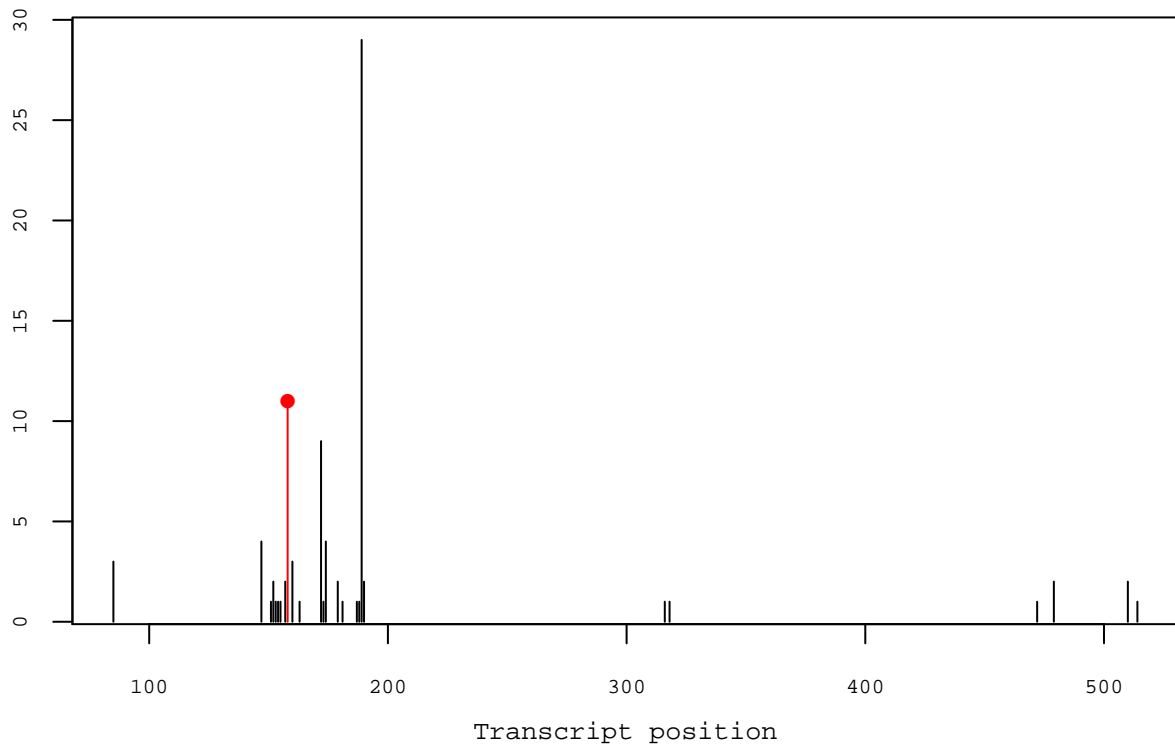


5' ATGCTACGTGACACCTCCTCATTGAAGTACTG '3
||o||||| ||||| |||||
3' CGGTGCACTATGGAGGAATAACTT '5

Fragment Abundance



Cleavage site: 158 Tag abundance: 11 Weighted abundance: 5.5 Category: 2
sRNA abundance: 8 Alignment score: 3.5 MFE ratio: 0.751 p-value: 0.004