbrenneri   -----GTTCCAGTTTTTTTCCG---------------CGGTAATAACGCGAGCAAGTCCTATCACCGGGAGAAAAACTGGAGT----------------
                   *   ** *  *  * *               ******  *  *   * * *    **********  **  ***
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ ++++++++++++++++++++++++++++++++++++++++++++ NM_133957
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ ++++++++++++++++++++++++++++++++++++++++++++ NM_018823
ppacificus  .(((((.(((((..((.(((((((.((((.(((((((((((.((((........... )))).))))))))))).)))))).))))))))))))))))))      1,000
                                                                                                                        -54.30
cbrenneri        .(((((((((((((((.                ((((.(((..((......))..)))).))))))))))))))))))).                      1,000
                                                                                                                        -29.00
```

ppacificus	chromosome:chrUn:118860787:118860884:1	Same_strand|Intronic_non-coding|NM_133957|Nfat5 ## {Repeats: no}
cbrenneri	chromosome:chrUn:170984147:170984284:-1	Opposite_strand|Intronic_coding|NM_171042

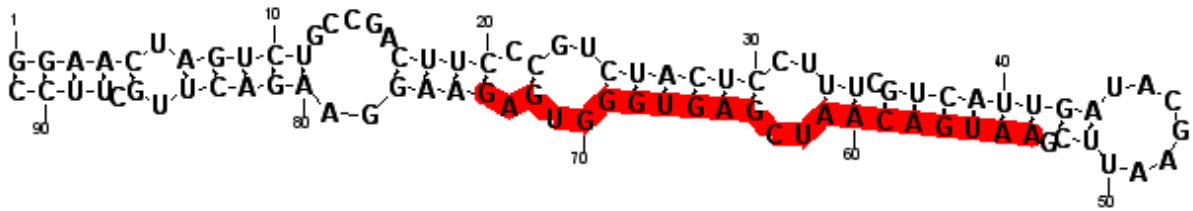
block13895 [novel_cloningOK_randfoldOK]

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	0.008	no	no	0.48/0.50	20/21/1.00	0.0	0.0	11	0	1	0	17	3	3arm	2	nd	0.14	2	12	1	na	na

Families

Member of family novel5 (seed AUGACAA): block4989_novel, block11618_novel, block13895_novel



```
                                                                                                                reads   miRBase family seed
seed        ------------------------------------------------------------AUGACAA------------------------------   11      novel
seed        ------------------------------------------------------------UGACAAU------------------------------   1       novel
                                                                                                                len     cloning frequencies
                                                                                                                        PS312
            ------------------------------------------------------------AATGACAATC-GAGTGGGTGAG-----------------   21      11
            ------------------------------------------------------------ATGACAATC-GAGTGGGTGAG-----------------   20      1
ppacificus  GGAACTAGTCTGCCGACTTCCCGTCTACTCCTTTCGTCATTGATACG---AATTCG--AATGACAATC-GAGTGGGTGAGAAGGAAGACTTGCTTCC
cbriggsae   ----------------------GATCGTCGTCTTCTTTGTCTGAAAC----AAAACATTCATGACAATT-GGATTGATATGT----------------
celegans    --------------------CCTCCTCACTTCCTCTATTGTTGCTACCGTAAACACGGTCATGACAACTAGAGTGGGGATG-----------------
cbrenneri   --------------------CAATTGGGTCTTCTTGTCATTGACAGC---GATACGGTAATGACAAGC-AAGTGCCAATTC----------------
                                                 *   **  *      *  *    *******      *
            ---------------------------------------------------   ------  ---------- ---------------------------------  NM_080760
            ---------------------------------------------------   ------  ---------- ---------------------------------  NM_004392
            ---------------------------------------------------   ------  ---------- ---------------------------------  NM_018823
            ---------------------------------------------------   ------  ---------- ---------------------------------  NM_133957
            ---------------------------------------------------   ------  ---------- ---------------------------------  NM_080759
            ---------------------------------------------------   ------  ---------- ---------------------------------  NM_135607
            ++++++++++++++++++++++++++++++++++++++++++++++++++   ++++++  ++++++++++ +++++++++++++++++++++++++++++++++  NM_214682
            ++++++++++++++++++++++++++++++++++++++++++++++++++   ++++++  ++++++++++ +++++++++++++++++++++++++++++++++  NM_001062082
            ---------------------------------------------------   ------  ---------- ---------------------------------  NM_012634
            ++++++++++++++++++++++++++++++++++++++++++++++++++   ++++++  ++++++++++ +++++++++++++++++++++++++++++++++  NM_001026560
            ++++++++++++++++++++++++++++++++++++++++++++++++++   ++++++  ++++++++++ +++++++++++++++++++++++++++++++++  NM_001085355
ppacificus  (((((..(((((.....((((.(((((((((..((.(((((((((....   ...)).  )))))))).. )))))))))..))))..))))))...))))      1.000 -29.40
cbriggsae                          ....(((((((...(((((((((..    ......)))).)))))).. )))).))).....                     1.000 -11.50
celegans                         ..(((((((....((((((((((..(((((....)))))).)))))))..))))))).))))))))))))..              1.000 -21.60
cbrenneri                         .(((((((..(((((((((((((....(   (...)).))))))))))). )))..)))))))).                    1.000 -17.30
```

ppacificus	chromosome:chrUn:118297111:118297201:1	Opposite_strand|Intronic_coding|NM_080760|DACH1 ## Opposite_strand|Intronic_non-coding|NM_018823|Nfat5

		## Same_strand|Intronic_non-coding|NM_214682|pscd1 ## Same_strand|Intronic_coding|NM_001062082|Os05g0413400 ## {Repeats: no}
cbriggsae	chromosome:chrIV:14996380:14996510:1	Same_strand|Intronic_coding|NM_080629 ## Opposite_strand|Intronic_coding|NM_067727
celegans	chromosome:chrII:6170019:6170149:1	intergenic
cbrenneri	chromosome:chrUn:90188826:90188956:-1	Same_strand|Intronic_coding|NM_001123230 ## Opposite_strand|Intronic_coding|NM_009930 ## Opposite_strand|Exonic_coding|NM_001089437 ## Opposite_strand|Boundary_coding|NM_207068

---

sblock241 [novel_cloningOK_multiarm_DicerOK_randfoldOK]

Hairpin parameters

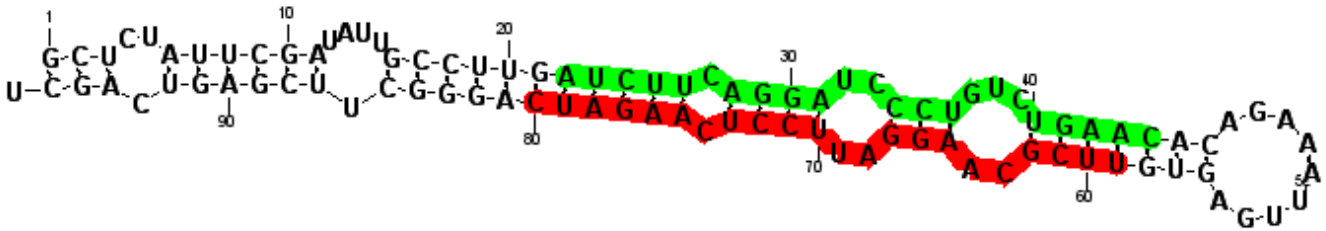
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.43/0.48	21/23/1.00	0.0 0.0	0.0 0.0	1 18	0 0	1 1	0 0	21 17	2 3	5arm 3arm	10 10	nd nd	0.26 0.23	3 2	21	1	1	1

Clusters

Located in cluster 21: sblock239_novel, sblock240_novel, sblock241_novel, sblock242_novel, sblock243_novel

Families

Member of family novel2 (seed UCGCAAG): sblock239_novel, sblock240_novel, sblock241_novel, sblock242_novel, sblock243_novel, sblock5_novel, sblock6_novel, sblock9_novel, sblock7_cand



```
                                                                                                   reads   miRBase family seed
seed      ------------------------------------------------------------UCGCAAG------------------------------   19      novel
seed      ------------------------------------------------------------CGCAAGG------------------------------   1       novel
seed      -----------------------UCUUCAG-------------------------------------------------------------------   1       novel
                                                                                                   len     cloning frequencies
                                                                                                           PS312
          ------------------------------------------------------------TTCGCAAGGATTCCTCAAGATC-----------------   22      18
          ---------------------ATCTTCAGGATCCCTGTCTGAAC-------------------------------------------------------   23      1
          ------------------------------------------------------------TCGCAAGGATTCCTCAAGATC-----------------   21      1
          ------------------------------------------------------------TTCGCAAGGATTCCTCAAGAT------------------   21      1
ppacificus GCTCTATTCGATATTGCCTTGATCTTCAGGATCCCTGTCTGAACACAGAAATTGAGTGTTCGCAAGGATTCCTCAAGATCAGGGCTTCGAGTCAGCT
cremanei   --TTTTTT--------GC-CCACTCACTGAACAGTTAC-------CAACTCTTATGCGTTCGCAAGTGGGTCCCGAGAGAATAGATAT------GT-
cjaponica  GGCCTATC--------GCGCAACCTATTATAGGCCTATC---GCGCAAAACCTGTGGGATC-------GGTCGCAAGGAAGCGTCATT------GCC
               * *          *   *        *    *         **     *  * * **          * * **                 *
```

```
                 ------------------------------------------------------------------------------------------------------ NM_077023
ppacificus       (((..((((((....((((((((((.((((..(((...(((((((.........)))))))..)))..)))).)))))))))))).))))))).))).      1.000
                                                                                                                          -44.50
cremanei           ((((((        (( ((((((...((((((.((...        ..........)))))))..)))))))...))))))........      ..      0.824
                                                                                                                          -15.02
cjaponica        (((..(((.        ((((..(((.....((((.(((   .((((.....)))).))).       ))))...)))..)))).)).      )))      1.000
                                                                                                                          -26.00
```

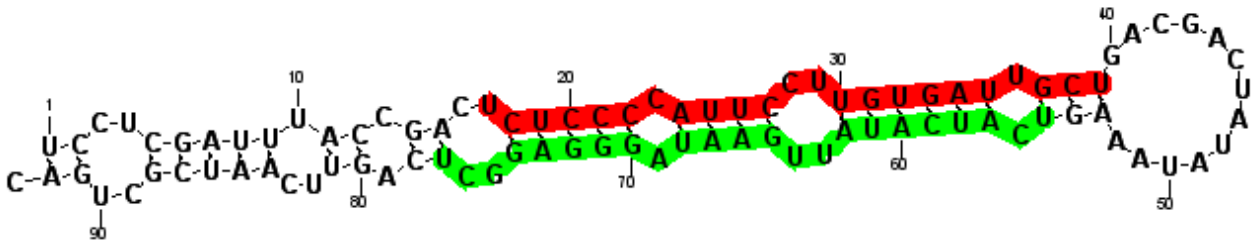
ppacificus	chromosome:chrUn:70645228:70645324:1	Opposite_strand|Intronic_coding|NM_077023|sulp-3 ## {SimpF: trf}
cremanei	chromosome:chrUn:88568187:88568258:-1	Opposite_strand|Intronic_coding|NM_001029143 ## Same_strand|Intronic_coding|NM_074134
cjaponica	chromosome:chrUn:9659736:9659872:1	intergenic

---

sblock3 [novel_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	0.003	no	no	0.39/0.48	23/23/1.00	0.0 0.0	0.0 0.0	1 1	0 0	1 1	0 0	16 16	0 2	5arm 3arm	1 1	nd nd	0.22 0.26	2 2	2	1	2	2



```
                                                                                                                                reads   miRBase
                                                                                                                                        family seed
seed             ----------------------CUCCCCA------------------------------------------------------------------------------   1       novel
seed             ------------------------------------------------------------CAUCAUA------------------------------------------   1       novel
                                                                                                                                len     cloning
                                                                                                                                        frequencies
                                                                                                                                        PS312
                 ---------------------TCTCCCCATTCCTTGTGATTGCT------------------------------------------------------------------   23      1
                 ------------------------------------------------------------TCATCATATTGAATAGGGAGGCT----------------------   23      1
ppacificus       ----TCCTCGATTTACCGA-CTCTCCCCATTCCTTGTGATTGCTGACGACTATATAAAGTCATCATATTGAATAGGGAGGCTCAGTTCAATCGCTGAC
cbrenneri        GGAAATCTCTGTACACTGATCGATACACATTCTC-----------------------AATCATCATATCGTA----------CAGTTTTCT-------
                       ***  *  ** ** *  * * *****                          * ********* * *          *****   *
                 +++++   +++++++++++++++ ++++++++++++++
```

ppacificus	chromosome:chrUn:2933733:2933825:-1	Same_strand|Intronic_coding|NM_141224|CG12586 ## Opposite_strand|Intronic_coding|NM_001103493|CG32654 ## Opposite_strand|Intronic_non-coding|NM_001108564|Agl ## {Repeats: no}
cbrenneri	chromosome:chrUn:24644941:24645073:-1	Same_strand|Intronic_coding|NM_207130

---

block10249 [novel_cloningOK_randfoldOK]

Hairpin parameters

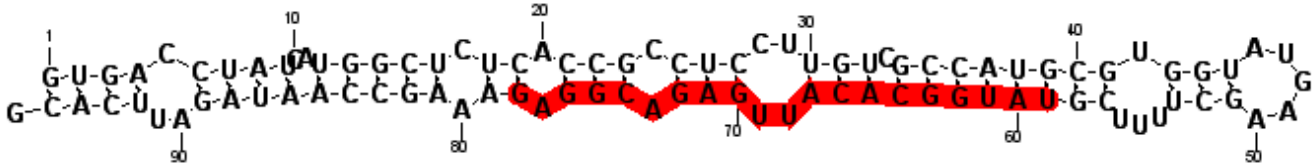
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.50/0.50	20/20/1.00	0.0	0.0	6	0	1	0	18	8	3arm	2	nd	0.20	2	6	1	na	na

Clusters

Located in cluster 20: block10249_novel, block10251_cand

Families

Member of family miR-228 (seed AUGGCAC): block373_novel, block2819_novel, block10249_novel, block374_cand, block8794_cand, block10251_cand



