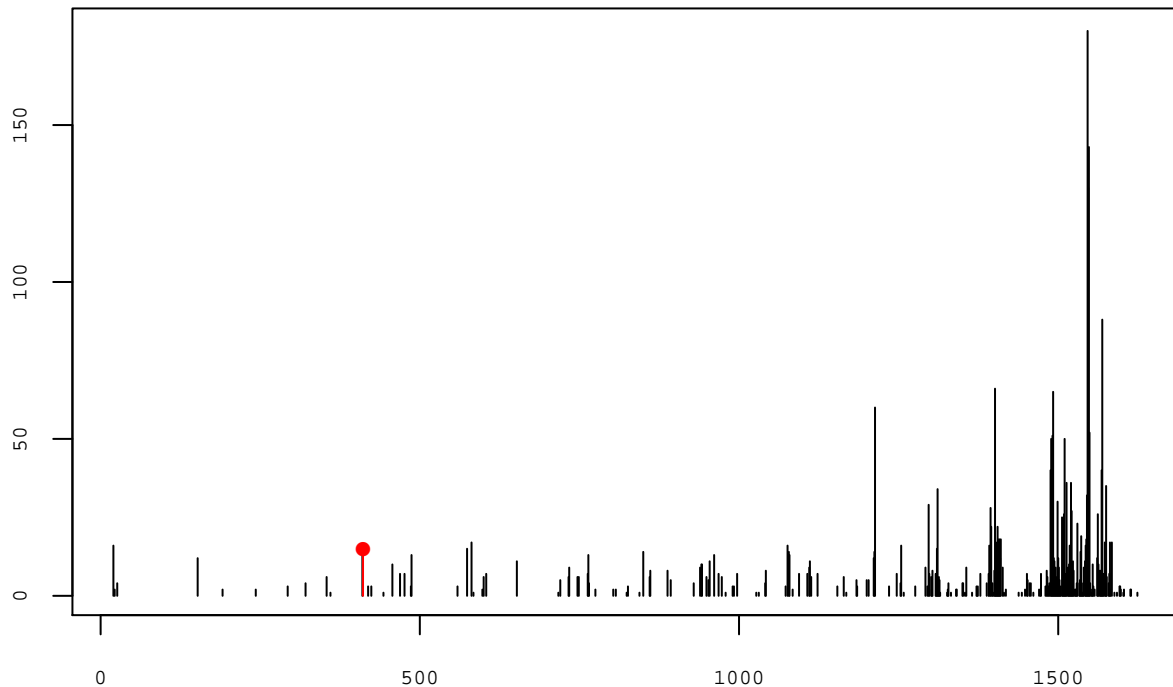


PggD14842_c14_g1_i1

5' AAGCCGAGTTCCTCCAAACACTTCATTTC AAT '3
|||||||o|||||||
3' CTCAAGGGGGTTGTGAAGTC '5

Fragment Abundance



Transcript position

Cleavage site: 411 Tag abundance: 15 Weighted abundance: 15 Category: 2
sRNA abundance: 31 Alignment score: 1.5 MFE ratio: 0.877 p-value: 0.031