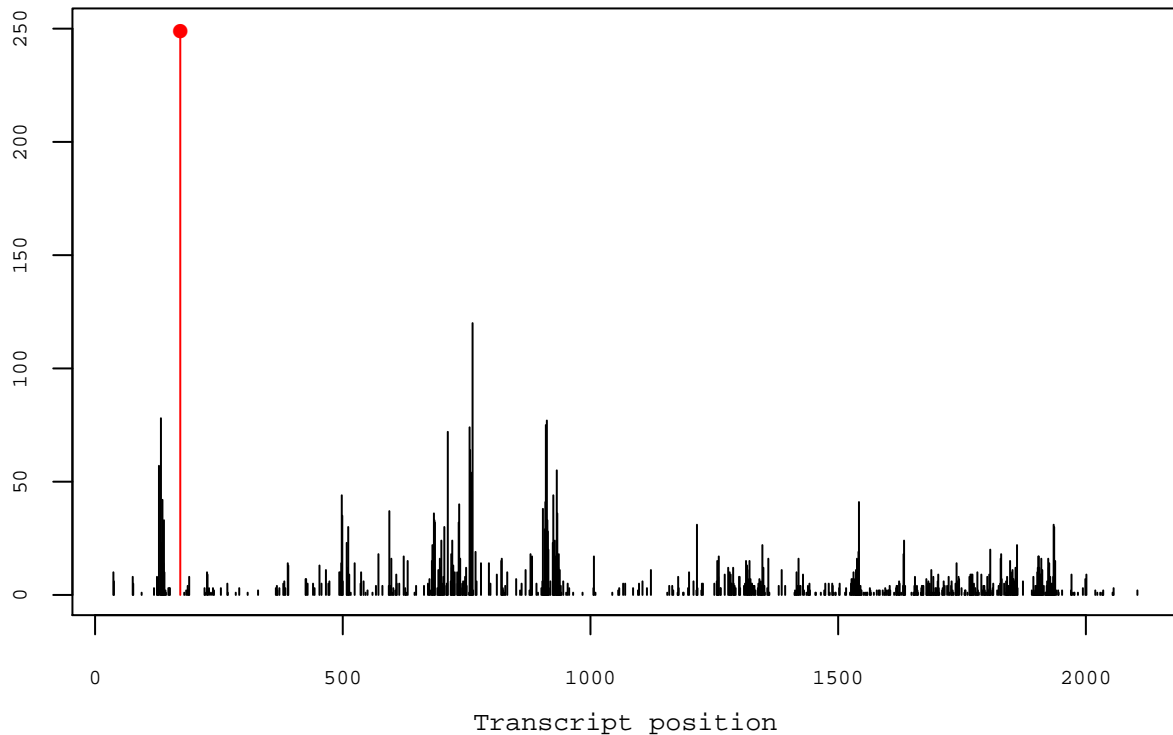


5' ATCCTCTCCTCTTCGTGCGCCTTCCAAACCCA '3
||||| |o||| |||||
3' AGGAGACGTACGGGGAAGGT '5

Fragment Abundance



Cleavage site: 172 Tag abundance: 249 Weighted abundance: 249 Category: 0
sRNA abundance: 8 Alignment score: 4 MFE ratio: 0.727 p-value: 0