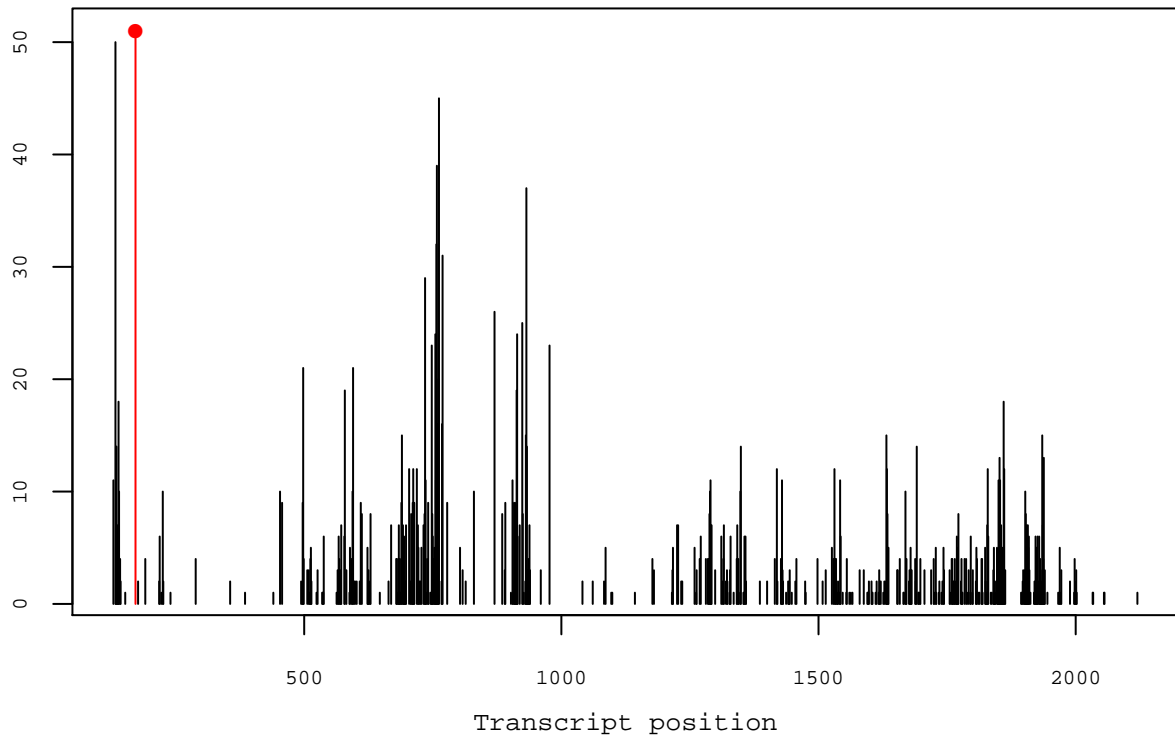


5' ATCCTCTCCTCTTCGTGCGCCTTCCAAACCCA '3
||||| |o||| |||||
3' GGAGACGTACGGGGAAGGT '5

Fragment Abundance



Cleavage site: 172 Tag abundance: 51 Weighted abundance: 51 Category: 0
sRNA abundance: 27 Alignment score: 4 MFE ratio: 0.714 p-value: 0.001