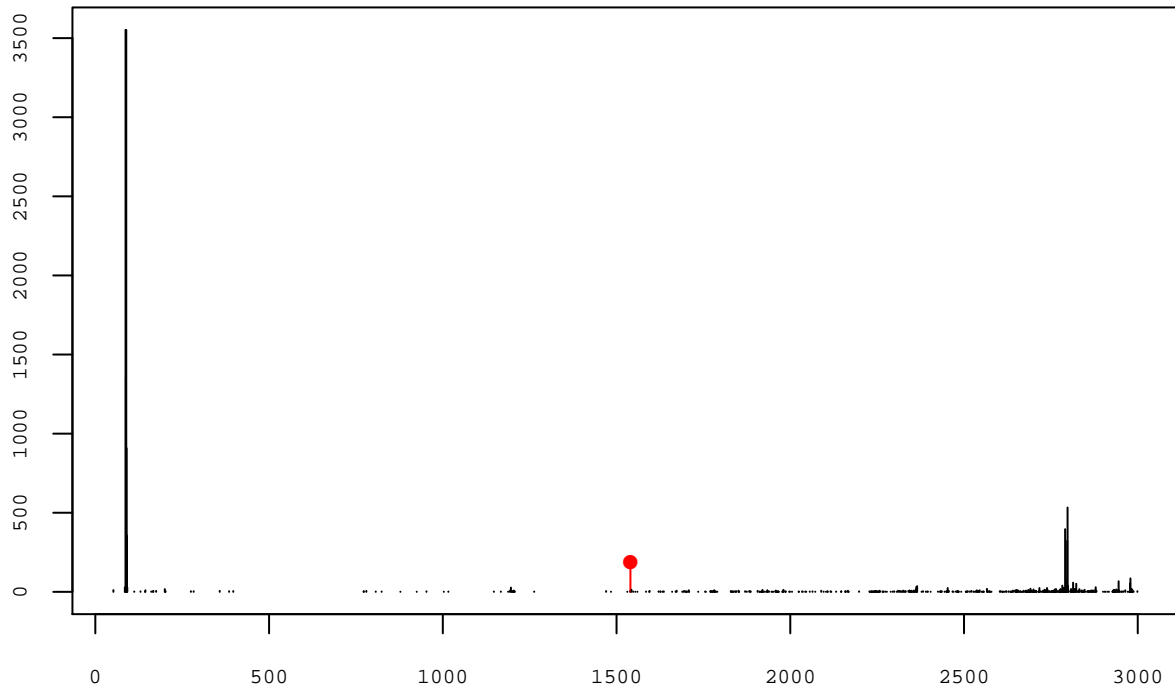


PggD3876_c10_g1_i1

5' GCGCATGGGATATTGGCGCGGCTCAATCACCA '3
| | | | | | | | | | ○ | | | | | | |
3' CGCTATAACCGTGCCGAGTT '5

Fragment Abundance



Transcript position

Cleavage site: 1540 Tag abundance: 190 Weighted abundance: 157 Category: 2
sRNA abundance: 83 Alignment score: 2 MFE ratio: 0.894 p-value: 0.036