

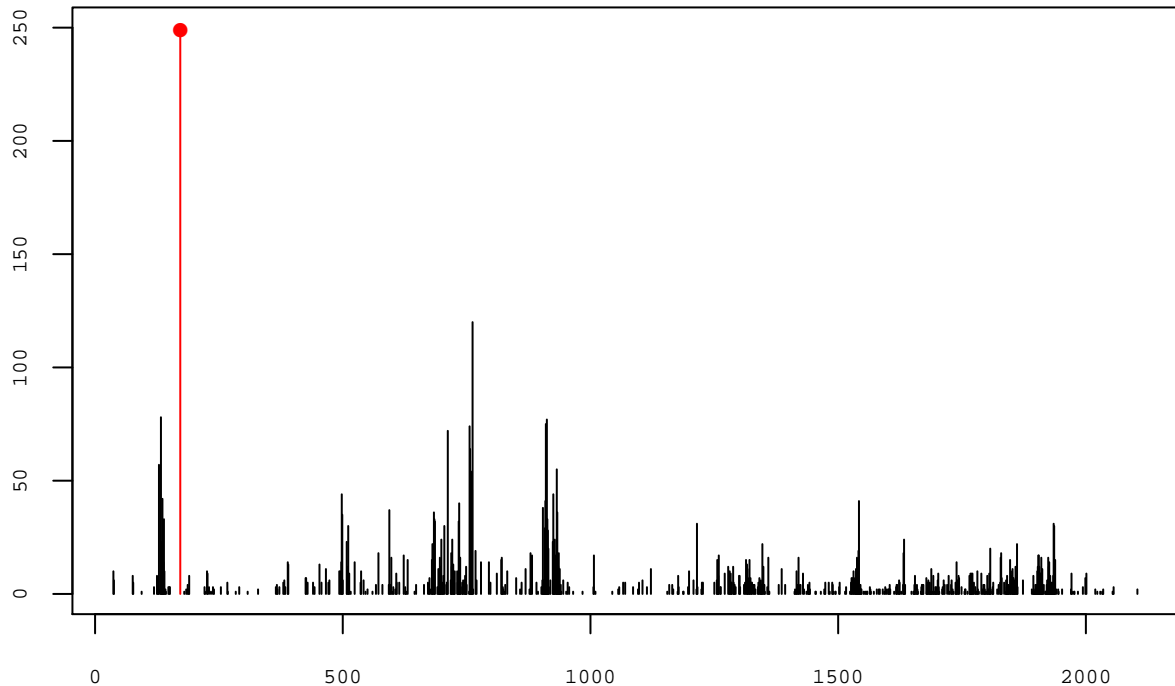
PggD4925\_c7\_g1\_i2

5' ATCCTCTCCTCTTCGTGCGCCTTCCAAACCCA '3

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3' GGAGACGTACGGGGAAGGT '5

Fragment Abundance



Transcript position

Cleavage site: 172 Tag abundance: 249 Weighted abundance: 249 Category: 0  
sRNA abundance: 12 Alignment score: 4 MFE ratio: 0.714 p-value: 0