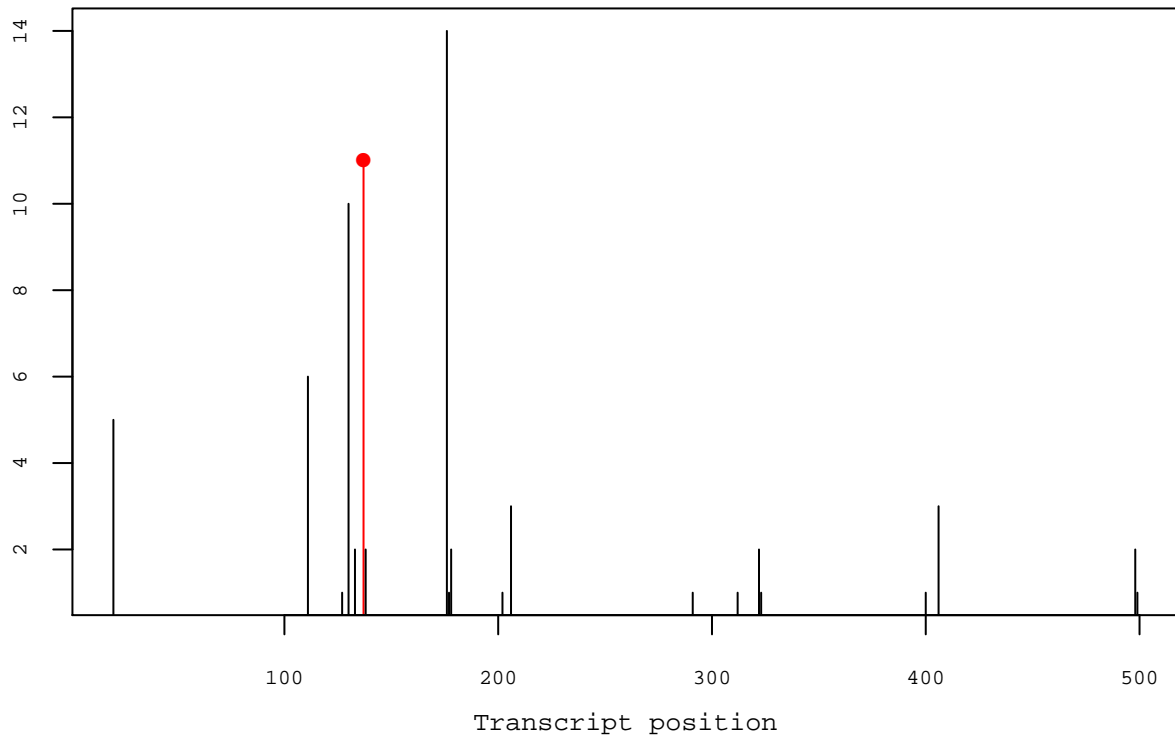


5' TAGATCACCGTGATCTACGGTCAGGATCGGAC '3  
 ||||| ||||| |o| |||||  
 3' CTAGTGCCACTAGATGTCAGTCCT '5

Fragment Abundance



Cleavage site: 137 Tag abundance: 11 Weighted abundance: 5 Category: 2  
 sRNA abundance: 32 Alignment score: 2 MFE ratio: 0.849 p-value: 0.015