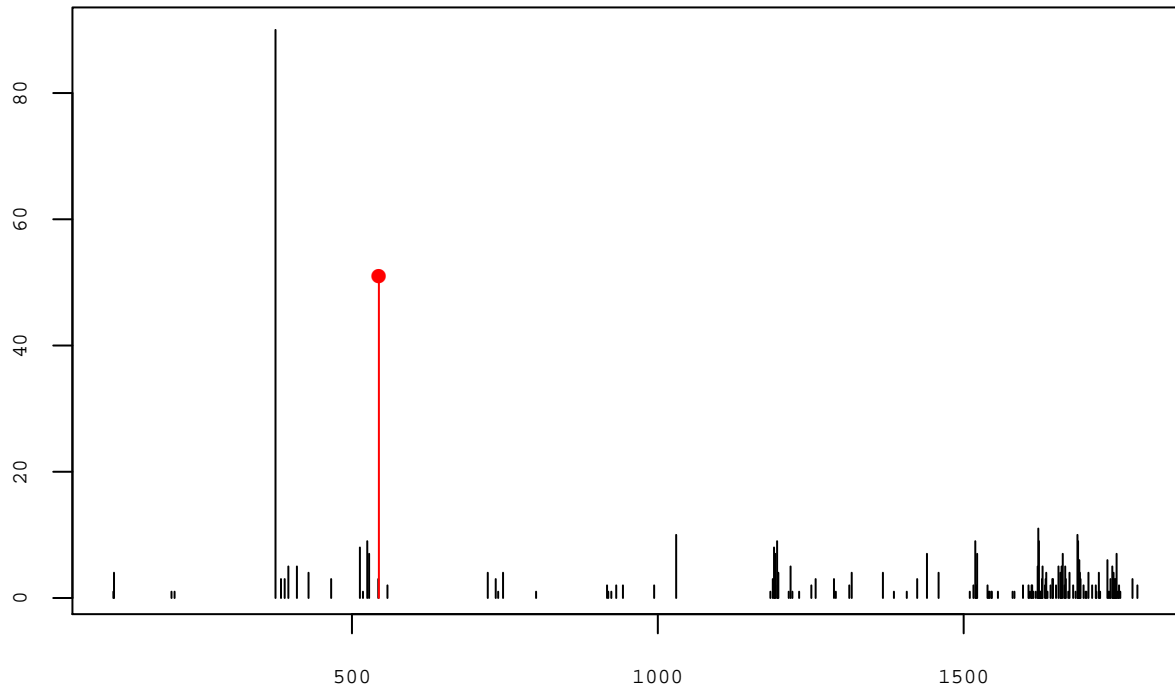


PggD7691_c15_g1_i1

5' TCCCTCTCGATATTGGCTCGGCTCAATTCCT 3'
||||| |||||
3' TCTATAACCGTGCCGAGTT 5'

Fragment Abundance



Transcript position

Cleavage site: 544 Tag abundance: 51 Weighted abundance: 51 Category: 2
sRNA abundance: 48 Alignment score: 3 MFE ratio: 0.869 p-value: 0.04