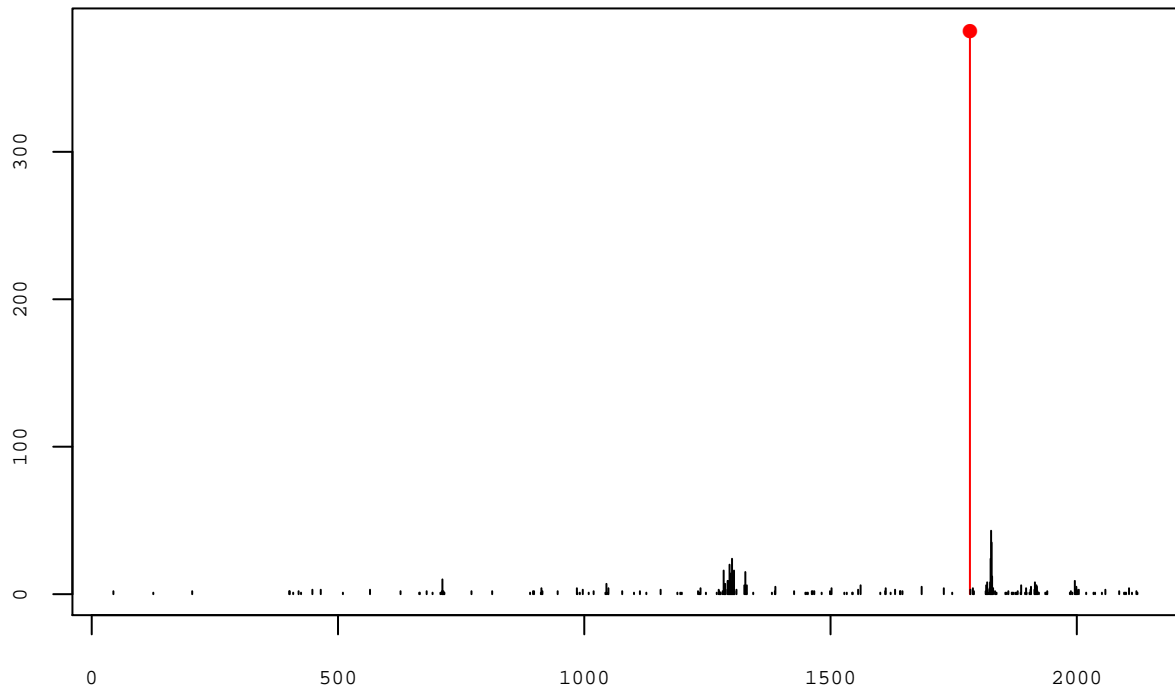


PggD620_c8_g1_i1

5' CGCTGGA-GCAGCATCATCAGGATTCTTATC '3
| | | | | | | | | | | | | | | | | |
3' TACGTCGTAGTAGTTCTAAGC '5

Fragment Abundance



Transcript position

Cleavage site: 1783 Tag abundance: 382 Weighted abundance: 382 Category: 0
sRNA abundance: 186 Alignment score: 3 MFE ratio: 0.926 p-value: 0.008