```
                                                                                                                reads   miRBase family seed
seed        ------------------------------------------------------------AUGGCAC------------------------------   6       miR-228
                                                                                                                len     cloning frequencies
                                                                                                                        PS312
            ------------------------------------------------------------TATGGCACATTGAGACGGAG------------------   20      6
ppacificus  GTGACCTATCATGGCTCTCACCGCCTCCTTGTCGCCATGCGTGGTATGAAGCTTTTCGTATGGCACATTGAGACGGAGAAAGCCAATAGATTCACG
cjaponica   -----------------TCGGCTGCTTCCTG--GCCACACTTGTTCTGAA-TTTGTGGAATGGCACATG---------------AATGGAGTCG-G
                              **  *  ** * **  ****  * ** * ****  ** * * ********               *** ** **  *
            ---------------------------------------------------------------------------------------------------- NM_001065794
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_017398
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_172493
ppacificus  ((((.(((((..((((((.((.((((.((((..(((.(((((((((.((((.....)))...)))))))))))..))))).))).)).)).))))))))..))))).      1.000 -42.00
cjaponica                        .((((((..(((.((  (((((((..((.....) )..)))...)))))).)).)                ))...))))) .      0.994 -15.20
```

ppacificus	chromosome:chrUn:65098861:65098956:1	Opposite_strand|Intronic_non-coding|NM_001065794|Os07g0239400 ## Same_strand|Intronic_coding|NM_017398|Diap2 ## {Repeats: no}
cjaponica	chromosome:chrUn:32319539:32319674:1	Opposite_strand|Exonic_coding|NM_066551 ## Opposite_strand|Intronic_coding|NM_007842

---

sblock5 [novel_cloningOK_multiarm_DicerOK_randfoldOK]

Hairpin parameters

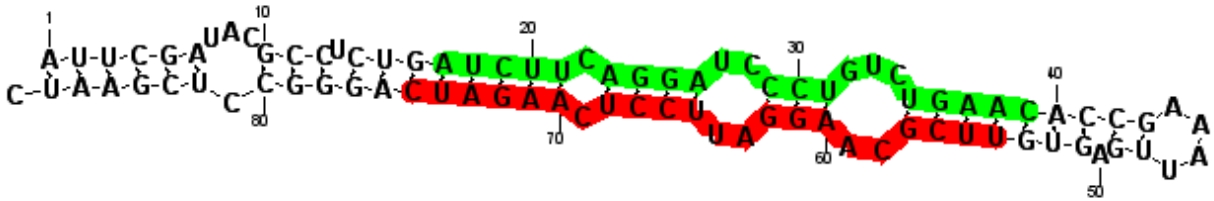
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.43/0.48	21/23/1.00	0.0 0.0	0.0 0.0	1 18	0 0	1 1	0 0	16 13	4 6	5arm 3arm	10 10	nd nd	0.26 0.23	3 2	21	1	1	1

Clusters

Located in cluster 2: sblock5_novel, sblock6_novel, sblock7_cand, sblock8_novel, sblock9_novel

Families

Member of family novel2 (seed UCGCAAG): sblock239_novel, sblock240_novel, sblock241_novel, sblock242_novel, sblock243_novel, sblock5_novel, sblock6_novel, sblock9_novel, sblock7_cand



```
                                                                                                   reads   miRBase family seed
seed      ------------------------------------------------------------UCGCAAG---------------------------   19      novel
seed      ------------------------------------------------------------CGCAAGG---------------------------   1       novel
seed      -----------------UCUUCAG-----------------------------------------------------------------------   1       novel
                                                                                                   len     cloning frequencies
                                                                                                           PS312
          ------------------------------------------------------------TTCGCAAGGATTCCTCAAGATC-------------   22      18
          ----------------ATCTTCAGGATCCCTGTCTGAAC------------------------------------------------------   23      1
          ------------------------------------------------------------TTCGCAAGGATTCCTCAAGAT--------------   21      1
          ------------------------------------------------------------TCGCAAGGATTCCTCAAGATC-------------   21      1
ppacificus  ATTCGATACGCCTCTGATCTTCAGGATCCCTGTCTGAACACC-----GAAATTGAGTGTTCGCAAGGATTCCTCAAGATCAGGGCCTCGAATC
cremanei    ------------------TTTTTTGCCCACTCACTGAACAGTTACCAACTCTTATGCGTTCGCAAGTGGGTCCCGAGAGAATAGATATGT---
cjaponica   GGCCTAT-CGCGCAACCTATTATAGGCCTATCGCGCAAAACCTGTGGGAT------CGGTCGCAAGGAAGCGTC------ATTGCC-------
                          **   *  *  *  *  ** *                 * *******       *      *  *
            ------------------------------------------------     ------------------------------------------------------ NM_141281
            ------------------------------------------------     ------------------------------------------------------ NM_077023
ppacificus  ((((((...((((.(((((((.((((..((((...((((((((     (....)).)))))))..))))..)))).))))))))))).))))))).          1.000
                                                                                                                          -39.70
cremanei                        ((((((((((((...(((((.((.............)))))))..)))))))...))))))..........                0.824
                                                                                                                          -15.02
cjaponica   (((..(( .(((((..((((.....((((.(((.((((.....)))))).)))      .)))))...))))..)))))).      )).)))                1.000
                                                                                                                          -26.00
```

ppacificus	chromosome:chrUn:8759292:8759379:-1	Opposite_strand|Intronic_coding|NM_141281|PEK ## {SimpF: trf}
cremanei	chromosome:chrUn:88568187:88568258:-1	Opposite_strand|Intronic_coding|NM_001029143 ## Same_strand|Intronic_coding|NM_074134
cjaponica	chromosome:chrUn:9659741:9659868:1	intergenic

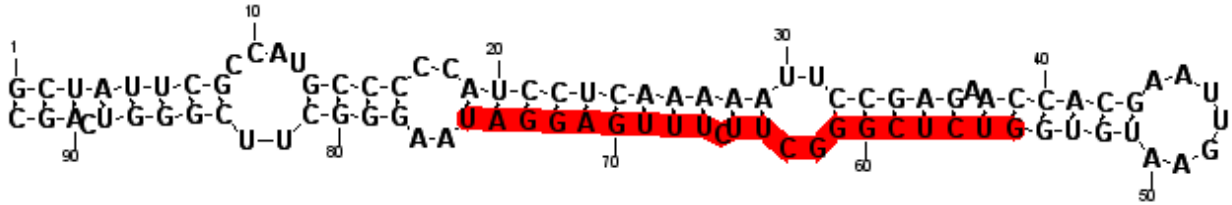
block7033 [novel_cloningOK_randfoldOK]

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	0.52/0.52	21/21/1.00	0.0	0.0	5	0	1	0	17	4	3arm	1	nd	0.19	2	5	1	na	na

Clusters

Located in cluster 15: block7032_cand, block7033_novel



```
                                                                                                                                  reads   miRBase family seed
seed        ------------------------------------------------------UCUCGGG-----------------------------                            5       novel
                                                                                                                                  len     cloning frequencies
                                                                                                                                          PS312
            -------------------------------------------------------GTCTCGGGCTTCTTTGAGGAT-----------------                            21      5
ppacificus  GCTATTCGCCATGCCCCCATCCTCAAAAATTCCGAGAACCACGAATTGAATGTGGTCTCGGGCTTCTTTGAGGATAAGGGCTTCGGGTCAGC
cbrenneri   -----------TGTTGACA-----AAAAAAGACGAATGGCATAATCAGAAATTATTCTCGGGCGTTTTTG------------TCAGAT----
cjaponica   -------ACCAACCTGCCA----AGAAGATGTCAAG--------CTGTTATCGATTCTCGGGGGTTT---------------GCGGAT----
                              **      ** *   * *              *     *******  * *                 * * *
            ++++++
```

block9544 [novel_cloningOK_randfoldOK]

Hairpin parameters

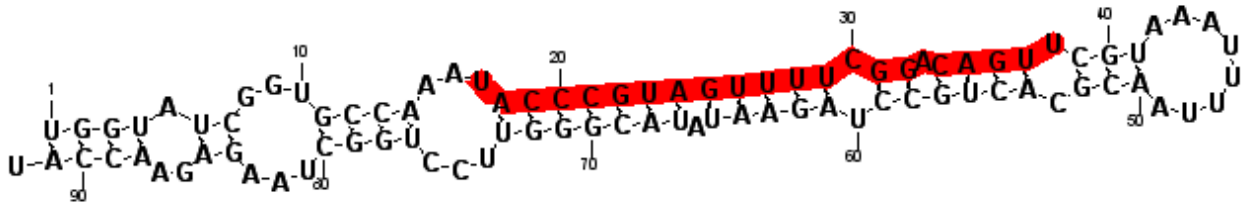
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.45/0.45	22/22/1.00	0.0	0.0	9	0	1	0	16	3	5arm	1	nd	0.14	1	9	1	na	na

Clusters

Located in cluster 17: block9537_cand, block9538_novel, block9539_novel, block9540_novel, sblock213_novel, block9543_cand, block9544_novel

Families

Member of family miR-51/52/55 (seed ACCCGUA): block7028_novel, block7029_novel, block9544_novel, block15318_novel, block15319_novel, sblock162_novel, sblock213_novel, sblock279_novel, sblock280_novel, block9543_cand



```
                                                                                                   reads   miRBase family seed
seed        -----------------ACCCGUA-------------------------------------------------------------   9     miR-51/52/55
                                                                                                   len     cloning frequencies
                                                                                                                PS312
            ----------------TACCCGTAGTTTTCGGACAGTT-------------------------------------------------  22    9
ppacificus  TGGTATCGGTGCCAAATACCCGTAGTTTTCGGACAGTTCGTAAATTTTAACGCACTGCCTAGAATATACGGGTTCCTGGCTAAGAGAACCAT
cjaponica   ----------------AACCCGTAGTTTTTAAAGG---CGCATACCAAAA---ATTGATTTAAATCTAGCGGGTC-----------------
                             ************   *     ** * *    **   * **  *  *** **  ** **
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_008140
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_001108780
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_204691
            ---------------------------------------------------------------------------------------------- NM_001086814
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_144499
            ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_000172
ppacificus  ((((.((...((((...(((((((((((.((.((((.(((........))).)))))).)))))).)))))))...)))).)).)))).      1.000 -35.80
cjaponica                   .(((((((((..(((((((..   ..(((........   ..)).)))))).))).)))))).                0.881 -10.70
```

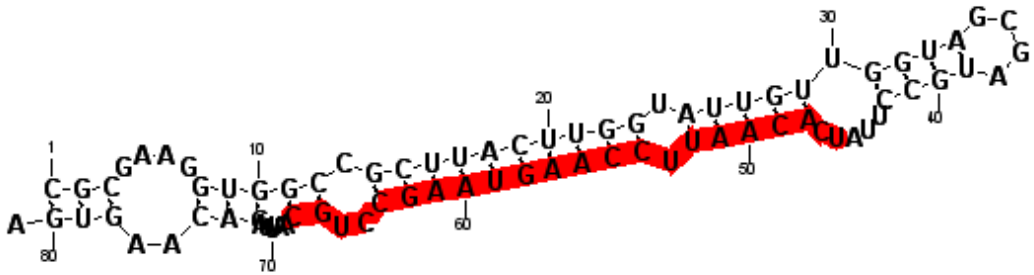
ppacificus	chromosome:chrUn:49877409:49877500:1	Same_strand|Intronic_coding|NM_008140|Gnat1 ## Opposite_strand|Intronic_non-coding|NM_001086814|pl10 ## {Repeats: no}
cjaponica	chromosome:chrUn:24364588:24364719:-1	Opposite_strand|Intronic_coding|NM_065165

---

block1073 [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	0.006	no	no	0.43/0.45	21/22/1.00	0.0	0.0	15	0	1	0	14	7	3arm	1	nd	0.23	2	17	1	na	na



```
                                                                                                                reads   miRBase family seed
seed            ------------------------------------------------------CACAAUU-----------------------------      17      novel
                                                                                                                len     cloning frequencies
                                                                                                                                PS312
                ------------------------------------------------------TCACAATTCCA-AGTAAGCCTGC--------------     22      15
                ------------------------------------------------------TCACAATTCCA-AGTAAGCCTG---------------     21      2
ppacificus      -----CGCGAAGGTGGCCGCTTACTTGGTATTGTTGGTAGCGATGCCT---TATCACAATTCCA-AGTAAGCCTGCAATTACACAAGTGA
cremanei        ------ACGAGAATGATTTTGTCTTTGTTTT---------CAAACACTGAAATTCACAATTCGA-ATTATTTTCCC--------------
celegans        ------AAAGAGATACGTAATTAATTGGTTAGACTAG--ACGTAGTCT---ATTCACAATTCCCTAGTGTCTTTTT--------------
cbrenneri       ACTGTTTCAGGAATTGGAAATTGTTTGATAT-------------GTCT-----TCACAATTCCA-ATTTTGACTGT--------------
                            *       *  *** *                 **     *********   * *
          -----     -------------------------------------------   ------------- ------------------------------ NM_001055806
          +++++     +++++++++++++++++++++++++++++++++++++++++++   +++++++++++++ +++++++++++++++++++++++++++++ NM_001452
ppacificus          ((....(((((.(((((((((.(((((.((((....))))).   ....))))).))) )))))))..)).....))).)))).      0.470 -27.50
cremanei             ..(((((((.((((...(((((((         ((.....))))).....))))..))) )))))))))..                  0.994 -11.20
celegans             ((((((((((.....(((((..(((((((.   ...)))))))   ).....)))))).....))))))))))                 1.000 -18.70
cbrenneri       ......(((.(((((((.((((((..((...              .)).     ..)))))))))) )))))))....                  0.996 -12.00
```

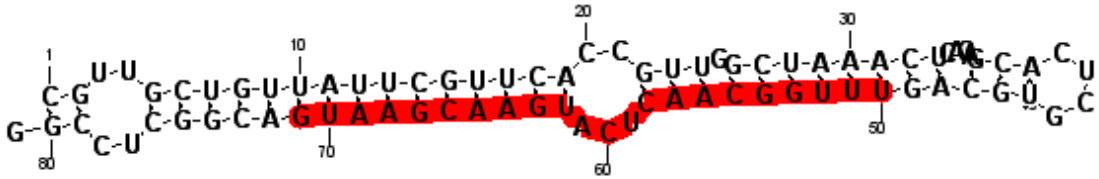
ppacificus	chromosome:chrUn:35607547:35607627:-1	Opposite_strand|Intronic_coding|NM_001055806|Os03g0197300 ## Same_strand|Intronic_coding|NM_001452|FOXF2 ## {Repeats: no}
cremanei	chromosome:chrUn:56429588:56429708:1	Opposite_strand|Boundary_non-coding|NM_113200 ## Opposite_strand|Boundary_coding|NM_068785 ## Opposite_strand|Intronic_coding|NM_003530 ## Same_strand|Intronic_coding|NM_001111216
celegans	chromosome:chrV:11270653:11270717:-1	intergenic
cbrenneri	chromosome:chrUn:125558030:125558150:-1	Same_strand|Intronic_coding|NM_001083196

---

block6369 [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	0.41/0.41	22/22/1.00	0.0	0.0	7	0	1	0	10	5	3arm	1	nd	0.14	3	7	1	na	na



