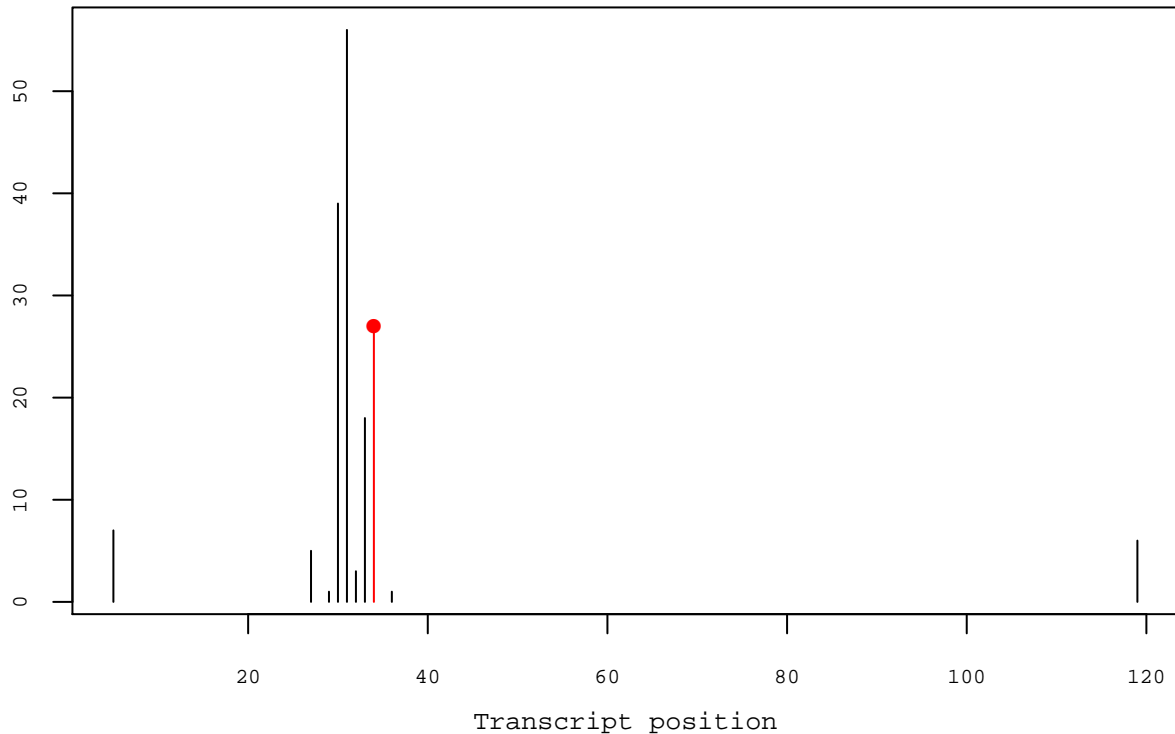


PggD5575_c505_g1_i1

5' TGTACCCTCCGAATAACCTAAAAATGTACGCAA '3
||||| ||||| ||||| ||||| |||||
3' ATGGTAGGCTTATTGGATTATACA '5

Fragment Abundance



Cleavage site: 34 Tag abundance: 27 Weighted abundance: 13.5 Category: 2
sRNA abundance: 14 Alignment score: 3 MFE ratio: 0.766 p-value: 0.014