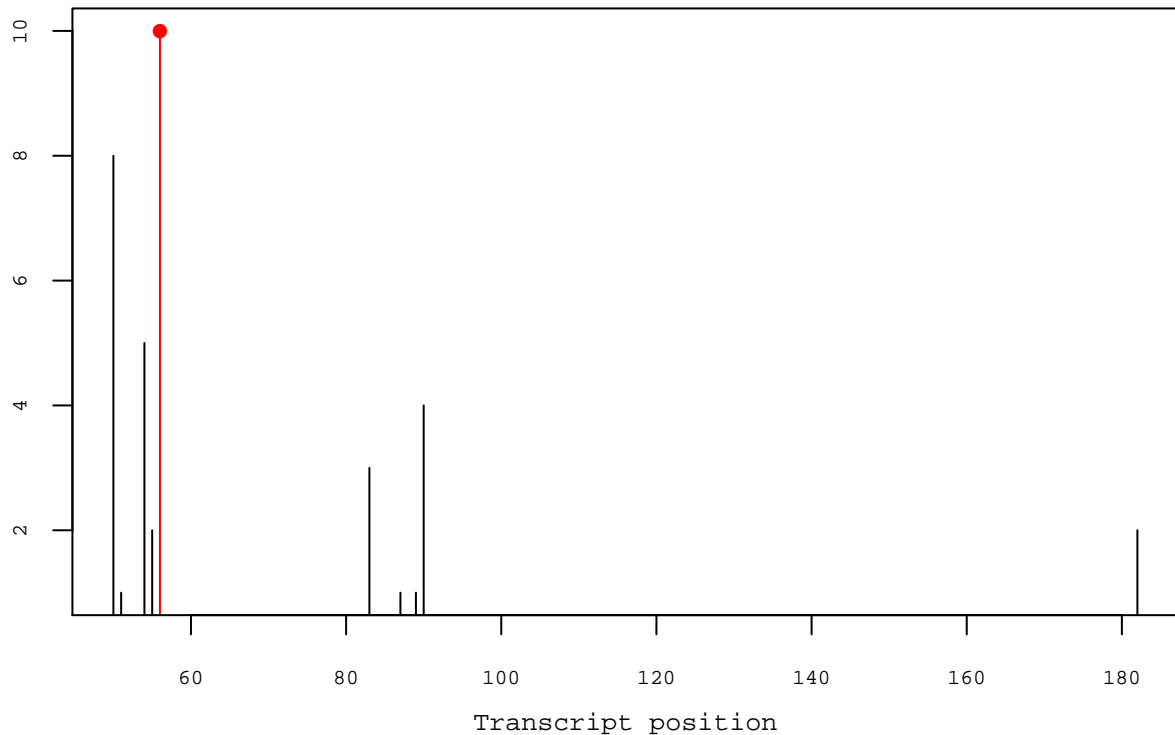


5' ATCATGATCAACAGTCAGGATCGGACACCGCA '3

|||| || ||||| |||o|||

3' CTAGATGCCAGTCCTAGTCTG '5

Fragment Abundance



Cleavage site: 56 Tag abundance: 10 Weighted abundance: 2.5 Category: 0
sRNA abundance: 34 Alignment score: 3 MFE ratio: 0.712 p-value: 0.013