```
                                                                                                                reads   miRBase family seed
seed          ------------------------------------------------------------UUGGCAA------------------------      7       novel
                                                                                                                len     cloning frequencies
                                                                                                                                PS312
              ------------------------------------------------------------TTTGGCAACTCATGAACGAATG----------     22      7
ppacificus    -----CGTTGCTGTTATTCGTTCACCGTTGGCTAAACTCAGAGCACTCGTGCA----GTTTGGCAACTCATGAACGAATGACGGCTCCGG
cremanei      -----CTATCCTTTTTTTTCTTC--------CTAAATACACAACATTTATGTCTCTGTTTTGGCAA-GAGTAAAAGGATAA---------
cjaponica     GAGTGCGATGGCATTG---------------CAGAAT---GGGCGATCGCCCATTCGGTTTGGCAACTCGCCGACCACTC----------
                   *  *    **                *  **       *  *           *******       *    *
         +++++     ++++++++++++++++++++++++++++++++++++++++++    ++++++++++++++++++++++++++++++++++++++ NM_001088036
         +++++     ++++++++++++++++++++++++++++++++++++++++++    ++++++++++++++++++++++++++++++++++++++ NM_011821
         +++++     ++++++++++++++++++++++++++++++++++++++++++    ++++++++++++++++++++++++++++++++++++++ NM_009203
         +++++     ++++++++++++++++++++++++++++++++++++++++++    ++++++++++++++++++++++++++++++++++++++ NM_001079844
ppacificus         ((..(((((((((((((((..((((.((((((((....(((....))))    )))))))))...))))))))))))))..)).      1.000 -37.70
cremanei           .((((((((..(((((.        (((((.(((..(((....)))...))))))))).))  )))).))))))))).               1.000 -17.10
cjaponica     (((((...(((((.(((                (.((((   ((((....)))))))))......))))...)))))..))))))             0.690 -27.30
```

ppacificus	chromosome:chrUn:147878155:147878235:-1	Same_strand|Intronic_non-coding|NM_001088036|LOC397877 ## {Repeats: no}
cremanei	chromosome:chrUn:141697968:141698088:-1	intergenic
cjaponica	chromosome:chrUn:146071586:146071706:1	intergenic ## {SimpF: trf}

---

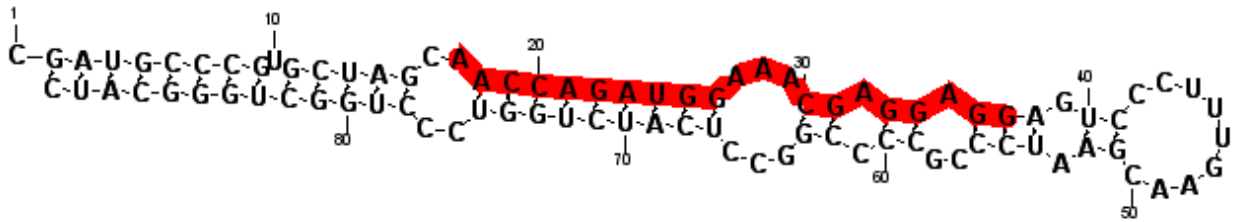
block9538 [novel_cloningOK_randfoldOK]

Hairpin parameters

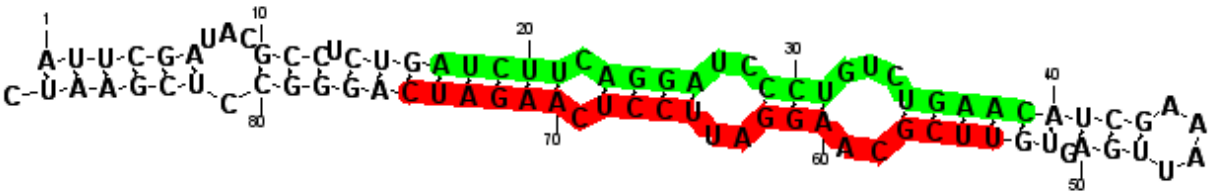
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.004	no	no	0.52/0.52	21/21/1.00	0.0	0.0	5	0	1	0	16	4	5arm	1	nd	0.24	3	5	1	na	na

Clusters

Located in cluster 17: block9537_cand, block9538_novel, block9539_novel, block9540_novel, sblock213_novel, block9543_cand, block9544_novel



```
                                                                                                                reads   miRBase family seed
seed        -----------------ACCAGAU-------------------------------------------------------------------------   5       novel
                                                                                                                len     cloning frequencies
                                                                                                                        PS312
            ----------------AACCAGATGGAAACGAGGAGG-------------------------------------------------------------   21      5
ppacificus  CGATGCCCGTGCTAGCAACCAGATGGAAACGAGGAGGAGTCCCTTTGAACGAATCCCGCCCCGGCCTCATCTGGTCCCTGGCTGGGCATC
cbrenneri   ----------------GACCAGATGGAACCAAGTGTGAAGATATTGATGAGTGTTCCATTTGGGCTGGATCTGGC---------------
                             *********** * **    **     **     *  * **     ***   ******
            ++++++
```



```
                                                                                                                reads   miRBase family seed
seed      -------------------------------------------------------UCGCAAG---------------------------              19      novel
seed      ------------------UCUUCAG-------------------------------------------------------------------              1       novel
seed      -------------------------------------------------------CGCAAGG--------------------------              1       novel
                                                                                                                len     cloning frequencies
                                                                                                                                PS312
          -------------------------------------------------------TTCGCAAGGATTCCTCAAGATC-------------      22      18
          -------------------------------------------------------TCGCAAGGATTCCTCAAGATC-------------      21      1
          -----------------ATCTTCAGGATCCCTGTCTGAAC-------------------------------------------------      23      1
          -------------------------------------------------------TTCGCAAGGATTCCTCAAGAT--------------      21      1
ppacificus  -ATTCGATACGCCTCTGATCTTCAGGATCCCTGTCTGAACATCGAAATTGAGTGTTCGCAAGGATTCCTCAAGATCAGGGCCTCGAATC
cremanei    --TTTTTTGC-CCACTCACTGAACAGTTACC------AACTCTTAT-----GCGTTCGCAAGTGGGTCCCGAGAGAATAGATATGT---
cjaponica   GGCCTATCGCGCAACCTATTATAGGCCTATCGCGCAAAACCTGTGG---GATCGGTCGCAAGGAAGCGTC------ATTGCC-------
                     * *  *  *         *  *      ***             * *******       *      *  *
            ----- ------------------------------------------------------------------------------------ NM_077023
ppacificus   ((((((...(((.(((((((.((((..(((...(((((((((....))).)))))).))))..))))).))))))))))).))))))).   1.000
                                                                                                          -37.70
cremanei      (((((((( (((((...(((((.((....      .........     )))))))..)))))))...)))))).........        0.824
                                                                                                          -15.02
cjaponica   (((..(((.(((((..(((.....((((.(((.((((.....)))).   )))).)))).)...)))..)))).      )).)))       1.000
                                                                                                          -26.00
```

ppacificus	chromosome:chrUn:70645509:70645596:1	Opposite_strand|Intronic_coding|NM_077023|sulp-3 ## {SimpF: trf}
cremanei	chromosome:chrUn:88568187:88568258:-1	Opposite_strand|Intronic_coding|NM_001029143 ## Same_strand|Intronic_coding|NM_074134
cjaponica	chromosome:chrUn:9659741:9659868:1	intergenic

---

sblock6 [novel_cloningOK_multiarm_DicerOK_randfoldOK]

Hairpin parameters

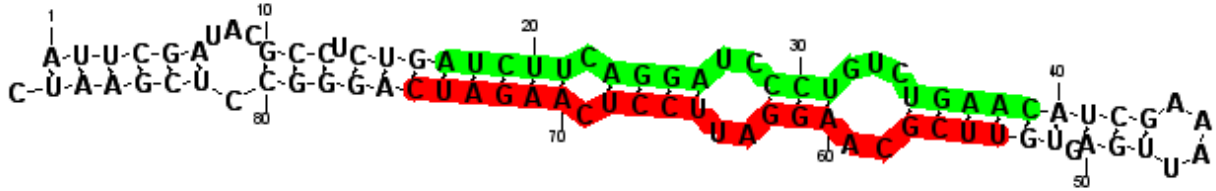
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.43/0.48	21/23/1.00	0.0 0.0	0.0 0.0	1 18	0 0	1 1	0 0	16 13	4 6	5arm 3arm	10 10	nd nd	0.26 0.23	3 2	21	1	1	1

Clusters

Located in cluster 2: sblock5_novel, sblock6_novel, sblock7_cand, sblock8_novel, sblock9_novel

Families

Member of family novel2 (seed UCGCAAG): sblock239_novel, sblock240_novel, sblock241_novel, sblock242_novel, sblock243_novel, sblock5_novel, sblock6_novel, sblock9_novel, sblock7_cand



```
                                                                                                                reads   miRBase family seed
seed        ------------------------------------------------------UCGCAAG---------------------------            19      novel
seed        ------------------UCUUCAG-------------------------------------------------------------------------  1       novel
seed        ------------------------------------------------------CGCAAGG---------------------------            1       novel
                                                                                                                len     cloning frequencies
                                                                                                                                PS312
            -------------------------------------------------------TTCGCAAGGATTCCTCAAGATC-------------         22      18
            -------------------------------------------------------TCGCAAGGATTCCTCAAGATC-------------         21      1
            -----------------ATCTTCAGGATCCCTGTCTGAAC-----------------------------------------------------   23      1
            -------------------------------------------------------TTCGCAAGGATTCCTCAAGAT--------------         21      1
ppacificus  -ATTCGATACGCCTCTGATCTTCAGGATCCCTGTCTGAACATCGAAATTGAGTGTTCGCAAGGATTCCTCAAGATCAGGGCCTCGAATC
cremanei    --TTTTTTGC-CCACTCACTGAACAGTTACC------AACTCTTAT-----GCGTTCGCAAGTGGGTCCCGAGAGAATAGATATGT---
cjaponica   GGCCTATCGCGCAACCTATTATAGGCCTATCGCGCAAAACCTGTGG---GATCGGTCGCAAGGAAGCGTC------ATTGCC-------
                     * *  *  *         *  *      ***             * *******       *      *  *
            ----- ------------------------------------------------------------------------------------- NM_141281
            ----- ------------------------------------------------------------------------------------- NM_077023
ppacificus   ((((((...((((.((((((((.((((..(((...((((((((((....)))).)))))).))))..)))).)))))))))))).))))))).   1.000
                                                                                                          -37.70
cremanei      ((((((( (((((...((((((.((....      .........     )))))))..)))))))...))))))..........          0.824
                                                                                                          -15.02
cjaponica   (((..((.((((..(((.....((((.(((.((((.....)))))).   )))).)))))...)))).)))))).      )).)))        1.000
                                                                                                          -26.00
```

ppacificus	chromosome:chrUn:8759423:8759510:-1	Opposite_strand|Intronic_coding|NM_141281|PEK ## {SimpF: trf}
cremanei	chromosome:chrUn:88568187:88568258:-1	Opposite_strand|Intronic_coding|NM_001029143 ## Same_strand|Intronic_coding|NM_074134
cjaponica	chromosome:chrUn:9659741:9659868:1	intergenic

---

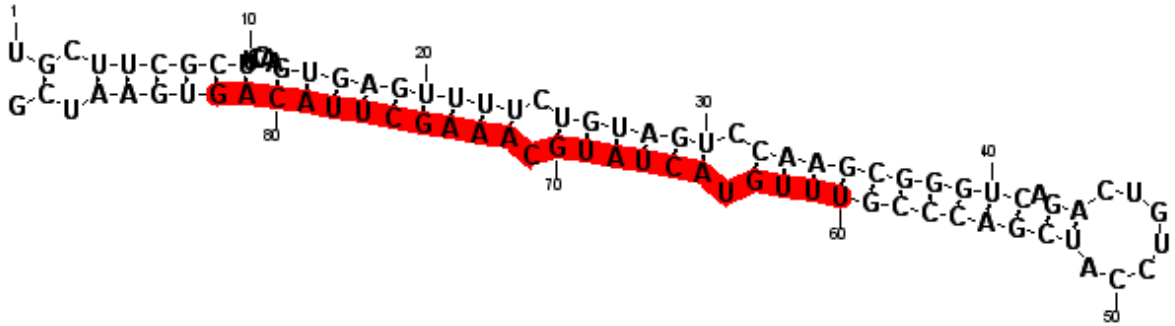
block2936 [novel_cloningOK_randfoldOK]

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	0.32/0.35	19/23/0.80	0.0	0.0	4	0	1	0	7	8	3arm	1	nd	0.09	1	5	1	na	na

Families

Member of family miR-239a (seed UUGUACU): cbr-mir-239b, cbr-mir-239b, block2936_novel



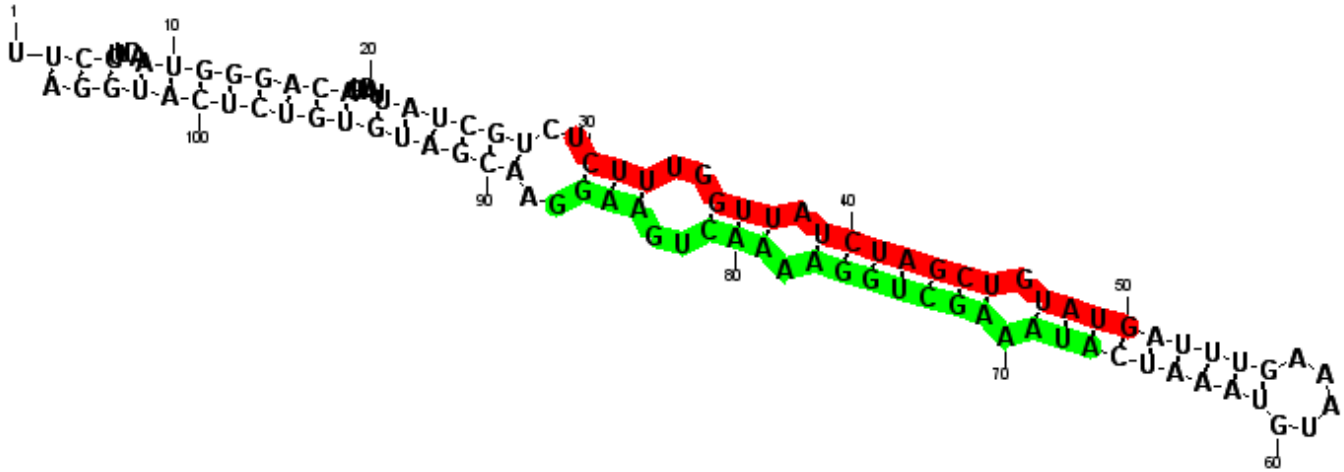
		reads	miRBase family seed
seed	----------UUGUACU----------	4	miR-239a
seed	----------UGUACUA----------	1	novel
		len	cloning frequencies
			PS312
	----------TTTGTACTATGCAAAGCTTACAG-------	23	4
	----------TTGTACTATGCAAAGCTTA----------	19	1
ppacificus	tgcttcgcttccaagtgagttttctgtagtccaagcgggtcagactgtccatcgacccgTTTGTACTATGCAAAGCTTACAGtgaatcg		
	**********		
	++++++

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	0.33/0.40	19/24/0.98	0.0 0.4	0.0 0.0	90 5	0 0	1 1	0 0	28 18	5 6	5arm 3arm	1 1	nd nd	0.18 0.29	2 2	102	1	1	0

Families

Member of family miR-75/79 (seed UAAAGCU): cel-mir-79, sblock75_novel, block675_cand, block15135_cand



