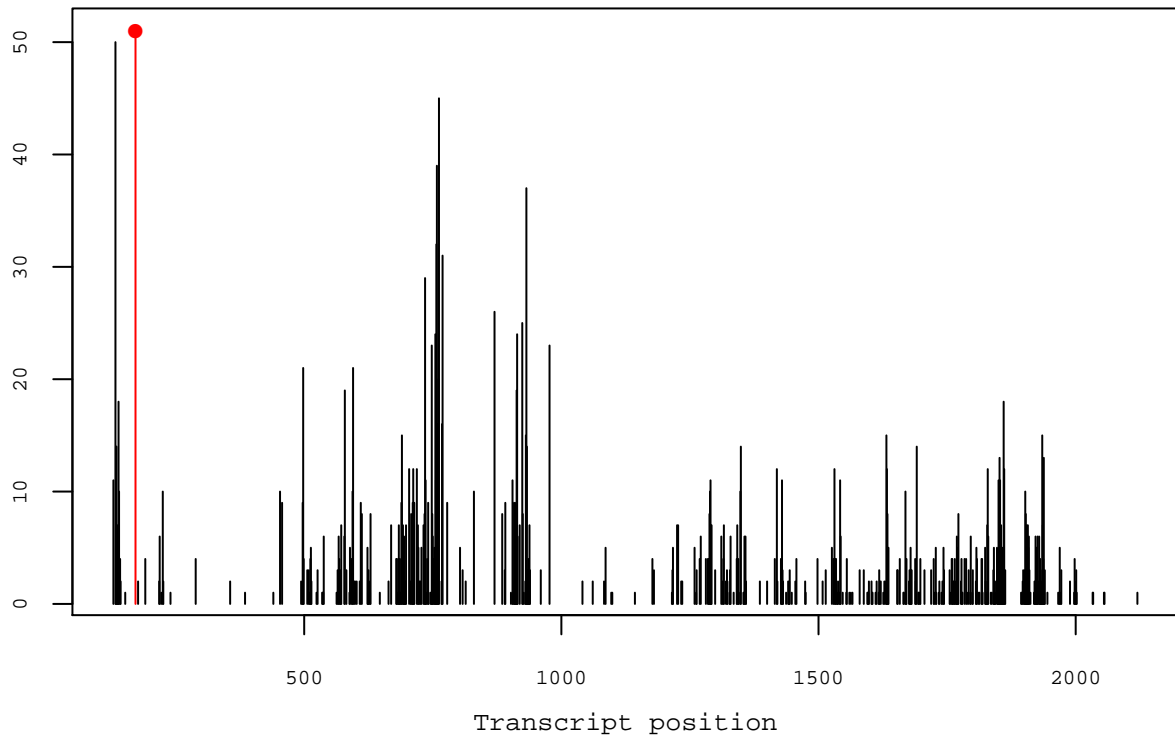


PggD4925_c7_g1_i2

5' ATCCTCTCCTCTTCGTGCGCCTTCCAAACCCA '3
||||| |o| | |||||
3' AGGAGACGTACGGGGAAGGT '5

Fragment Abundance



Cleavage site: 172 Tag abundance: 51 Weighted abundance: 51 Category: 0
sRNA abundance: 6 Alignment score: 4 MFE ratio: 0.727 p-value: 0.001