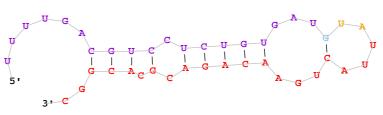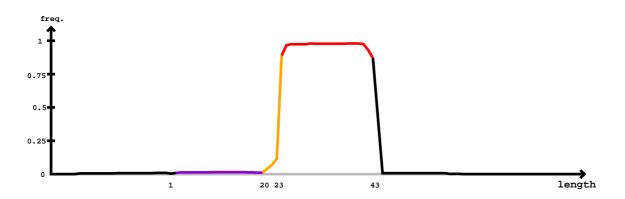| Provisional ID	: NW_025322615.1_Acropora_millepora_isolate_JS-1_unplaced_genomic_scaffold_Amil_v2.1_Sc0000015_whole_genome_shotgun_sequer
Score total	: 268.2
Score for star read(s)	: 3.9
Score for read counts	: 264.2
Score for mfe	: -2.8
Score for randfold	: 0
Score for cons. seed	: 3
Total read count	: 530
Mature read count	: 525
Loop read count	: 0
Star read count	: 5

Star   **Mature**

```
5'- ugugucacugauguucuuaccacguuuugacguccucugugauguauuacugaacagacgcacggcgacauggaaucuauuuguuuuauacaaguaauaguuuucacua  -3'    obs
    ugugucacugauguucuuaccacguuuugacguccucugugauguauuacugaacagacgcacggcgacauggaaucuauuuguuuuauacaaguaauaguuuucacua         exp
    .(((..(((((..((((((.....(((..((.((((((.((.(((((....))))).))...))))))..))).....))))).(((((((.....))))))).)))...))).. reads  mm    sample
....ucacugauguucuuaccac.........................................................................................   3      0      seq
.........guucuuaccacguuuugacgucAucugug..........................................................................   1      1      seq
...............cacguuuugacguccucug..............................................................................   1      0      seq
....................uuuugacguccucugugau.........................................................................   3      0      seq
.....................uuugacguccucugugau.........................................................................   2      0      seq
.........................uccucugugauUuauuacuga..................................................................   1      1      seq
...............................uauuacugaacagacgcac..............................................................   1      0      seq
...............................uauuacugaacagacgcacg.............................................................  15      0      seq
...............................uauuacugaacagacgcacgg............................................................   5      0      seq
...............................uauuacugaacagacgcacgU............................................................   1      1      seq
...............................uauuacugaacagacgcacgA............................................................   4      1      seq
...............................uauuacugaacagacgcacggc...........................................................   5      0      seq
...............................uauuacugaacagacgcacggU...........................................................   5      1      seq
...............................uauuacugaacagacgcacggcC..........................................................   1      1      seq
................................auuacugaacagacgcaU..............................................................   1      1      seq
................................auuacugaacagacgcacg.............................................................   3      0      seq
................................auuacugaacagacgcacgg............................................................   6      0      seq
................................auuacugaacagacgcacggc...........................................................   6      0      seq
................................auuacugaacagacgcacggU...........................................................   7      1      seq
................................auuacugaacagacgcacggcg..........................................................   1      0      seq
................................auuacugaacagacgcacggcU..........................................................   1      1      seq
.................................uuacugaGcagacgcacg............................................................   1      1      seq
.................................uuacugaacagacgcacg............................................................   5      0      seq
.................................Cuacugaacagacgcacgg...........................................................   1      1      seq
.................................uuacugaacagacgcacgg...........................................................  14      0      seq
.................................uuacugaacagacgcacggU..........................................................  113     1      seq
.................................uuacugaGcagacgcacggc..........................................................   3      1      seq
.................................uuacCgaacagacgcacggc..........................................................   1      1      seq
.................................uuaUugaacagacgcacggc..........................................................   1      1      seq
.................................uuacugaacagacgcacgCc..........................................................   1      1      seq
.................................uuacugaacagGcgcacggc..........................................................   4      1      seq
.................................uuacugaacagacgcacggG..........................................................   3      1      seq
.................................uuacugaacagacgcacggA..........................................................  23      1      seq
```

ugugucacugauguucuuaccacguuuugacguccucugugauguauuacugaacagacgcacggcgacauggaaucuauuuguuuuauacaaguaauaguuuucacua

Sequence	Count	Mismatch	
....uCacugaacagacgcacggc...	1	1	seq
....uAacugaacagacgcacggc...	1	1	seq
....uuacugaacagacgcacggc...	231	0	seq
....uuacugaacagacgcacggcU..	9	1	seq
....uuacugaacagacgcacggcC..	2	1	seq
....uuacugaacagacgcGcggcg...	1	1	seq
....uuacugaacagacgcacggcg...	2	0	seq
....uacugaacagacgcacgg...	2	0	seq
....uacugaacagacgcacggc..	12	0	seq
....uacugaacagacgcaUggc..	1	1	seq
....uacugaacagacgcacggA..	4	1	seq
....uacugaacagacgcacggU..	7	1	seq
....uacugaacagacgcacggcg...	1	0	seq
....uacugaacagacgcacggcC...	1	1	seq
....uacugaacagacgcacggcU...	14	1	seq
....acugaacagacgcacggc..	2	0	seq
....acugaacagacgcacggU..	1	1	seq
....acugaacagacgcacggcU...	1	1	seq
....aacagacgcacggcgGcauggaaucuauu...........................	2	1	seq
....aacagacgcacggcgacauggaaucuauu...........................	1	0	seq
....cacggcgacauggaaucuauuugu........................	1	0	seq