```
                                                                                                                                                                reads
seed     -------------------------------CUUUGGU-------------------------------------------------------------------------------------------------------   95
seed     ------------------------------------------------------------------------------------UAAAGCU-------------------------------------------------   3
seed     ------------------------------------------------------------------------------------AAAGCUG-------------------------------------------------   2
seed     -----------------------------------UGGUUAU-------------------------------------------------------------------------------------------------------   1
seed     -----------------------------------GGUUAUC-------------------------------------------------------------------------------------------------------   1
                                                                                                                                                                len
         ------------------------------TCTTTGGTTATCT-------------AGCTGTATG-------------------------------------------------------------------------------   22
         ------------------------------TCTTTGGTTATCT-------------AGCTGTAT--------------------------------------------------------------------------------   21
         ------------------------------------------------------------------------------------ATAAAGCTGGAAAACTGAAGG-----------------------------------   21
         ------------------------------------------------------------------------------------TAAAGCTGGAAAACTGAAGG-----------------------------------   20
         ------------------------------TCTTTGGTTATCT-------------AGCTGTATGAT------------------------------------------------------------------------   24
         ----------------------------------TTGGTTATCT-------------AGCTGTATG--------------------------------------------------------------------------   19
         ---------------------------------TGGTTATCT-------------AGCTGTATGA-------------------------------------------------------------------------   19
ppacificus TTCCTTCAATGGGACAGTCATTATCGTC---TCTTTGGTTATCT-------------AGCTGTATGATTTGAAATGTAAATCATAAAGCTGGAAAACTGAAGGAACGA----TGTGTCTCATGGA
cremanei   -------------------------------TCTTTGGT----G-------------AATATTGTTATCTGAAAACGAAATCGTTTTCGGAACAGA---ATAGAACGA----AACGA--------
cbriggsae  ------GAGTTGGAGGATCATTTTCTCGCTGTCTTTGGTCTCCTGCTGTGGATGTACAGCAATGTTGTGCTGTTCGAGCATGGCAGACACGAAGATTCCGTGGAAGGATCCTGATGACTC-----
celegans   ------------------------------TCTTTGGTTTTC----------------CAATCTTTCTCGTAGTATAGACTATTGAAAAGAAAAA----------GA----GGAAGCTGAAGG-
cjaponica  ------------------------------TCTTTGGT-----------------------TATCAGGCGGAATGAAAGATTTT-----GAAAGATTGATACCGCCA----GGTAAGTTTTGG-
                                         *******                        * *                                                *
ppacificus .(((....(((((((((.....((((((.   .((((..((((.(((             ((((.(((((((((.....)))))))))..))))))).))))..))))..))))    )))))))))))) 1.000
                                                                                                                                                  -44.80
cremanei                                 (((((.((    .              ..((((....((((((((((....))))))))))....)   )))..)).)    )).))         0.992
                                                                                                                                                  -15.40
```

```
cbriggsae   ((((((.((((((.(((((.((..(((((((((((((((((.((((((((((...)))))))).)))))))))).)).)))).)))))))..)).)))))))))))..))))))   0.825
                                                                                                                                -50.40
celegans                                .(((..((((((                ...(((((.(((((((....)))))).)))))))....          ..    )))))))..)))).   0.999
                                                                                                                                -15.50
cjaponica                               .......(                       ((((.(((((.((....(((((.     ...)))))).)).)))))).    )))))).......   0.967
                                                                                                                                -12.30
```

ppacificus	chromosome:chrUn:79981546:79981650:-1	{Repeats: no}
cremanei	chromosome:chrUn:12087335:12087479:-1	Same_strand|Intronic_coding|NM_001071615
cbriggsae	chromosome:chrUn:4246294:4246407:-1	intergenic
celegans	chromosome:chrIV:10150717:10150861:-1	intergenic
cjaponica	chromosome:chrUn:28857221:28857365:1	intergenic

---

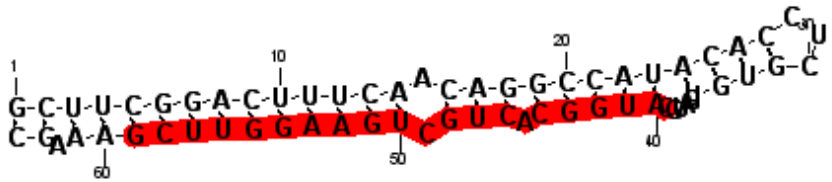
block2819 [novel_cloningOK_randfoldOK]

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	0.57/0.57	21/21/1.00	0.0	0.0	8	0	1	0	5	8	3arm	1	nd	0.10	1	8	1	na	na

Families

Member of family miR-228 (seed AUGGCAC): block373_novel, block2819_novel, block10249_novel, block374_cand, block8794_cand, block10251_cand



```
                                                                                   reads     miRBase family seed
   seed        ---------------------------------------AUGGCAC------------------      8        miR-228
                                                                                    len      cloning frequencies
                                                                                                     PS312
               ---------------------------------------CATGGCACTGCTGAAGGTTCG-----   21          8
ppacificus     gcttcggactttcaacaggccatacacctcgtgtgatgCATGGCACTGCTGAAGGTTCGaaagc
               ************************************************************
             ++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++++ NM_001069093
ppacificus     ((((((((((((((.(((((((((((...)))).....)))))).)))).))))))))))))..))   1.000 -28.80
```

ppacificus	chromosome:chrUn:74608390:74608453:-1	Same_strand|Intronic_coding|NM_001069093|Os09g0103700 ## {Repeats: no}

---

block10919 [novel_cloningOK_randfoldOK]

Hairpin parameters

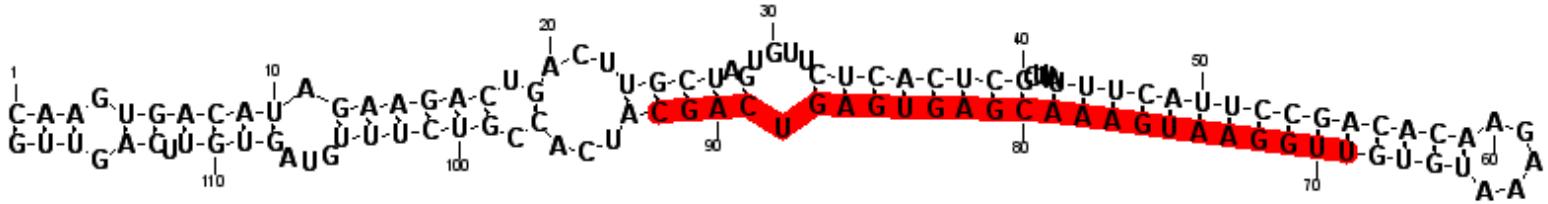
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.43/0.48	20/24/1.00	0.6	0.8	10	0	1	0	26	4	3arm	2	nd	0.08	2	12	1	na	na

Clusters

Located in cluster 23: block10919_novel, block10920_novel, block10921_cand

Families

Member of family novel12 (seed UGGAAUG): block10919_novel, block10920_novel



```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
```

		reads	m f
seed	----------UGGAAUG----------	6	n
seed	----------GGAAUGA----------	6	n
		len	c f
	----------TGGAATGAAACGAGTGAGTCAGC----------	23	4
	----------T---TGGAATGAAACGAGTGAGTCAGC----------	24	2
	----------T---TGGAATGAAACGAGTGAGTC----------	21	2
	----------T---TGGAATGAAACGAGTGAGTCAG----------	23	2
	----------TGGAATGAAACGAGTGAGTCAG----------	22	1
	----------TGGAATGAAACGAGTGAGTC----------	20	1

```
ppacificus CAAGTGACATAGAAGACTGACTTGCTAGTGTTCTCACTCGCTTATTTCATTCCGACACAAGAAATGTGT---TGGAATGAAACGAGTGAGTCAGCATCACCGTCTTTG--TAGTGTTCAGTTG
cjaponica  ---ACGCTATG------CGATTTTCT--TTTTCTCAA-AAATTATTTCATTT---CACGTTGAATTTGCACGTGGAATGAAATAATTTGGTGACCAAAATGAAAATTGGATAGCGT-------
                 *  **        ** ** **  * ******     *********    ***    *** **    *********  * *  ** * **  *      ***  *** **

ppacificus (((.(((((((.(((((((.....(((((.....(((((((((....(((((((((((((((.....))))))   ))))))))))))))))))..))))).....))))))).  ..)))))..)).))))  0.820 -48.10
cjaponica     (((((((.      (((((((((  (((..((((. (((((((((((((   ((((.((......))))))))))))))))))))))))..))))..))))).))))))))).))))))))        0.999 -43.40
```

ppacificus	chromosome:chrUn:75760177:75760294:1	{Repeats: no}
cjaponica	chromosome:chrUn:71593210:71593310:-1	Opposite_strand|Intronic_coding|NM_136816

---

block6540 [novel_cloningOK_randfoldOK]

Hairpin parameters

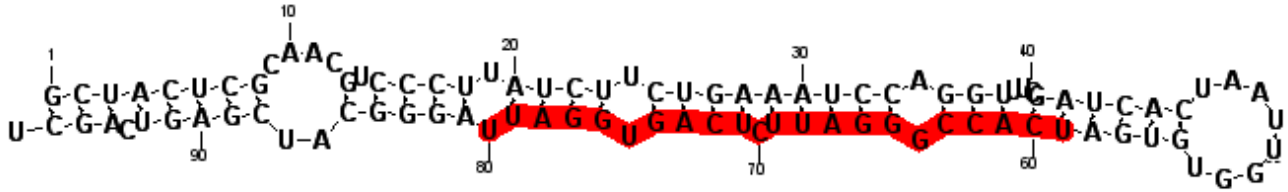
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.50/0.50	18/22/0.92	0.0	0.0	12	0	1	0	17	4	3arm	2	nd	0.23	2	13	1	na	na

Clusters

Located in cluster 13: block6539_novel, block6540_novel, block6541_novel, block6542_novel

Families

Member of family miR-35/36/38/39/40/41 (seed CACCGGG): cbr-mir-39, block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel, block6540_novel, block6541_novel, block13918_novel, block16473_novel, block19_cand



```
                                                                                                                reads   miRB
                                                                                                                        fami
seed    ----------------------------------------------------------------------CACCGG--G-------------------------------------  12    miR-
                                                                                                                        /38/
                                                                                                                        /40/
seed    ---------------------------------------------------------------------UCACCGG-----------------------------------------  1     nove
                                                                                                                len     clon
                                                                                                                        freq
                                                                                                                        P
        ----------------------------------------------------------------------TCACCGG--GATTCTCAGTGGATT------------------------ 22    12
        ---------------------------------------------------------------------ATCACCGG--GATTCTCAGT------------------------------ 18    1
ppacificus --------------GCTACTCGCAACGTCCCTTATCTTCTGAAATCCAGGTTTCGATCACTAATTGGTGTGATCACCGG--GATTCTCAGTGGATTAGGGCATCGAGTCAGCT-------
cbriggsae  ATGGTCTGGGTCGGACCTTTGCCAATTTTCTCCGCGGTGATACTCCAATGCGACGA-------------TTATCACCGGGTGAAAACTGGTAGAG-----GTCCGAGCCAGTCAGACCAT
cbrenneri  ----------------TTTCATGAAATATTTCAACGTTGAGACACCTAAGTTTT---------TTAGTTTTTTCACCGG--GAAATTTCGGGAAA-------------------------
                                **            *   *   * * *                  *  *******  **      *   *
ppacificus              ((((((((.....((((.(((..(((((((((.(((...((((((.......))))))))).)  ))))).))))..))))).))))...)))))).))).       1.000
                                                                                                                                -40.20
cbriggsae  ((((((((((((((((((((((.(((((.((.(((((((.((.........))             .))))))))))).))))).))))))))     ))))))).))...))))))))) 1.000
                                                                                                                                -58.70
cbrenneri                  .(((.((((((.((((..((.((((...((((((...)         ))))...))))))).)))  )))))))))).))).                      0.908
                                                                                                                                -11.10
```

ppacificus	chromosome:chrUn:158037196:158037292:-1	{SimpF: trf}
cbriggsae	chromosome:chrX:15335080:15335181:1	intergenic
cbrenneri	chromosome:chrUn:114149095:114149231:1	intergenic

---

block6541 [novel_cloningOK_randfoldOK]

Hairpin parameters

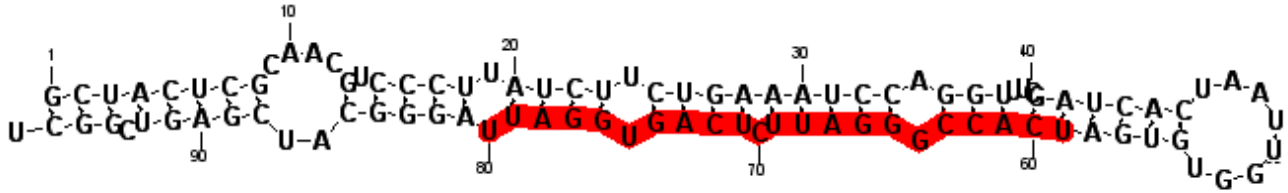
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.50/0.50	18/22/0.92	0.0	0.0	12	0	1	0	17	4	3arm	2	nd	0.23	2	13	1	na	na

Clusters

Located in cluster 13: block6539_novel, block6540_novel, block6541_novel, block6542_novel

Families

Member of family miR-35/36/38/39/40/41 (seed CACCGGG): cbr-mir-39, block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel, block6540_novel, block6541_novel, block13918_novel, block16473_novel, block19_cand



```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
```

		reads	miRB fami
seed	----------CACCGG--G----------	12	miR- /38/ /40/
seed	----------UCACCGG----------	1	nove
		len	clon freq
			P
	----------TCACCGG--GATTCTCAGTGGATT----------	22	12
	----------ATCACCGG--GATTCTCAGT----------	18	1

```
ppacificus ---------------GCTACTCGCAACGTCCCTTATCTTCTGAAATCCAGGTTTCGATCACTAATTGGTGTGATCACCGG--GATTCTCAGTGGATTAGGGCATCGAGTCGGCT-------
cbriggsae  ATGGTCTGGGTCGGACCTTTGCCAATTTTCTCCGCGGTGATACTCCAATGCGACGA-------------TTATCACCGGGTGAAAACTGGTAGA-----GGTCCGAGCCAGTCAGACCAT
cbrenneri  ----------------TTTCATGAAATATTTCAACGTTGAGACACCTAAGTTTT----------TTAGTTTTTTCACCGGG-AAATTTCGGGAAA-------------------------
                                 **            *   *   * * *                  *  *******   *      *   *

