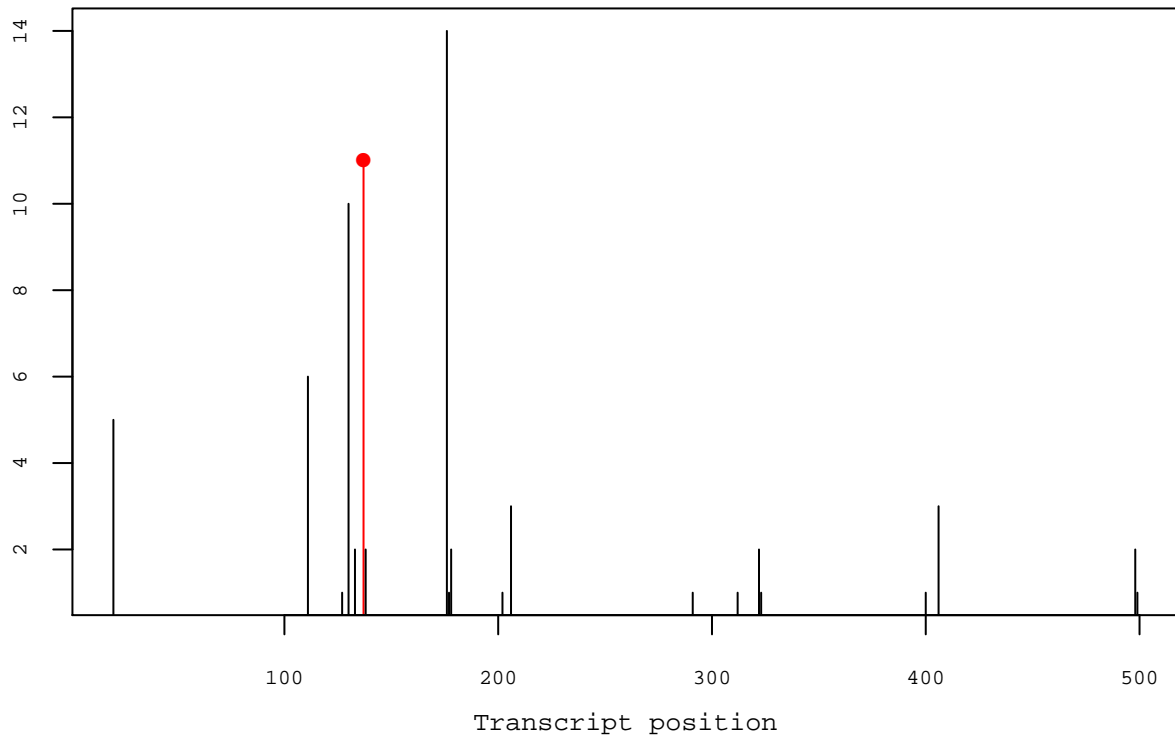


5' TAGATCACCGTGATCTACGGTCAGGATCGGAC '3
 ||||| ||o|||||||o|
 3' CTAGTGCCATTAGATGCCAGTCTT '5

Fragment Abundance



Cleavage site: 137 Tag abundance: 11 Weighted abundance: 5 Category: 2
 sRNA abundance: 32 Alignment score: 2.5 MFE ratio: 0.843 p-value: 0.015