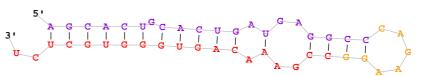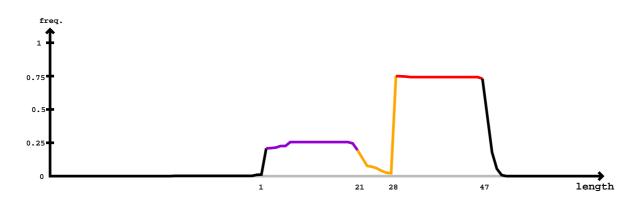| Provisional ID	: NW_025322681.1_Acropora_millepora_isolate_JS-1_unplaced_genomic_scaffold_Amil_v2.1_Sc0000192_whole_genome_shotgun_sequer
Score total	: 250.9
Score for star read(s)	: 3.9
Score for read counts	: 246.4
Score for mfe	: 1.2
Score for randfold	: 0
Score for cons. seed	: -0.6
Total read count	: 495
Mature read count	: 378
Loop read count	: 0
Star read count	: 117

Star **Mature**

```
5'- acacucgagguagucuuauaggcuuaccuucauccuagcuaucagcacugcacugaugaggcccagaaggccgaaacagugggugcucuaagugacguuuuguuugcuuuuuu  -3'   obs
     acacucgagguagucuuauaggcuuaccuucauccuagcuaucagcacugcacugaugaggcccagaaggccgaaacagugggugcucuaagugacguuuuguuugcuuuuuu        exp
     .(((((.((((((((((.....)))).))))))............(((((((.(((((.(..(((((.....)))).).).)))))))))))...))))...............     reads     mm     sample
```

sequence	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
...................................agcacugcacugaugaggA...	2	1	seq
...................................agcacugcacugaugaggc...	23	0	seq
...................................agcacugcacugaugaggcc..	25	0	seq
...................................agcacugcacugaugaggcG..	4	1	seq
...................................agcacugcacugaugaggccG...	1	1	seq
...................................agcacugcacugaugaggccc...	8	0	seq
...................................agcacugcacugaugaggccA...	18	1	seq
...................................agcacugcacugaugaggccca..	3	0	seq
...................................agcacugcacugaugaAgcccag...	2	1	seq
...................................agcacugcacugaugaggcccaga..	2	0	seq
...................................agcacugcacugaugaggcccagaa...	1	0	seq
...................................agcaGugcacugaugaggcccagaa...	1	1	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
....acugcacugaugaggcccaga.......................................	2	0	seq
....aUugcacugaugaggcccaga.......................................	1	1	seq
....acugcacugaugaggcccagaa......................................	2	0	seq
....ugcacugaugaggcccag...	2	0	seq
....ugcacugaugaggcccaU...	2	1	seq

acacucgagguagucuuauaggcuuaccuucauccuagcuaucagcacugcacugaugaggcccagaaggccgaaacagugggugcucuaagugacguuuuguuugcuuuuuu

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