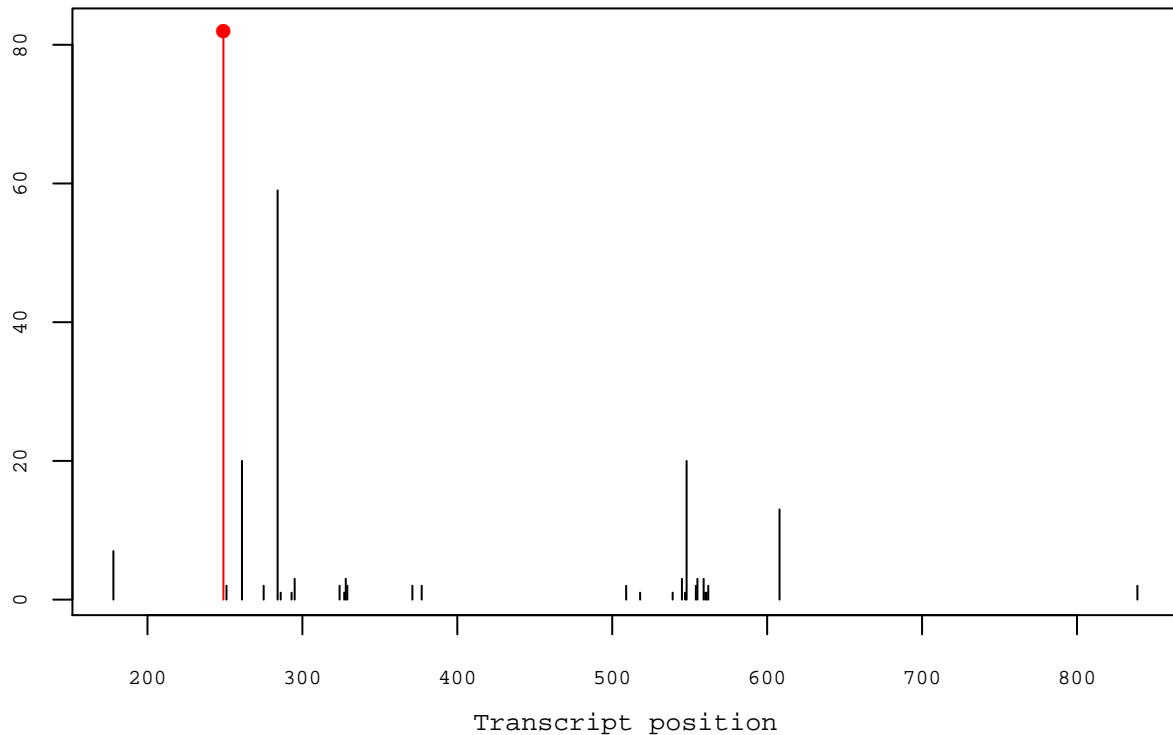


PggD11120_c28_g1_i1

5' GGTTCAGTTC AATAAAGCTGTGGGAAATTAC '3

||||| | ||||| | |
3' TCAAGTTC TTTGACACCTT '5

Fragment Abundance



Cleavage site: 249 Tag abundance: 82 Weighted abundance: 41 Category: 0
sRNA abundance: 117 Alignment score: 3 MFE ratio: 0.785 p-value: 0.013