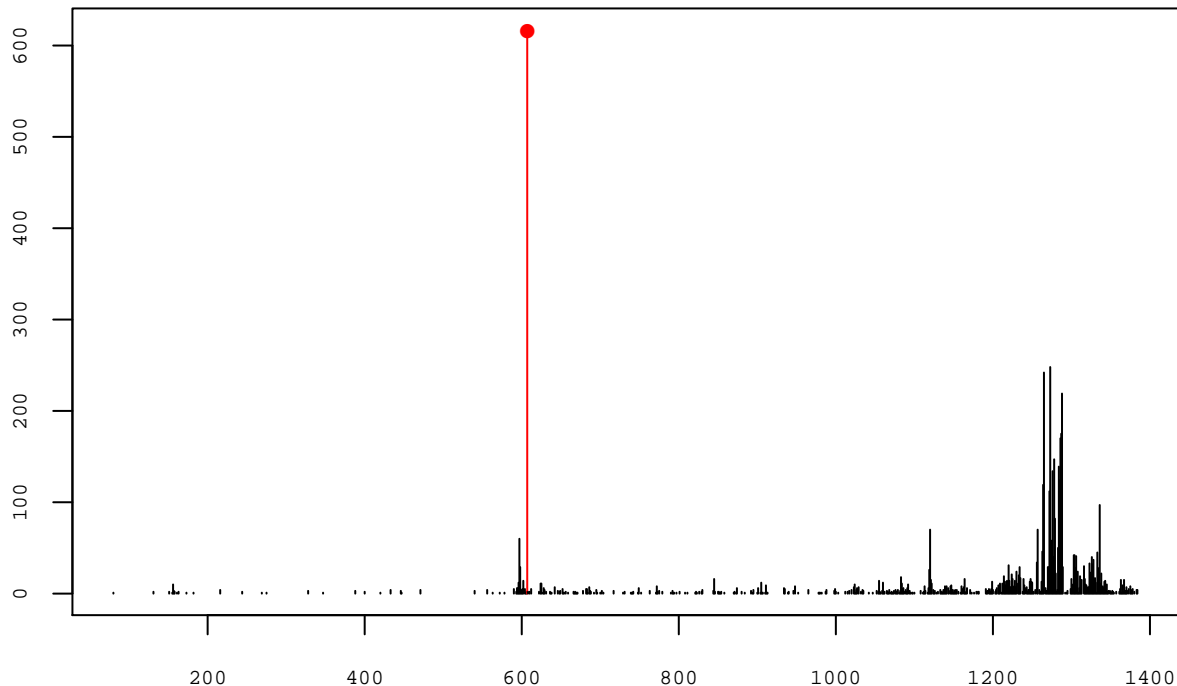


PggD4125_c99_g1_i1

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

Fragment Abundance



Transcript position

Cleavage site: 607 Tag abundance: 616 Weighted abundance: 154 Category: 0
sRNA abundance: 197 Alignment score: 3 MFE ratio: 0.826 p-value: 0.008