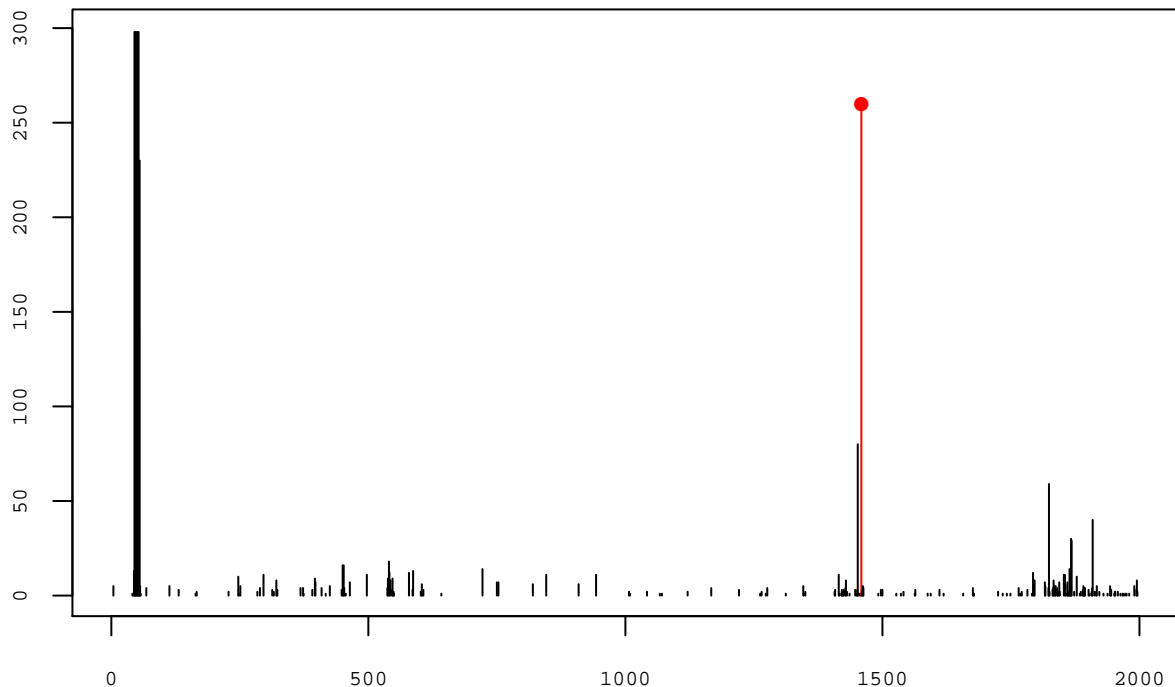


PggD12401_c1_g1_i2

5' GACTCTGATTGTGCTCTCTCTCTCTGTCATC 3'
| o|||o||| |||||
3' TCCGACATGAGAGAGAGAAGA 5'

Fragment Abundance



Transcript position

Cleavage site: 1459 Tag abundance: 260 Weighted abundance: 52 Category: 0
sRNA abundance: 37 Alignment score: 3 MFE ratio: 0.752 p-value: 0.008