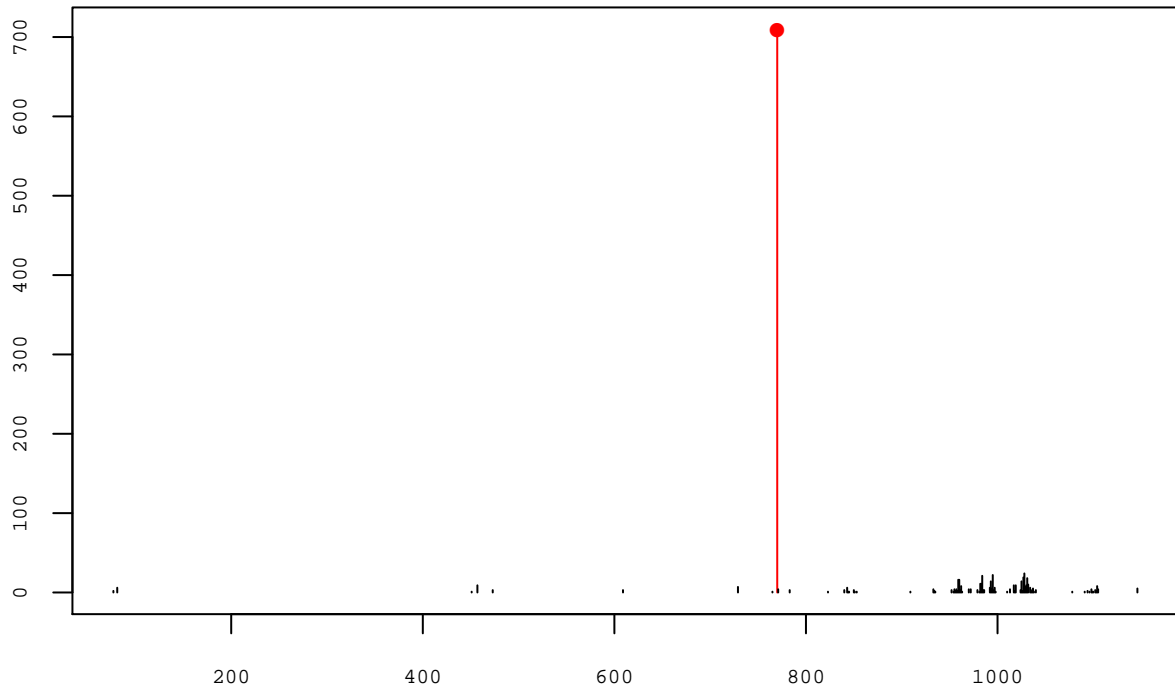


PggD1928_c0_g1_i2

5' AAGGCATTACGTGCCCTGCTTCTCCACAGTGG '3
o |||||
3' ACGTGCACGGGACGAAGAGGT '5

Fragment Abundance



Transcript position

Cleavage site: 770 Tag abundance: 709 Weighted abundance: 354.5 Category: 0
sRNA abundance: 235 Alignment score: 2.5 MFE ratio: 0.867 p-value: 0.006