ppacificus                (((((((.....((((.(((..(((((((((.(((...((((((.......)))))))))).)  ))))).))))..))))).))))...)))))).))).        1.000
                                                                                                                                      -39.90
cbriggsae  ((((((((((((((((((((((.(((((.((.(((((((.((.........))              .)))))))))).)))))).)))))))     )))))))).))...))))))))) 1.000
                                                                                                                                      -58.70
cbrenneri                   .(((.((((((.((((..((.(((((...((((((...)          ))))...)))))).))))  ))))))))).))).                        0.908
                                                                                                                                      -11.10
```

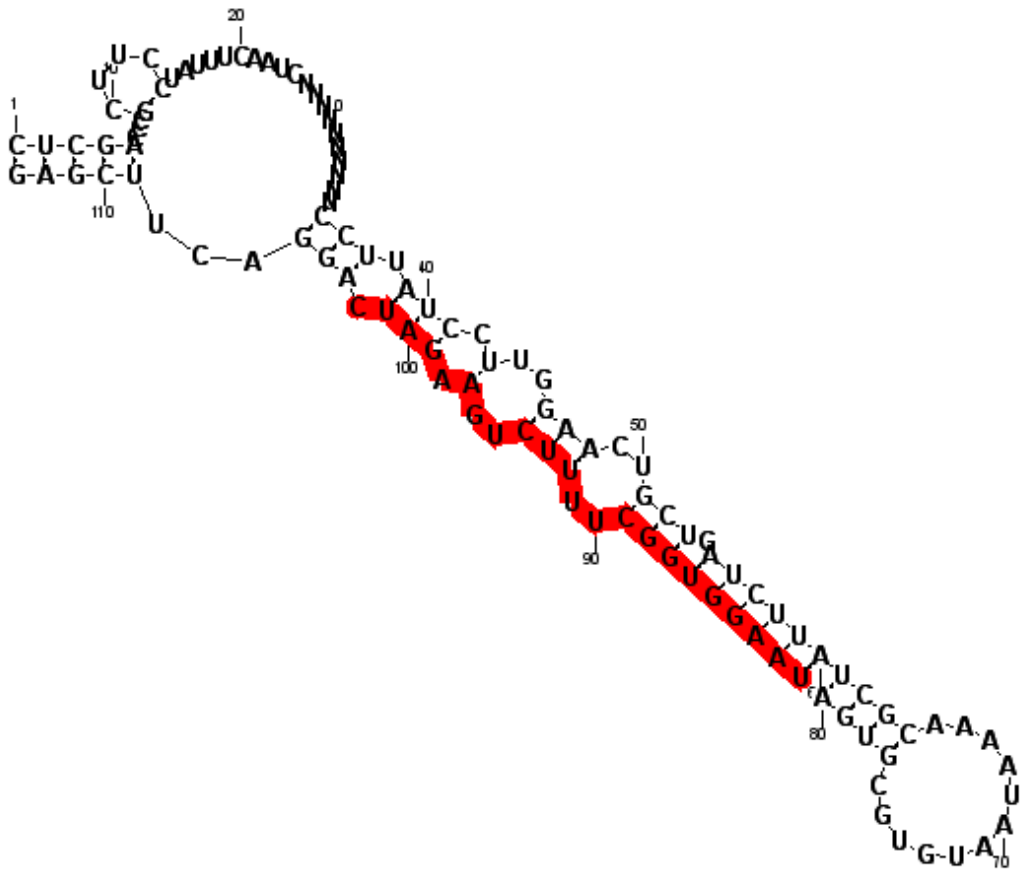
ppacificus	chromosome:chrUn:158037323:158037419:-1	{SimpF: trf}
cbriggsae	chromosome:chrX:15335080:15335181:1	intergenic
cbrenneri	chromosome:chrUn:114149095:114149231:1	intergenic

---

block5657 [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	0.38/0.41	21/22/1.00	0.0	0.0	14	0	1	0	11	4	3arm	1	nd	0.18	2	15	1	na	na



		reads	miRBase family
seed	----------AAGGUGG----------	15	novel
		len	cloning frequen
			PS31
	----------TAAGGTGGCTTTTCTGAAGATC----------	22	14
	----------TAAGGTGGCTTTTCTGAAGAT----------	21	1

```
ppacificus CTCGACCCGCTTCCTATTTCAATCNNNNNNNNNNCCTTATCCTTGGAACTGCTGATCTTATCGCAAA----ATAATGTGCGTGATAAGGTGGCTTTTCTGAAGATCAGGACTTCGAG
cbrenneri  ----------------------------------TGTCATGCCGGGA----TTGATCATTTCACATATTTTATTGTGTGCGTGA-AAGGTGGAATTCC-----------GTTTGAAG
                                               * ** *  ***     ***** * ** ** *    **  ********* *******  ** *             **  **

ppacificus (((((.............................(((.(((.(((((((..(((.(((((((((...    .........)))))))))))))..)))))).))).))).))))) 0.430
                                                                                                                                  -25.55
cbrenneri                                     ..(((...(((((    ((.(((.(((((((.(((........))).)))) )))))).)).))))           )..)))).. 0.999
                                                                                                                                  -16.40
```

ppacificus	chromosome:chrUn:133907025:133907137:-1	{Repeats: no}
cbrenneri	chromosome:chrUn:74128333:74128485:-1	intergenic

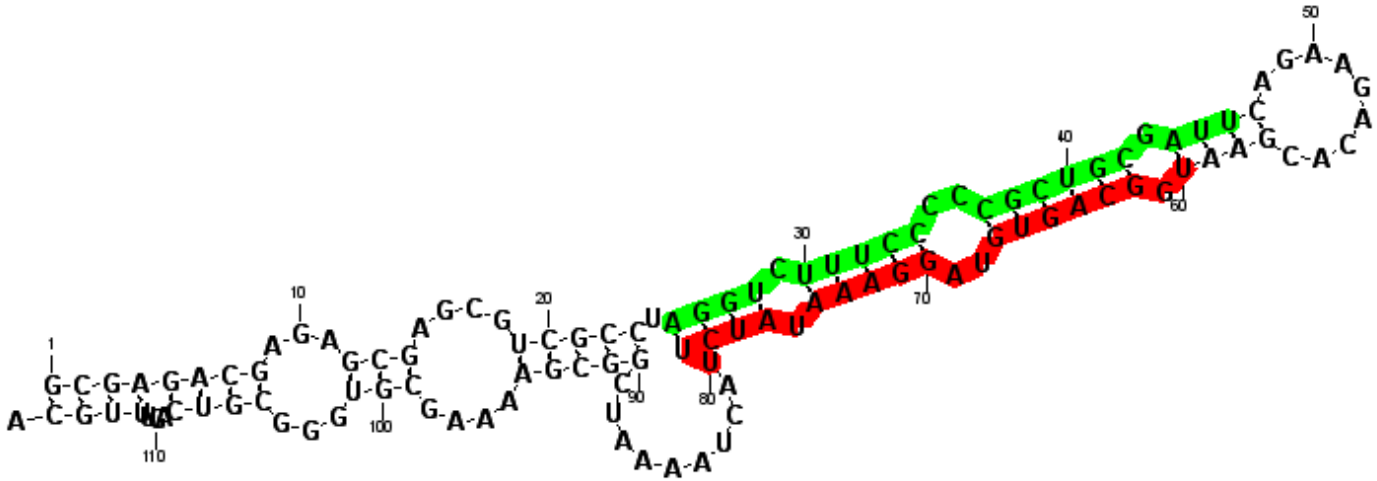
sblock395 [novel_cloningHIGH_multiarm_DicerOK_randfoldOK]

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	0.009	no	no	0.36/0.59	18/24/0.98	0.0 0.0	0.0 0.0	1 51	0 0	1 1	0 0	24 36	1 3	5arm 3arm	2 2	nd nd	0.18 0.29	2 2	60	1	2	1

Families

Member of family novel7 (seed GGUCUUU): sblock21_novel, sblock395_novel



```
                                                                                                                                                                                reads   miRBase family s
seed    ------------------------------------------------------------GGCAGUG------------------------------------------------------   58      miR-34
seed    ------------------------------------------------------------UGGCAGU------------------------------------------------------    1      novel
seed    -------------------------GGUCUUU-------------------------------------------------------------------------------------------    1      novel
                                                                                                                                                len     cloning frequenc
                                                                                                                                                        PS312
        ------------------------------------------------------------TGGCAGTGTAGGAAATATCTT-------------------------------------   21      51
        ------------------------------------------------------------TGGCAGTGTAGGAAATATCTTAC-----------------------------------   23      3
        ------------------------AGGTCTTTCCCCCGCTGCGATT-------------------------------------------------------------------------   22      1
        -----------------------------------------------------------ATGGCAGTGTAGGAAATATCTT-------------------------------------   22      1
        ------------------------------------------------------------TGGCAGTGTAGGAAATATCTTA------------------------------------   22      1
        ------------------------------------------------------------TGGCAGTGTAGGAAATAT----------------------------------------   18      1
        ------------------------------------------------------------TGGCAGTGTAGGAAATATCT--------------------------------------   20      1
        ------------------------------------------------------------TGGCAGTGTAGGAAATATCTTACT----------------------------------   24      1
ppacificus gcgagacgagagcgagcgtcgcctaggtctttcccccgctgcgattcagaagacacgaaTGGCAGTGTAGGAAATATCTTactaaaatcggcgaaaagcgtgggcgtcagtttgca
           ****************************************************************************************************************
ppacificus ((((((((...(((....(((((.((((.(((((..((((((.((((.........))))).)))))))..)))))).)))).........))))))....)))...)))))...))))). 0.520
                                                                                                                                                -43.40
```

ppacificus	chromosome:chrUn:165706450:165706565:1	{Repeats: no}

---

block6542 [novel_cloningOK_randfoldOK]

Hairpin parameters

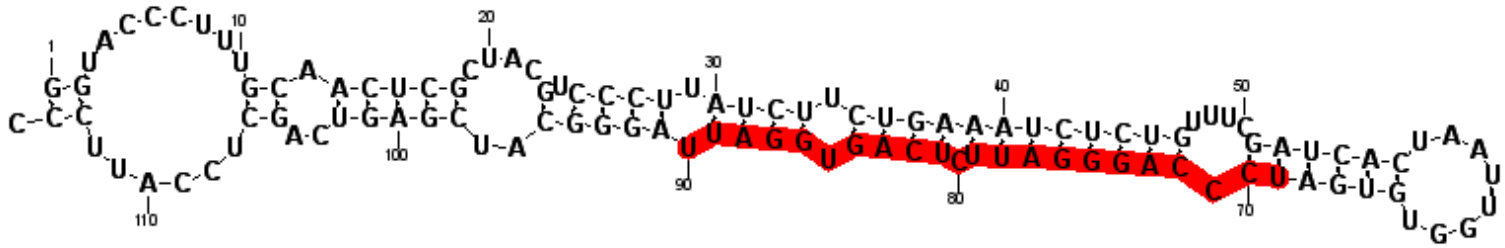
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.002	no	no	0.50/0.50	22/22/1.00	0.0	0.0	22	0	1	0	25	4	3arm	1	nd	0.23	2	22	1	na	na

Clusters

Located in cluster 13: block6539_novel, block6540_novel, block6541_novel, block6542_novel

Families

Member of family novel8 (seed CCCAGGG): block6539_novel, block6542_novel



```
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
```

		reads	miRBase family se
seed	----------CCCAGGG----------	22	novel
		len	cloning frequenci
			PS312
	----------TCCCAGGGATTCTCAGTGGATT----------	22	22

```
ppacificus GGTACCCTTTGCAACTCGCTACGTCCCTTATCTTCTGAAATCTCTGTTTCGATCACTAATTGGTGTGATCCCAGGGATTCTCAGTGGATTAGGGCATCGAGTCAGCTCCATTCCC
cbrenneri  -AAACCCCCGAAAA---------------AAACCCGGAAAAATTTTTTT-------------------TCCCAGGG-TTTTCCGGGGTTT-------------------------
              ****     **               *    * ****  * * ***                   ******** ** ** * ** **

ppacificus ((........((.(((((.....((((.((((..(((((((((((....((((((........)))))).))))))))).))))..))))..))))...))))))..)).....)). 0.950
                                                                                                                                  -37.94
cbrenneri   (((((((.((...                ((((((((((((.....)))                   )))..))) )))))).))))))                           1.000
                                                                                                                                  -22.10
```

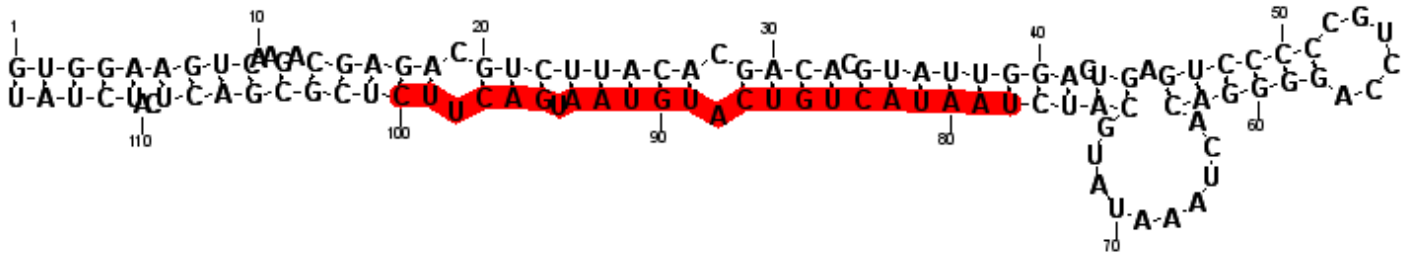
ppacificus	chromosome:chrUn:158037442:158037556:-1	{SimpF: trf}
cbrenneri	chromosome:chrUn:14975122:14975276:-1	Opposite_strand|Intronic_coding|NM_059756

---

block954 [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	0.30/0.30	23/23/1.00	0.0	0.0	26	0	1	0	15	20	3arm	1	nd	0.13	1	26	1	na	na



```
                                                                                                                                                reads   miRBase family se
seed    ------------------------------------------------------------------------------AAUACUG------------------------------   26      miR-236
                                                                                                                                                len     cloning frequenci
                                                                                                                                                        PS312
        ------------------------------------------------------------------------------TAATACTGTCATGTAATGACTTC---------------   23      26
ppacificus gtggaagtcaagacgagacgtcttacacgacacgtattggagtgagtcccccgtccaggggacactaaatatgcatcTAATACTGTCATGTAATGACTTCtcgcgactcatctat
           ***********************************************************************************************************************
ppacificus (((((((((....((((((.(((((((.((((.(((((((.(((((.....)))))).....)))))))))))))).))))).))).))))).))))..)))))  0.880
                                                                                                                                                -43.50
```

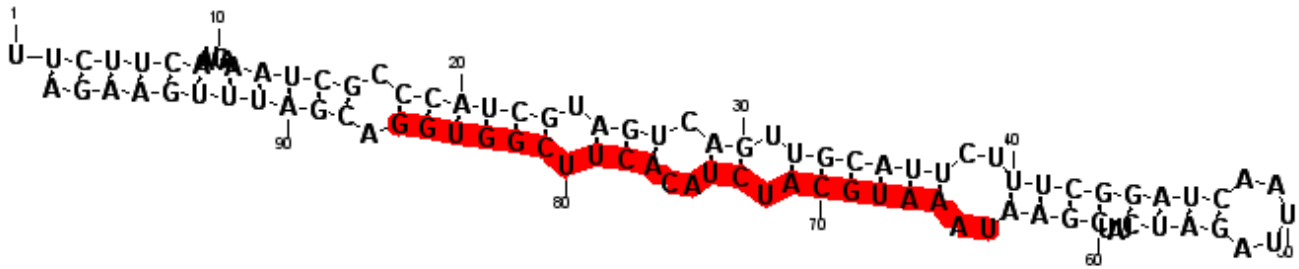
ppacificus	chromosome:chrUn:31908649:31908763:-1	{Repeats: no}

---

block9384 [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	0.42/0.43	23/24/1.00	0.0	0.0	8	0	1	0	12	11	3arm	1	nd	0.26	2	9	1	na	na



		reads	miRBase family seed
seed	----------AAAUGCA----------	8	miR-232
seed	----------UAAAUGC----------	1	novel
		len	cloning frequencies
			PS312
	----------TAAATGCATCTACACTTCGGTGG----------	23	8
	----------ATAAATGCATCTACACTTCGGTGG----------	24	1

