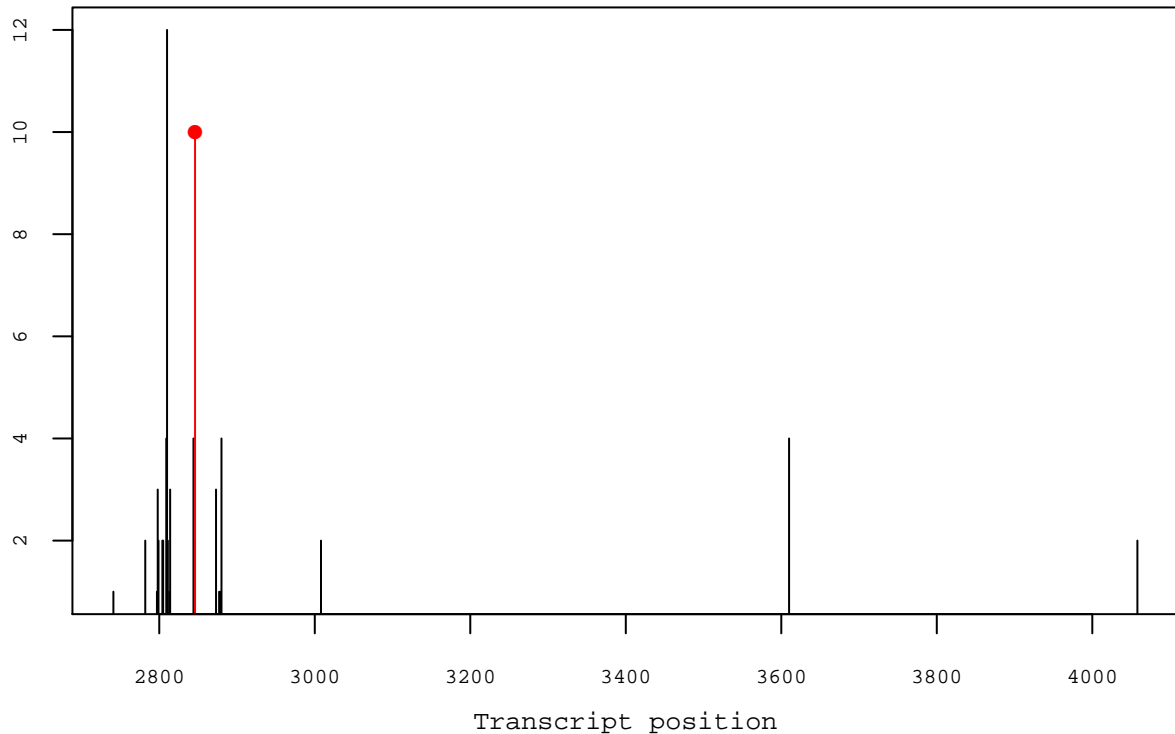


5' ACTGTGATCTACGGCCAGGATCGGACACCGCA '3
o|||||||o |||||
3' GCACTAGATGCTAGTCCTAGCCTG '5

Fragment Abundance



Cleavage site: 2846 Tag abundance: 10 Weighted abundance: 2.5 Category: 2
sRNA abundance: 304 Alignment score: 3.5 MFE ratio: 0.859 p-value: 0.003