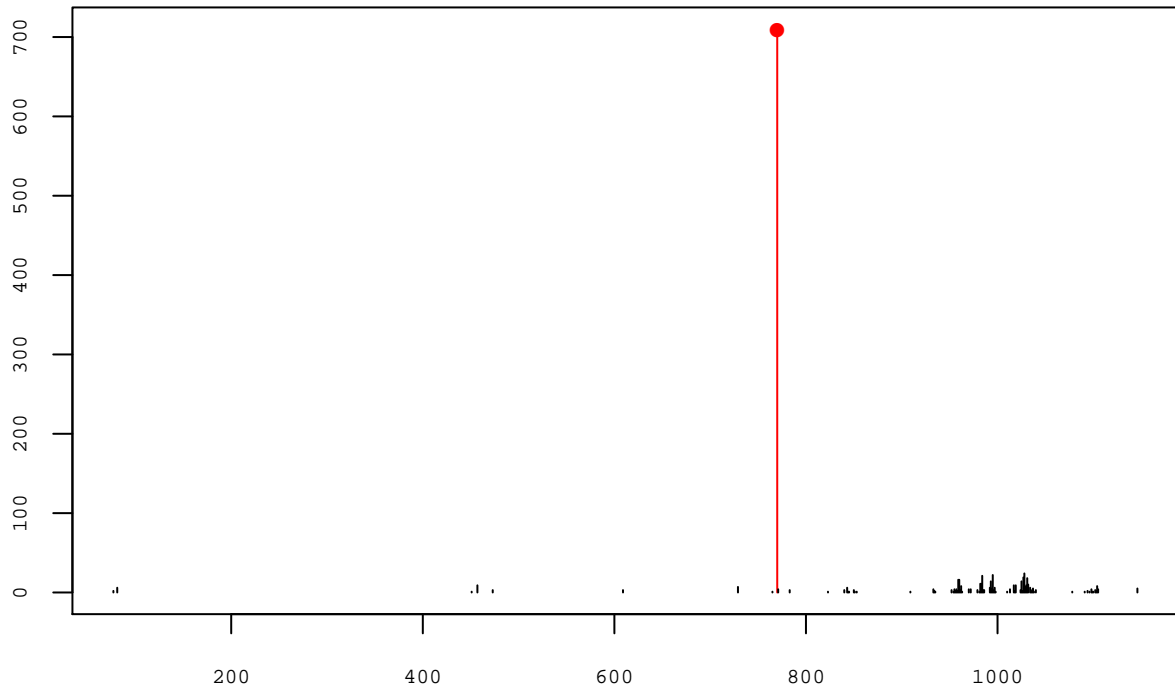


PggD1928_c0_g1_i2

5' AAGGCATTACGTGCCCTGCTTCTCCACAGTGG 3'
o |||||
3' CGTGCACGGGACGAAGAGGT 5'

Fragment Abundance



Transcript position

Cleavage site: 770 Tag abundance: 709 Weighted abundance: 354.5 Category: 0
sRNA abundance: 45 Alignment score: 1.5 MFE ratio: 0.899 p-value: 0.006