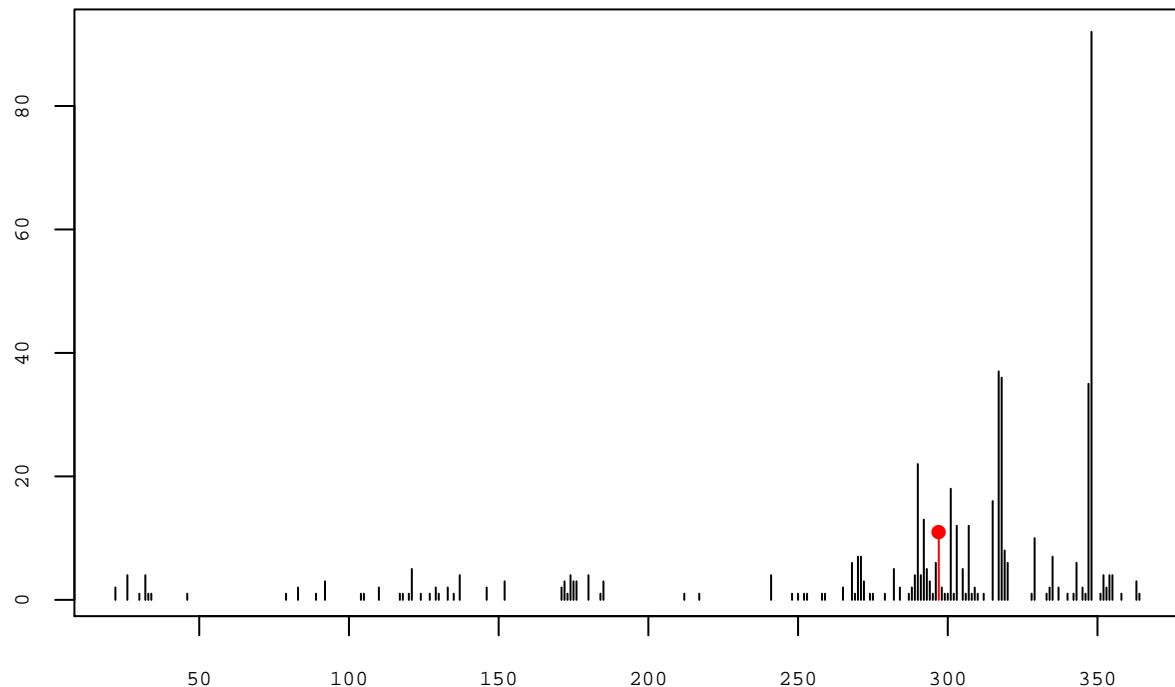


PggD7012_c274_g1_i1

5' CTTAAGAATAGCTTATGCCGCACGTAGAACTA '3
||| ||| o | o | ||| ||| ||| |||
3' TTCTTATTGGATTCGGCGTGCAT '5

Fragment Abundance



Transcript position

Cleavage site: 297 Tag abundance: 11 Weighted abundance: 11 Category: 2
sRNA abundance: 6 Alignment score: 3 MFE ratio: 0.834 p-value: 0.03