```
ppacificus ------TTCTTCAATGAAATCGCCCATCGTAGTCAGTTGCATTCTTTCGGATCAATT--------AGATCTATCGAATAAATGCATCTACACTTCGGTGGACGATTTGAAGA
cremanei   ------------------------------GATTTTTTGGTATTCAATCGGATTATAT---------TCGAATTCGAACAAATGCAAATACCGAAAAGTC-------------
cbriggsae  ------CACTGGAGCGAA-----------------TTTGCAATTTTTTAAACTATTT----------CCTTTTTTTAAAAATGCAAATTCGCTCTACTG-------------
celegans   ----------------ATGATGTGAATCGTGTTTTTTTACAATGATTACAATGATTT------------TTTTTTAAGAAATGCACAAAATTCATTCAT-------------
cbrenneri  GTTCAGAACTACCAC--------------------TGTATATTTCTCTGAATGACACAGTGTATGTGATTTTTCCTGTAAATGCAGTACTATTTTGAAC-------------
cjaponica  GCTGCTTCCTTACAT-------------GTATTCTTTCTTTTTTCTTCAAATA--------------------TGAATAAATGCATTATTAGGTAGCGC-------------
                                                 *       *                          *******
ppacificus       .(((((((....(((((.(((((((.(((.((.(((((((..(((((((((....        .))))...))))..)))))))..))..))))..))))))..))))))))))) 1.000 -35.40
cremanei                                  ((((((((((((((((.(((((((....         ...)))))))).....))..))))))))))))))              0.946 -16.30
cbriggsae        ((.(((((((((                  ((((((..(((((((((.....          ......))))))))))))))))))))))))..))              1.000 -24.00
celegans                   ((((.((((((.(((((((((((.((.((((.....)))).            ..)).)))))))).))))...))))))))))                0.977 -11.00
cbrenneri  ((((((((.((..((                    (((((.......(((.((((((.....)))))..)).)))......)))))))..))))))))))                0.713 -16.14
cjaponica  (((((((...((.((             ((((((..(((...(((....)))).. .))))..))))))))))..))))))))..                1.000 -14.60
```

ppacificus	chromosome:chrUn:48100069:48100166:1	{Repeats: no}
cremanei	chromosome:chrUn:80350887:80351024:-1	Opposite_strand|Intronic_coding|NM_211666 ## Same_strand|Intronic_coding|NM_069875
cbriggsae	chromosome:chrUn:1788308:1788445:1	Same_strand|Intronic_coding|NM_070482
celegans	chromosome:chrX:8595573:8595710:1	Opposite_strand|Intronic_coding|F18E9.7
cbrenneri	chromosome:chrUn:89916265:89916402:-1	intergenic
cjaponica	chromosome:chrUn:138877944:138878081:1	intergenic

---

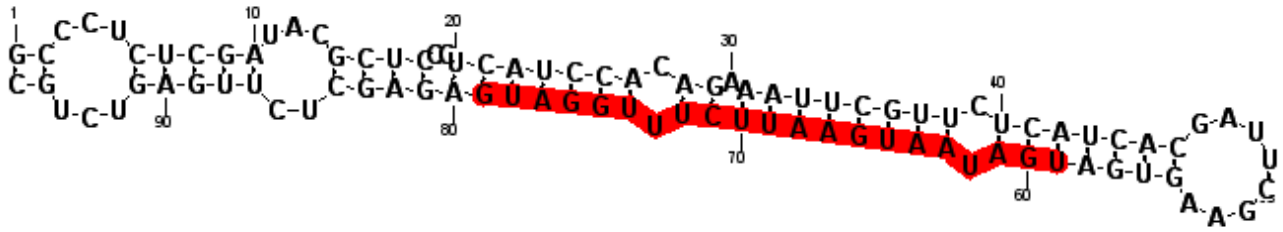
block10683 [novel_cloningOK_randfoldOK]

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	0.29/0.29	21/21/1.00	0.0	0.0	9	0	1	0	17	4	3arm	1	nd	0.10	1	9	1	na	na

Clusters

Located in cluster 22: block10683_novel, block10684_cand, block10685_cand



```
                                                                                                                reads   miRBase family seed
seed            ------------------------------------------------------------------GAUAAUG------------------------------   9       novel
                                                                                                                len     cloning frequencies
                                                                                                                        PS312
                ------------------------------------------------------------------TGATAATGAATTCTTTGGATG-----------------   21      9
ppacificus      GCCCTCTCGATACGCTCCCTCATCCACAG-AAATTCGTTCTCAT--CACGATTCGA------AGTG--ATGATAATGAATTCTTTGGATGAGAGCTCTTGAGTCTGC
cremanei        -----------------GCTCCAGTAGGG-ACACTTATTTTCA------GATCAAACATGGGGATA--TTGATAATGATAGCTACTGG----------------TGC
cbriggsae       --------------------CGACGACGATAAATACGTTCCAGCTGGACTATTAAAC-----AGTG--CAGATAATGTAATTTCTTCAATA----------------
celegans        --------------------CCAAATCGG-ATATTCATTTCATT--GTCGAT----------GGTGATATGATAATGAGTGAT----------------GGATTTGC
cjaponica       --------------------GCACATCA--AAGTTCGTTGTACC--GGCGATTTTAC-----GATG--ATGATAATGAATTTTTTGT-----------------CGC
                                                *      **           **            *     *******     *
ppacificus      ((...((((((...((((..(((((((.(( .(((((((((.((((  (((.......      .)))  )))).))))))))))).))))))))))..))))))...))  1.000 -39.50
cremanei                        ((.(((((((.. ....((((((.(((      ((((.........))).  )))).)))))...))))))))                .))  0.750 -16.10
cbriggsae                          ....((.((....((((((....(((.(((.......     )))).  )))..))))))...)).)).....                  0.992 -10.80
celegans                           .(((((((.. .(((((((((((.(  ((((..          ..))))))))).))))))))..                .)))))))..  0.989 -14.70
cjaponica                          ((((((..(  ((((((((((..(  (.((......)      ).))  ...))))))))))))).)))                  .))  0.852 -12.50
```

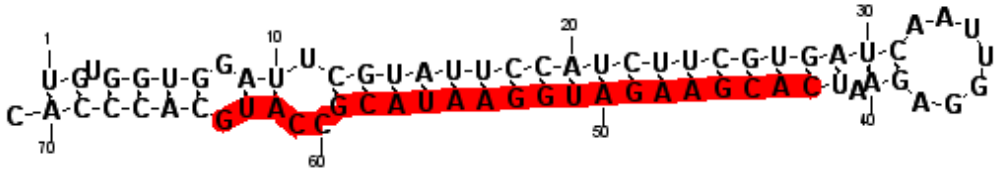
ppacificus	chromosome:chrUn:70959103:70959198:1	{Repeats: no}
cremanei	chromosome:chrUn:45154183:45154318:1	Opposite_strand|Boundary_non-coding|NM_070915 ## Opposite_strand|Exonic_coding|NM_074490
cbriggsae	chromosome:chrV:9044075:9044210:1	Opposite_strand|Intronic_coding|NM_001011629 ## Same_strand|Intronic_coding|NM_062593
celegans	chromosome:chrV:4762905:4763040:1	Same_strand|Exonic_coding|C18G1.3
cjaponica	chromosome:chrUn:14651215:14651350:1	intergenic

---

block13316 [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	0.48/0.50	20/22/1.00	0.0	0.0	25	0	1	0	7	4	3arm	1	nd	0.14	2	33	1	na	na



```
                                                                                                                reads   miRBase family
                                                                                                                        seed
seed   ------------------------------------------------------------ACGAAGA--------------------------------   28      novel
seed   -------------------------------------------------------------CGAAGA----U----------------------------   4       novel
seed   --------------------------------------------------------------GAAGA----UG---------------------------   1       novel
                                                                                                                len     cloning
                                                                                                                        frequencies
                                                                                                                        PS312
       ------------------------------------------------------------CACGAAGA----TGGAATACGCCATG---------------22      25
       -------------------------------------------------------------ACGAAGA----TGGAATACGCCATG---------------21      4
       ------------------------------------------------------------CACGAAGA----TGGAATACGCCAT----------------21      2
       -------------------------------------------------------------CGAAGA----TGGAATACGCCATG---------------20      1
       ------------------------------------------------------------CACGAAGA----TGGAATACGCCA-----------------20      1
ppacificus --------TGTGGTGGATTCGTATTCCA---------TCTTCGTGATCAATTGGAGAATCACGAAGA----TGGAATACGCCATGCACCCAC--------
cremanei   ------------ATGGTTACATGCTCCA---------TTTTACAGCTCGATAGAAGCA-AACGAAGA---TGGAAATCCACCAG----------------
cbriggsae  -------------TGAGCTCACATAC-----------TCTTCGTAATTTTTAG----ATTACGAAGAG-AGATGATTTCACAGA----------CAGTAT
celegans   TTCTTAGATTTGGTGG---TGTATTCCACATTTCCGGTCTGCGTGATCACT----GTATCACGAAGA--CTTTGAAT-CGTCAT-CTCCGACTTCAAGAG
cbrenneri  -----------------CTCGTTTTCTCCT-------GTTGTTCGATTCATAATTGTGAAACGAAGAACAGAGGAAACCGC-------------------
cjaponica  -------------TAAGAAATTGTT------------TCTTTTTGATCATTCAGATTGTCACGAAGAT-GCTTAATTTCGTC------------------
                                                  *      *   *         *******       *   *

ppacificus         ((.(((((.((.(((((((((         (((((((((((.......)).)))))))))    )))))))))..)).)))))).         1.000
                                                                                                                   -37.30
cremanei               .((((...((..((((         ((((...((((....)).)). ....))))   )))).)).)..)))).                0.994
                                                                                                                   -13.00
cbriggsae               ((((.((((....(          ((((((((((....)    )))))))))) ...))).)))).... ......              0.973
                                                                                                                   -18.60
celegans   .(((((.((.(((((.((   ((.....((((((..(((((.(((((((....    ..)))))).)))  )).)))) .)))))  ).)))).)).)))))  0.881
                                                                                                                   -24.00
cbrenneri                   ...(((((((.((       (((.((((.((((((....)))))).)))).))))))))))))...                   1.000
                                                                                                                   -22.60
cjaponica               ...(((((((..            (((((.(((.((.......)))))).)))))). ...))))))))...                 0.999
                                                                                                                   -11.30
```

ppacificus	chromosome:chrUn:111743640:111743710:1	{Repeats: no}
cremanei	chromosome:chrUn:21310585:21310695:-1	Same_strand|Intronic_coding|NM_180914 ## Opposite_strand|Intronic_coding|NM_001031159
cbriggsae	chromosome:chrV:5188622:5188682:-1	Same_strand|Intronic_coding|NM_062569
celegans	chromosome:chrX:4533911:4533999:-1	Opposite_strand|Exonic_coding|C07A12.3a
cbrenneri	chromosome:chrUn:50585408:50585518:-1	intergenic
cjaponica	chromosome:chrUn:69107145:69107255:-1	Opposite_strand|Intronic_coding|NM_171458

sblock280 [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	0.002	no	no	0.52/0.68	21/22/1.00	0.0 0.0	0.0 0.0	4 57	0 0	1 1	0 0	19 20	3 5	5arm 3arm	1 1	nd nd	0.18 0.18	2 2	63	1	1	2

Clusters

Located in cluster 24: sblock279_novel, sblock280_novel

Families

Member of family miR-51/52/55 (seed ACCCGUA): block7028_novel, block7029_novel, block9544_novel, block15318_novel, block15319_novel, sblock162_novel, sblock213_novel, sblock279_novel, sblock280_novel, block9543_cand

```
                                                                                                                reads   miRBase family seed
seed    ----------------------------------------------------------ACCCGUA-----------------------------------     57      miR-51/52/55
seed    --------------------CGAUGAC-------------------------------------------------------------------------------     4       novel
seed    ----------------------------------------------------------CCCGUAG-----------------------------------      2       novel
                                                                                                                len     cloning frequencies
                                                                                                                                PS312
        ---------------------------------------------------------CACCCGTAGTCCGTTATCGTCT--------------------     22      57
        --------------------ACGATGACCGCTCGACGGGAGC-------------------------------------------------------------     22      4
        ---------------------------------------------------------ACCCGTAGTCCGTTATCGTCT--------------------     21      2
ppacificus aatgagggagtgattgaacacgatgaccgctcgacgggagcatccattgcgagattgCACCCGTAGTCCGTTATCGTCTtcaaccaactccaatctcat
           ****************************************************************************************************
ppacificus .(((((((((..(((((.(((((((.(((..(((((.(((((........)))).)).)))))))..)))))))).)))))...)))))...))))) 0.990
                                                                                                                -37.80
```

ppacificus	chromosome:chrUn:94125873:94125971:1	{Repeats: no}

sblock279 [novel_cloningHIGH_multiarm_DicerOK_randfoldOK]

Hairpin parameters

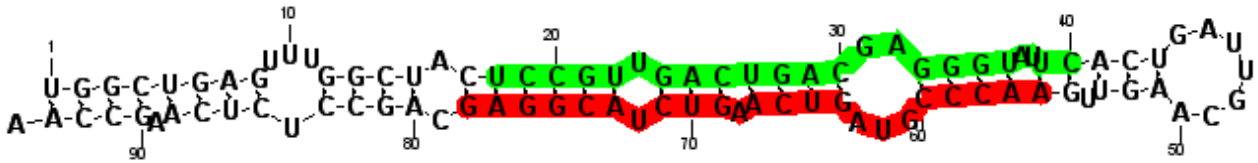
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.44/0.52	18/23/0.96	0.0 0.0	0.3 0.0	6 46	0 0	1 1	0 0	17 16	3 5	5arm 3arm	1 1	nd nd	0.22 0.26	2 3	57	1	1	1

Clusters

Located in cluster 24: sblock279_novel, sblock280_novel

Families

Member of family miR-51/52/55 (seed ACCCGUA): block7028_novel, block7029_novel, block9544_novel, block15318_novel, block15319_novel, sblock162_novel, sblock213_novel, sblock279_novel, sblock280_novel, block9543_cand



```
                                                                                                    reads   miRBase family seed
seed   -------------------------------------------------------ACCCGUA------------------------------   50    miR-51/52/55
seed   ------------------CCGUUGA-------------------------------------------------------------------   6     novel
seed   ------------------CGUUGAC------------------------------------------------------------------   1     novel
                                                                                                    len   cloning frequencies
                                                                                                                PS312
       -------------------------------------------------------AACCCGTAGTCAAGTCTACGGAG----------------  23    46
       -----------------TCCGTTGACTGACGAGGGTATTC-------------------------------------------------------  23    4
       -------------------------------------------------------AACCCGTAGTCAAGTCTA---------------------  18    2
       -------------------------------------------------------AACCCGTAGTCAAGTCTACGG------------------  21    2
       -----------------TCCGTTGACTGACGAGGGTATT--------------------------------------------------------  22    2
       ------------------CCGTTGACTGACGAGGGTATT---------------------------------------------------------  21    1
ppacificus tggctgagtttggctactccgttgactgacgagggtattcactgattgcaagttgAACCCGTAGTCAAGTCTACGGAGcagcctctcaagccaa
           ****************************************************************************************
ppacificus ((((((((...((((.(((((((.(((((((..((((..(((((.......)))).)))))))...)))).))).)))))).))))).)))).  1.000 -46.70
```

ppacificus	chromosome:chrUn:94125746:94125839:1	{Repeats: no}

---

block5167 [novel_cloningHIGH_randfoldOK]

Hairpin parameters

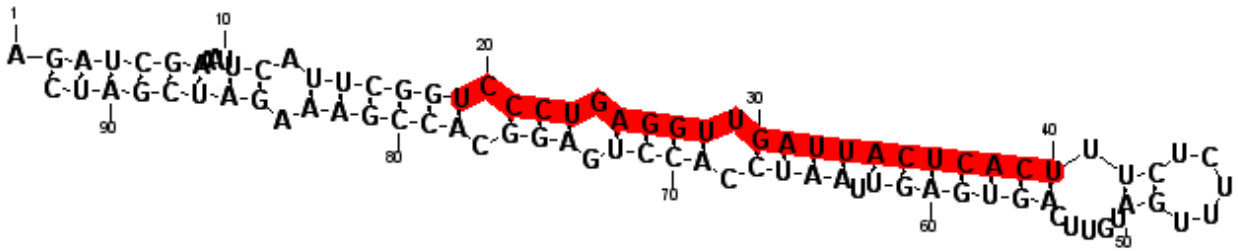
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.45/0.45	22/22/1.00	0.0	0.0	27	0	1	0	18	3	5arm	1	nd	0.18	1	27	1	na	na

Clusters

Located in cluster 11: block5166_novel, block5167_novel

Families

Member of family lin-4 (seed CCCUGAG): cbr-lin-4, block5167_novel, block8798_cand, sblock281_cand



		reads	miRBase family seed
seed	----------CCCUGAG----------	27	lin-4
		len	cloning frequencies
			PS312
	----------TCCCTGAGGTTGATTACTCACT----------	22	27

