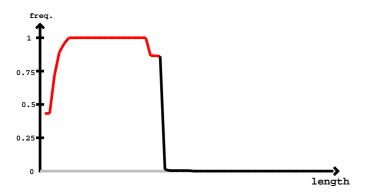miRBase precursor : chromosome_2_6103
Total read count : 245
chromosome_2_6103 read count 244
remaining reads : 1

```
      chromosome_2_6103
5'- uggaagcacaguucguuuugacaacacuuaaaguugucaauaaaaacuaugcaacccacu  -3'   exp
    .((..((((.(((((....((((((((((.......))))))))))....))))).)))..))....   reads   mm        sample
    uggaagcacaguucguuuugG.....................................         1       1         seq
    uggaagcacaguucguuuuga.....................................         19      0         seq
    uggaagcacagGucguuuuga.....................................         1       1         seq
    uggaagcacaguGcguuuuga.....................................         1       1         seq
    uggaagcacGguucguuuuga.....................................         1       1         seq
    uggaagcacaguucUuuuuga.....................................         1       1         seq
    Aggaagcacaguucguuuuga.....................................         3       1         seq
    uggaagcacaguucAuuuuga.....................................         4       1         seq
    Aggaagcacaguucguuuugacaa..................................         5       1         seq
    uggaGgcacaguucguuuugacaa..................................         2       1         seq
    uggaagcacaguucguuuugUcaa..................................         1       1         seq
    uggaagcacaguucAuuuugacaa..................................         25      1         seq
    uggaagcacaguucguuuAacaa...................................         2       1         seq
    uUgaagcacaguucguuuugacaa..................................         2       1         seq
    Gggaagcacaguucguuuugacaa..................................         2       1         seq
    uggaagcacaguucguuuugacaa..................................         30      0         seq
    Cggaagcacaguucguuuugacaa..................................         1       1         seq
    uggaagcacaguGcguuuugacaa..................................         1       1         seq
    uggaagcacaguucguCuugacaa..................................         1       1         seq
    uggaagcacaguucguuuugacaaG.................................         2       1         seq
    uggaagcacaguucguuuugacaacacuAa............................         1       1         seq
    .ggaagcacaguucguuuuga.....................................         1       0         seq
    .Agaagcacaguucguuuugacaa..................................         17      1         seq
    .ggaagcacaguucguuuugacaa..................................         24      0         seq
    .ggaagcacaguucAuuuugacaa..................................         16      1         seq
    .ggaaAcacaguucguuuugacaa..................................         1       1         seq
    .ggaagcacaguucguuuugacaG..................................         1       1         seq
    .ggaagcacagGucguuuugacaa..................................         1       1         seq
    .Ugaagcacaguucguuuugacaa..................................         9       1         seq
    ..Uaagcacaguucguuuuga.....................................         1       1         seq
    ..gaagcacaguucguuuugacaa..................................         23      0         seq
    ..Uaagcacaguucguuuugacaa..................................         10      1         seq
    ..gaagcacaguucAuuuugacaa..................................         6       1         seq
    ..Aaagcacaguucguuuugacaa..................................         2       1         seq
    ...Gagcacaguucguuuugaca...................................         1       1         seq
```

uggaagcacaguucguuuugacaacacuuaaaguugucaauaaaaacuaugcaacccacu

```
...aagcacaguucguuuugacaa.....................................    10    0    seq
...aagcacaguucAuuuugacaa.....................................     4    1    seq
...Gagcacaguucguuuugacaa.....................................     1    1    seq
....agcacagGucguuuugacaa.....................................     1    1    seq
....agcacaguucguuuugacaa.....................................     6    0    seq
....agcacaguucAuuuugacaa.....................................     4    1    seq
```