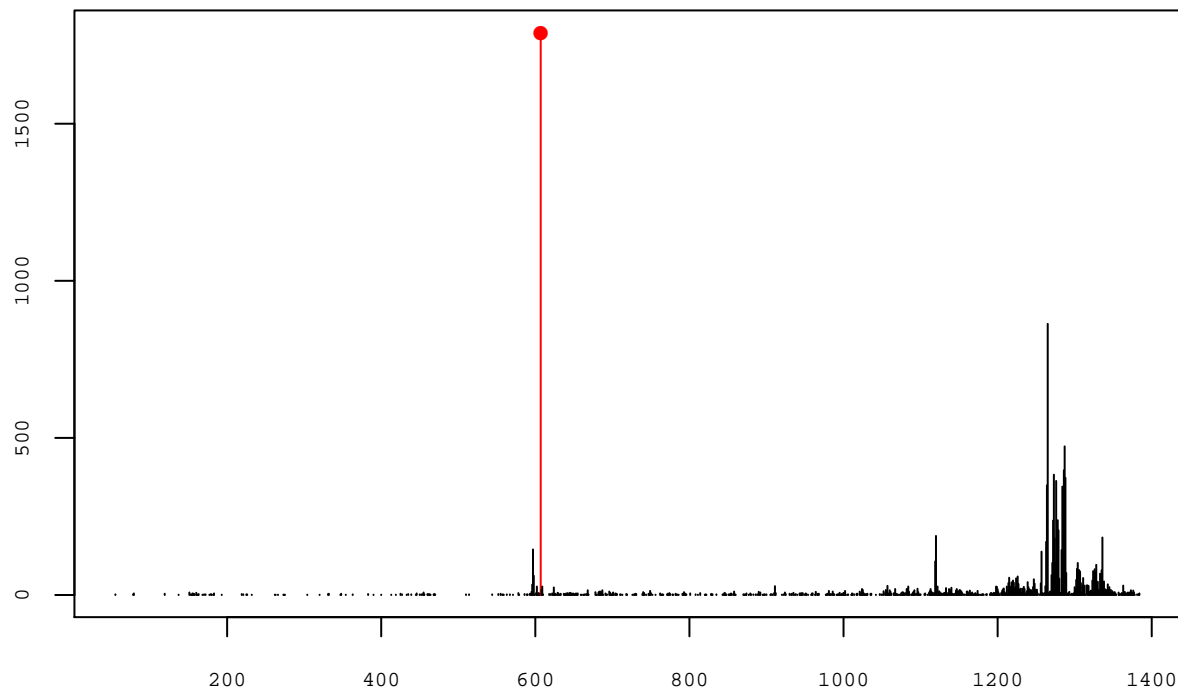


PggD4125_c99_g1_i1

5' AAGAACCGTTCAAGAAAGCCTGTGGAAATCTC 3'
| | | | | | | | | | | | | | | | | | | |
3' GTCAAGTTCTTTTCG-ACACCTT 5'

Fragment Abundance



Transcript position

Cleavage site: 607 Tag abundance: 1789 Weighted abundance: 447.25 Category: 0
sRNA abundance: 470 Alignment score: 3 MFE ratio: 0.826 p-value: 0.008