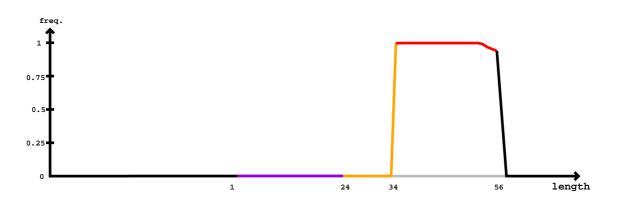| Provisional ID	: NC_058069.1_Acropora_millepora_isolate_JS-1_chromosome_4_Amil_v2.1_whole_genome_shotgun_sequence_167435
Score total	: 1452.5
Score for star read(s)	: 3.9
Score for read counts	: 1444
Score for mfe	: 1.7
Score for randfold	: 0
Score for cons. seed	: 3
Total read count	: 2844
Mature read count	: 2840
Loop read count	: 0
Star read count	: 4


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

	reads	mm	sample
..............ucaccaggcucucaguaucac.	1	0	seq
...............ucaccaggcucucaguaucaca.	1	0	seq
..........................ugguAgaaguccucaaucacccu.	4	1	seq
....uuuacgcagugugauuggagacuuuuaucgu.	1	0	seq
....gcagugugauuggagacuuuuaucgu.	1	0	seq
....cagugugauuggagacuuuuaucgu.	1	0	seq
....ugugGuuggagacuuuua.	1	1	seq
....Cgugauuggagacuuuua.	1	1	seq
....ugugauuggagacuuuuU.	2	1	seq
....ugugauuggagacuuuua.	15	0	seq
....ugugauuggagacuuuuC.	1	1	seq
....ugugauuggagacCuuuau.	1	1	seq
....ugugauuggagacuuuuUu.	2	1	seq
....ugugauuggagacuuuuau.	54	0	seq
....ugugauuggagacuuuuaC.	9	1	seq
....ugugauuggagacuuuuauc.	37	0	seq
....ugugGuuggagacuuuuauc.	1	1	seq
....ugugauuggagacuuuuauA.	4	1	seq
....ugugauuggagacuuuuaucg.	25	0	seq
....ugugauuggagacuuuuaucA.	12	1	seq
....ugugauuggagacuuuuaucU.	1	1	seq
....ugugauuggagacCuuuaucg.	1	1	seq
....ugugauuggagacuCuuaucg.	1	1	seq
....ugugauuggagacuuuuaucAu.	11	1	seq
....ugugauuggagacuuuuUucgu.	1	1	seq
....ugugauuggagacuuuuauAgu.	1	1	seq
....ugugauuggagacuuCuaucgu.	5	1	seq
....Agugauuggagacuuuuaucgu.	8	1	seq
....ugugauuggagacuuuCaucgu.	7	1	seq
....ugugauuggagacuuuuauUgu.	2	1	seq
....ugugauuggagacuuuuaucgA.	86	1	seq
....ugugauuggagacuuuuaucCu.	27	1	seq
....ugugGuuggagacuuuuaucgu.	9	1	seq

aaaucuuugaggaucucaccaggcucucaguaucacaugguggaaguccucaaucacccucuuuacgcagugugauuggagacuuuuaucguggccugagugcacuuu

Sequence	Count	Flag	Type
....ugugauuggagacuuuuGucgu................	1	1	seq
....uUugauuggagacuuuuaucgu................	8	1	seq
....ugugauuggagacuuuuaGcgu................	1	1	seq
....ugugauuggagacuuuuaucgG................	40	1	seq
....ugugauuggGgacuuuuaucgu................	7	1	seq
....ugugauuggagacuuuuaucgu................	1690	0	seq
....ugugauuggagacuuuuaCcgu................	3	1	seq
....ugugauuggagGcuuuuaucgu................	9	1	seq
....Cgugauuggagacuuuuaucgu................	11	1	seq
....ugugauuggagacuuAuaucgu................	2	1	seq
....ugugauuggagacuuuuaucgC................	364	1	seq
....ugugauuggagacuuuuaucUu................	2	1	seq
....ugCgauuggagacuuuuaucgu................	4	1	seq
....ugugauCggagacuuuuaucgu................	7	1	seq
....ugugauuggagacuCuuaucgu................	7	1	seq
....ugugauugAagacuuuuaucgu................	4	1	seq
....ugugauuAgagacuuuuaucgu................	4	1	seq
....ugugauuggagacCuuuaucgu................	8	1	seq
....ugugaCuggagacuuuuaucgu................	4	1	seq
....uAugauuggagacuuuuaucgu................	2	1	seq
....ugugauuggagacuuuuaucguC................	38	1	seq
....ugugauuggagacuuuuaucguA................	37	1	seq
....ugugauuggagacuuuuaucguU................	253	1	seq
....ugugauuggagacuuuuaucgug................	3	0	seq
....ugugauuggagacuuuuaucgCg................	1	1	seq
....ugugauuggagacuuuuaucgugU...............	1	1	seq
....ugugauuggagacuuuuaucgugC...............	1	1	seq
....gugauuggagacuuuuaucgu................	2	0	seq
....ugauuggagacuuuuaucgu................	1	0	seq