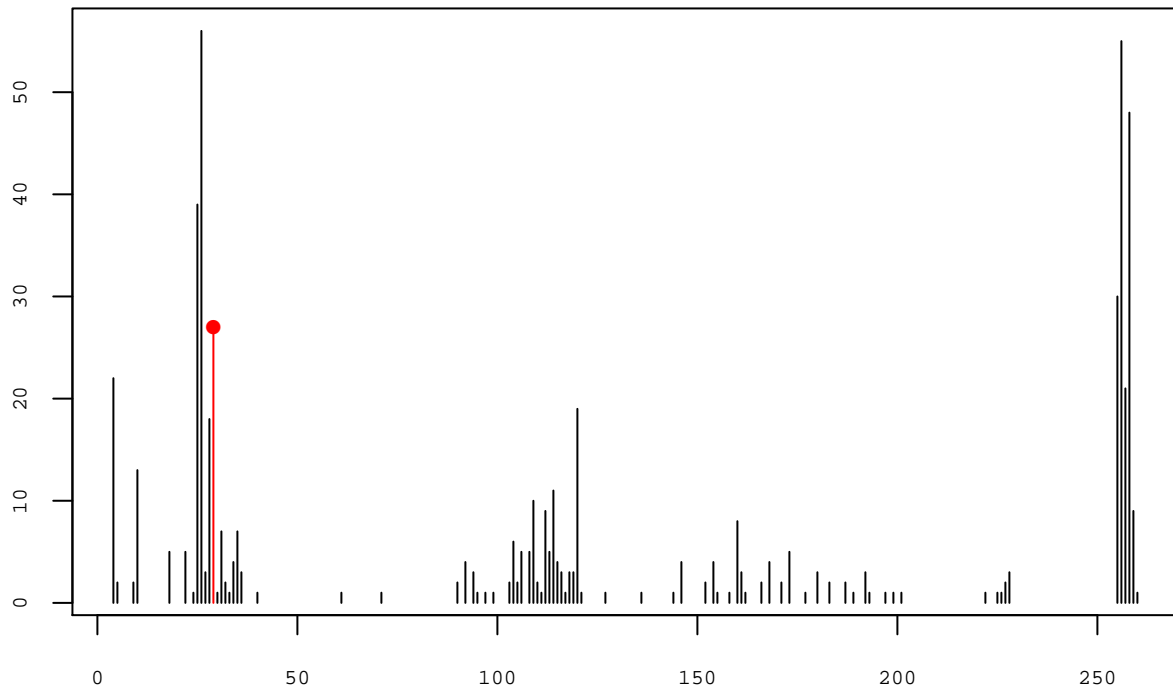


5' CGTACCATT CGAATAACCTAAAATGTACGCAA '3
||| ||| |o| ||| ||| ||| ||| |||
3' ATGGTAGGCTTATTGGATTATACA '5

Fragment Abundance



Transcript position

Cleavage site: 29 Tag abundance: 27 Weighted abundance: 13.5 Category: 2
sRNA abundance: 14 Alignment score: 2.5 MFE ratio: 0.806 p-value: 0.025