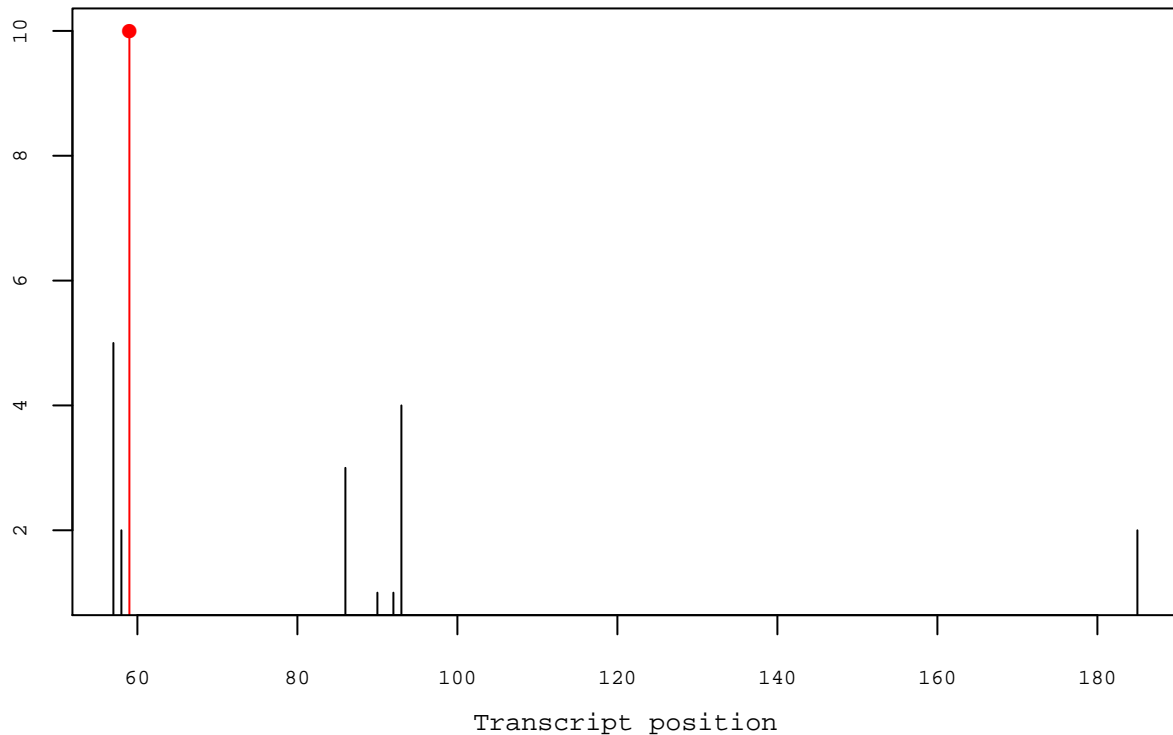


5' TTCGTGATCTATGGTCAGGATCGGACACCGCA '3  
||| ||| |o|o| ||| ||| |||  
3' GCACTAGATGCTAGTCCTAGCCTG '5

Fragment Abundance



Cleavage site: 59 Tag abundance: 10 Weighted abundance: 2.5 Category: 0  
sRNA abundance: 304 Alignment score: 1.5 MFE ratio: 0.948 p-value: 0.003