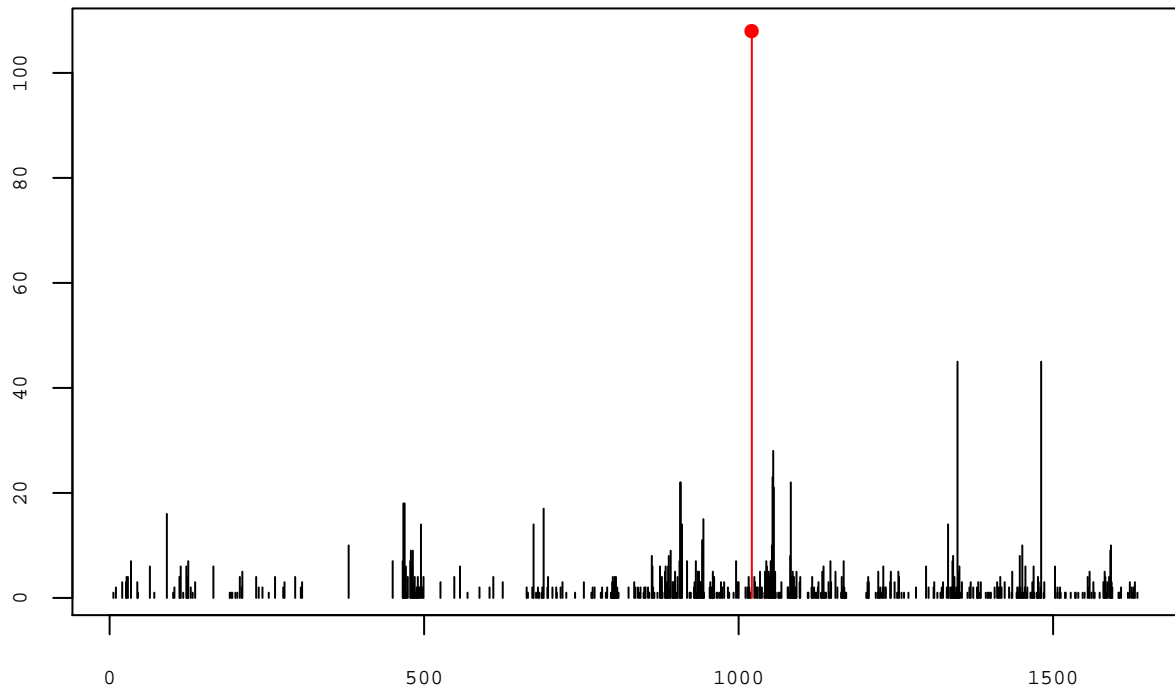


PggD13513_c39_g1_i1

5' GGTTC TTCAGTGTGCAAGTGATGTGAAACATT '3
 ||||| |||||
3' GTCACACGTTCTCTAC-CTT '5

Fragment Abundance



Transcript position

Cleavage site: 1021 Tag abundance: 108 Weighted abundance: 36 Category: 0
sRNA abundance: 14 Alignment score: 4 MFE ratio: 0.752 p-value: 0.004