```
ppacificus agatcgaaattcattcggTCCCTGAGGTTGATTACTCACTttctctttgatgttcagtgagttaatccacctgaggcaccgaaagatcgatc
           ***********************************************************************************************
ppacificus .(((((...((.(((((((.(((.((((.(((((((((((.((.....)).....)))))))).)))).)))).))).)))))).)))))))) 1.000 -39.50
```

ppacificus	chromosome:chrUn:124787015:124787106:-1	{Repeats: no}

---

block4438 [novel_cloningHIGH_randfoldOK]

Hairpin parameters

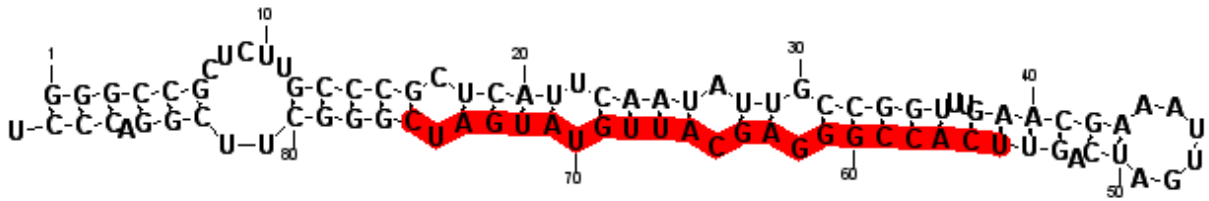
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.002	no	no	0.48/0.53	19/22/0.96	0.0	0.0	48	0	1	0	14	5	3arm	8	nd	0.18	1	52	1	na	na

Clusters

Located in cluster 9: block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel

Families

Member of family miR-35/36/38/39/40/41 (seed CACCGGG): cbr-mir-39, block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel, block6540_novel, block6541_novel, block13918_novel, block16473_novel, block19_cand



		reads	miRBase family seed
seed	----------CACCGGG----------	52	miR-35/36/38/39/40/41
		len	cloning frequencies
			PS312

```
                 -------------------------------------------------------TCACCGGGAGCATTGTATGATC--------------- 22          48
                 -------------------------------------------------------TCACCGGGAGCATTGTATG----------------- 19          2
                 -------------------------------------------------------TCACCGGGAGCATTGTATGAT---------------- 21          2
ppacificus GGGCCGCTCTTGCCCGCTCATTCAATATTGCCGGTTTGAACGAAATTGATC-AGTTCACCGGGAGCATTGTATGATCGGGCTTCGGACCCT
cremanei   -----------GCTCG---ACGTCATACTCTCGTGTTGATCCACATTAATCTGGTTCACCGGGAGCATT------TTGGAGGT--------
                      ** **   *    *** *  **  **** * * *** ***  ****************      * **   *
ppacificus ((((((.....(((((.((((.((((.((.(((((..((((((.....)) .)))))))))).)).)))).)))).))))..))).))). 1.000 -39.20
cremanei              ..(((.   .((..((.(((((((.((.((.(((.......))).)))))))))).)).      .))..)).         0.983 -15.00
```

ppacificus	chromosome:chrUn:105940516:105940605:-1	{SimpF: trf}
cremanei	chromosome:chrUn:56134520:56134649:-1	intergenic

---

block4440 [novel_cloningHIGH_randfoldOK]

Hairpin parameters

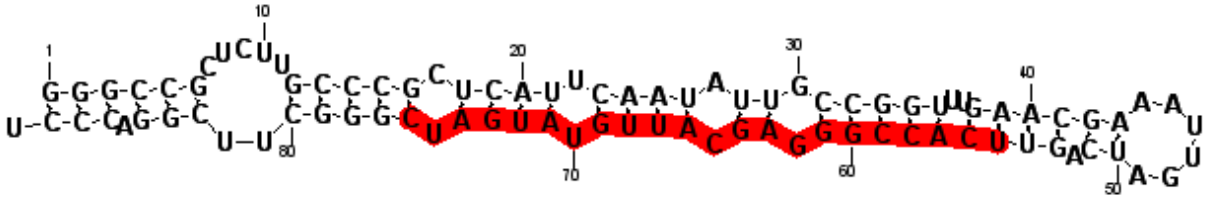
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.002	no	no	0.48/0.53	19/22/0.96	0.0	0.0	48	0	1	0	14	5	3arm	8	nd	0.18	1	52	1	na	na

Clusters

Located in cluster 9: block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel

Families

Member of family miR-35/36/38/39/40/41 (seed CACCGGG): cbr-mir-39, block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel, block6540_novel, block6541_novel, block13918_novel, block16473_novel, block19_cand



```
                                                                                                   reads     miRBase family seed
seed             -------------------------------------------------------CACCGGG----------------------------- 52        miR-35/36/38/39/40/41
                                                                                                    len      cloning frequencies
                                                                                                                     PS312
                 -------------------------------------------------------TCACCGGGAGCATTGTATGATC--------------- 22          48
                 -------------------------------------------------------TCACCGGGAGCATTGTATG----------------- 19          2
                 -------------------------------------------------------TCACCGGGAGCATTGTATGAT---------------- 21          2
ppacificus GGGCCGCTCTTGCCCGCTCATTCAATATTGCCGGTTTGAACGAAATTGATC-AGTTCACCGGGAGCATTGTATGATCGGGCTTCGGACCCT
cremanei   -----------GCTCG---ACGTCATACTCTCGTGTTGATCCACATTAATCTGGTTCACCGGGAGCATT------TTGGAGGT--------
                      ** **   *    *** *  **  **** * * *** ***  ****************      * **   *
ppacificus ((((((.....(((((.((((.((((.((.(((((..((((((.....)) .)))))))))).)).)))).)))).))))..))).))). 1.000 -39.20
cremanei              ..(((.   .((..((.(((((((.((.((.(((.......))).)))))))))).)).      .))..)).         0.983 -15.00
```

ppacificus	chromosome:chrUn:105940740:105940829:-1	{SimpF: trf}

cremanei	chromosome:chrUn:56134520:56134649:-1	intergenic

---

block4442 [novel_cloningHIGH_randfoldOK]

Hairpin parameters

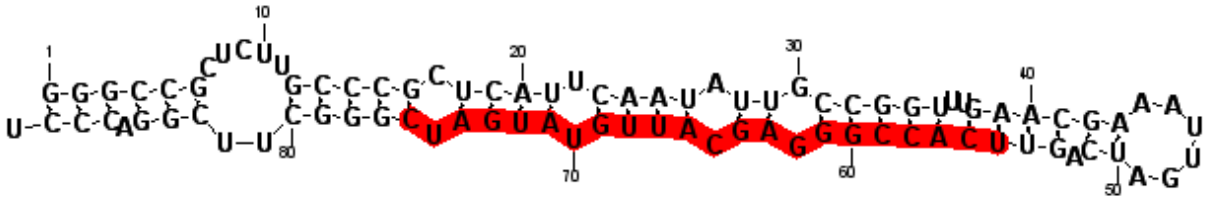
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.002	no	no	0.48/0.53	19/22/0.96	0.0	0.0	48	0	1	0	14	5	3arm	8	nd	0.18	1	52	1	na	na

Clusters

Located in cluster 9: block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel

Families

Member of family miR-35/36/38/39/40/41 (seed CACCGGG): cbr-mir-39, block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel, block6540_novel, block6541_novel, block13918_novel, block16473_novel, block19_cand



```
                                                                                                                reads   miRBase family seed
   seed   -------------------------------------------------------CACCGGG----------------------------          52     miR-35/36/38/39/40/41
                                                                                                                len     cloning frequencies
                                                                                                                                   PS312
          -------------------------------------------------------TCACCGGGAGCATTGTATGATC--------------- 22            48
          -------------------------------------------------------TCACCGGGAGCATTGTATG----------------- 19            2
          -------------------------------------------------------TCACCGGGAGCATTGTATGAT--------------- 21            2
ppacificus GGGCCGCTCTTGCCCGCTCATTCAATATTGCCGGTTTGAACGAAATTGATC-AGTTCACCGGGAGCATTGTATGATCGGGCTTCGGACCCT
cremanei   -----------GCTCG---ACGTCATACTCTCGTGTTGATCCACATTAATCTGGTTCACCGGGAGCATT------TTGGAGGT--------
                      ** **   *    *** *  **  **** * * *** ***  ****************      * **   *
ppacificus ((((((.....(((((.((((.((((.((.(((((..((((((.....)) .)))))))))).)).)))).)))).)))))..))).)))). 1.000 -39.20
cremanei              ..((.   .((..((.(((((((.((.((.((((.......))).)))))))))).)).      .))..)).         0.983 -15.00
```

ppacificus	chromosome:chrUn:105940964:105941053:-1	{SimpF: trf}
cremanei	chromosome:chrUn:56134520:56134649:-1	intergenic

---

block4444 [novel_cloningHIGH_randfoldOK]

Hairpin parameters

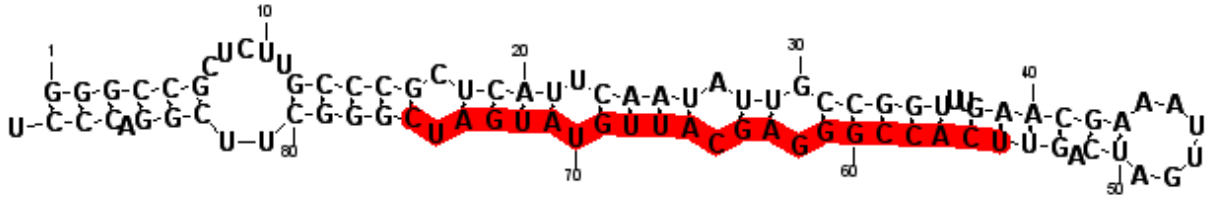
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.002	no	no	0.48/0.53	19/22/0.96	0.0	0.0	48	0	1	0	14	5	3arm	8	nd	0.18	1	52	1	na	na

Clusters

Located in cluster 9: block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel

Families

Member of family miR-35/36/38/39/40/41 (seed CACCGGG): cbr-mir-39, block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel, block6540_novel, block6541_novel, block13918_novel, block16473_novel, block19_cand



```
                                                                                                   reads     miRBase family seed
seed            ------------------------------------------------------CACCGGG-----------------------------  52        miR-35/36/38/39/40/41
                                                                                                   len       cloning frequencies
                                                                                                                        PS312
                ------------------------------------------------------TCACCGGGAGCATTGTATGATC--------------  22        48
                ------------------------------------------------------TCACCGGGAGCATTGTATG-----------------  19        2
                ------------------------------------------------------TCACCGGGAGCATTGTATGAT---------------  21        2
ppacificus      GGGCCGCTCTTGCCCGCTCATTCAATATTGCCGGTTTGAACGAAATTGATC-AGTTCACCGGGAGCATTGTATGATCGGGCTTCGGACCCT
cremanei        -----------GCTCG---ACGTCATACTCTCGTGTTGATCCACATTAATCTGGTTCACCGGGAGCATT------TTGGAGGT--------
                           ** **   *    *** *  **  **** * * *** ***  ****************      * **   *
ppacificus      ((((((.....(((((.((((.((((.((.(((((..((((((......)) .)))))))))).)).)))).)))).)))))..))).)))). 1.000 -39.20
cremanei                   ..((.   .((..((.(((((((.((.((.(((........))).)))))))))).)).      .))..)).         0.983 -15.00
```

ppacificus	chromosome:chrUn:105941188:105941277:-1	{SimpF: trf}
cremanei	chromosome:chrUn:56134520:56134649:-1	intergenic

---

block4446 [novel_cloningHIGH_randfoldOK]

Hairpin parameters

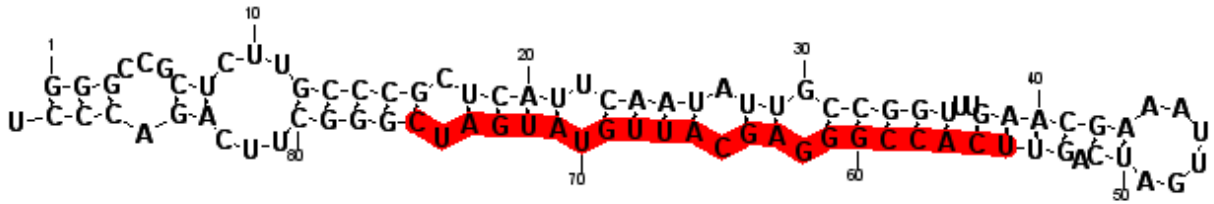
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.002	no	no	0.48/0.53	19/22/0.96	0.0	0.0	48	0	1	0	14	5	3arm	8	nd	0.18	1	52	1	na	na

Clusters

Located in cluster 9: block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel

Families

Member of family miR-35/36/38/39/40/41 (seed CACCGGG): cbr-mir-39, block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel, block6540_novel, block6541_novel, block13918_novel, block16473_novel, block19_cand



