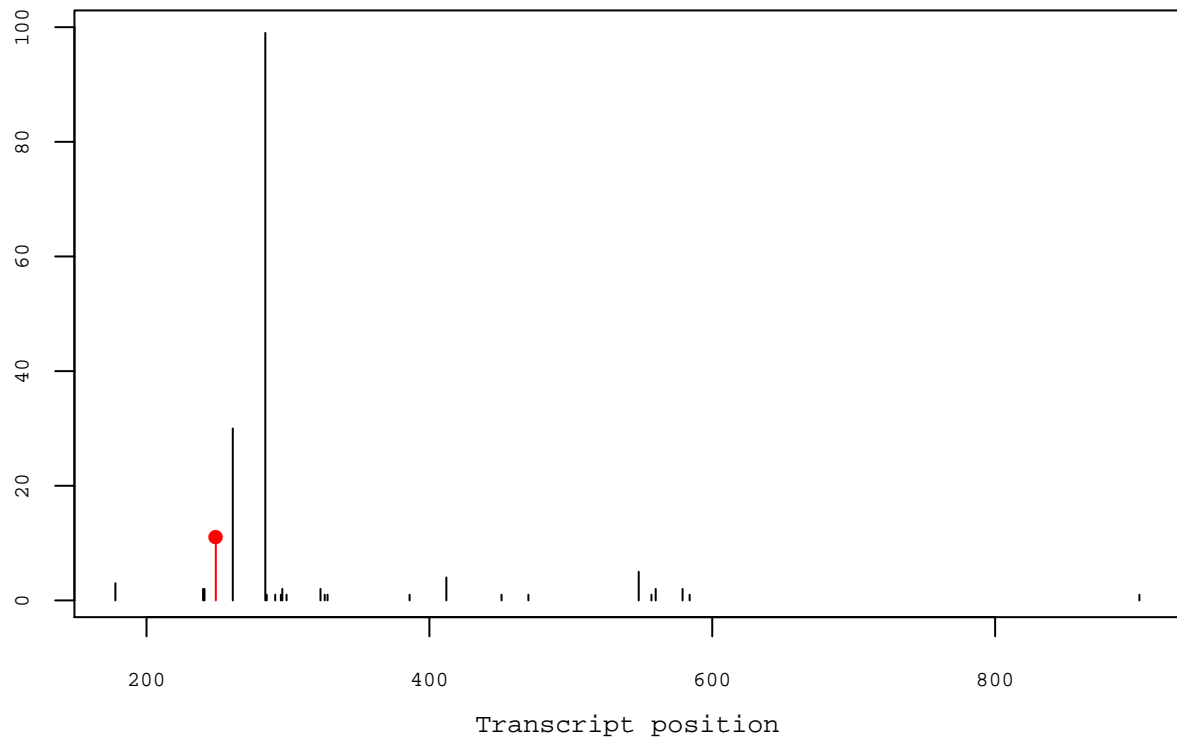


PggD11120\_c28\_g1\_i1

5' GGTTCAGTTC AATAAAGCTGTGGGAAATTAC '3  
||||| ||||| |  
3' CGTCAAGTTC TTTGACACCTT '5

Fragment Abundance



Cleavage site: 249 Tag abundance: 11 Weighted abundance: 5.5 Category: 3  
sRNA abundance: 9 Alignment score: 3 MFE ratio: 0.818 p-value: 0.036