

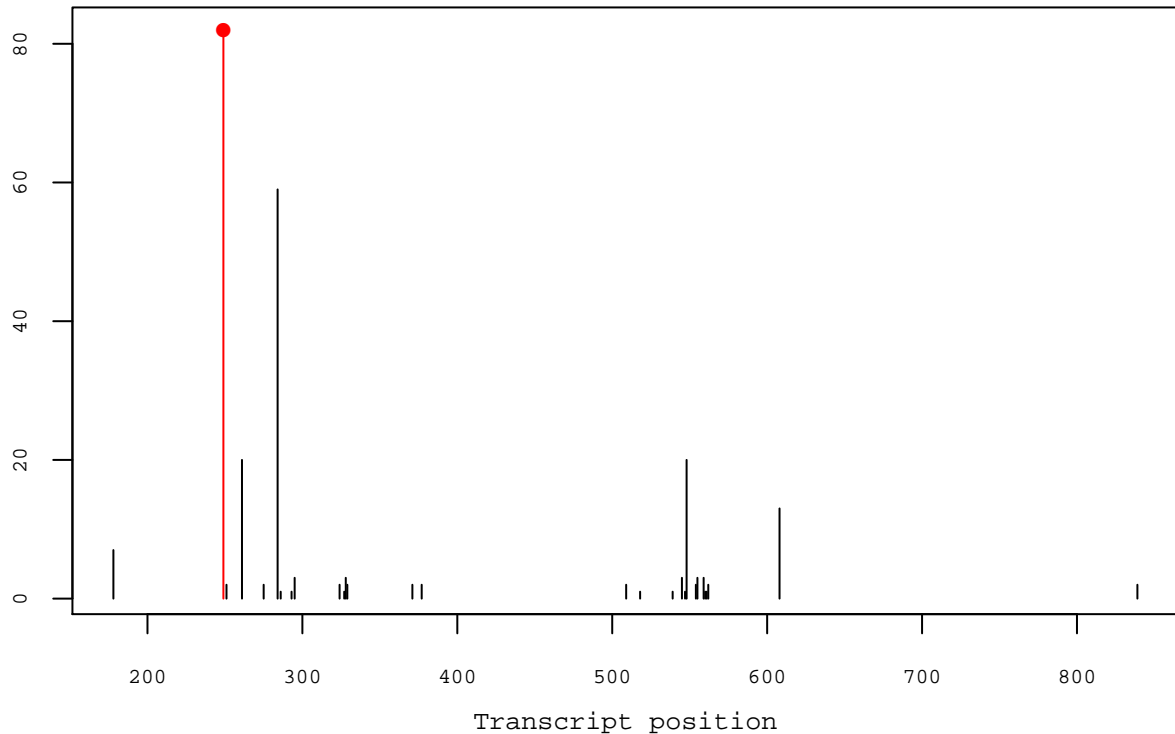
PggD11120\_c28\_g1\_i1

5' GGTTCAGTTC AATAAAGCTGTGGGAAATTAC '3

||||| | | | | | | | | | | | | | | | | |

3' GTCAAGTTCTTTCGACACCTT '5

Fragment Abundance



Cleavage site: 249 Tag abundance: 82 Weighted abundance: 41 Category: 0  
srna abundance: 197 Alignment score: 3 MFE ratio: 0.801 p-value: 0.008