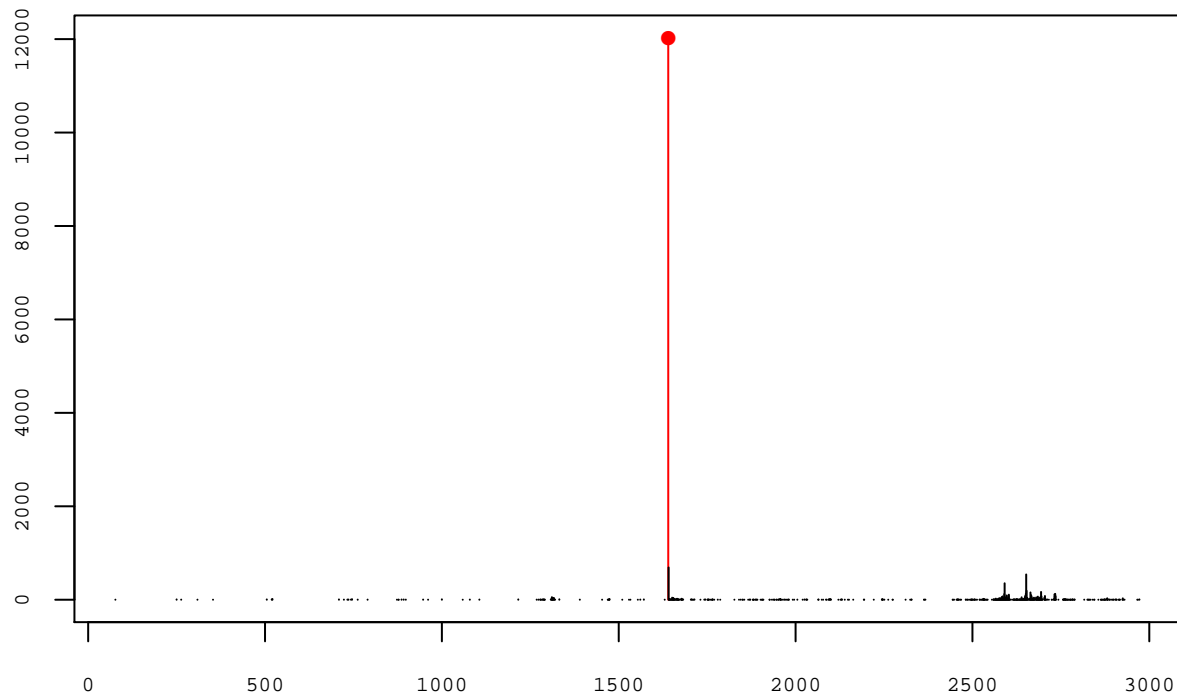


PggD1242_c13_g1_i2

5' GCAGCTAGCATAACAGGGAGCCAGGCAAATTCT '3
| | | | | | | | | | | | | | | | | | | | | |
3' ACCGTATGTCCCTCGGTCCGT '5

Fragment Abundance



Transcript position

Cleavage site: 1640 Tag abundance: 12026 Weighted abundance: 6013 Category: 0
sRNA abundance: 237 Alignment score: 1 MFE ratio: 0.914 p-value: 0.001