```
                                                                                                reads     miRBase family seed
seed    -------------------------------------------------------CACCGGG----------------------------  52        miR-35/36/38/39/40/41
                                                                                                 len      cloning frequencies
                                                                                                                  PS312
        -------------------------------------------------------TCACCGGGAGCATTGTATGATC--------------  22        48
        -------------------------------------------------------TCACCGGGAGCATTGTATG-----------------  19        2
        -------------------------------------------------------TCACCGGGAGCATTGTATGAT---------------  21        2
ppacificus GGGCCGCTCTTGCCCGCTCATTCAATATTGCCGGTTTGAACGAAATTGATC-AGTTCACCGGGAGCATTGTATGATCGGGCTTCAGACCCT
cremanei   -----------GCTCG---ACGTCATACTCTCGTGTTGATCCACATTAATCTGGTTCACCGGGAGCATT------TTGGAGGT--------
                      ** **   *    *** *  **  **** * * *** ***  ****************      * **   *
ppacificus (((...((...(((((.((((.((((.((.(((((..((((((.....)) .)))))))))).)).)))).)))).)))))...)).)))). 1.000 -35.40
cremanei              ..((.   .((..((.(((((((.((.((.(((.......))).)))))))))).)).      .))..)).         0.983 -15.00
```

ppacificus	chromosome:chrUn:105941412:105941501:-1	{SimpF: trf}
cremanei	chromosome:chrUn:56134520:56134649:-1	intergenic

---

block4449 [novel_cloningHIGH_randfoldOK]

Hairpin parameters

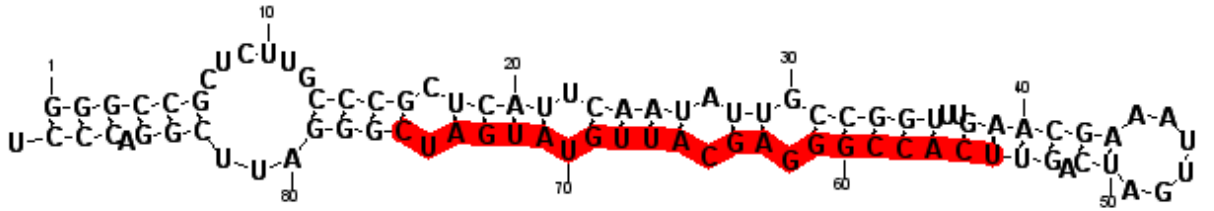
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.003	no	no	0.48/0.53	19/22/0.96	0.0	0.0	48	0	1	0	14	5	3arm	8	nd	0.18	1	52	1	na	na

Clusters

Located in cluster 9: block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel

Families

Member of family miR-35/36/38/39/40/41 (seed CACCGGG): cbr-mir-39, block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel, block6540_novel, block6541_novel, block13918_novel, block16473_novel, block19_cand



```
                                                                                                   reads     miRBase family seed
   seed   ------------------------------------------------------CACCGGG----------------------------  52      miR-35/36/38/39/40/41
                                                                                                    len      cloning frequencies
                                                                                                                     PS312
          -------------------------------------------------------TCACCGGGAGCATTGTATGATC--------------- 22      48
          -------------------------------------------------------TCACCGGGAGCATTGTATG----------------- 19      2
          -------------------------------------------------------TCACCGGGAGCATTGTATGAT---------------- 21      2
ppacificus GGGCCGCTCTTGCCCGCTCATTCAATATTGCCGGTTTGAACGAAATTGATC-AGTTCACCGGGAGCATTGTATGATCGGGATTCGGACCCT
cremanei   -----------GCTCG---ACGTCATACTCTCGTGTTGATCCACATTAATCTGGTTCACCGGGAGCATT------TTGGAGGT--------
                      ** **   *    *** *  **  **** * * *** ***  ****************      * **   *
ppacificus ((((((.....((((.((((.((((.((.(((((..((((((.....)) .)))))))))).)).)))).)))).))))...))).))). 1.000 -36.00
cremanei              ..((.   .((..((.(((((((.((.((.(((.......))).)))))))))).)).      .))..)).         0.983 -15.00
```

ppacificus	chromosome:chrUn:105941937:105942026:-1	{SimpF: trf}
cremanei	chromosome:chrUn:56134520:56134649:-1	intergenic

---

block4451 [novel_cloningHIGH_randfoldOK]

Hairpin parameters

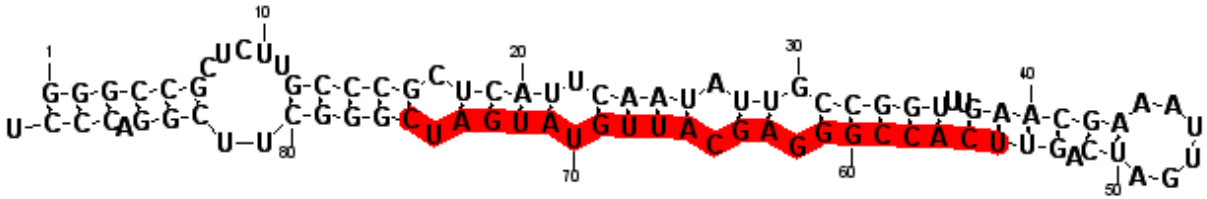
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.002	no	no	0.48/0.53	19/22/0.96	0.0	0.0	48	0	1	0	14	5	3arm	8	nd	0.18	1	52	1	na	na

Clusters

Located in cluster 9: block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel

Families

Member of family miR-35/36/38/39/40/41 (seed CACCGGG): cbr-mir-39, block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel, block6540_novel, block6541_novel, block13918_novel, block16473_novel, block19_cand



```
                                                                                                   reads     miRBase family seed
   seed   ------------------------------------------------------CACCGGG----------------------------  52      miR-35/36/38/39/40/41
                                                                                                    len      cloning frequencies
                                                                                                                     PS312
          -------------------------------------------------------TCACCGGGAGCATTGTATGATC--------------- 22      48
          -------------------------------------------------------TCACCGGGAGCATTGTATG----------------- 19      2
          -------------------------------------------------------TCACCGGGAGCATTGTATGAT---------------- 21      2
ppacificus GGGCCGCTCTTGCCCGCTCATTCAATATTGCCGGTTTGAACGAAATTGATC-AGTTCACCGGGAGCATTGTATGATCGGGCTTCGGACCCT
cremanei   -----------GCTCG---ACGTCATACTCTCGTGTTGATCCACATTAATCTGGTTCACCGGGAGCATT------TTGGAGGT--------
                      ** **   *    *** *  **  **** * * *** ***  ****************      * **   *
ppacificus ((((((.....(((((.((((.((((.((.(((((..((((((.....)) .)))))))))).)).)))).)))).))))))..))).))). 1.000 -39.20
```

```
cremanei              ..((.   .((..((.(((((((.((.((.(((.......))).))))))))))).)).      .))..)).        0.983 -15.00
```

ppacificus	chromosome:chrUn:105942162:105942251:-1	{SimpF: trf}
cremanei	chromosome:chrUn:56134520:56134649:-1	intergenic

---

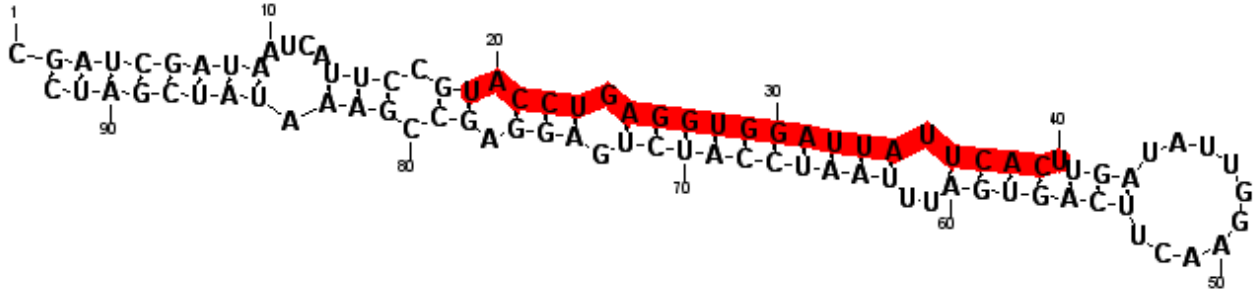
block5166 [novel_cloningOK_randfoldOK]

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	0.39/0.41	22/23/1.00	0.0	0.0	6	0	1	0	18	3	5arm	1	nd	0.18	1	7	1	na	na

Clusters

Located in cluster 11: block5166_novel, block5167_novel



```
                                                                                                                    reads     miRBase family seed
seed            -------------------ACCUGAG-------------------------------------------------------------------------  7         novel
                                                                                                                     len      cloning frequencies
                                                                                                                                      PS312
                -------------------TACCTGAGGTGGATTATTCACT-------------------------------------------------------  22        6
                -------------------TACCTGAGGTGGATTATTCACTT------------------------------------------------------  23        1
ppacificus      CGATCGATAATCATTCCGTACCTGAGGTGGATTATTCACTTGATATTGGAACTTCAGTGATTTAATCCATCTGAGGAGCCGAAATATCGATC
celegans        -------------------TACCTGAGCAGG-------ACGTGAGACCAAATAGTTGCGAAATTAGTCTTTTT-------CACTGCATAGGTT
                                   ********  **       ** *** *    *   *     * *** **  * *       *     ** * *
ppacificus      .(((((((((....((((.((.((((.(((((((((.((((.(((.........)))))))..))))))))))).))).)).)).)))))))) 1.000 -36.30
celegans                           .(((((.(((((       (...((((((....((((((....))))))))))..)       ).)))))..)))))). 1.000 -17.70
```

ppacificus	chromosome:chrUn:124786846:124786937:-1	{Repeats: no}
celegans	chromosome:chrX:16412008:16412139:-1	Same_strand|Intronic_coding|T24D11.1

---

block6539 [novel_cloningOK_randfoldOK]

Hairpin parameters

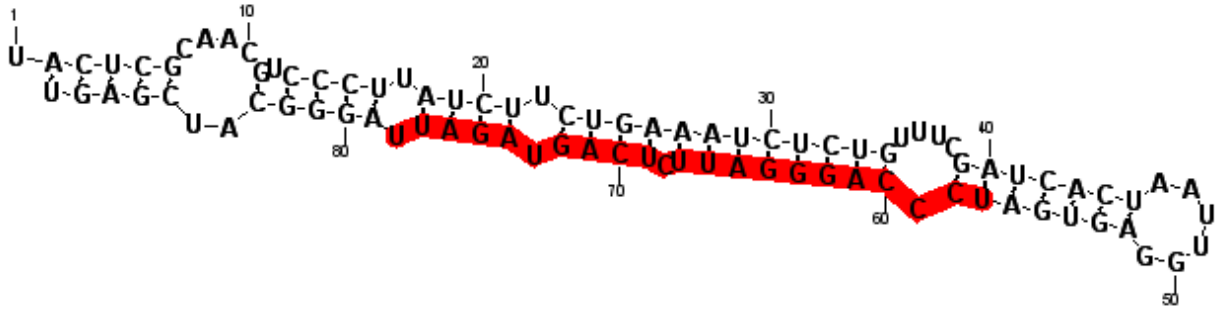
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.45/0.45	22/22/1.00	0.0	0.0	15	0	1	0	12	5	3arm	1	nd	0.18	1	15	1	na	na

Clusters

Located in cluster 13: block6539_novel, block6540_novel, block6541_novel, block6542_novel

Families

Member of family novel8 (seed CCCAGGG): block6539_novel, block6542_novel



```
                                                                                                    reads     miRBase family seed
seed      ---------------------------------------------------------CCCAGGG--------------------------  15        novel
                                                                                                    len       cloning frequencies
                                                                                                              PS312
          ---------------------------------------------------------TCCCAGGGATTCTCAGTAGATT------------ 22        15
ppacificus TACTCGCAACGTCCCTTATCTTCTGAA-ATCTCTGTTTCGATCACTAATTGGAGTGATCCCAGGGATTCTCAGTAGATTAGGGCATCGAGT
cremanei   AACTCTCTATGGTCC--ATCTGCCGAATCGATCTGCATCGA--GTTGATTT-------CCCAGGG-ACGTCTGACGATTT-----------
cjaponica  TTTTGGCA---------ATTTGCCCA--CTATCTGGCT-----ATTAGCCG-------CCCAGGGCAGATCTGCCGAAT------------
              *  *          ** * *  *     ****  *       *            *******    ** *  ** *
ppacificus .(((((.....((((.((((.(((((  (((((((....(((((((.....)))))))).))))))).))))).))))).))))...))))) 1.000 -36.40
cremanei   ...((((....((((  ..((((..(((((((.((......)  ))))))))       ..))))) )).....)).)).)...           0.951 -13.30
cjaponica  .(((((((         ((((((((.  .....((((.     ....))))       ....)))))))))).))))))).             1.000 -24.90
```

ppacificus	chromosome:chrUn:158037074:158037163:-1	{SimpF: trf}
cremanei	chromosome:chrUn:145214541:145214670:-1	Same_strand|Boundary_coding|NM_059406 ## Same_strand|Intronic_coding|NM_007741
cjaponica	chromosome:chrUn:88309678:88309807:-1	Opposite_strand|Intronic_coding|NM_068771

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block4453 [novel_cloningHIGH_randfoldOK]

Hairpin parameters

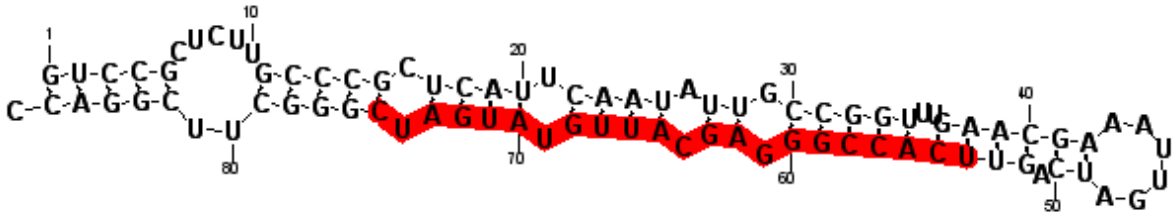
miRNA	randfold	RNA	rep	GC min/max	len min/max /mir_range	5'var	3'var	reads	reads edited	libs	libs edited	base distance	loop distance	position	locations	exon distance	unpaired	max bulge	total reads	total libs	dicer	drosha
no	0.001	no	no	0.48/0.53	19/22/0.96	0.0	0.0	48	0	1	0	12	5	3arm	8	nd	0.18	1	52	1	na	na

Clusters

Located in cluster 9: block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel

Families

Member of family miR-35/36/38/39/40/41 (seed CACCGGG): cbr-mir-39, block4438_novel, block4440_novel, block4442_novel, block4444_novel, block4446_novel, block4449_novel, block4451_novel, block4453_novel, block6540_novel, block6541_novel, block13918_novel, block16473_novel, block19_cand



```
                                                                                                                   reads   miRBase family seed
seed            ------------------------------------------------------CACCGGG---------------------------          52      miR-35/36/38/39/40/41
                                                                                                                   len     cloning frequencies
                                                                                                                           PS312
                ------------------------------------------------------TCACCGGGAGCATTGTATGATC------------ 22              48
                ------------------------------------------------------TCACCGGGAGCATTGTATGAT------------- 21              2
                ------------------------------------------------------TCACCGGGAGCATTGTATG---------------- 19              2
ppacificus      GTCCGCTCTTGCCCGCTCATTCAATATTGCCGGTTTGAACGAAATTGATC-AGTTCACCGGGAGCATTGTATGATCGGGCTTCGGACC
cremanei        GCTCG-------------ACGTCATACTCTCGTGTTGATCCACATTAATCTGGTTCACCGGGAGCATT------------TTGGAGGT
                *  **             *    *** *  **  **** * * *** ***  ***************             ** *
ppacificus      (((((.....(((((.((((.(((((.((.(((((..((((((.....)) .)))))))))).)).)))).)))).)))))..)))))). 1.000 -37.20
cremanei        ..((.             .((..((.(((((((.((.((.(((.......))).))))))))))).)).            .))..)). 0.983 -15.00
```

ppacificus	chromosome:chrUn:105942388:105942474:-1	{SimpF: trf}
cremanei	chromosome:chrUn:56134522:56134648:-1	intergenic