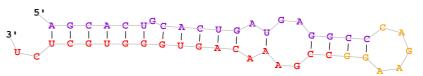Provisional ID   : NW_025322681.1_Acropora_millepora_isolate_JS-1_unplaced_genomic_scaffold_Amil_v2.1_Sc0000192_whole_genome_shotgun_sequen
Score total   :   250.9
Score for star read(s) :   3.9
Score for read counts   :   246.4
Score for mfe   :   1.2
Score for randfold   :   0
Score for cons. seed   :   -0.6
Total read count   :   495
Mature read count   :   378
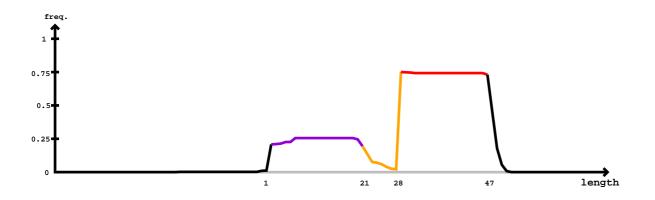Loop read count   :   0
Star read count   :   117


```
5'- acacucgagguagucuuauaggcuuaccuucauccuagcuaucagcacugcacugaugaggcccagaaggccgaaacagugggugcucuaagugacguuuuguuugcuuuuuu  -3'   obs
    acacucgagguagucuuauaggcuuaccuucauccuagcuaucagcacugcacugaugaggcccagaaggccgaaacagugggugcucuaagugacguuuuguuugcuuuuuu         exp
    .(((((.(((((((((.....))).)))))).............(((((.(((((.(..(((((.....))))..).)))))))))))...)))).................    reads    mm    sample
    ......................uaccuucauccuagcuaucagcacugc....................................................................    1      0     seq
    ..................................ucagcacugcacugaugagg..............................................................    2      0     seq
    ..................................ucagcacugcacugaugaggc.............................................................    1      0     seq
    ..................................ucagcacugcacugaugaggcc............................................................    1      0     seq
    ...................................cagcacugcacugaugaggcc...........................................................    1      0     seq
    ....................................agcacugcacugaugagC.............................................................    1      1     seq
    ....................................agcacugcacugaugagg.............................................................    2      0     seq
    ....................................agcacugcacugaugaggc............................................................    23     0     seq
    ....................................agcacugcacugaugaggA............................................................    2      1     seq
    ....................................agcacugcacugaugaggcG...........................................................    4      1     seq
    ....................................agcacugcacugaugaggcc...........................................................    25     0     seq
    ....................................agcacugcacugaugaggccA..........................................................    18     1     seq
    ....................................agcacugcacugaugaggccG..........................................................    1      1     seq
    ....................................agcacugcacugaugaggccc..........................................................    8      0     seq
    ....................................agcacugcacugaugaggccca.........................................................    3      0     seq
    ....................................agcacugcacugaugaAgcccag........................................................    2      1     seq
    ....................................agcacugcacugaugaggcccaga.......................................................    2      0     seq
    ....................................agcaGugcacugaugaggcccagaa......................................................    1      1     seq
    ....................................agcacugcacugaugaggcccagaa......................................................    1      0     seq
    ....................................agcacugcacugaugaggcccagaagg....................................................    3      0     seq
    ....................................agcacAgcacugaugaggcccagaagg....................................................    1      1     seq
    ....................................agcacugcacugaugaggcccagaaggA...................................................    1      1     seq
    ....................................agcacugcacugaugaAgcccagaaggc...................................................    1      1     seq
    ....................................agcacugcacugaugaggcccagaaggccg.................................................    1      0     seq
    .....................................gcacugcacugaugaggcccagaaggccg.................................................    1      0     seq
    .......................................cacugcacugaugaggccA........................................................    1      1     seq
    .......................................cacugcacugaugaggcccaga.....................................................    1      0     seq
    ........................................acugcacugaugaggccc........................................................    1      0     seq
    ........................................aUugcacugaugaggcccaga.....................................................    1      1     seq
    ........................................acugcacugaugaggcccaga.....................................................    2      0     seq
    ........................................acugcacugaugaggcccagaa....................................................    2      0     seq
    .........................................ugcacugaugaggcccag......................................................    2      0     seq
    .........................................ugcacugaugaggcccaU......................................................    2      1     seq
```

```
acacucgagguagucuuauaggcuuaccuucauccuagcuaucagcacugcacugaugaggcccagaaggccgaaacagugggugcucuaagugacguuuuguuugcuuuuuu
```

Sequence	Count	Mismatch	
................ugcacugaugaggcccaga..	4	0	seq
................ugcacugaugaggcccagaa...	3	0	seq
................ugcacugaugaggcccagaag..	2	0	seq
................ugcacugaugaggcccagaagg...	2	0	seq
.................acugaugaggcccagaaggcc...	1	0	seq
.................................ccgaaacagugggugcCc..	1	1	seq
.................................ccgaaacagugggugcuc..	4	0	seq
.................................ccgaaacagugggugcuU..	1	1	seq
................................cUgaaacagugggugcucu..	2	1	seq
................................ccgaaacagugggugUucu..	1	1	seq
.................................ccgaaacagugggugcucG...	2	1	seq
.................................ccgGaacagugggugcucu...	1	1	seq
.................................ccgaaacagugggugcucu...	170	0	seq
.................................ccgaaacagugggugcucC...	48	1	seq
.................................ccgaaacGgugggugcucu...	1	1	seq
.................................Ucgaaacagugggugcucu...	3	1	seq
.................................ccgaaacaAugggugcucu...	2	1	seq
.................................ccgaaacagugggugcGcu...	1	1	seq
.................................ccgaaacagugggugcAcu...	1	1	seq
.................................ccgaaGcagugggugcucu...	1	1	seq
.................................ccgaaacagugggugcuUu...	1	1	seq
.................................ccgaaacagugggugcucA...	25	1	seq
.................................ccgaaacagugggugcCcu...	8	1	seq
.................................ccgaaacagugggugcucuU..	2	1	seq
.................................ccgaaacagugggugcucua..	9	0	seq
.................................ccgaaacagugggugcucuC..	2	1	seq
.................................ccgaaacagugggugcucuaC...	6	1	seq
.................................ccgaaacagugggugcucuaa...	21	0	seq
.................................ccgaaacagugggugcucuaU...	36	1	seq
.................................ccgaaacagugggugcucuaaC..	2	1	seq
.................................ccgaaacagugggugcucuaaU..	4	1	seq
.................................ccgaaacagugggugcucuaGg..	18	1	seq
.................................ccgaaacagugggugcucuaagu..	4	0	seq
................................cgaaacagugggugcucu...	1	0	seq