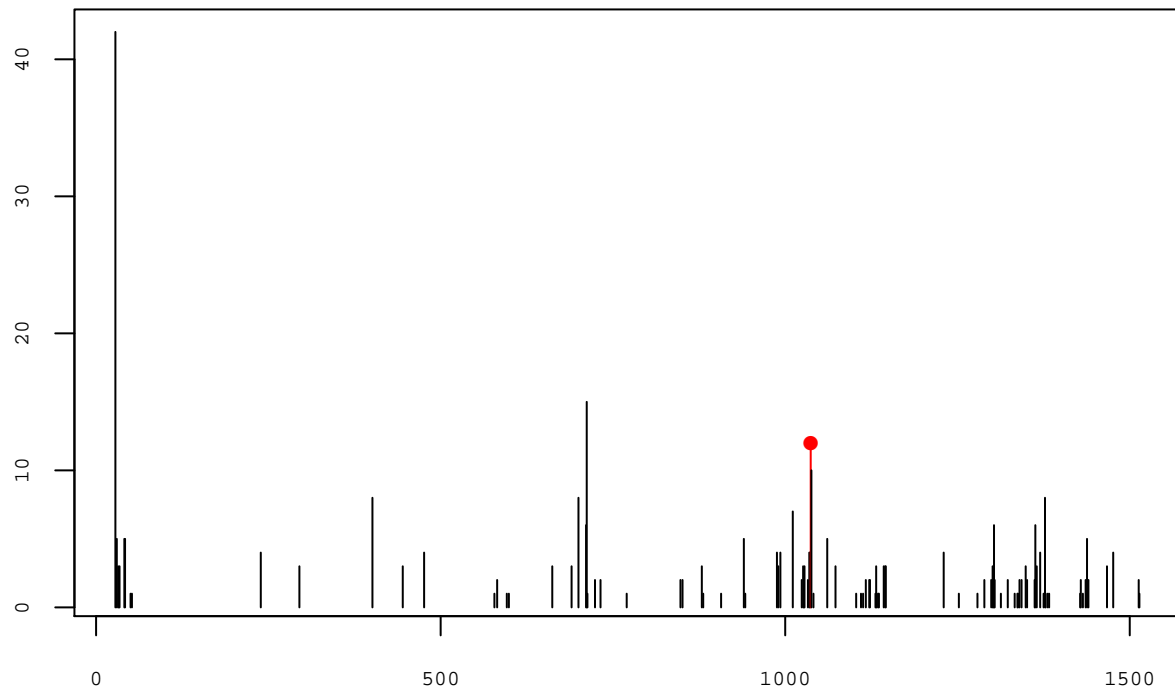


PggD1644_c0_g1_i1

```
5' CACCATTGGAGTCCTAATGCATTAGAACTCAT '3
   |||||
3' GGTAACCTCATGATTACGTAGTCA '5
```

Fragment Abundance



Transcript position

Cleavage site: 1037 Tag abundance: 12 Weighted abundance: 12 Category: 2
sRNA abundance: 5 Alignment score: 3 MFE ratio: 0.818 p-value: 0.048