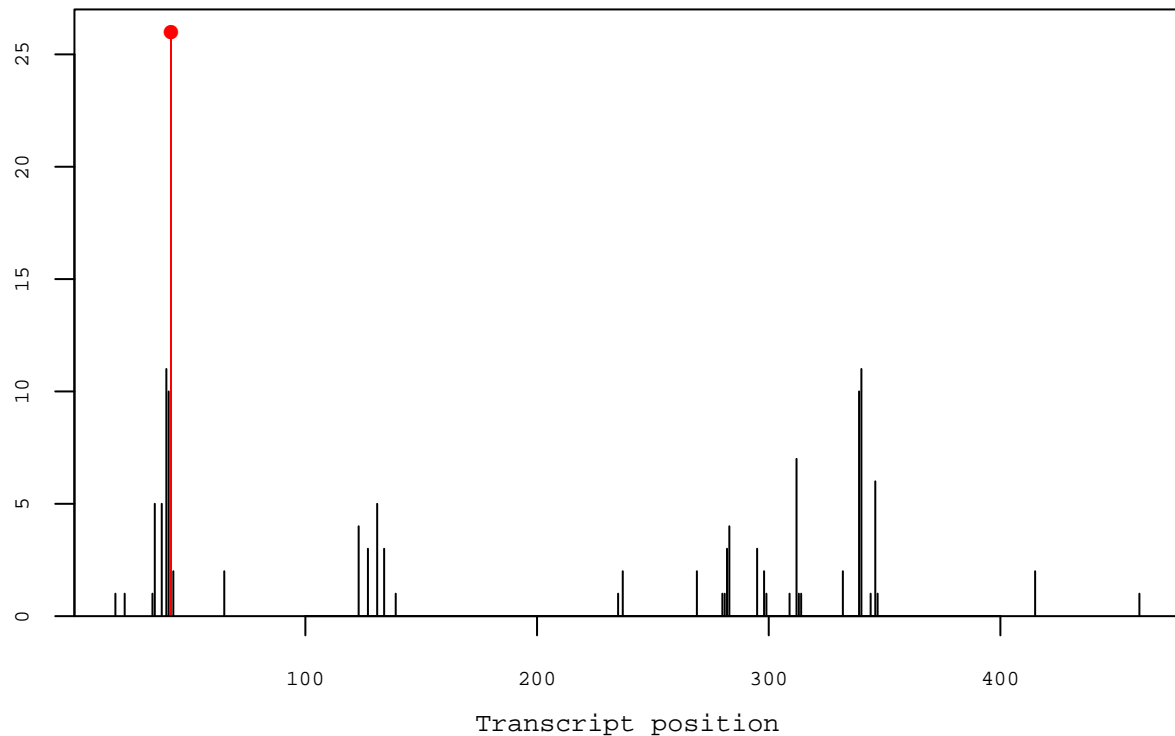


5' GAACACGAGTTGTTACGAACAAA-GAGTCCTT '3
 |||||o|||||||o
 3' TGTGCTCGACAAGTGCTTGTATTAT '5

Fragment Abundance



Cleavage site: 42 Tag abundance: 26 Weighted abundance: 4.143 Category: 0
 sRNA abundance: 23 Alignment score: 2 MFE ratio: 0.895 p-value: 0.014