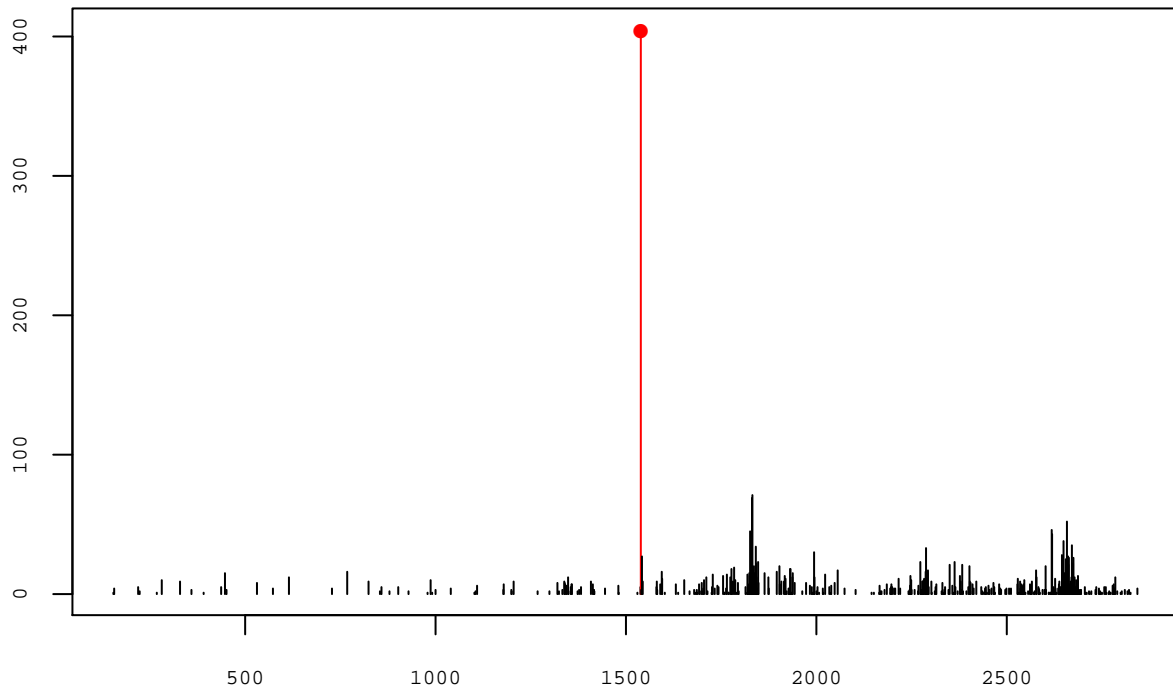


PggD2305_c3_g1_i1

5' GCACATGGGATATTGGCGGGCTCAATCACCA '3
| | | | | | | | | | | | | | | | | |
3' TCACTATAACCGCGCCGAGTT '5

Fragment Abundance



Transcript position

Cleavage site: 1539 Tag abundance: 404 Weighted abundance: 371 Category: 0
sRNA abundance: 20 Alignment score: 2 MFE ratio: 0.886 p-value: 0.001